



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/31, 15/62, C07K 14/295, 16/12, 19/00, A01K 67/027, A61K 39/118, G01N 33/53, C12Q 1/68</b>	<b>A2</b>	<b>(11) International Publication Number:</b> <b>WO 99/27105</b>  <b>(43) International Publication Date:</b> 3 June 1999 (03.06.99)
<b>(21) International Application Number:</b> PCT/IB98/01890  <b>(22) International Filing Date:</b> 20 November 1998 (20.11.98)  <b>(30) Priority Data:</b> 97/14673                      21 November 1997 (21.11.97)      FR 60/107,078                    4 November 1998 (04.11.98)      US  <b>(71) Applicant (for all designated States except US):</b> GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR).  <b>(72) Inventor; and</b> <b>(75) Inventor/Applicant (for US only):</b> GRIFFAIS, Rémy [FR/FR]; 51, boulevard Romain Roland, F-92120 Montrouge (FR).  <b>(74) Agents:</b> MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> <i>CHLAMYDIA PNEUMONIAE</i> GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION  <b>(57) Abstract</b>  <p>The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of <i>Chlamydia pneumoniae</i>, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the <i>Chlamydia pneumoniae</i> genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing <i>Chlamydia pneumoniae</i> infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular <i>Chlamydia pneumoniae</i>, infections.</p>		

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakhstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		



**CHLAMYDIA PNEUMONIAE GENOMIC SEQUENCE AND POLYPEPTIDES,**  
**FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS,**  
**PREVENTION AND TREATMENT OF INFECTION**

5

The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of *Chlamydia pneumoniae*, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the *Chlamydia pneumoniae* genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing *Chlamydia pneumoniae* infection.

15 The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular *Chlamydia pneumoniae*, infections.

20 Comparative analysis of the sequence of the gene encoding the ribosomal 16S RNA has been widely used for the phylogenetic study of prokaryotes. This approach has made it possible to classify the Chlamydiae among the eubacteria, among which they represent a well-isolated group, with, nevertheless, a very weak link with the planctomyces. The Chlamydiae thus exhibit some unique characteristics within the eubacteria, in particular their development cycle and the structure of their

25 membranes. They have a unique two-phase cell cycle: the elementary body, a small extracellular form, attaches to the host and is phagocytosed; in the phagosome, it is converted to the replicative intracellular form, the reticulate body. The Chlamydiae are obligate intracellular bacteria which multiply in eukaryotic cells at the expense of their energy reserves and nucleotide pools; they are responsible for a wide variety of diseases in mammals and birds. The Chlamydiae are the only

30 members of the order Chlamydiales, of the family Chlamydiaceae and of the genus Chlamydia. Within the genus *Chlamydia*, four species are currently described: *Chlamydia trachomatis*, *Chlamydia psittaci*, *Chlamydia pneumoniae* and *Chlamydia pecorum*. These bacteria are grouped together and share biological and biochemical properties. Among them, only the first three infect humans, *Chlamydia pecorum* being a pathogen of ruminants.

35 The species *Chlamydia psittaci* infects many animals, in particular birds, and is transmissible to humans. It is responsible for atypical pneumonia, for hepatic and renal dysfunction, for endocarditis and for conjunctivitis.

The species *Chlamydia trachomatis* is the best characterized. Besides a murine strain, it is divided into two groups which are distinguishable by the nature of the diseases for which they are responsible: trachoma, genital attack and venereal lymphogranulomatosis. There are fifteen human serotypes of *Chlamydia trachomatis* (A, K) and LGV (L1, L2, L3). Strains A to C are mainly found in eye infections, whereas strains D to K and LGV are essentially responsible for genital entry infections. It should be mentioned that the LGV strains are responsible for systemic diseases. Historically, it was in 1906 that Halberstaeder and Von Provaseck discovered, in trachoma patients, the presence of inclusions in the cytoplasm of the cells derived from conjunctival scrapings. In 1940, Rake and Jones described these same inclusions in certain cells obtained by puncturing the ganglia from a patient suffering from venereal granulomatosis. Characterization of the *Chlamydia trachomatis* microorganism was only successfully carried out in 1957, after a series of isolations in cell cultures.

It was in 1983 that *Chlamydia pneumoniae* was recognized as a human pathogen (Grayston JT et al., 1986); since then, special attention has been paid to this bacterium and it is estimated (Gaydos CA et al., 1994) that 10% of pneumonias, and 5% of bronchitides and sinusites are attributable to *Chlamydia pneumoniae* (Aldous MB et al., 1992). More recently, the association of this bacterium with the pathogenesis of asthmatic disease and of cardiovascular impairments is increasingly of interest.

Serological studies have made it possible to observe that *Chlamydia pneumoniae* infection is common in children between 5 and 16 years of age. Before this age, it is rare to find antibodies; the increase in the number of individuals carrying antibodies is then correlated with age up to 20 years. Accordingly, 50% of adults are carriers of antibodies, it being possible for this prevalence to be as high as 75%. These figures are all the more striking since a first infection induces antibody levels of which the persistence over time is limited to 3 or at most 5 years, which suggests frequent reinfection during the entire lifespan. The annual seroconversion rate is about 8% between 8 and 12 years and about 6% between 12 and 16 years (Haidl et al., 1994). Before the age of 15 years, the seroprevalence of the disease is identical between both sexes. After this age, men are more frequently infected than women; this is true in all regions worldwide where such studies have been carried out.

These infections are geographically highly widespread, as shown by numerous studies carried out throughout the world (Kanamoto Y et al., 1991; Tong CY et al., 1993). Developed countries of the north such as Canada, Denmark and Norway have the lowest infection rates; conversely, the highest prevalence rates are found in the less developed countries of tropical regions where the infection may occur before the age of 5 years.

Humans are the only known reservoir for *Chlamydia pneumoniae* and it is probable that the infection is caused by direct transmission, respiratory secretions probably being responsible for this low-yield transmission (Aldous et al., 1992). The chain of transmission may also appear to be indirect (Kleemola M et al., 1988), suggesting that the infection is caused by an effective transmission, but also that asymptomatic carriers exist, which could explain the high prevalence of the disease.

Other studies (Mordhorst CH et al., 1992) show that the efficiency of the transmission varies according to the individuals and list cases of infection affecting all or the majority of members of one family or of a group of families. The period of incubation is several weeks, significantly longer in this regard than that of many other respiratory pathogenic agents. Although under conditions of high  
5 relative humidity the infectivity of *Chlamydia pneumoniae* in the open air decreases rapidly, suggesting a direct mode of transmission under these conditions, it is probable that the transmission occurs in some cases indirectly since the microorganism can survive for up to 30 hours in a hostile environment (Falsey et al., 1993).

Clinical manifestations due to *Chlamydia pneumoniae* are essentially respiratory  
10 diseases. Pneumonia and bronchitis are the most frequent because they are clinically patent: since etiological diagnosis is evoked in this case, the infectious agent is identified. The asymptomatic diseases are probably numerous (Grayston JT et al., 1992; Grayston JT et al., 1986; Thom DH et al., 1990). The disease then progresses via bronchitis or pneumonia; fever is absent at the time of examination but is sometimes reported by the patient. The degree of seriousness of the disease is  
15 variable and in hospitalized patients, it is common to observe pleural effusion; a generalized infection may also be observed and, in severe cases, anatomicopathological examination shows *Chlamydia pneumoniae* diseases.

Other syndromes such as sinusitis (Hashiguchi K et al., 1992), purulent otitis media (Ogawa H et al., 1992), or pharyngitis (Huovinen P et al., 1989) have been described, as well as  
20 infections with respiratory impairments similar to asthma (Hahn DL et al., 1991). *Chlamydia pneumoniae* has also been associated with sarcoidosis, with erythema nodosum (Sundelof et al., 1993) and one case of Guillain-Barré syndrome has even been described (Haidl et al., 1992). The involvement of *Chlamydia pneumoniae* in Reiter's syndrome has also been evaluated (Braun J et al., 1994).

25 The association of *Chlamydia pneumoniae* with coronary diseases and with myocardial infarction was first suspected from the observation of the high antibody level in 71% of patients having a heart disease (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M et al., 1993; Thomas GN et al., 1997). Studies carried out in several countries have shown similar results in patients with atheromatous impairments (Shor A et al., 1992; Kuo CC et al., 1993; Puolakkainen M  
30 et al., 1993; Grayston JT et al., 1996; Casas-Ciria J et al., 1996; Thomas GN et al., 1997; Jackson LA et al., 1997) and in patients with carotid impairments. Anatomicopathological and microbiological studies have detected *Chlamydia pneumoniae* in the vessels. The electron microscope has made it possible to visualize the bacterium (Ladany S et al., 1989), which has in fact been demonstrated by other techniques such as PCR (Campbell LA et al., 1992; Kuo CC et al., 1993; Kuo CC et al., 1988). It  
35 also appears that the bacterium is more frequently found in old atheromatous lesions. Other studies carried out on young subjects from 15 to 35 years have given the opportunity to study the coronary arteries of people without atherosclerosis, this observation not being possible in older subjects (the

onset of the atheromatous disease is early). In these young subjects, the PCR studies did not find *Chlamydia pneumoniae* in subjects free of atheromatous disease, but revealed the presence of *Chlamydia pneumoniae* in two of the eleven subjects who showed early lesions and in six of the seven subjects who developed atheroma plaques. These studies therefore show that the atheroma plaque is very strongly correlated with the presence of *Chlamydia pneumoniae*, but the role played by the bacterium in vascular pathology is not yet defined.

The data relating to controlled clinical studies analysing the effect of treatments in *Chlamydia pneumoniae* infections are limited in number. Unlike penicillin, ampicillin or the sulphamides, erythromycin, tetracycline or doxycycline show an antibiotic activity *in vitro* against *Chlamydia pneumoniae*. However, a treatment at high doses should be continued for several weeks in order to avoid a recurrence of the infection. Accordingly, the use of two new macrolides, clarithromycin and azithromycin, whose diffusion, bioavailability and half-life allow shorter and better tolerated cures, is nowadays preferred. In the absence of definitive proof based on the results of clinical studies, an effective, without recurrences, and well-tolerated treatment of *Chlamydia pneumoniae* infections therefore remains desirable.

An even more important need up until now relates to a specific and sensitive diagnosis, which can be carried out conveniently and rapidly, allowing early screening for the infection. Methods based on *Chlamydia pneumoniae* culture are slow and require a considerable know-how because of the difficulty involved in the collection, preservation and storage of the strain under appropriate conditions. Methods based on antigen detection (EIA, DFA) or on nucleic acid amplification (PCR) provide tests which are more suitable for laboratory practice. A reliable, sensitive and convenient test, which allows distinction between serogroups and a fortiori between *Chlamydia pneumoniae* species is therefore highly desirable.

This is all the more important since the symptoms of *Chlamydia pneumoniae* infection appear slowly, since all the pathologies associated with these infections have not yet been identified, and since, as has been mentioned above, an association is suspected between these infections and serious chronic infections, asthma or atherosclerosis.

No vaccine is yet available against *Chlamydia pneumoniae*: this is due to the labile nature of the antigens specific to the strain, which has so far prevented their specific identification.

Although the number of studies and of animal models developed is high, the antigens used have not induced sufficient protective immunity to lead to the development of human vaccines. In the case of *Chlamydia pneumoniae*, the role of the immune defense in the physiology and pathology of the disease should probably be understood in order to develop satisfactory vaccines.

More detailed information relating to the biology of these strains, their interactions with their hosts, the associated phenomena of infectivity and those of escaping the immune defenses of the host in particular, and finally their involvement in the development of the these associated pathologies, will allow a better understanding of these mechanisms. In the light of the preceding text which shows

in particular the limitations of the means of controlling *Chlamydia pneumoniae* infection, it is therefore at present essential, on the one hand, to develop molecular tools, in particular from a better genetic knowledge of *Chlamydia pneumoniae*, but also to develop new preventive and therapeutic treatments, new diagnostic methods and new vaccine strategies which are specific, effective and tolerated. This is precisely the object of the present invention.

The subject of the present invention is the nucleotide sequence having the sequence SEQ ID No. 1 of the *Chlamydia pneumoniae* genome. However, the invention is not limited to SEQ ID No. 1, but encompasses genomes and nucleotides encoding polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the subject of the present invention encompasses nucleotide sequences characterized in that they are chosen from:

a) the nucleotide sequence of SEQ ID No. 1, a nucleotide sequence exhibiting at least 99.9% identity with the sequence SEQ ID No. 1, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. \_\_\_, the nucleotide sequence of a clone insert within ATCC Deposit No. \_\_\_;

b) a nucleotide sequence homologous to the sequence SEQ ID No. 1;

c) a polynucleotide sequence that hybridizes to the nucleotide sequence of a) under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10<sup>6</sup> cpm of <sup>32</sup>P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a

temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 5 Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety.

- 10 d) a nucleotide sequence complementary to the sequence SEQ ID No. 1 or complementary to a nucleotide sequence as defined in a), b) or c) and a nucleotide sequence of their corresponding RNA;
- e) a nucleotide sequence of a representative fragment of the sequence SEQ ID No. 1, or of a representative fragment of the nucleotide sequence as defined in a), b), c) or d);
- f) a nucleotide sequence comprising a sequence as defined in a), b), c), d) or e);
- 15 g) a nucleotide sequence capable of being obtained from a nucleotide sequence as defined in a), b), c), d), e) or f); and
- h) a modified nucleotide sequence of a nucleotide sequence as defined in a), b), c), d), e), f) or g).

Nucleotide sequence, polynucleotide or nucleic acid are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of 20 transcription of the said DNAs.

It should be understood that the present invention does not relate to the genomic nucleotide sequences of *Chlamydia pneumoniae* taken in their natural environment, that is to say in the natural state. They are sequences which may have been isolated, purified or partially purified, by separation methods such as, for example, ion-exchange chromatography, molecular size exclusion 25 chromatography or affinity chromatography, or alternatively fractionation techniques based on solubility in various solvents, or by genetic engineering methods such as amplification, cloning or subcloning, it being possible for the sequences of the invention to be carried by vectors.

The nucleotide sequence SEQ ID No. 1 was obtained by sequencing the *Chlamydia pneumoniae* genome by the method of directed sequencing after fluorescent automated sequencing of 30 the inserts of clones and assembling of these sequences of nucleotide fragments (inserts) by means of softwares (cf. Examples). In spite of the high precision of the sequence SEQ ID No. 1, it is possible that it does not perfectly, 100% represent the nucleotide sequence of the *Chlamydia pneumoniae* genome and that a few rare sequencing errors or uncertainties still remain in the sequence SEQ ID No. 1. In the present invention, the presence of an uncertainty for an amino acid is designated 35 by "Xaa" and that for a nucleotide is designated by "N" in the sequence listing below. These few rare errors or uncertainties could be easily detected and corrected by persons skilled in the art using the entire chromosome and/or its representative fragments according to the invention and standard

amplification, cloning and sequencing methods, it being possible for the sequences obtained to be easily compared, in particular by means of a computer software and using computer-readable media for recording the sequences according to the invention as described, for example, below. After correcting these possible rare errors or uncertainties, the corrected nucleotide sequence obtained would still exhibit at least 99.9% identity with the sequence SEQ ID No. 1. Such rare sequencing uncertainties are not present within the DNA contained within ATCC Deposit No. \_\_\_ or \_\_\_, and whatever rare sequence uncertainties that exist within SEQ ID No. 1 can routinely be corrected utilizing the DNA of the ATCC deposits.

Homologous nucleotide sequence for the purposes of the present invention is understood to mean a nucleotide sequence having a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, this percentage being purely statistical and it being possible for the differences between the two nucleotide sequences to be distributed randomly and over their entire length. The said homologous sequences exhibiting a percentage identity with the bases of the nucleotide sequence SEQ ID No. 1 of at least 80%, preferably 90% and 95%, may comprise, for example, the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the Chlamydia family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the genomic sequence or to the sequences of its representative fragments of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. In the present invention, the terms family and genus are mutually interchangeable, the terms variant, serotype, strain and subspecies are also mutually interchangeable. These homologous sequences may thus correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Thompson *et al.*, 1994, *Nucleic Acids Res.* 22(2):4673-4680; Higgins *et al.*, 1996, *Methods Enzymol.* 266:383-402; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272; Altschul *et al.*, 1997,

*Nuc. Acids Res.* 25:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

- (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- 5 (2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3)BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4)TBLASTN compares a query protein sequence against a nucleotide sequence database
- 10 translated in all six reading frames (both strands); and
- (5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science* 256:1443-1445; Henikoff and Henikoff, 1993, *Proteins* 17:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 20 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, 25 Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268).

Nucleotide sequence complementary to a sequence of the invention is understood to mean any DNA whose nucleotides are complementary to those of the sequence of the invention, and whose orientation is reversed (antiparallel sequence).

30 The present invention further comprises fragments of the sequences of a) through f), above. Representative fragments of the sequences according to the invention will be understood to mean any nucleotide fragment having at least 8 successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. It is understood that such fragments refer only to portions of SEQ 35 ID No. 1 that are not currently listed in a publicly available database.

Among these representative fragments, those capable of hybridizing under stringent conditions with a nucleotide sequence according to the invention are preferred. Hybridization under



stringent conditions means that the temperature and ionic strength conditions are chosen such that they allow hybridization to be maintained between two complementary DNA fragments.

By way of illustration, high stringency conditions for the hybridization step for the purposes of defining the nucleotide fragments described above, are advantageously the following.

5           The hybridization is carried out at a preferred temperature of 65EC in the presence of SSC buffer, 1 × SSC corresponding to 0.15 M NaCl and 0.05 M Na citrate. The washing steps may be, for example, the following:

2 × SSC, 0.1% SDS at room temperature followed by three washes with 1 × SSC, 0.1% SDS; 0.5 × SSC, 0.1% SDS; 0.1 × SSC, 0.1% SDS at 68EC for 15 minutes.

10           Intermediate stringency conditions, using, for example, a temperature of 60EC in the presence of a 5 × SSC buffer, or of low stringency, for example a temperature of 50EC in the presence of a 5 × SSC buffer, respectively require a lower overall complementarity for the hybridization between the two sequences.

15           The stringent hybridization conditions described above for a polynucleotide of about 300 bases in size will be adapted by persons skilled in the art for larger- or smaller-sized oligonucleotides, according to the teaching of Sambrook et al., 1989.

20           Among the representative fragments according to the invention, those which can be used as primer or probe in methods which make it possible to obtain homologous sequences or their representative fragments according to the invention, or to reconstitute a genomic fragment found to be incomplete in the sequence SEQ ID No. 1 or carrying an error or an uncertainty, are also preferred, these methods, such as the polymerase chain reaction (PCR), cloning and sequencing of nucleic acid being well known to persons skilled in the art. These homologous nucleotide sequences corresponding to mutations or to inter- or intra-species variations, as well as the complete genomic sequence or one of its representative fragments capable of being reconstituted, of course form part of  
25           the invention.

          Among the said representative fragments, those which can be used as primer or probe in methods allowing diagnosis of the presence of *Chlamydia pneumoniae* or one of its associated microorganisms as defined below are also preferred.

30           The representative fragments capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the host cell and/or organism, are also preferred. Replication cycle is intended to designate invasion, multiplication, intracellular localization, in particular retention in the vacuole and inhibition of the process of fusion to the lysosome, and propagation of *Chlamydia pneumoniae* or one  
35           of its associated microorganisms from host cells to host cells.

          Among the said representative fragments, those corresponding to nucleotide sequences corresponding to open reading frames, called ORF sequences (ORF for open reading frame), and

encoding polypeptides, such as for example, but without being limited thereto, the ORF sequences which will be later described, are finally preferred.

The representative fragments according to the invention may be obtained, for example, by specific amplification, such as PCR, or after digestion, with appropriate restriction enzymes, of nucleotide sequences according to the invention; these methods are in particular described in the manual by Sambrook et al., 1989. The said representative fragments may also be obtained by chemical synthesis when they are not too large in size and according to methods well known to persons skilled in the art. For example, such fragments can be obtained by isolating fragments of the genomic DNA of ATCC Deposit No. \_\_\_\_ or a clone insert present at this ATCC Deposit No. \_\_\_\_.

10 The representative fragments according to the invention may be used, for example, as primer, to reconstitute some of the said representative fragments, in particular those in which a portion of the sequence is likely to be missing or imperfect, by methods well known to persons skilled in the art such as amplification, cloning or sequencing techniques.

Modified nucleotide sequence will be understood to mean any nucleotide sequence obtained by mutagenesis according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the normal sequences, for example mutations in the regulatory and/or promoter sequences for the expression of a polypeptide, in particular leading to a modification of the level of expression of the said polypeptide or to a modulation of the replicative cycle.

Modified nucleotide sequence will also be understood to mean any nucleotide sequence encoding a modified polypeptide as defined below.

The subject of the present invention also includes *Chlamydia pneumoniae* nucleotide sequences characterized in that they are chosen from a nucleotide sequence of an open reading frame (ORF), that is, the ORF2 to ORF1297 sequences.

The ORF2 to ORF1297 nucleotide sequences are defined in Tables 1 and 2, *infra*, by their position on the sequence SEQ ID No. 1. For example, the ORF2 sequence is defined by the nucleotide sequence between the nucleotides at position 42 and 794 on the sequence SEQ ID No. 1, ends included. ORF2 to ORF1297 have been identified via homology analyses as well as via analyses of potential ORF start sites, as discussed in the examples below. It is to be understood that each identified ORF of the invention comprises a nucleotide sequence that spans the contiguous nucleotide sequence from the ORF stop codon immediately 3' to the stop codon of the preceding ORF and through the 5' codon to the next stop codon of SEQ ID No.:1 in-frame to the ORF nucleotide sequence. Table 2, *infra*, lists the beginning, end and potential start site of each of ORFs 1-1297. In one embodiment, the ORF comprises the contiguous nucleotide sequence spanning from the potential ORF start site downstream (that is, 3') to the ORF stop codon (or the ORF codon immediately adjacent to and upstream of the ORF stop codon). ORF2 to ORF1297 encode the polypeptides of SEQ ID No. 2 to SEQ ID No. 1291 and of SEQ ID No. 6844 to SEQ ID No. 6849, respectively.

Upon introduction of minor frameshifts, certain individual ORFs can comprise larger

“combined” ORFs. A list of such putative “combined” ORFs is shown in Table 3, below. For example, a combined ORF can comprise ORF 25, ORF 26 and ORF 27, including intervening in-frame, nucleotide sequences. The order of ORFs (5' to 3'), within each “combined” ORF is as listed. It is to be understood that when ORF2 to ORF1297 are referred to herein, such reference is also meant to include “combined” ORFs. Polypeptide sequences encoded by such “combined” ORFs are also part of the present invention.

**Table 3**

- ORF 25, ORF 26, ORF 27;
- 10 ORF 28, ORF 29, ORF 30;
- ORF 31, ORF 32;
- ORF 33, ORF 35;
- ORF 466, ORF 467;
- ORF 468, ORF 469;
- 15 ORF 477, ORF 476, ORF 474;
- ORF 480, ORF 482;
- ORF 483, ORF 485, ORF 486, ORF 500;
- ORF 503, ORF 504, ORF 505;
- ORF 506, ORF 507;
- 20 ORF 1211, ORF 647;
- ORF 1286, ORF 1039;
- ORF 691, ORF 690;
- ORF 105, ORF 106;
- ORF 170, ORF 171; ORF 394, ORF 393;
- 25 ORF 453, ORF 452, ORF 451;
- ORF 526, ORF 525;
- ORF 757, ORF 756, ORF 755;
- ORF 856, ORF 855;
- ORF 958, ORF 957;
- 30 ORF 915, ORF 914, ORF 913;
- ORF 543, ORF 544;
- ORF 1266, ORF 380;
- ORF 745, ORF 744;
- ORF 777, ORF 776;
- 35 ORF 343, ORF 1297, and representative fragments.

Table 1 also depicts the results of homology searches that compared the sequences of the

polypeptides encoded by each of the ORFs to sequences present in public published databases. It is understood that those polypeptides listed in Table 1 as exhibiting greater than about 95% identity to a polypeptide present in a publicly disclosed database are not considered part of the present invention; likewise in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention. In another embodiment, it is understood that those polypeptides listed in Table 1 as exhibiting greater than about 99% identity to a polypeptide present in a publicly disclosed database are not considered part of the invention; likewise, in this embodiment, those nucleotide sequences encoding such polypeptides are not considered part of the invention.

The invention also relates to the nucleotide sequences characterized in that they comprise a nucleotide sequence chosen from:

- a) an ORF2 to ORF1297, a "combined" ORF nucleotide sequence, the nucleotide sequence of the genomic DNA contained within ATCC Deposit No. \_\_\_\_\_ or the nucleotide sequence of a clone insert in ATCC Deposit No. \_\_\_\_\_ according to the invention;
- b) a homologous nucleotide sequence exhibiting at least 80% identity across an entire ORF2 to ORF1297 nucleotide sequence according to the invention or as defined in a);
- c) a polynucleotide sequence that hybridizes to ORF2 to ORF1297 under conditions of high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10<sup>6</sup> cpm of <sup>32</sup>P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate

stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia pneumoniae* polypeptide.

- d) complementary or RNA nucleotide sequence corresponding to an ORF2 to ORF1297 sequence according to the invention or as defined in a), b) or c);
- e) a nucleotide sequence of a representative fragment of an ORF2 to ORF1297 sequence according to the invention or of a sequence as defined in a), b), c) or d);
- f) a nucleotide sequence capable of being obtained from an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d) or e); and
- g) a modified nucleotide sequence of an ORF2 to ORF1297 sequence according to the invention or as defined in a), b), c), d), e) or f);

As regards the homology with the ORF2 to ORF1297 nucleotide sequences, the homologous sequences exhibiting a percentage identity with the bases of one of the ORF2 to ORF1297 nucleotide sequences of at least 80%, preferably 90% and 95%, are preferred. Such homologous sequences are identified routinely via, for example, the algorithms described above and in the examples below. The said homologous sequences correspond to the homologous sequences as defined above and may comprise, for example, the sequences corresponding to the ORF sequences of a bacterium belonging to the *Chlamydia* family, including the species *Chlamydia trachomatis*, *Chlamydia psittaci* and *Chlamydia pecorum* mentioned above, as well as the sequences corresponding to the ORF sequences of a bacterium belonging to the variants of the species *Chlamydia pneumoniae*. These homologous sequences may likewise correspond to variations linked to mutations within the same species or between species and may correspond in particular to truncations, substitutions, deletions and/or additions of at least one nucleotide. The said homologous sequences may also correspond to variations linked to the degeneracy of the genetic code or to a bias in the genetic code which is specific to the family, to the species or to the variant and which are likely to be present in *Chlamydia*.

The invention comprises polypeptides encoded by a nucleotide sequence according to the invention, preferably by a representative fragment of the sequence SEQ ID No. 1 and corresponding to an ORF sequence, in particular the *Chlamydia pneumoniae* polypeptides, characterized in that they are chosen from the sequences SEQ ID No. 2 to SEQ ID No. 1291 or SEQ ID No. 6844 to SEQ ID No.

6849 and representative fragments thereof. However, the invention is not limited to polypeptides encoded by ORFs in SEQ ID No. 1 and its corresponding ORF sequences, but encompasses polypeptides of strain variants, polymorphisms, allelic variants, and mutants.

Thus, the invention also comprises the polypeptides characterized in that they comprise a  
5 polypeptide chosen from:

- a) a polypeptide encoded by a polynucleotide sequence in SEQ ID No. 1 (e.g., any polypeptide encoded by a polynucleotide sequence corresponding to ORF2 to ORF1297 and/or representative fragments thereof) according to the invention;
- b) a polypeptide homologous to a polypeptide according to the invention, or as defined in a);
- 10 c) a polypeptide encoded by a polynucleotide sequence that hybridizes to SEQ ID No. 1 or ORF2 to ORF1297 under high or intermediate stringency as described below:

(i) By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65EC in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll,  
15 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65EC, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10<sup>6</sup> cpm of <sup>32</sup>P-labeled probe. Alternatively, the hybridization step can be performed at 65EC in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37EC for 1 h in a solution containing  
20 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50EC for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68EC for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989,  
25 Molecular Cloning, A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably such polypeptide represents a homolog of a polypeptide encoded by ORF2 to ORF1297. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such  
30 sequences encode a *Chlamydia pneumoniae* polypeptide.

(ii) By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60EC in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50EC and the hybridized probes are  
35 detectable by autoradiography. Other conditions of intermediate stringency which may be used are well known in the art and as cited in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual,

Second Edition, Cold Spring Harbor Press, N.Y., pp. 9.47-9.57; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. are incorporated herein in their entirety. Preferably, such sequences encode a homolog of a polypeptide encoded by one of ORF2 to ORF1297. In one embodiment, such sequences encode a *Chlamydia*  
5 *pneumoniae* polypeptide.

- d) a fragment of at least 5 amino acids of a polypeptide according to the invention, or as defined in a), b) or c);
- e) a biologically active fragment of a polypeptide according to the invention, or as defined in a), b), c) or d); and
- 10 f) a modified polypeptide of a polypeptide according to the invention, as defined in a), b), c), d) or e).

In the present description, the terms polypeptide, peptide and protein are interchangeable.

It should be understood that the invention does not relate to the polypeptides in natural form, that is to say that they are not taken in their natural environment but that they may have been  
15 isolated or obtained by purification from natural sources, or alternatively obtained by genetic recombination, or else by chemical synthesis and that they may, in this case, comprise nonnatural amino acids, as will be described below.

Homologous polypeptide will be understood to designate the polypeptides exhibiting, in relation to the natural polypeptide, certain modifications such as in particular a deletion, addition or  
20 substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, and/or a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequence exhibits at least 80%, preferably 90%, homology or identity with the amino acid sequences of the polypeptides according to the invention are preferred. In the case of a substitution, one or more consecutive or nonconsecutive amino acids are replaced by "equivalent"  
25 amino acids. The expression "equivalent" amino acid is intended here to designate any amino acid capable of being substituted for one of the amino acids in the basic structure without, however, essentially modifying the biological activities of the corresponding peptides and as will be defined later.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the  
30 variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-2448; Altschul et al., 1990, *J. Mol. Biol.* 215(3):403-410; Thompson et al., 1994, *Nucleic Acids Res.* 22(2):4673-4680; Higgins et al., 1996, *Methods Enzymol.* 266:383-402; Altschul et al., 1990, *J. Mol. Biol.* 215(3):403-  
35 410; Altschul et al., 1993, *Nature Genetics* 3:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see,

e.g., Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res.* 25:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

- 5 (1)BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2)BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3)BLASTX compares the six-frame conceptual translation products of a query  
10 nucleotide sequence (both strands) against a protein sequence database;
- (4)TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5)TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

15 The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet  
20 *et al.*, 1992, *Science* 256:1443-1445; Henikoff and Henikoff, 1993, *Proteins* 17:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment  
25 pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268).

Equivalent amino acids may be determined either based on their structural homology  
30 with the amino acids for which they are substituted, or on results of comparative tests of biological activity between the various polypeptides which may be carried out.

By way of example, there may be mentioned the possibilities of substitutions which may be carried out without resulting in a substantial modification of the biological activity of the corresponding modified polypeptides; the replacements, for example, of leucine with valine or  
35 isoleucine, of aspartic acid with glutamic acid, of glutamine with asparagine, of arginine with lysine, and the like, the reverse substitutions naturally being feasible under the same conditions.

The homologous polypeptides also correspond to the polypeptides encoded by the



homologous nucleotide sequences as defined above and thus comprise in the present definition the mutated polypeptides or polypeptides corresponding to inter- or intra-species variations which may exist in *Chlamydia*, and which correspond in particular to truncations, substitutions, deletions and/or additions of at least one amino acid residue.

5                   Biologically active fragment of a polypeptide according to the invention will be understood to designate in particular a polypeptide fragment, as defined below, exhibiting at least one of the characteristics of the polypeptides according to the invention, in particular in that it is:

- capable of eliciting an immune response directed against *Chlamydia pneumoniae*; and/or
- capable of being recognized by an antibody specific for a polypeptide according to the invention;
- 10                   and/or
- capable of binding to a polypeptide or to a nucleotide sequence of *Chlamydia pneumoniae*; and/or
- capable of modulating, regulating, inducing or inhibiting the expression of a gene of *Chlamydia pneumoniae* or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia pneumoniae* or one of its associated microorganisms in the
- 15                   host cell and/or organism; and/or
- capable of generally exerting an even partial physiological activity, such as for example a structural activity (cellular envelope, ribosome), an enzymatic (metabolic) activity, a transport activity, an activity in the secretion or in the virulence.

A polypeptide fragment according to the invention is understood to designate a  
20 polypeptide comprising a minimum of 5 amino acids, preferably 10 amino acids or preferably 15 amino acids. It is to be understood that such fragments refer only to portions of polypeptides encoded by ORF2 to ORF1297 that are not currently listed in a publicly available database.

The polypeptide fragments according to the invention may correspond to isolated or purified fragments which are naturally present in *Chlamydia pneumoniae* or which are secreted by  
25 *Chlamydia pneumoniae*, or may correspond to fragments capable of being obtained by cleaving the said polypeptide with a proteolytic enzyme, such as trypsin or chymotrypsin or collagenase, or with a chemical reagent, such as cyanogen bromide (CNBr) or alternatively by placing the said polypeptide in a highly acidic environment, for example at pH 2.5. Such polypeptide fragments may be equally well prepared by chemical synthesis, using hosts transformed with an expression vector according to  
30 the invention containing a nucleic acid allowing the expression of the said fragments, placed under the control of appropriate elements for regulation and/or expression.

"Modified polypeptide" of a polypeptide according to the invention is understood to designate a polypeptide obtained by genetic recombination or by chemical synthesis as will be described below, exhibiting at least one modification in relation to the normal sequence. These  
35 modifications may in particular affect amino acids responsible for a specificity or for the efficiency of the activity, or responsible for the structural conformation, for the charge or for the hydrophobicity, and for the capacity for multimerization and for membrane insertion of the polypeptide according to

the invention. It is thus possible to create polypeptides with an equivalent, an increased or a reduced activity, and with an equivalent, a narrower or a broader specificity. Among the modified polypeptides, there may be mentioned the polypeptides in which up to 5 amino acids may be modified, truncated at the N- or C-terminal end, or alternatively deleted, or else added.

5 As is indicated, the modifications of the polypeptide may have in particular the objective:

- of making it capable of modulating, regulating, inhibiting or inducing the expression of a gene of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms, and/or capable of modulating the replication cycle of *Chlamydia*, in particular of *Chlamydia pneumoniae* and its variants, or one of its associated microorganisms,  
10 in the host cell and/or organism,
- of allowing its use in methods of biosynthesis or of biodegradation, or its incorporation into vaccine compositions,
- of modifying its bioavailability as a compound for therapeutic use.

The said modified polypeptides may also be used on any cell or microorganism for which  
15 the said modified polypeptides will be capable of modulating, regulating, inhibiting or inducing gene expression, or of modulating the growth or the replication cycle of the said cell or of the said microorganism. The methods allowing demonstration of the said modulations on eukaryotic or prokaryotic cells are well known to persons skilled in the art. The said cells or microorganisms will be chosen, in particular, from tumour cells or infectious microorganisms and the said modified  
20 polypeptides may be used for the prevention or treatment of pathologies linked to the presence of the said cells or of the said microorganisms. It is also clearly understood that the nucleotide sequences encoding the said modified polypeptides may be used for the said modulations, for example by the intermediacy of vectors according to the invention and which are described below, so as to prevent or to treat the said pathologies.

25 The above modified polypeptides may be obtained using combinatory chemistry, in which it is possible to systematically vary portions of the polypeptide before testing them on models, cell cultures or microorganisms for example, so as to select the compounds which are the most active or which exhibit the desired properties.

Chemical synthesis also has the advantage of being able to use:

- 30
- nonnatural amino acids, or
  - nonpeptide bonds.

Accordingly, in order to extend the life of the polypeptides according to the invention, it may be advantageous to use nonnatural amino acids, for example in the D form, or alternatively amino acid analogues, in particular sulphur-containing forms for example.

35 Finally, the structure of the polypeptides according to the invention, its homologous or modified forms, as well as the corresponding fragments may be integrated into chemical structures of the polypeptide type and the like. Accordingly, it may be advantageous to provide at the N- and C-

terminal ends compounds which are not recognized by proteases.

Also forming part of the invention are the nucleotide sequences encoding a polypeptide according to the invention. Described below are ORF nucleotide sequences encoding polypeptides exhibiting particularly preferable characteristics. For each group of preferred ORFS described below, it is to be understood that in addition to the individual ORFs listed, in instances wherein such ORFS are present as part of "combined" ORFs, the "combined" ORFs are also to be included within the preferred group.

More particularly, the subject of the invention is nucleotide sequences, characterized in that they encode a polypeptide of the cellular envelope, preferably of the outer cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, such as for example the predominant proteins of the outer membrane, the adhesion proteins or the proteins entering into the composition of the Chlamydia wall. Among these sequences, the sequences comprising a nucleotide sequence chosen from the following sequences are most preferred:

ORF15; ORF25; ORF26; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF35;  
ORF68; ORF124; ORF275; ORF291; ORF294; ORF327; ORF342; ORF364; ORF374; ORF380;  
ORF414; ORF439; ORF466; ORF467; ORF468; ORF469; ORF470; ORF472; ORF474; ORF476;  
ORF477; ORF478; ORF479; ORF480; ORF482; ORF485; ORF500; ORF501; ORF503; ORF504;  
ORF505; ORF506; ORF520; ORF578; ORF580; ORF581; ORF595; ORF596; ORF597; ORF737;  
ORF830; ORF834; ORF836; ORF893; ORF917; ORF932; ORF976; ORF1035; ORF1045; ORF1090  
and one of their representative fragments.

The structure of the cytoplasmic membranes and of the wall of bacteria is dependent on the associated proteins. The structure of the cytoplasmic membrane makes it impermeable to water, to water-soluble substances and to small-sized molecules (ions, small inorganic molecules, peptides or proteins). To enter into or to interfere with a cell or a bacterium, a ligand must establish a special relationship with a protein anchored in the cytoplasmic membrane (the receptor). These proteins which are anchored on the membrane play an important role in metabolism since they control the exchanges in the bacterium. These exchanges apply to molecules of interest for the bacterium (small molecules such as sugars and small peptides) as well as undesirable molecules for the bacterium such as antibiotics or heavy metals.

The double lipid layer structure of the membrane requires the proteins which are inserted therein to have hydrophobic domains of about twenty amino acids forming an alpha helix. Predominantly hydrophobic and potentially transmembrane regions may be predicted from the primary sequence of the proteins, itself deduced from the nucleotide sequence. The presence of one or more putative transmembrane domains raises the possibility for a protein to be associated with the cytoplasmic membrane and to be able to play an important metabolic role therein or alternatively for the protein thus exposed to be able to exhibit potentially protective epitopes.

If the proteins inserted into the membrane exhibit several transmembrane domains

capable of interacting with one another via electrostatic bonds, it then becomes possible for these proteins to form pores which go across the membrane which becomes permeable for a number of substances. It should be noted that proteins which do not have transmembrane domains may also be anchored by the intermediacy of fatty acids in the cytoplasmic membrane, it being possible for the breaking of the bond between the protein and its anchor in some cases to be responsible for the release of the peptide outside the bacterium.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having between 1 and 3 transmembrane domains and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF2; ORF3; ORF6; ORF9; ORF10; ORF11; ORF13; ORF14; ORF16; ORF18; ORF19; ORF20;  
 ORF21; ORF22; ORF25; ORF27; ORF28; ORF29; ORF30; ORF31; ORF32; ORF33; ORF34;  
 ORF35; ORF37; ORF39; ORF41; ORF42; ORF44; ORF45; ORF46; ORF47; ORF48; ORF49;  
 ORF50; ORF53; ORF54; ORF56; ORF57; ORF59; ORF60; ORF61; ORF62; ORF63; ORF64;  
 15 ORF65; ORF66; ORF69; ORF72; ORF73; ORF74; ORF76; ORF77; ORF78; ORF79; ORF80;  
 ORF82; ORF84; ORF85; ORF86; ORF88; ORF89; ORF90; ORF91; ORF92; ORF93; ORF95;  
 ORF96; ORF98; ORF99; ORF100; ORF101; ORF102; ORF103; ORF104; ORF105; ORF106;  
 ORF107; ORF108; ORF114; ORF117; ORF118; ORF122; ORF123; ORF124; ORF125; ORF129;  
 ORF130; ORF131; ORF132; ORF133; ORF134; ORF135; ORF137; ORF138; ORF139; ORF140;  
 20 ORF141; ORF142; ORF143; ORF145; ORF146; ORF147; ORF150; ORF151; ORF152; ORF156;  
 ORF157; ORF158; ORF159; ORF160; ORF161; ORF162; ORF164; ORF166; ORF167; ORF170;  
 ORF173; ORF175; ORF176; ORF178; ORF179; ORF180; ORF182; ORF183; ORF184; ORF185;  
 ORF186; ORF187; ORF188; ORF189; ORF190; ORF191; ORF192; ORF194; ORF195; ORF196;  
 ORF197; ORF198; ORF199; ORF200; ORF201; ORF202; ORF205; ORF207; ORF208; ORF209;  
 25 ORF210; ORF212; ORF215; ORF219; ORF220; ORF224; ORF226; ORF227; ORF228; ORF231;  
 ORF232; ORF233; ORF234; ORF235; ORF236; ORF238; ORF239; ORF240; ORF241; ORF242;  
 ORF244; ORF247; ORF251; ORF252; ORF253; ORF255; ORF256; ORF257; ORF258; ORF260;  
 ORF262; ORF263; ORF266; ORF267; ORF268; ORF269; ORF270; ORF273; ORF274; ORF276;  
 ORF278; ORF279; ORF280; ORF281; ORF282; ORF283; ORF284; ORF286; ORF287; ORF289;  
 30 ORF290; ORF291; ORF293; ORF294; ORF297; ORF304; ORF305; ORF307; ORF308; ORF309;  
 ORF310; ORF311; ORF313; ORF314; ORF315; ORF316; ORF318; ORF319; ORF320; ORF321;  
 ORF322; ORF323; ORF324; ORF325; ORF326; ORF331; ORF332; ORF336; ORF338; ORF339;  
 ORF341; ORF344; ORF345; ORF346; ORF350; ORF352; ORF353; ORF356; ORF357; ORF358;  
 ORF359; ORF360; ORF362; ORF365; ORF366; ORF367; ORF370; ORF372; ORF373; ORF376;  
 35 ORF377; ORF378; ORF379; ORF381; ORF382; ORF383; ORF384; ORF385; ORF386; ORF387;  
 ORF390; ORF392; ORF393; ORF394; ORF396; ORF398; ORF399; ORF400; ORF404; ORF408;  
 ORF410; ORF411; ORF413; ORF416; ORF417; ORF418; ORF420; ORF422; ORF424; ORF427;

ORF428; ORF429; ORF430; ORF431; ORF433; ORF434; ORF437; ORF440; ORF441; ORF442;  
ORF443; ORF444; ORF445; ORF447; ORF450; ORF451; ORF452; ORF455; ORF456; ORF459;  
ORF460; ORF461; ORF462; ORF463; ORF464; ORF465; ORF467; ORF469; ORF471; ORF474;  
ORF475; ORF476; ORF477; ORF479; ORF482; ORF483; ORF484; ORF485; ORF486; ORF487;  
5 ORF488; ORF491; ORF493; ORF494; ORF497; ORF498; ORF499; ORF503; ORF508; ORF509;  
ORF510; ORF512; ORF514; ORF515; ORF516; ORF517; ORF518; ORF520; ORF521; ORF523;  
ORF525; ORF527; ORF528; ORF529; ORF530; ORF531; ORF533; ORF534; ORF535; ORF536;  
ORF537; ORF540; ORF541; ORF543; ORF544; ORF545; ORF546; ORF548; ORF549; ORF551;  
ORF553; ORF554; ORF555; ORF556; ORF557; ORF558; ORF559; ORF560; ORF562; ORF563;  
10 ORF564; ORF565; ORF566; ORF569; ORF571; ORF573; ORF576; ORF577; ORF581; ORF583;  
ORF584; ORF585; ORF586; ORF588; ORF591; ORF592; ORF594; ORF595; ORF596; ORF597;  
ORF599; ORF600; ORF603; ORF605; ORF608; ORF614; ORF615; ORF620; ORF621; ORF622;  
ORF623; ORF624; ORF625; ORF629; ORF630; ORF631; ORF633; ORF634; ORF637; ORF642;  
ORF644; ORF645; ORF647; ORF648; ORF652; ORF654; ORF655; ORF657; ORF658; ORF659;  
15 ORF660; ORF661; ORF664; ORF665; ORF666; ORF667; ORF670; ORF671; ORF672; ORF673;  
ORF674; ORF676; ORF679; ORF681; ORF684; ORF687; ORF688; ORF689; ORF690; ORF693;  
ORF694; ORF695; ORF696; ORF697; ORF698; ORF699; ORF700; ORF701; ORF703; ORF705;  
ORF706; ORF707; ORF708; ORF710; ORF712; ORF715; ORF716; ORF717; ORF718; ORF719;  
ORF721; ORF722; ORF723; ORF725; ORF726; ORF727; ORF728; ORF729; ORF730; ORF731;  
20 ORF733; ORF736; ORF737; ORF738; ORF740; ORF741; ORF742; ORF743; ORF747; ORF748;  
ORF750; ORF752; ORF754; ORF755; ORF756; ORF757; ORF759; ORF760; ORF761; ORF762;  
ORF763; ORF764; ORF765; ORF766; ORF767; ORF768; ORF772; ORF774; ORF775; ORF777;  
ORF781; ORF783; ORF788; ORF791; ORF792; ORF793; ORF794; ORF795; ORF796; ORF797;  
ORF798; ORF799; ORF802; ORF803; ORF806; ORF807; ORF808; ORF809; ORF810; ORF811;  
25 ORF813; ORF814; ORF815; ORF816; ORF817; ORF819; ORF820; ORF821; ORF823; ORF824;  
ORF827; ORF829; ORF830; ORF831; ORF833; ORF834; ORF835; ORF837; ORF844; ORF845;  
ORF846; ORF847; ORF848; ORF849; ORF850; ORF851; ORF852; ORF854; ORF855; ORF856;  
ORF857; ORF859; ORF860; ORF862; ORF865; ORF866; ORF868; ORF869; ORF870; ORF871;  
ORF872; ORF874; ORF877; ORF878; ORF879; ORF880; ORF881; ORF882; ORF884; ORF885;  
30 ORF888; ORF889; ORF890; ORF891; ORF892; ORF894; ORF895; ORF896; ORF897; ORF899;  
ORF900; ORF902; ORF903; ORF904; ORF905; ORF909; ORF910; ORF912; ORF913; ORF914;  
ORF915; ORF917; ORF918; ORF919; ORF921; ORF923; ORF924; ORF926; ORF927; ORF928;  
ORF929; ORF930; ORF931; ORF937; ORF938; ORF939; ORF941; ORF943; ORF948; ORF951;  
ORF952; ORF953; ORF958; ORF960; ORF963; ORF964; ORF965; ORF968; ORF970; ORF974;  
35 ORF975; ORF977; ORF979; ORF980; ORF981; ORF983; ORF984; ORF985; ORF987; ORF989;  
ORF992; ORF993; ORF997; ORF998; ORF999; ORF1001; ORF1002; ORF1004; ORF1005;  
ORF1009; ORF1013; ORF1014; ORF1015; ORF1016; ORF1019; ORF1021; ORF1023; ORF1024;

ORF1029; ORF1031; ORF1033; ORF1034; ORF1039; ORF1041; ORF1042; ORF1045;  
 ORF1047; ORF1049; ORF1051; ORF1052; ORF1053; ORF1054; ORF1056; ORF1059; ORF1061;  
 ORF1062; ORF1063; ORF1064; ORF1065; ORF1067; ORF1075; ORF1077; ORF1078; ORF1079;  
 ORF1080; ORF1081; ORF1089; ORF1095; ORF1097; ORF1098; ORF1099; ORF1101; ORF1102;  
 5 ORF1103; ORF1106; ORF1107; ORF1108; ORF1109; ORF1110; ORF1113; ORF1116; ORF1118;  
 ORF1119; ORF1121; ORF1123; ORF1124; ORF1126; ORF1128; ORF1130; ORF1131; ORF1133;  
 ORF1134; ORF1136; ORF1137 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,  
 characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or one of its  
 10 representative fragments, having between 4 and 6 transmembrane domains and in that they comprise a  
 nucleotide sequence chosen from the following sequences:

ORF5; ORF7; ORF8; ORF15; ORF36; ORF38; ORF51; ORF55; ORF58; ORF67; ORF70; ORF81;  
 ORF97; ORF110; ORF111; ORF115; ORF119; ORF126; ORF128; ORF148; ORF155; ORF163;  
 ORF165; ORF168; ORF169; ORF171; ORF172; ORF174; ORF177; ORF181; ORF193; ORF203;  
 15 ORF213; ORF214; ORF216; ORF217; ORF221; ORF222; ORF225; ORF229; ORF243; ORF246;  
 ORF248; ORF254; ORF261; ORF285; ORF288; ORF292; ORF296; ORF298; ORF299; ORF301;  
 ORF303; ORF317; ORF328; ORF329; ORF351; ORF354; ORF355; ORF364; ORF371; ORF374;  
 ORF375; ORF391; ORF395; ORF401; ORF403; ORF405; ORF409; ORF414; ORF419; ORF421;  
 ORF423; ORF425; ORF438; ORF448; ORF453; ORF458; ORF466; ORF468; ORF470; ORF480;  
 20 ORF489; ORF490; ORF496; ORF501; ORF504; ORF505; ORF506; ORF511; ORF513; ORF519;  
 ORF526; ORF532; ORF538; ORF539; ORF547; ORF550; ORF561; ORF568; ORF570; ORF574;  
 ORF578; ORF579; ORF580; ORF582; ORF589; ORF593; ORF598; ORF601; ORF604; ORF610;  
 ORF613; ORF617; ORF626; ORF632; ORF635; ORF638; ORF640; ORF641; ORF646; ORF649;  
 ORF650; ORF651; ORF686; ORF711; ORF724; ORF732; ORF734; ORF744; ORF745; ORF749;  
 25 ORF751; ORF769; ORF770; ORF771; ORF773; ORF776; ORF779; ORF780; ORF785; ORF787;  
 ORF789; ORF801; ORF805; ORF812; ORF822; ORF825; ORF826; ORF839; ORF841; ORF843;  
 ORF853; ORF861; ORF875; ORF876; ORF886; ORF893; ORF898; ORF906; ORF907; ORF908;  
 ORF920; ORF922; ORF925; ORF933; ORF935; ORF936; ORF944; ORF946; ORF947; ORF954;  
 ORF959; ORF961; ORF966; ORF967; ORF972; ORF978; ORF995; ORF996; ORF1000; ORF1003;  
 30 ORF1010; ORF1011; ORF1012; ORF1017; ORF1020; ORF1030; ORF1036; ORF1038; ORF1043;  
 ORF1046; ORF1048; ORF1050; ORF1058; ORF1071; ORF1073; ORF1084; ORF1085; ORF1086;  
 ORF1087; ORF1091; ORF1092; ORF1094; ORF1096; ORF1100; ORF1104; ORF1111; ORF1112;  
 ORF1114; ORF1117; ORF1122; ORF1125 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
 35 invention, characterized in that they encode a *Chlamydia pneumoniae* transmembrane polypeptide or  
 one of its representative fragments, having at least 7 transmembrane domains and in that they  
 comprise a nucleotide sequence chosen from the following sequences:

ORF17; ORF52; ORF68; ORF83; ORF87; ORF109; ORF112; ORF113; ORF120; ORF121;  
 ORF127; ORF153; ORF204; ORF211; ORF218; ORF223; ORF275; ORF277; ORF295; ORF300;  
 ORF302; ORF306; ORF327; ORF335; ORF342; ORF343; ORF347; ORF349; ORF361; ORF363;  
 ORF369; ORF380; ORF388; ORF389; ORF397; ORF415; ORF432; ORF439; ORF446; ORF449;  
 5 ORF472; ORF478; ORF500; ORF522; ORF524; ORF567; ORF575; ORF602; ORF606; ORF609;  
 ORF636; ORF639; ORF643; ORF653; ORF668; ORF692; ORF702; ORF704; ORF713; ORF720;  
 ORF778; ORF784; ORF800; ORF836; ORF838; ORF842; ORF864; ORF867; ORF883; ORF901;  
 ORF916; ORF932; ORF934; ORF940; ORF942; ORF950; ORF956; ORF971; ORF973; ORF976;  
 ORF988; ORF994; ORF1018; ORF1028; ORF1035; ORF1037; ORF1044; ORF1055; ORF1057;  
 10 ORF1068; ORF1069; ORF1070; ORF1072; ORF1082; ORF1088; ORF1105; ORF1132; ORF1135  
 and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,  
 characterized in that they encode a *Chlamydia pneumoniae* surface exposed polypeptide (e.g., an outer  
 membrane protein) or one of its representative fragments, said nucleotide sequences comprising a  
 15 nucleotide sequence chosen from the following sequences:

ORF 15, ORF 25, ORF 26, ORF 27, ORF 28, ORF 29, ORF 30, ORF 31, ORF 32, ORF 33, ORF 35,  
 ORF 36, ORF 1257, ORF 280, ORF 291, ORF 314, ORF 354, ORF 380, ORF 1266, ORF 466, ORF  
 467, ORF 468, ORF 469, ORF 470, ORF 472, ORF 474, ORF 476, ORF 477, ORF 478, ORF 479,  
 ORF 480, ORF 482, ORF 483, ORF 485, ORF 486, ORF 500, ORF 501, ORF 503, ORF 504, ORF  
 20 505, ORF 506, ORF 507, ORF 1268, ORF 1269, ORF 543, ORF 544, ORF 578, ORF 579, ORF 580,  
 ORF 581, ORF 595, ORF 596, ORF 597, ORF 1271, ORF 633, ORF 637, ORF 699, ORF 706, ORF  
 737, ORF 744, ORF 1273, ORF 751, ORF 775, ORF 776, ORF 777, ORF 793, ORF 815, ORF 830,  
 ORF 1221, ORF 849, ORF 851, ORF 852, ORF 874, ORF 891, ORF 922, ORF 940, ORF 1231, ORF  
 1281, ORF 1035, ORF 1079, ORF 1087, ORF 1108, and one of their representative fragments.

25 Preferably, the invention relates to the nucleotide sequences according to the invention,  
 characterized in that they encode a *Chlamydia pneumoniae* lipoprotein or one of its representative  
 fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following  
 sequences:

ORF 3, ORF 10, ORF 11, ORF 16, ORF 1254, ORF 1255, ORF 38, ORF 1256, ORF 62, ORF 85,  
 30 ORF 1258, ORF 115, ORF 1151, ORF 151, ORF 1259, ORF 173, ORF 1261, ORF 186, ORF 194,  
 ORF 205, ORF 214, ORF 216, ORF 217, ORF 238, ORF 1177, ORF 280, ORF 291, ORF 317, ORF  
 327, ORF 354, ORF 364, ORF 367, ORF 414, ORF 432, ORF 1192, ORF 460, ORF 1267, ORF 1268,  
 ORF 520, ORF 536, ORF 1270, ORF 576, ORF 597, ORF 603, ORF 609, ORF 637, ORF 1272, ORF  
 652, ORF 1213, ORF 699, ORF 705, ORF 706, ORF 708, ORF 711, ORF 727, ORF 1274, ORF 800,  
 35 ORF 814, ORF 825, ORF 829, ORF 830, ORF 831, ORF 844, ORF 849, ORF 1275, ORF 1276, ORF  
 1277, ORF 872, ORF 878, ORF 880, ORF 891, ORF 892, ORF 1278, ORF 1279, ORF 1280, ORF  
 941, ORF 942, ORF 1282, ORF 1283, ORF 952, ORF 988, ORF 998, ORF 1009, ORF 1285, ORF

1235, ORF 1028, ORF 1056, ORF 1070, ORF 1287, ORF 1087, ORF 1288, ORF 1289, ORF 1098, ORF 1246, ORF 1291, ORF 1108, ORF 1109, ORF 1112, ORF 1133, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention,  
5 characterized in that they encode a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 316, ORF 564, ORF 610, ORF 647, ORF 1211, ORF 688, ORF 924, and one of their representative fragments.

Preferably the invention relates to additional LPS-related nucleotide sequences according  
10 to the invention, characterized in that they encode:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octulosonic acid)-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 177, ORF 1156, ORF 245, ORF 767, and one of their representative fragments;

15 (b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 74, and one of its representative fragments;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the  
20 following sequences: ORF 1286, ORF 1039, and one of their representative fragments; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences: ORF 689, ORF 690, ORF 691, ORF 1037, and one of their representative fragments.

25 Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide containing RGD (Arg-Gly-Asp) attachment sites or one of its representative fragments.

(a) RGD-containing proteins that are outer membrane proteins, are more likely to play a  
30 role in cell attachment. ORFs that encoded a protein containing an RGD sequence and also were classified as outer membrane proteins are ORF 468 and its representative fragments.

(b) An RGD-encoding ORF that showed homology to *cds1*, *cds2*, and *copN* type III  
35 virulence loci in *Chlamydia psittaci* (Hsia, R. et al. (1997), Type III secretion genes identity a putative virulence locus of *Chlamydia*. Molecular Microbiology 25:351-359) is ORF 350, and its representative fragments.



(c) The outer membrane of *Chlamydia* is made of cysteine-rich proteins that form a network of both intra and inter molecular disulfide links. This contributes to the integrity of the membrane since *Chlamydia* lacks the peptidoglycan layer that other gram-negative bacteria have. Cysteine-rich proteins that have the RGD sequence are also considered to be potential vaccine candidates. Cysteine-rich proteins were defined as proteins that had more than 3.0% cysteine in their primary amino acid sequence, above the mean genomic ORF cysteine content. The corresponding ORFs are: ORF 1290, ORF 1294, ORF 1296, and one of their representative fragments.

(d) The outer membrane of *Chlamydia* may also contain small proteins that have cysteines in their N- and C-terminus that may contribute to the network formed by disulfide linkages. These proteins may be anchored in the outer membrane via their N-terminus and may have their C-terminus exposed, which then can interact with the host cells. Alternatively, these proteins may be anchored in the outer membrane via both N-and C-terminus and may have regions in the middle that may be exposed which can in turn interact with the host cells. ORFs encoding polypeptides that contain cysteines in their first 30 amino acids and also contain an RGD sequence are: ORF 105, ORF 106, ORF 114, ORF 170, ORF 171, ORF 1264, ORF 268, ORF 1265, ORF 350, ORF 393, ORF 394, ORF 451, ORF 452, ORF 453, ORF 473, ORF 499, ORF 515, ORF 519, ORF 525, ORF 526, ORF 538, ORF 611, ORF 645, ORF 686, ORF 700, ORF 746, ORF 755, ORF 756, ORF 757, ORF 789, ORF 814, ORF 855, ORF 856, ORF 878, ORF 957, ORF 958, ORF 989, ORF 1290, and one of their representative fragments.

(e) RGD-containing ORFs homologous to RGD-containing ORFs from *Chlamydia trachomatis* are:

ORF 114, ORF 468, ORF 755, ORF 756, ORF 757, ORF 855, ORF 856, ORF 905, ORF 913, ORF 914, ORF 915, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* Type III or other, non-type III secreted polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence chosen from the following sequences:

ORF 25, ORF 28, ORF 29, ORF 33, ORF 308, ORF 309, ORF 343, ORF 344, ORF 345, ORF 367, ORF 414, ORF 415, ORF 480, ORF 550, ORF 579, ORF 580, ORF 581, ORF 597, ORF 699, ORF 744, ORF 751, ORF 776, ORF 866, ORF 874, ORF 883, ORF 884, ORF 888, ORF 891, ORF 1293,

and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, said nucleotide sequences comprising a nucleotide sequence  
5 chosen from the following sequences: ORF 267, ORF 271, ORF 419, ORF 590, ORF 932, ORF 1292, ORF 1295, and one of their representative fragments.

Preferably, the invention relates to the nucleotide sequences according to the invention, characterized in that they encode *Chlamydia pneumoniae* polypeptides not found in *Chlamydia trachomatis* (Blastp.  $P > e^{-10}$ ), said nucleotide sequences comprising a nucleotide sequence chosen from  
10 the following sequences: ORF 7, ORF 8, ORF 9, ORF 16, ORF 17, ORF 18, ORF 19, ORF 20, ORF 21, ORF 22, ORF 1254, ORF 23, ORF 1255, ORF 24, ORF 1139, ORF 1140, ORF 46, ORF 47, ORF 51, ORF 60, ORF 1256, ORF 61, ORF 62, ORF 63, ORF 64, ORF 1257, ORF 65, ORF 66, ORF 67, ORF 68, ORF 1143, ORF 1145, ORF 83, ORF 84, ORF 1146, ORF 85, ORF 86, ORF 87, ORF 1258, ORF 116, ORF 117, ORF 125, ORF 1148, ORF 143, ORF 1150, ORF 1151, ORF 144, ORF 145, ORF  
15 147, ORF 148, ORF 149, ORF 150, ORF 152, ORF 1259, ORF 162, ORF 166, ORF 1154, ORF 167, ORF 1261, ORF 1156, ORF 1157, ORF 178, ORF 179, ORF 1158, ORF 182, ORF 183, ORF 184, ORF 185, ORF 1159, ORF 186, ORF 1160, ORF 187, ORF 188, ORF 189, ORF 190, ORF 1161, ORF 1162, ORF 191, ORF 192, ORF 194, ORF 195, ORF 1163, ORF 196, ORF 201, ORF 202, ORF 209, ORF 212, ORF 221, ORF 224, ORF 1167, ORF 226, ORF 227, ORF 228, ORF 229, ORF 230, ORF  
20 231, ORF 232, ORF 1169, ORF 1170, ORF 1171, ORF 234, ORF 235, ORF 236, ORF 1172, ORF 243, ORF 251, ORF 252, ORF 1176, ORF 253, ORF 255, ORF 254, ORF 256, ORF 1177, ORF 1178, ORF 262, ORF 263, ORF 1264, ORF 278, ORF 279, ORF 1180, ORF 280, ORF 290, ORF 291, ORF 292, ORF 296, ORF 1181, ORF 297, ORF 298, ORF 300, ORF 1265, ORF 322, ORF 324, ORF 325, ORF 370, ORF 1186, ORF 371, ORF 372, ORF 1187, ORF 373, ORF 378, ORF 1266, ORF 382, ORF  
25 383, ORF 384, ORF 385, ORF 386, ORF 1188, ORF 1189, ORF 391, ORF 392, ORF 398, ORF 400, ORF 403, ORF 1191, ORF 423, ORF 435, ORF 445, ORF 450, ORF 1193, ORF 456, ORF 460, ORF 461, ORF 465, ORF 1196, ORF 471, ORF 473, ORF 475, ORF 481, ORF 484, ORF 487, ORF 488, ORF 489, ORF 490, ORF 491, ORF 492, ORF 493, ORF 494, ORF 495, ORF 496, ORF 497, ORF 498, ORF 499, ORF 502, ORF 1267, ORF 1268, ORF 508, ORF 510, ORF 509, ORF 512, ORF 515,  
30 ORF 519, ORF 1197, ORF 521, ORF 1198, ORF 522, ORF 524, ORF 528, ORF 534, ORF 537, ORF 1269, ORF 1270, ORF 548, ORF 551, ORF 557, ORF 1201, ORF 1203, ORF 562, ORF 566, ORF 593, ORF 595, ORF 600, ORF 1271, ORF 604, ORF 611, ORF 612, ORF 614, ORF 616, ORF 625, ORF 627, ORF 628, ORF 629, ORF 631, ORF 641, ORF 1272, ORF 648, ORF 1212, ORF 663, ORF 685, ORF 707, ORF 714, ORF 715, ORF 716, ORF 717, ORF 722, ORF 746, ORF 1273, ORF 761,  
35 ORF 764, ORF 770, ORF 1217, ORF 783, ORF 1274, ORF 803, ORF 815, ORF 1220, ORF 835, ORF 1221, ORF 844, ORF 845, ORF 846, ORF 847, ORF 848, ORF 849, ORF 850, ORF 851, ORF 1275, ORF 852, ORF 862, ORF 1276, ORF 1277, ORF 873, ORF 1223, ORF 892, ORF 919, ORF 1225,

ORF 1278, ORF 926, ORF 1228, ORF 1229, ORF 1230, ORF 1279, ORF 1281, ORF 1282, ORF 1283, ORF 948, ORF 950, ORF 949, ORF 951, ORF 980, ORF 982, ORF 1233, ORF 999, ORF 1000, ORF 1001, ORF 1002, ORF 1008, ORF 1285, ORF 1235, ORF 1016, ORF 1019, ORF 1027, ORF 1036, ORF 1241, ORF 1048, ORF 1049, ORF 1050, ORF 1053, ORF 1054, ORF 1064, ORF 1076, ORF 1091, ORF 1288, ORF 1093, ORF 1289, ORF 1101, ORF 1103, ORF 1245, ORF 1246, ORF 1247, ORF 1290, ORF 1291, ORF 1115, ORF 1116, ORF 1118, ORF 1120, ORF 1249, ORF 1121, ORF 1250, ORF 1126, ORF 1251, ORF 1127, ORF 1128, ORF 1130, ORF 1129, ORF 1131, ORF 1136, ORF 1253, ORF 1292, ORF 1294, ORF 1295, ORF 1296, and one of their representative fragments.

10 Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, such as for example triose phosphate isomerase or pyruvate kinase, and in that they comprise a nucleotide sequence chosen from the following sequences:

15 ORF2; ORF55; ORF56; ORF69; ORF75; ORF80; ORF100; ORF110; ORF114; ORF120; ORF121; ORF157; ORF160; ORF161; ORF172; ORF180; ORF181; ORF198; ORF200; ORF225; ORF248; ORF249; ORF276; ORF277; ORF318; ORF319; ORF320; ORF323; ORF331; ORF347; ORF375; ORF376; ORF381; ORF393; ORF394; ORF395; ORF396; ORF409; ORF446; ORF447; ORF448; ORF449; ORF513; ORF516; ORF571; ORF647; ORF662; ORF697; ORF718; ORF793; ORF794; ORF808; ORF809; ORF838; ORF839; ORF840; ORF853; ORF854; ORF918; ORF923; ORF929; ORF931; ORF938; ORF939; ORF958; ORF959; ORF960; ORF966; ORF995; ORF1021; ORF1040; ORF1041; ORF1042; ORF1085; ORF1100; ORF1102; ORF1117; ORF1118; ORF1119; ORF1120; ORF1135 and one of their representative fragments.

25 Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, such as for example CTP synthetase or GMP synthetase, and in that they comprise a nucleotide sequence chosen from the following sequences:

30 ORF77; ORF78; ORF138; ORF189; ORF190; ORF233; ORF246; ORF338; ORF412; ORF421; ORF438; ORF607; ORF648; ORF657; ORF740; ORF783; ORF967; ORF989; ORF990; ORF992; ORF1011; ORF1058; ORF1059; ORF1073; ORF1074 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, such as for example DNA polymerases or DNA topoisomerases, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF14; ORF59; ORF70; ORF71; ORF97; ORF113; ORF137; ORF141; ORF169; ORF285; ORF287;

ORF288; ORF313; ORF326; ORF358; ORF411; ORF443; ORF548; ORF569; ORF601; ORF651;  
ORF654; ORF658; ORF659; ORF664; ORF665; ORF694; ORF698; ORF704; ORF760; ORF762;  
ORF763; ORF786; ORF787; ORF788; ORF801; ORF802; ORF812; ORF819; ORF822; ORF870;  
ORF897; ORF898; ORF902; ORF908; ORF916; ORF954; ORF955; ORF961; ORF983; ORF996;  
5 ORF1007; ORF1012; ORF1013; ORF1014; ORF1015; ORF1038; ORF1137 and one of their  
representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its  
representative fragments which is involved in the metabolism of amino acids or polypeptides, such as  
10 for example serine hydroxymethyl transferase or the proteins which load amino acids onto transfer  
RNAs, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF99; ORF111; ORF127; ORF134; ORF140; ORF174; ORF175; ORF176; ORF353; ORF377;  
ORF404; ORF523; ORF539; ORF559; ORF561; ORF586; ORF598; ORF609; ORF636; ORF687;  
ORF700; ORF701; ORF759; ORF790; ORF857; ORF861; ORF904; ORF936; ORF952; ORF962;  
15 ORF963; ORF964; ORF965; ORF991; ORF1003; ORF1004; ORF1005; ORF1018; ORF1067;  
ORF1110; ORF1111; ORF1112; ORF1114; ORF1121; ORF1122; ORF1123; ORF1124; ORF1125  
and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its  
20 representative fragments which is involved in the metabolism of polypeptides, such as for example  
protein kinases or proteases, and in that they comprise a nucleotide sequence chosen from the  
following sequences:

ORF4; ORF44; ORF45; ORF48; ORF54; ORF112; ORF130; ORF155; ORF163; ORF212; ORF257;  
ORF307; ORF343; ORF405; ORF416; ORF458; ORF540; ORF541; ORF542; ORF543; ORF544;  
25 ORF560; ORF594; ORF652; ORF699; ORF723; ORF747; ORF817; ORF827; ORF871; ORF909;  
ORF910; ORF911; ORF912; ORF1023; ORF1051; ORF1052; ORF1081 and one of their  
representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its  
30 representative fragments which is involved in the metabolism of fatty acids, such as for example  
succinyl-CoA-synthesizing proteins or phosphatidylserine synthetase, and in that they comprise a  
nucleotide sequence chosen from the following sequences:

ORF76; ORF284; ORF308; ORF309; ORF310; ORF311; ORF312; ORF425; ORF433; ORF565;  
ORF688; ORF690; ORF691; ORF767; ORF797; ORF894; ORF895; ORF994; ORF1020; ORF1030;  
35 ORF1033; ORF1034; ORF1046; ORF1047; ORF1057 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its

representative fragments which is involved in the synthesis of the wall, such as for example KDO transferase, and the proteins responsible for the attachment of certain sugars onto the exposed proteins, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF49; ORF50; ORF177; ORF178; ORF245; ORF610; ORF972; ORF974; ORF978; ORF1037 and  
5 one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, such as for example initiation factors, RNA polymerases or certain chaperone proteins, and in that  
10 they comprise a nucleotide sequence chosen from the following sequences:

ORF90; ORF92; ORF131; ORF151; ORF199; ORF333; ORF334; ORF336; ORF379; ORF589;  
ORF590; ORF619; ORF630; ORF649; ORF739; ORF741; ORF806; ORF821; ORF843; ORF968;  
ORF971; ORF1061 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
15 invention, characterized in that they encode a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative fragments, such as for example the ribosomal proteins L21, L27 and S10, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF93; ORF94; ORF95; ORF136; ORF259; ORF332; ORF348; ORF583; ORF584; ORF588;  
ORF591; ORF592; ORF663; ORF666; ORF667; ORF669; ORF670; ORF671; ORF672; ORF673;  
20 ORF674; ORF675; ORF676; ORF677; ORF678; ORF679; ORF680; ORF681; ORF683; ORF684;  
ORF738; ORF781; ORF1008; ORF1024; ORF1025; ORF1066 and one of their representative  
fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* transport polypeptide or one of  
25 its representative fragments, such as for example the proteins for transporting amino acids, sugars and certain oligopeptides, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF40; ORF41; ORF52; ORF105; ORF106; ORF107; ORF109; ORF133; ORF210; ORF211;  
ORF214; ORF215; ORF216; ORF217; ORF218; ORF219; ORF220; ORF223; ORF242; ORF260;  
30 ORF293; ORF299; ORF366; ORF369; ORF575; ORF602; ORF638; ORF639; ORF640; ORF643;  
ORF653; ORF702; ORF703; ORF724; ORF732; ORF855; ORF856; ORF901; ORF906; ORF933;  
ORF942; ORF1043; ORF1086; ORF1105 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the  
invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its  
35 representative fragments which is involved in the virulence process, such as for example the proteins analogous to the *Escherichia coli* vacB protein, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF546; ORF550; ORF778; ORF779; ORF886 and one of their representative fragments.

Preferably, the invention also relates to the nucleotide sequences according to the invention, characterized in that they encode a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, such as  
5 for example proteins homologous to proteins in the secretory system of certain bacteria such as the Salmonellae or the Yersiniae, and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF751; ORF874; ORF875; ORF876; ORF883; ORF884; ORF885 and one of their representative fragments.

10 Preferably, the invention also relates to a nucleotide sequence according to the invention, characterized in that they encode a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of  $>10^{-5}$ ), and in that they comprise a nucleotide sequence chosen from the following sequences:

ORF7; ORF8; ORF17; ORF18; ORF19; ORF20; ORF22; ORF23; ORF24; ORF51; ORF60; ORF63;  
15 ORF65; ORF66; ORF67; ORF83; ORF84; ORF86; ORF87; ORF125; ORF143; ORF144; ORF179;  
ORF182; ORF184; ORF185; ORF187; ORF221; ORF252; ORF254;; ORF278; ORF279; ORF387;  
ORF388; ORF397; ORF1048; ORF1049; ORF1050; ORF1128; ORF1130; ORF1131 and one of their representative fragments.

Also forming part of the invention are polypeptides encoded by the polynucleotides of  
20 the invention, as well as fusion polypeptides comprising such polypeptides. In one embodiment, the polypeptides and fusion polypeptides immunoreact with seropositive serum of an individual infected with *Chlamydia pneumoniae*. For example, described below, are polypeptide sequences exhibiting particularly preferable characteristics. For each group of preferred polypeptides described below, it is to be understood that in addition to the individual polypeptides listed, in instances wherein such  
25 polypeptides are encoded as part of "combined" ORFs, such "combined" polypeptides are also to be included within the preferred group.

The subject of the invention is also a polypeptide according to the invention, characterized in that it is a polypeptide of the cellular envelope, preferably of the outer cellular envelope, of *Chlamydia pneumoniae* or one of its representative fragments. According to the  
30 invention, the said polypeptide is preferably chosen from the polypeptides having the following sequences:

SEQ ID No. 15; SEQ ID No. 25; SEQ ID No. 26; SEQ ID No. 27; SEQ ID No. 28; SEQ ID No. 29;  
SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 35; SEQ ID No. 68;  
SEQ ID No. 124; SEQ ID No. 275; SEQ ID No. 291; SEQ ID No. 294; SEQ ID No. 327; SEQ ID  
35 No. 342; SEQ ID No. 364; SEQ ID No. 374; SEQ ID No. 380; SEQ ID No. 414; SEQ ID No. 439;  
SEQ ID No. 466; SEQ ID No. 467; SEQ ID No. 468; SEQ ID No. 469; SEQ ID No. 470; SEQ ID  
No. 472; SEQ ID No. 474; SEQ ID No. 476; SEQ ID No. 477; SEQ ID No. 478; SEQ ID No. 479;

SEQ ID No. 480; SEQ ID No. 482; SEQ ID No. 485; SEQ ID No. 500; SEQ ID No. 501;  
SEQ ID No. 503; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 520; SEQ ID  
No. 578; SEQ ID No. 580; SEQ ID No. 581; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597;  
SEQ ID No. 737; SEQ ID No. 830; SEQ ID No. 834; SEQ ID No. 836; SEQ ID No. 893; SEQ ID  
5 No. 917; SEQ ID No. 932; SEQ ID No. 976; SEQ ID No. 1035; SEQ ID No. 1045; SEQ ID No. 1090  
and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,  
characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its  
representative fragments, having between 1 and 3 transmembrane domains, and in that it is chosen  
10 from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 3; SEQ ID No. 6; SEQ ID No. 9; SEQ ID No. 10; SEQ ID No. 11;  
SEQ ID No. 13; SEQ ID No. 14; SEQ ID No. 16; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20;  
SEQ ID No. 21; SEQ ID No. 22; SEQ ID No. 25; SEQ ID No. 27; SEQ ID No. 28; SEQ ID  
No. 29; SEQ ID No. 30; SEQ ID No. 31; SEQ ID No. 32; SEQ ID No. 33; SEQ ID No. 34;  
15 SEQ ID No. 35; SEQ ID No. 37; SEQ ID No. 39; SEQ ID No. 41; SEQ ID No. 42; SEQ ID  
No. 44; SEQ ID No. 45; SEQ ID No. 46; SEQ ID No. 47; SEQ ID No. 48; SEQ ID No. 49;  
SEQ ID No. 50; SEQ ID No. 53; SEQ ID No. 54; SEQ ID No. 56; SEQ ID No. 57; SEQ ID  
No. 59; SEQ ID No. 60; SEQ ID No. 61; SEQ ID No. 62; SEQ ID No. 63; SEQ ID No. 64;  
SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 69; SEQ ID No. 72; SEQ ID No. 73; SEQ ID  
20 No. 74; SEQ ID No. 76; SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 79; SEQ ID No. 80;  
SEQ ID No. 82; SEQ ID No. 84; SEQ ID No. 85; SEQ ID No. 86; SEQ ID No. 88; SEQ ID  
No. 89; SEQ ID No. 90; SEQ ID No. 91; SEQ ID No. 92; SEQ ID No. 93; SEQ ID No. 95;  
SEQ ID No. 96; SEQ ID No. 98; SEQ ID No. 99; SEQ ID No. 100; SEQ ID No. 101; SEQ ID  
No. 102; SEQ ID No. 103; SEQ ID No. 104; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107;  
25 SEQ ID No. 108; SEQ ID No. 114; SEQ ID No. 117; SEQ ID No. 118; SEQ ID No. 122; SEQ ID  
No. 123; SEQ ID No. 124; SEQ ID No. 125; SEQ ID No. 129; SEQ ID No. 130; SEQ ID No. 131;  
SEQ ID No. 132; SEQ ID No. 133; SEQ ID No. 134; SEQ ID No. 135; SEQ ID No. 137; SEQ ID  
No. 138; SEQ ID No. 139; SEQ ID No. 140; SEQ ID No. 141; SEQ ID No. 142; SEQ ID No. 143;  
SEQ ID No. 145; SEQ ID No. 146; SEQ ID No. 147; SEQ ID No. 150; SEQ ID No. 151; SEQ ID  
30 No. 152; SEQ ID No. 156; SEQ ID No. 157; SEQ ID No. 158; SEQ ID No. 159; SEQ ID No. 160;  
SEQ ID No. 161; SEQ ID No. 162; SEQ ID No. 164; SEQ ID No. 166; SEQ ID No. 167; SEQ ID  
No. 170; SEQ ID No. 173; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 178; SEQ ID No. 179;  
SEQ ID No. 180; SEQ ID No. 182; SEQ ID No. 183; SEQ ID No. 184; SEQ ID No. 185; SEQ ID  
No. 186; SEQ ID No. 187; SEQ ID No. 188; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 191;  
35 SEQ ID No. 192; SEQ ID No. 194; SEQ ID No. 195; SEQ ID No. 196; SEQ ID No. 197; SEQ ID  
No. 198; SEQ ID No. 199; SEQ ID No. 200; SEQ ID No. 201; SEQ ID No. 202; SEQ ID No. 205;  
SEQ ID No. 207; SEQ ID No. 208; SEQ ID No. 209; SEQ ID No. 210; SEQ ID No. 212; SEQ ID

No. 215; SEQ ID No. 219; SEQ ID No. 220; SEQ ID No. 224; SEQ ID No. 226; SEQ ID  
No. 227; SEQ ID No. 228; SEQ ID No. 231; SEQ ID No. 232; SEQ ID No. 233; SEQ ID No. 234;  
SEQ ID No. 235; SEQ ID No. 236; SEQ ID No. 238; SEQ ID No. 239; SEQ ID No. 240; SEQ ID  
No. 241; SEQ ID No. 242; SEQ ID No. 244; SEQ ID No. 247; SEQ ID No. 251; SEQ ID No. 252;  
5 SEQ ID No. 253; SEQ ID No. 255; SEQ ID No. 256; SEQ ID No. 257; SEQ ID No. 258; SEQ ID  
No. 260; SEQ ID No. 262; SEQ ID No. 263; SEQ ID No. 266; SEQ ID No. 267; SEQ ID No. 268;  
SEQ ID No. 269; SEQ ID No. 270; SEQ ID No. 273; SEQ ID No. 274; SEQ ID No. 276; SEQ ID  
No. 278; SEQ ID No. 279; SEQ ID No. 280; SEQ ID No. 281; SEQ ID No. 282; SEQ ID No. 283;  
SEQ ID No. 284; SEQ ID No. 286; SEQ ID No. 287; SEQ ID No. 289; SEQ ID No. 290; SEQ ID  
10 No. 291; SEQ ID No. 293; SEQ ID No. 294; SEQ ID No. 297; SEQ ID No. 304; SEQ ID No. 305;  
SEQ ID No. 307; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID No. 311; SEQ ID  
No. 313; SEQ ID No. 314; SEQ ID No. 315; SEQ ID No. 316; SEQ ID No. 318; SEQ ID No. 319;  
SEQ ID No. 320; SEQ ID No. 321; SEQ ID No. 322; SEQ ID No. 323; SEQ ID No. 324; SEQ ID  
No. 325; SEQ ID No. 326; SEQ ID No. 331; SEQ ID No. 332; SEQ ID No. 336; SEQ ID No. 338;  
15 SEQ ID No. 339; SEQ ID No. 341; SEQ ID No. 344; SEQ ID No. 345; SEQ ID No. 346; SEQ ID  
No. 350; SEQ ID No. 352; SEQ ID No. 353; SEQ ID No. 356; SEQ ID No. 357; SEQ ID No. 358;  
SEQ ID No. 359; SEQ ID No. 360; SEQ ID No. 362; SEQ ID No. 365; SEQ ID No. 366; SEQ ID  
No. 367; SEQ ID No. 370; SEQ ID No. 372; SEQ ID No. 373; SEQ ID No. 376; SEQ ID No. 377;  
SEQ ID No. 378; SEQ ID No. 379; SEQ ID No. 381; SEQ ID No. 382; SEQ ID No. 383; SEQ ID  
20 No. 384; SEQ ID No. 385; SEQ ID No. 386; SEQ ID No. 387; SEQ ID No. 390; SEQ ID No. 392;  
SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 396; SEQ ID No. 398; SEQ ID No. 399; SEQ ID  
No. 400; SEQ ID No. 404; SEQ ID No. 408; SEQ ID No. 410; SEQ ID No. 411; SEQ ID No. 413;  
SEQ ID No. 416; SEQ ID No. 417; SEQ ID No. 418; SEQ ID No. 420; SEQ ID No. 422; SEQ ID  
No. 424; SEQ ID No. 427; SEQ ID No. 428; SEQ ID No. 429; SEQ ID No. 430; SEQ ID No. 431;  
25 SEQ ID No. 433; SEQ ID No. 434; SEQ ID No. 437; SEQ ID No. 440; SEQ ID No. 441; SEQ ID  
No. 442; SEQ ID No. 443; SEQ ID No. 444; SEQ ID No. 445; SEQ ID No. 447; SEQ ID No. 450;  
SEQ ID No. 451; SEQ ID No. 452; SEQ ID No. 455; SEQ ID No. 456; SEQ ID No. 459; SEQ ID  
No. 460; SEQ ID No. 461; SEQ ID No. 462; SEQ ID No. 463; SEQ ID No. 464; SEQ ID No. 465;  
SEQ ID No. 467; SEQ ID No. 469; SEQ ID No. 471; SEQ ID No. 474; SEQ ID No. 475; SEQ ID  
30 No. 476; SEQ ID No. 477; SEQ ID No. 479; SEQ ID No. 482; SEQ ID No. 483; SEQ ID No. 484;  
SEQ ID No. 485; SEQ ID No. 486; SEQ ID No. 487; SEQ ID No. 488; SEQ ID No. 491; SEQ ID  
No. 493; SEQ ID No. 494; SEQ ID No. 497; SEQ ID No. 498; SEQ ID No. 499; SEQ ID No. 503;  
SEQ ID No. 508; SEQ ID No. 509; SEQ ID No. 510; SEQ ID No. 512; SEQ ID No. 514; SEQ ID  
No. 515; SEQ ID No. 516; SEQ ID No. 517; SEQ ID No. 518; SEQ ID No. 520; SEQ ID No. 521;  
35 SEQ ID No. 523; SEQ ID No. 525; SEQ ID No. 527; SEQ ID No. 528; SEQ ID No. 529; SEQ ID  
No. 530; SEQ ID No. 531; SEQ ID No. 533; SEQ ID No. 534; SEQ ID No. 535; SEQ ID No. 536;  
SEQ ID No. 537; SEQ ID No. 540; SEQ ID No. 541; SEQ ID No. 543; SEQ ID No. 544; SEQ ID



No. 545; SEQ ID No. 546; SEQ ID No. 548; SEQ ID No. 549; SEQ ID No. 551; SEQ ID No. 553; SEQ ID No. 554; SEQ ID No. 555; SEQ ID No. 556; SEQ ID No. 557; SEQ ID No. 558; SEQ ID No. 559; SEQ ID No. 560; SEQ ID No. 562; SEQ ID No. 563; SEQ ID No. 564; SEQ ID No. 565; SEQ ID No. 566; SEQ ID No. 569; SEQ ID No. 571; SEQ ID No. 573; SEQ ID No. 576; 5 SEQ ID No. 577; SEQ ID No. 581; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 585; SEQ ID No. 586; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 594; SEQ ID No. 595; SEQ ID No. 596; SEQ ID No. 597; SEQ ID No. 599; SEQ ID No. 600; SEQ ID No. 603; SEQ ID No. 605; SEQ ID No. 608; SEQ ID No. 614; SEQ ID No. 615; SEQ ID No. 620; SEQ ID No. 621; SEQ ID No. 622; SEQ ID No. 623; SEQ ID No. 624; SEQ ID No. 625; SEQ ID No. 629; SEQ ID 10 No. 630; SEQ ID No. 631; SEQ ID No. 633; SEQ ID No. 634; SEQ ID No. 637; SEQ ID No. 642; SEQ ID No. 644; SEQ ID No. 645; SEQ ID No. 647; SEQ ID No. 648; SEQ ID No. 652; SEQ ID No. 654; SEQ ID No. 655; SEQ ID No. 657; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 660; SEQ ID No. 661; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 676; 15 SEQ ID No. 679; SEQ ID No. 681; SEQ ID No. 684; SEQ ID No. 687; SEQ ID No. 688; SEQ ID No. 689; SEQ ID No. 690; SEQ ID No. 693; SEQ ID No. 694; SEQ ID No. 695; SEQ ID No. 696; SEQ ID No. 697; SEQ ID No. 698; SEQ ID No. 699; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 703; SEQ ID No. 705; SEQ ID No. 706; SEQ ID No. 707; SEQ ID No. 708; SEQ ID No. 710; SEQ ID No. 712; SEQ ID No. 715; SEQ ID No. 716; SEQ ID No. 717; SEQ ID No. 718; SEQ ID 20 No. 719; SEQ ID No. 721; SEQ ID No. 722; SEQ ID No. 723; SEQ ID No. 725; SEQ ID No. 726; SEQ ID No. 727; SEQ ID No. 728; SEQ ID No. 729; SEQ ID No. 730; SEQ ID No. 731; SEQ ID No. 733; SEQ ID No. 736; SEQ ID No. 737; SEQ ID No. 738; SEQ ID No. 740; SEQ ID No. 741; SEQ ID No. 742; SEQ ID No. 743; SEQ ID No. 747; SEQ ID No. 748; SEQ ID No. 750; SEQ ID No. 752; SEQ ID No. 754; SEQ ID No. 755; SEQ ID No. 756; SEQ ID No. 757; SEQ ID No. 759; 25 SEQ ID No. 760; SEQ ID No. 761; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 764; SEQ ID No. 765; SEQ ID No. 766; SEQ ID No. 767; SEQ ID No. 768; SEQ ID No. 772; SEQ ID No. 774; SEQ ID No. 775; SEQ ID No. 777; SEQ ID No. 781; SEQ ID No. 783; SEQ ID No. 788; SEQ ID No. 791; SEQ ID No. 792; SEQ ID No. 793; SEQ ID No. 794; SEQ ID No. 795; SEQ ID No. 796; SEQ ID No. 797; SEQ ID No. 798; SEQ ID No. 799; SEQ ID No. 802; SEQ ID No. 803; SEQ ID 30 No. 806; SEQ ID No. 807; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 810; SEQ ID No. 811; SEQ ID No. 813; SEQ ID No. 814; SEQ ID No. 815; SEQ ID No. 816; SEQ ID No. 817; SEQ ID No. 819; SEQ ID No. 820; SEQ ID No. 821; SEQ ID No. 823; SEQ ID No. 824; SEQ ID No. 827; SEQ ID No. 829; SEQ ID No. 830; SEQ ID No. 831; SEQ ID No. 833; SEQ ID No. 834; SEQ ID No. 835; SEQ ID No. 837; SEQ ID No. 844; SEQ ID No. 845; SEQ ID No. 846; SEQ ID No. 847; 35 SEQ ID No. 848; SEQ ID No. 849; SEQ ID No. 850; SEQ ID No. 851; SEQ ID No. 852; SEQ ID No. 854; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 857; SEQ ID No. 859; SEQ ID No. 860; SEQ ID No. 862; SEQ ID No. 865; SEQ ID No. 866; SEQ ID No. 868; SEQ ID No. 869; SEQ ID

No. 870; SEQ ID No. 871; SEQ ID No. 872; SEQ ID No. 874; SEQ ID No. 877; SEQ ID No. 878; SEQ ID No. 879; SEQ ID No. 880; SEQ ID No. 881; SEQ ID No. 882; SEQ ID No. 884; SEQ ID No. 885; SEQ ID No. 888; SEQ ID No. 889; SEQ ID No. 890; SEQ ID No. 891; SEQ ID No. 892; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 896; SEQ ID No. 897; SEQ ID No. 899;  
 5 SEQ ID No. 900; SEQ ID No. 902; SEQ ID No. 903; SEQ ID No. 904; SEQ ID No. 905; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 912; SEQ ID No. 913; SEQ ID No. 914; SEQ ID No. 915; SEQ ID No. 917; SEQ ID No. 918; SEQ ID No. 919; SEQ ID No. 921; SEQ ID No. 923; SEQ ID No. 924; SEQ ID No. 926; SEQ ID No. 927; SEQ ID No. 928; SEQ ID No. 929; SEQ ID No. 930; SEQ ID No. 931; SEQ ID No. 937; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 941; SEQ ID  
 10 No. 943; SEQ ID No. 948; SEQ ID No. 951; SEQ ID No. 952; SEQ ID No. 953; SEQ ID No. 958; SEQ ID No. 960; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 968; SEQ ID No. 970; SEQ ID No. 974; SEQ ID No. 975; SEQ ID No. 977; SEQ ID No. 979; SEQ ID No. 980; SEQ ID No. 981; SEQ ID No. 983; SEQ ID No. 984; SEQ ID No. 985; SEQ ID No. 987; SEQ ID No. 989; SEQ ID No. 992; SEQ ID No. 993; SEQ ID No. 997; SEQ ID No. 998; SEQ ID No. 999;  
 15 SEQ ID No. 1001; SEQ ID No. 1002; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1009; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1016; SEQ ID No. 1019; SEQ ID No. 1021; SEQ ID No. 1023; SEQ ID No. 1024; SEQ ID No. 1029; SEQ ID No. 1031; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1039; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1045; SEQ ID No. 1047; SEQ ID No. 1049; SEQ ID No. 1051; SEQ ID No. 1052;  
 20 SEQ ID No. 1053; SEQ ID No. 1054; SEQ ID No. 1056; SEQ ID No. 1059; SEQ ID No. 1061; SEQ ID No. 1062; SEQ ID No. 1063; SEQ ID No. 1064; SEQ ID No. 1065; SEQ ID No. 1067; SEQ ID No. 1075; SEQ ID No. 1077; SEQ ID No. 1078; SEQ ID No. 1079; SEQ ID No. 1080; SEQ ID No. 1081; SEQ ID No. 1089; SEQ ID No. 1095; SEQ ID No. 1097; SEQ ID No. 1098; SEQ ID No. 1099; SEQ ID No. 1101; SEQ ID No. 1102; SEQ ID No. 1103; SEQ ID No. 1106;  
 25 SEQ ID No. 1107; SEQ ID No. 1108; SEQ ID No. 1109; SEQ ID No. 1110; SEQ ID No. 1113; SEQ ID No. 1116; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1121; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1126; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131; SEQ ID No. 1133; SEQ ID No. 1134; SEQ ID No. 1136; SEQ ID No. 1137 and one of their representative fragments.

30 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its respective fragments, having between 4 and 6 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 5; SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 15; SEQ ID No. 36; SEQ ID No. 38;  
 35 SEQ ID No. 51; SEQ ID No. 55; SEQ ID No. 58; SEQ ID No. 67; SEQ ID No. 70; SEQ ID No. 81; SEQ ID No. 97; SEQ ID No. 110; SEQ ID No. 111; SEQ ID No. 115; SEQ ID No. 119; SEQ ID No. 126; SEQ ID No. 128; SEQ ID No. 148; SEQ ID No. 155; SEQ ID No. 163; SEQ ID

No. 165; SEQ ID No. 168; SEQ ID No. 169; SEQ ID No. 171; SEQ ID No. 172; SEQ ID No. 174; SEQ ID No. 177; SEQ ID No. 181; SEQ ID No. 193; SEQ ID No. 203; SEQ ID No. 213; SEQ ID No. 214; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 221; SEQ ID No. 222; SEQ ID No. 225; SEQ ID No. 229; SEQ ID No. 243; SEQ ID No. 246; SEQ ID No. 248; SEQ ID No. 254; 5 SEQ ID No. 261; SEQ ID No. 285; SEQ ID No. 288; SEQ ID No. 292; SEQ ID No. 296; SEQ ID No. 298; SEQ ID No. 299; SEQ ID No. 301; SEQ ID No. 303; SEQ ID No. 317; SEQ ID No. 328; SEQ ID No. 329; SEQ ID No. 351; SEQ ID No. 354; SEQ ID No. 355; SEQ ID No. 364; SEQ ID No. 371; SEQ ID No. 374; SEQ ID No. 375; SEQ ID No. 391; SEQ ID No. 395; SEQ ID No. 401; SEQ ID No. 403; SEQ ID No. 405; SEQ ID No. 409; SEQ ID No. 414; SEQ ID No. 419; SEQ ID 10 No. 421; SEQ ID No. 423; SEQ ID No. 425; SEQ ID No. 438; SEQ ID No. 448; SEQ ID No. 453; SEQ ID No. 458; SEQ ID No. 466; SEQ ID No. 468; SEQ ID No. 470; SEQ ID No. 480; SEQ ID No. 489; SEQ ID No. 490; SEQ ID No. 496; SEQ ID No. 501; SEQ ID No. 504; SEQ ID No. 505; SEQ ID No. 506; SEQ ID No. 511; SEQ ID No. 513; SEQ ID No. 519; SEQ ID No. 526; SEQ ID No. 532; SEQ ID No. 538; SEQ ID No. 539; SEQ ID No. 547; SEQ ID No. 550; SEQ ID No. 561; 15 SEQ ID No. 568; SEQ ID No. 570; SEQ ID No. 574; SEQ ID No. 578; SEQ ID No. 579; SEQ ID No. 580; SEQ ID No. 582; SEQ ID No. 589; SEQ ID No. 593; SEQ ID No. 598; SEQ ID No. 601; SEQ ID No. 604; SEQ ID No. 610; SEQ ID No. 613; SEQ ID No. 617; SEQ ID No. 626; SEQ ID No. 632; SEQ ID No. 635; SEQ ID No. 638; SEQ ID No. 640; SEQ ID No. 641; SEQ ID No. 646; SEQ ID No. 649; SEQ ID No. 650; SEQ ID No. 651; SEQ ID No. 686; SEQ ID No. 711; SEQ ID 20 No. 724; SEQ ID No. 732; SEQ ID No. 734; SEQ ID No. 744; SEQ ID No. 745; SEQ ID No. 749; SEQ ID No. 751; SEQ ID No. 769; SEQ ID No. 770; SEQ ID No. 771; SEQ ID No. 773; SEQ ID No. 776; SEQ ID No. 779; SEQ ID No. 780; SEQ ID No. 785; SEQ ID No. 787; SEQ ID No. 789; SEQ ID No. 801; SEQ ID No. 805; SEQ ID No. 812; SEQ ID No. 822; SEQ ID No. 825; SEQ ID No. 826; SEQ ID No. 839; SEQ ID No. 841; SEQ ID No. 843; SEQ ID No. 853; SEQ ID No. 861; 25 SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 886; SEQ ID No. 893; SEQ ID No. 898; SEQ ID No. 906; SEQ ID No. 907; SEQ ID No. 908; SEQ ID No. 920; SEQ ID No. 922; SEQ ID No. 925; SEQ ID No. 933; SEQ ID No. 935; SEQ ID No. 936; SEQ ID No. 944; SEQ ID No. 946; SEQ ID No. 947; SEQ ID No. 954; SEQ ID No. 959; SEQ ID No. 961; SEQ ID No. 966; SEQ ID No. 967; SEQ ID No. 972; SEQ ID No. 978; SEQ ID No. 995; SEQ ID No. 996; SEQ ID No. 1000; SEQ ID 30 No. 1003; SEQ ID No. 1010; SEQ ID No. 1011; SEQ ID No. 1012; SEQ ID No. 1017; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1036; SEQ ID No. 1038; SEQ ID No. 1043; SEQ ID No. 1046; SEQ ID No. 1048; SEQ ID No. 1050; SEQ ID No. 1058; SEQ ID No. 1071; SEQ ID No. 1073; SEQ ID No. 1084; SEQ ID No. 1085; SEQ ID No. 1086; SEQ ID No. 1087; SEQ ID No. 1091; SEQ ID No. 1092; SEQ ID No. 1094; SEQ ID No. 1096; SEQ ID No. 1100; SEQ ID 35 No. 1104; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1117; SEQ ID No. 1122; SEQ ID No. 1125 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention,

characterized in that it is a *Chlamydia pneumoniae* transmembrane polypeptide or one of its representative fragments, having at least 7 transmembrane domains, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 17; SEQ ID No. 52; SEQ ID No. 68; SEQ ID No. 83; SEQ ID No. 87; SEQ ID No. 109;  
 5 SEQ ID No. 112; SEQ ID No. 113; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 127; SEQ ID  
 No. 153; SEQ ID No. 204; SEQ ID No. 211; SEQ ID No. 218; SEQ ID No. 223; SEQ ID No. 275;  
 SEQ ID No. 277; SEQ ID No. 295; SEQ ID No. 300; SEQ ID No. 302; SEQ ID No. 306; SEQ ID  
 No. 327; SEQ ID No. 335; SEQ ID No. 342; SEQ ID No. 343; SEQ ID No. 347; SEQ ID No. 349;  
 SEQ ID No. 361; SEQ ID No. 363; SEQ ID No. 369; SEQ ID No. 380; SEQ ID No. 388; SEQ ID  
 10 No. 389; SEQ ID No. 397; SEQ ID No. 415; SEQ ID No. 432; SEQ ID No. 439; SEQ ID No. 446;  
 SEQ ID No. 449; SEQ ID No. 472; SEQ ID No. 478; SEQ ID No. 500; SEQ ID No. 522; SEQ ID  
 No. 524; SEQ ID No. 567; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 606; SEQ ID No. 609;  
 SEQ ID No. 636; SEQ ID No. 639; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 668; SEQ ID  
 No. 692; SEQ ID No. 702; SEQ ID No. 704; SEQ ID No. 713; SEQ ID No. 720; SEQ ID No. 778;  
 15 SEQ ID No. 784; SEQ ID No. 800; SEQ ID No. 836; SEQ ID No. 838; SEQ ID No. 842; SEQ ID  
 No. 864; SEQ ID No. 867; SEQ ID No. 883; SEQ ID No. 901; SEQ ID No. 916; SEQ ID No. 932;  
 SEQ ID No. 934; SEQ ID No. 940; SEQ ID No. 942; SEQ ID No. 950; SEQ ID No. 956; SEQ ID  
 No. 971; SEQ ID No. 973; SEQ ID No. 976; SEQ ID No. 988; SEQ ID No. 994; SEQ ID No. 1018;  
 SEQ ID No. 1028; SEQ ID No. 1035; SEQ ID No. 1037; SEQ ID No. 1044; SEQ ID No. 1055;  
 20 SEQ ID No. 1057; SEQ ID No. 1068; SEQ ID No. 1069; SEQ ID No. 1070; SEQ ID No. 1072;  
 SEQ ID No. 1082; SEQ ID No. 1088; SEQ ID No. 1105; SEQ ID No. 1132; SEQ ID No. 1135 and  
 one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a  
*Chlamydia pneumoniae* surface exposed polypeptide or one of its representative fragments, and in that  
 25 it is chosen from the polypeptides having the following sequences:

SEQ ID No. 15, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29,  
 SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32, SEQ ID No. 33, SEQ ID No. 35, SEQ ID No. 36,  
 SEQ ID No. 1257, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 314, SEQ ID No. 354, SEQ ID  
 No. 380, SEQ ID No. 1266, SEQ ID No. 466, SEQ ID No. 467, SEQ ID No. 468, SEQ ID No. 469,  
 30 SEQ ID No. 470, SEQ ID No. 472, SEQ ID No. 474, SEQ ID No. 476, SEQ ID No. 477, SEQ ID No.  
 478, SEQ ID No. 479, SEQ ID No. 480, SEQ ID No. 482, SEQ ID No. 483, SEQ ID No. 485, SEQ ID  
 No. 486, SEQ ID No. 500, SEQ ID No. 501, SEQ ID No. 503, SEQ ID No. 504, SEQ ID No. 505,  
 SEQ ID No. 506, SEQ ID No. 507, SEQ ID No. 1268, SEQ ID No. 1269, SEQ ID No. 543, SEQ ID  
 No. 544, SEQ ID No. 578, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 595,  
 35 SEQ ID No. 596, SEQ ID No. 597, SEQ ID No. 1271, SEQ ID No. 633, SEQ ID No. 637, SEQ ID  
 No. 699, SEQ ID No. 706, SEQ ID No. 737, SEQ ID No. 744, SEQ ID No. 1273, SEQ ID No. 751,  
 SEQ ID No. 775, SEQ ID No. 776, SEQ ID No. 777, SEQ ID No. 793, SEQ ID No. 815, SEQ ID No.

830, SEQ ID No. 1221, SEQ ID No. 849, SEQ ID No. 851, SEQ ID No. 852, SEQ ID No. 874, SEQ ID No. 891, SEQ ID No. 922, SEQ ID No. 940, SEQ ID No. 1231, SEQ ID No. 1281, SEQ ID No. 1035, SEQ ID No. 1079, SEQ ID No. 1087, SEQ ID No. 1108, and one of their representative fragments.

5 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* lipoprotein or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 3, SEQ ID No. 10, SEQ ID No. 11, SEQ ID No. 16, SEQ ID No. 1254, SEQ ID No. 1255, SEQ ID No. 38, SEQ ID No. 1256, SEQ ID No. 62, SEQ ID No. 85, SEQ ID No. 1258, SEQ ID  
10 No. 115, SEQ ID No. 1151, SEQ ID No. 151, SEQ ID No. 1259, SEQ ID No. 173, SEQ ID No. 1261, SEQ ID No. 186, SEQ ID No. 194, SEQ ID No. 205, SEQ ID No. 214, SEQ ID No. 216, SEQ ID No. 217, SEQ ID No. 238, SEQ ID No. 1177, SEQ ID No. 280, SEQ ID No. 291, SEQ ID No. 317, SEQ ID No. 327, SEQ ID No. 354, SEQ ID No. 364, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 432, SEQ ID No. 1192, SEQ ID No. 460, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 520, SEQ ID  
15 No. 536, SEQ ID No. 1270, SEQ ID No. 576, SEQ ID No. 597, SEQ ID No. 603, SEQ ID No. 609, SEQ ID No. 637, SEQ ID No. 1272, SEQ ID No. 652, SEQ ID No. 1213, SEQ ID No. 699, SEQ ID No. 705, SEQ ID No. 706, SEQ ID No. 708, SEQ ID No. 711, SEQ ID No. 727, SEQ ID No. 1274, SEQ ID No. 800, SEQ ID No. 814, SEQ ID No. 825, SEQ ID No. 829, SEQ ID No. 830, SEQ ID No. 831, SEQ ID No. 844, SEQ ID No. 849, SEQ ID No. 1275, SEQ ID No. 1276, SEQ ID No. 1277, SEQ  
20 ID No. 872, SEQ ID No. 878, SEQ ID No. 880, SEQ ID No. 891, SEQ ID No. 892, SEQ ID No. 1278, SEQ ID No. 1279, SEQ ID No. 1280, SEQ ID No. 941, SEQ ID No. 942, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 952, SEQ ID No. 988, SEQ ID No. 998, SEQ ID No. 1009, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1028, SEQ ID No. 1056, SEQ ID No. 1070, SEQ ID No. 1287, SEQ ID No. 1087, SEQ ID No. 1288, SEQ ID No. 1289, SEQ ID No. 1098, SEQ ID No. 1246, SEQ ID No.  
25 1291, SEQ ID No. 1108, SEQ ID No. 1109, SEQ ID No. 1112, SEQ ID No. 1133, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide (LPS) biosynthesis, and in that it is chosen from the polypeptides having the following sequences:

30 SEQ ID No. 316, SEQ ID No. 564, SEQ ID No. 610, SEQ ID No. 647, SEQ ID No. 1211, SEQ ID No. 688, SEQ ID No. 924, and one of their representative fragments.

Preferably, the invention relates to additional LPS-related polypeptides according to the invention, in that it is:

(a) a *Chlamydia pneumoniae* KDO (3-deoxy-D-manno-octylosonic acid)-related  
35 polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 177, SEQ ID No. 1156, SEQ ID No. 245, SEQ ID No. 767, and one of their representative fragments;

(b) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 74, and its representative fragment;

(c) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1286, SEQ ID No. 1039, and its representative fragment; and

(d) a *Chlamydia pneumoniae* lipid A component-related polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 689, SEQ ID No. 690, SEQ ID No. 691, SEQ ID No. 1037, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence and is also an outer membrane protein, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 468 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains an RGD sequence that shows homology to cds1, cds2, and copN type III virulence loci in *Chlamydia Psitacci*, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 350 and its representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments that is cysteine-rich and contains RGD sequence, and in that it is chosen from the polypeptides having the following sequences: SEQ ID No. 1290, SEQ ID No. 6846, SEQ ID No. 6848, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* outer membrane polypeptide that contains cysteines in their first 30 amino acids and also contain an RGD sequence, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 105, SEQ ID No. 106, SEQ ID No. 114, SEQ ID No. 170, SEQ ID No. 171, SEQ ID No. 1264, SEQ ID No. 268, SEQ ID No. 1265, SEQ ID No. 350, SEQ ID No. 393, SEQ ID No. 394, SEQ ID No. 451, SEQ ID No. 452, SEQ ID No. 453, SEQ ID No. 473, SEQ ID No. 499, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 525, SEQ ID No. 526, SEQ ID No. 538, SEQ ID No. 611, SEQ ID No. 645, SEQ ID No. 686, SEQ ID No. 700, SEQ ID No. 746, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 789, SEQ ID No. 814, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 878, SEQ ID No. 957, SEQ ID No. 958, SEQ ID No. 989, SEQ ID No. 1290, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a

*Chlamydia pneumoniae* polypeptide or one of its representative fragments that contains RGD sequences homologous to *Chlamydia trachomatis* polypeptides containing RGD sequences, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 114, SEQ ID No. 468, SEQ ID No. 755, SEQ ID No. 756, SEQ ID No. 757, SEQ ID No. 855, SEQ ID No. 856, SEQ ID No. 905, SEQ ID No. 913, SEQ ID No. 914, SEQ ID No. 915, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* Type III and non-Type III secreted polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

10 SEQ ID No. 25, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 33, SEQ ID No. 308, SEQ ID No. 309, SEQ ID No. 343, SEQ ID No. 344, SEQ ID No. 345, SEQ ID No. 367, SEQ ID No. 414, SEQ ID No. 415, SEQ ID No. 480, SEQ ID No. 550, SEQ ID No. 579, SEQ ID No. 580, SEQ ID No. 581, SEQ ID No. 597, SEQ ID No. 699, SEQ ID No. 744, SEQ ID No. 751, SEQ ID No. 776, SEQ ID No. 866, SEQ ID No. 874, SEQ ID No. 883, SEQ ID No. 884, SEQ ID No. 888, SEQ ID No. 891, SEQ ID No. 6845, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* cell wall anchored surface polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 267, SEQ ID No. 271, SEQ ID No. 419, SEQ ID No. 590, SEQ ID No. 932, SEQ ID No. 6844, SEQ ID No. 6847, and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments not found in *Chlamydia trachomatis* (Blastp  $P > e^{-10}$ ), and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 7, SEQ ID No. 8, SEQ ID No. 9, SEQ ID No. 16, SEQ ID No. 17, SEQ ID No. 18, SEQ ID No. 19, SEQ ID No. 20, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 1254, SEQ ID No. 23, SEQ ID No. 1255, SEQ ID No. 24, SEQ ID No. 1139, SEQ ID No. 1140, SEQ ID No. 46, SEQ ID No. 47, SEQ ID No. 51, SEQ ID No. 60, SEQ ID No. 1256, SEQ ID No. 61, SEQ ID No. 62, SEQ ID No. 63, SEQ ID No. 64, SEQ ID No. 1257, SEQ ID No. 65, SEQ ID No. 66, SEQ ID No. 67, SEQ ID No. 68, 30 SEQ ID No. 1143, SEQ ID No. 1145, SEQ ID No. 83, SEQ ID No. 84, SEQ ID No. 1146, SEQ ID No. 85, SEQ ID No. 86, SEQ ID No. 87, SEQ ID No. 1258, SEQ ID No. 116, SEQ ID No. 117, SEQ ID No. 125, SEQ ID No. 1148, SEQ ID No. 143, SEQ ID No. 1150, SEQ ID No. 1151, SEQ ID No. 144, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 148, SEQ ID No. 149, SEQ ID No. 150, SEQ ID No. 152, SEQ ID No. 1259, SEQ ID No. 162, SEQ ID No. 166, SEQ ID No. 1154, SEQ ID No. 167, 35 SEQ ID No. 1261, SEQ ID No. 1156, SEQ ID No. 1157, SEQ ID No. 178, SEQ ID No. 179, SEQ ID No. 1158, SEQ ID No. 182, SEQ ID No. 183, SEQ ID No. 184, SEQ ID No. 185, SEQ ID No. 1159, SEQ ID No. 186, SEQ ID No. 1160, SEQ ID No. 187, SEQ ID No. 188, SEQ ID No. 189, SEQ ID

No. 190, SEQ ID No. 1161, SEQ ID No. 1162, SEQ ID No. 191, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 195, SEQ ID No. 1163, SEQ ID No. 196, SEQ ID No. 201, SEQ ID No. 202, SEQ ID No. 209, SEQ ID No. 212, SEQ ID No. 221, SEQ ID No. 224, SEQ ID No. 1167, SEQ ID No. 226, SEQ ID No. 227, SEQ ID No. 228, SEQ ID No. 229, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 1169, SEQ ID No. 1170, SEQ ID No. 1171, SEQ ID No. 234, SEQ ID No. 235, SEQ ID No. 236, SEQ ID No. 1172, SEQ ID No. 243, SEQ ID No. 251, SEQ ID No. 252, SEQ ID No. 1176, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 1177, SEQ ID No. 1178, SEQ ID No. 262, SEQ ID No. 263, SEQ ID No. 1264, SEQ ID No. 278, SEQ ID No. 279, SEQ ID No. 1180, SEQ ID No. 280, SEQ ID No. 290, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 296, SEQ ID No. 1181, SEQ ID No. 297, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 1265, SEQ ID No. 322, SEQ ID No. 324, SEQ ID No. 325, SEQ ID No. 370, SEQ ID No. 1186, SEQ ID No. 371, SEQ ID No. 372, SEQ ID No. 1187, SEQ ID No. 373, SEQ ID No. 378, SEQ ID No. 1266, SEQ ID No. 382, SEQ ID No. 383, SEQ ID No. 384, SEQ ID No. 385, SEQ ID No. 386, SEQ ID No. 1188, SEQ ID No. 1189, SEQ ID No. 391, SEQ ID No. 392, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 403, SEQ ID No. 1191, SEQ ID No. 423, SEQ ID No. 435, SEQ ID No. 445, SEQ ID No. 450, SEQ ID No. 1193, SEQ ID No. 456, SEQ ID No. 460, SEQ ID No. 461, SEQ ID No. 465, SEQ ID No. 1196, SEQ ID No. 471, SEQ ID No. 473, SEQ ID No. 475, SEQ ID No. 481, SEQ ID No. 484, SEQ ID No. 487, SEQ ID No. 488, SEQ ID No. 489, SEQ ID No. 490, SEQ ID No. 491, SEQ ID No. 492, SEQ ID No. 493, SEQ ID No. 494, SEQ ID No. 495, SEQ ID No. 496, SEQ ID No. 497, SEQ ID No. 498, SEQ ID No. 499, SEQ ID No. 502, SEQ ID No. 1267, SEQ ID No. 1268, SEQ ID No. 508, SEQ ID No. 510, SEQ ID No. 509, SEQ ID No. 512, SEQ ID No. 515, SEQ ID No. 519, SEQ ID No. 1197, SEQ ID No. 521, SEQ ID No. 1198, SEQ ID No. 522, SEQ ID No. 524, SEQ ID No. 528, SEQ ID No. 534, SEQ ID No. 537, SEQ ID No. 1269, SEQ ID No. 1270, SEQ ID No. 548, SEQ ID No. 551, SEQ ID No. 557, SEQ ID No. 1201, SEQ ID No. 1203, SEQ ID No. 562, SEQ ID No. 566, SEQ ID No. 593, SEQ ID No. 595, SEQ ID No. 600, SEQ ID No. 1271, SEQ ID No. 604, SEQ ID No. 611, SEQ ID No. 612, SEQ ID No. 614, SEQ ID No. 616, SEQ ID No. 625, SEQ ID No. 627, SEQ ID No. 628, SEQ ID No. 629, SEQ ID No. 631, SEQ ID No. 641, SEQ ID No. 1272, SEQ ID No. 648, SEQ ID No. 1212, SEQ ID No. 663, SEQ ID No. 685, SEQ ID No. 707, SEQ ID No. 714, SEQ ID No. 715, SEQ ID No. 716, SEQ ID No. 717, SEQ ID No. 722, SEQ ID No. 746, SEQ ID No. 1273, SEQ ID No. 761, SEQ ID No. 764, SEQ ID No. 770, SEQ ID No. 1217, SEQ ID No. 783, SEQ ID No. 1274, SEQ ID No. 803, SEQ ID No. 815, SEQ ID No. 1220, SEQ ID No. 835, SEQ ID No. 1221, SEQ ID No. 844, SEQ ID No. 845, SEQ ID No. 846, SEQ ID No. 847, SEQ ID No. 848, SEQ ID No. 849, SEQ ID No. 850, SEQ ID No. 851, SEQ ID No. 1275, SEQ ID No. 852, SEQ ID No. 862, SEQ ID No. 1276, SEQ ID No. 1277, SEQ ID No. 873, SEQ ID No. 1223, SEQ ID No. 892, SEQ ID No. 919, SEQ ID No. 1225, SEQ ID No. 1278, SEQ ID No. 926, SEQ ID No. 1228, SEQ ID No. 1229, SEQ ID No. 1230, SEQ ID No. 1279, SEQ ID No. 1281, SEQ ID No. 1282, SEQ ID No. 1283, SEQ ID No. 948, SEQ ID No. 950, SEQ ID No. 949, SEQ ID No. 951, SEQ ID No. 980, SEQ ID No.



982, SEQ ID No. 1233, SEQ ID No. 999, SEQ ID No. 1000, SEQ ID No. 1001, SEQ ID No. 1002, SEQ ID No. 1008, SEQ ID No. 1285, SEQ ID No. 1235, SEQ ID No. 1016, SEQ ID No. 1019, SEQ ID No. 1027, SEQ ID No. 1036, SEQ ID No. 1241, SEQ ID No. 1048, SEQ ID No. 1049, SEQ ID No. 1050, SEQ ID No. 1053, SEQ ID No. 1054, SEQ ID No. 1064, SEQ ID No. 1076, SEQ ID No. 1091, 5 SEQ ID No. 1288, SEQ ID No. 1093, SEQ ID No. 1289, SEQ ID No. 1101, SEQ ID No. 1103, SEQ ID No. 1245, SEQ ID No. 1246, SEQ ID No. 1247, SEQ ID No. 1290, SEQ ID No. 1291, SEQ ID No. 1115, SEQ ID No. 1116, SEQ ID No. 1118, SEQ ID No. 1120, SEQ ID No. 1249, SEQ ID No. 1121, SEQ ID No. 1250, SEQ ID No. 1126, SEQ ID No. 1251, SEQ ID No. 1127, SEQ ID No. 1128, SEQ ID No. 1130, SEQ ID No. 1129, SEQ ID No. 1131, SEQ ID No. 1136, SEQ ID No. 1253, SEQ ID No. 10 6844, SEQ ID No. 6846, SEQ ID No. 6847, SEQ ID No. 6848, and one of their representative fragments

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of 15 cofactors, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 2; SEQ ID No. 55; SEQ ID No. 56; SEQ ID No. 69; SEQ ID No. 75; SEQ ID No. 80; SEQ ID No. 100; SEQ ID No. 110; SEQ ID No. 114; SEQ ID No. 120; SEQ ID No. 121; SEQ ID No. 157; SEQ ID No. 160; SEQ ID No. 161; SEQ ID No. 172; SEQ ID No. 180; SEQ ID No. 181; SEQ ID No. 198; SEQ ID No. 200; SEQ ID No. 225; SEQ ID No. 248; SEQ ID No. 249; SEQ ID 20 No. 276; SEQ ID No. 277; SEQ ID No. 318; SEQ ID No. 319; SEQ ID No. 320; SEQ ID No. 323; SEQ ID No. 331; SEQ ID No. 347; SEQ ID No. 375; SEQ ID No. 376; SEQ ID No. 381; SEQ ID No. 393; SEQ ID No. 394; SEQ ID No. 395; SEQ ID No. 396; SEQ ID No. 409; SEQ ID No. 446; SEQ ID No. 447; SEQ ID No. 448; SEQ ID No. 449; SEQ ID No. 513; SEQ ID No. 516; SEQ ID No. 571; SEQ ID No. 647; SEQ ID No. 662; SEQ ID No. 697; SEQ ID No. 718; SEQ ID No. 793; 25 SEQ ID No. 794; SEQ ID No. 808; SEQ ID No. 809; SEQ ID No. 838; SEQ ID No. 839; SEQ ID No. 840; SEQ ID No. 853; SEQ ID No. 854; SEQ ID No. 918; SEQ ID No. 923; SEQ ID No. 929; SEQ ID No. 931; SEQ ID No. 938; SEQ ID No. 939; SEQ ID No. 958; SEQ ID No. 959; SEQ ID No. 960; SEQ ID No. 966; SEQ ID No. 995; SEQ ID No. 1021; SEQ ID No. 1040; SEQ ID No. 1041; SEQ ID No. 1042; SEQ ID No. 1085; SEQ ID No. 1100; SEQ ID No. 1102; SEQ ID 30 No. 1117; SEQ ID No. 1118; SEQ ID No. 1119; SEQ ID No. 1120; SEQ ID No. 1135 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the intermediate metabolism of nucleotides or nucleic acids, and in that it is 35 chosen from the polypeptides having the following sequences:

SEQ ID No. 77; SEQ ID No. 78; SEQ ID No. 138; SEQ ID No. 189; SEQ ID No. 190; SEQ ID No. 233; SEQ ID No. 246; SEQ ID No. 338; SEQ ID No. 412; SEQ ID No. 421; SEQ ID No. 438;

SEQ ID No. 607; SEQ ID No. 648; SEQ ID No. 657; SEQ ID No. 740; SEQ ID No. 783; SEQ ID No. 967; SEQ ID No. 989; SEQ ID No. 990; SEQ ID No. 992; SEQ ID No. 1011; SEQ ID No. 1058; SEQ ID No. 1059; SEQ ID No. 1073; SEQ ID No. 1074 and one of their representative fragments.

5 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of nucleic acids, and in that it is chosen from the polypeptides having the following sequences:

10 SEQ ID No. 14; SEQ ID No. 59; SEQ ID No. 70; SEQ ID No. 71; SEQ ID No. 97; SEQ ID No. 113; SEQ ID No. 137; SEQ ID No. 141; SEQ ID No. 169; SEQ ID No. 285; SEQ ID No. 287; SEQ ID No. 288; SEQ ID No. 313; SEQ ID No. 326; SEQ ID No. 358; SEQ ID No. 411; SEQ ID No. 443; SEQ ID No. 548; SEQ ID No. 569; SEQ ID No. 601; SEQ ID No. 651; SEQ ID No. 654; SEQ ID No. 658; SEQ ID No. 659; SEQ ID No. 664; SEQ ID No. 665; SEQ ID No. 694; SEQ ID No. 698; SEQ ID No. 704; SEQ ID No. 760; SEQ ID No. 762; SEQ ID No. 763; SEQ ID No. 786; 15 SEQ ID No. 787; SEQ ID No. 788; SEQ ID No. 801; SEQ ID No. 802; SEQ ID No. 812; SEQ ID No. 819; SEQ ID No. 822; SEQ ID No. 870; SEQ ID No. 897; SEQ ID No. 898; SEQ ID No. 902; SEQ ID No. 908; SEQ ID No. 916; SEQ ID No. 954; SEQ ID No. 955; SEQ ID No. 961; SEQ ID No. 983; SEQ ID No. 996; SEQ ID No. 1007; SEQ ID No. 1012; SEQ ID No. 1013; SEQ ID No. 1014; SEQ ID No. 1015; SEQ ID No. 1038; SEQ ID No. 1137 and one of their representative 20 fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of amino acids or polypeptides, and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 99; SEQ ID No. 111; SEQ ID No. 127; SEQ ID No. 134; SEQ ID No. 140; SEQ ID No. 174; SEQ ID No. 175; SEQ ID No. 176; SEQ ID No. 353; SEQ ID No. 377; SEQ ID No. 404; SEQ ID No. 523; SEQ ID No. 539; SEQ ID No. 559; SEQ ID No. 561; SEQ ID No. 586; SEQ ID No. 598; SEQ ID No. 609; SEQ ID No. 636; SEQ ID No. 687; SEQ ID No. 700; SEQ ID No. 701; SEQ ID No. 759; SEQ ID No. 790; SEQ ID No. 857; SEQ ID No. 861; SEQ ID No. 904; SEQ ID 30 No. 936; SEQ ID No. 952; SEQ ID No. 962; SEQ ID No. 963; SEQ ID No. 964; SEQ ID No. 965; SEQ ID No. 991; SEQ ID No. 1003; SEQ ID No. 1004; SEQ ID No. 1005; SEQ ID No. 1018; SEQ ID No. 1067; SEQ ID No. 1110; SEQ ID No. 1111; SEQ ID No. 1112; SEQ ID No. 1114; SEQ ID No. 1121; SEQ ID No. 1122; SEQ ID No. 1123; SEQ ID No. 1124; SEQ ID No. 1125 and one of their representative fragments.

35 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of polypeptides, and in that it is chosen from the polypeptides

having the following sequences:

SEQ ID No. 4; SEQ ID No. 44; SEQ ID No. 45; SEQ ID No. 48; SEQ ID No. 54; SEQ ID No. 112; SEQ ID No. 130; SEQ ID No. 155; SEQ ID No. 163; SEQ ID No. 212; SEQ ID No. 257; SEQ ID No. 307; SEQ ID No. 343; SEQ ID No. 405; SEQ ID No. 416; SEQ ID No. 458; SEQ ID  
 5 No. 540; SEQ ID No. 541; SEQ ID No. 542; SEQ ID No. 543; SEQ ID No. 544; SEQ ID No. 560; SEQ ID No. 594; SEQ ID No. 652; SEQ ID No. 699; SEQ ID No. 723; SEQ ID No. 747; SEQ ID No. 817; SEQ ID No. 827; SEQ ID No. 871; SEQ ID No. 909; SEQ ID No. 910; SEQ ID No. 911; SEQ ID No. 912; SEQ ID No. 1023; SEQ ID No. 1051; SEQ ID No. 1052; SEQ ID No. 1081 and one of their representative fragments.

10 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the metabolism of fatty acids, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 76; SEQ ID No. 284; SEQ ID No. 308; SEQ ID No. 309; SEQ ID No. 310; SEQ ID  
 15 No. 311; SEQ ID No. 312; SEQ ID No. 425; SEQ ID No. 433; SEQ ID No. 565; SEQ ID No. 688; SEQ ID No. 690; SEQ ID No. 691; SEQ ID No. 767; SEQ ID No. 797; SEQ ID No. 894; SEQ ID No. 895; SEQ ID No. 994; SEQ ID No. 1020; SEQ ID No. 1030; SEQ ID No. 1033; SEQ ID No. 1034; SEQ ID No. 1046; SEQ ID No. 1047; SEQ ID No. 1057 and one of their representative fragments.

20 Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the synthesis of the wall, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 49; SEQ ID No. 50; SEQ ID No. 177; SEQ ID No. 178; SEQ ID No. 245; SEQ ID  
 25 No. 610; SEQ ID No. 972; SEQ ID No. 974; SEQ ID No. 978; SEQ ID No. 1037 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the transcription, translation and/or maturation process, and in that it is chosen  
 30 from the polypeptides having the following sequences:

SEQ ID No. 90; SEQ ID No. 92; SEQ ID No. 131; SEQ ID No. 151; SEQ ID No. 199; SEQ ID No. 333; SEQ ID No. 334; SEQ ID No. 336; SEQ ID No. 379; SEQ ID No. 589; SEQ ID No. 590; SEQ ID No. 619; SEQ ID No. 630; SEQ ID No. 649; SEQ ID No. 739; SEQ ID No. 741; SEQ ID No. 806; SEQ ID No. 821; SEQ ID No. 843; SEQ ID No. 968; SEQ ID No. 971; SEQ ID No. 1061  
 35 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* ribosomal polypeptide or one of its representative

fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 93; SEQ ID No. 94; SEQ ID No. 95; SEQ ID No. 136; SEQ ID No. 259; SEQ ID No. 332; SEQ ID No. 348; SEQ ID No. 583; SEQ ID No. 584; SEQ ID No. 588; SEQ ID No. 591; SEQ ID No. 592; SEQ ID No. 663; SEQ ID No. 666; SEQ ID No. 667; SEQ ID No. 669; SEQ ID  
5 No. 670; SEQ ID No. 671; SEQ ID No. 672; SEQ ID No. 673; SEQ ID No. 674; SEQ ID No. 675; SEQ ID No. 676; SEQ ID No. 677; SEQ ID No. 678; SEQ ID No. 679; SEQ ID No. 680; SEQ ID No. 681; SEQ ID No. 683; SEQ ID No. 684; SEQ ID No. 738; SEQ ID No. 781; SEQ ID No. 1008; SEQ ID No. 1024; SEQ ID No. 1025; SEQ ID No. 1066 and one of their representative fragments.

Preferably, the invention also relates to a polypeptide according to the invention,  
10 characterized in that it is a *Chlamydia pneumoniae* transport polypeptide or one of its representative fragments, and in that it is chosen from the polypeptides having the following sequences:

SEQ ID No. 40; SEQ ID No. 41; SEQ ID No. 52; SEQ ID No. 105; SEQ ID No. 106; SEQ ID No. 107; SEQ ID No. 109; SEQ ID No. 133; SEQ ID No. 210; SEQ ID No. 211; SEQ ID No. 214; SEQ ID No. 215; SEQ ID No. 216; SEQ ID No. 217; SEQ ID No. 218; SEQ ID No. 219; SEQ ID  
15 No. 220; SEQ ID No. 223; SEQ ID No. 242; SEQ ID No. 260; SEQ ID No. 293; SEQ ID No. 299; SEQ ID No. 366; SEQ ID No. 369; SEQ ID No. 575; SEQ ID No. 602; SEQ ID No. 638; SEQ ID No. 639; SEQ ID No. 640; SEQ ID No. 643; SEQ ID No. 653; SEQ ID No. 702; SEQ ID No. 703; SEQ ID No. 724; SEQ ID No. 732; SEQ ID No. 855; SEQ ID No. 856; SEQ ID No. 901; SEQ ID No. 906; SEQ ID No. 933; SEQ ID No. 942; SEQ ID No. 1043; SEQ ID No. 1086; SEQ ID  
20 No. 1105 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the virulence process, and in that it is chosen from the polypeptides having the following sequences:

25 SEQ ID No. 546; SEQ ID No. 550; SEQ ID No. 778; SEQ ID No. 779; SEQ ID No. 886 and one of their representative fragments.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a *Chlamydia pneumoniae* polypeptide or one of its representative fragments which is involved in the secretory system and/or which is secreted, and in that it is chosen from the  
30 polypeptides having the following sequences:

SEQ ID No. 751; SEQ ID No. 874; SEQ ID No. 875; SEQ ID No. 876; SEQ ID No. 883; SEQ ID No. 884; SEQ ID No. 885 and one of their representative fragments.

The secreted polypeptides, including the Type III and other, non-Type III secreted polypeptides, of the present invention, as well as the corresponding nucleotide sequences, may be  
35 detected by techniques known to persons skilled in the art, such as for example the techniques using cloning combined with vectors allowing the expression of the said polypeptides fused to export markers such as the *luc* gene for luciferase or the *PhoA* gene for alkaline phosphatase.

Preferably, the invention relates to a polypeptide according to the invention, characterized in that it is a polypeptide specific to *Chlamydia pneumoniae* or one of its representative fragments (with a Blast E value of  $>10^{-5}$ ), and in that it is chosen from the polypeptides having the following sequences:

- 5 SEQ ID No. 7; SEQ ID No. 8; SEQ ID No. 17; SEQ ID No. 18; SEQ ID No. 19; SEQ ID No. 20; SEQ ID No. 22; SEQ ID No. 23; SEQ ID No. 24; SEQ ID No. 51; SEQ ID No. 60; SEQ ID No. 63; SEQ ID No. 65; SEQ ID No. 66; SEQ ID No. 67; SEQ ID No. 83; SEQ ID No. 84; SEQ ID No. 86; SEQ ID No. 87; SEQ ID No. 125; SEQ ID No. 143; SEQ ID No. 144; SEQ ID No. 179; SEQ ID No. 182; SEQ ID No. 184; SEQ ID No. 185; SEQ ID No. 187; SEQ ID No. 221; 10 SEQ ID No. 252; SEQ ID No. 254; SEQ ID No. 278; SEQ ID No. 279; SEQ ID No. 387; SEQ ID No. 388; SEQ ID No. 397; SEQ ID No. 1048; SEQ ID No. 1049; SEQ ID No. 1050; SEQ ID No. 1128; SEQ ID No. 1130; SEQ ID No. 1131 and one of their representative fragments.

In general, in the present invention, the functional group to which a polypeptide of the invention belongs, as well as its corresponding nucleotide sequence, may be determined either by 15 comparative analogy with sequences already known, or by the use of standard techniques of biochemistry, of cytology combined with the techniques of genetic engineering such as immunoaffinity, localization by immunolabelling, differential extraction, measurement of enzymatic activity, study of the activity inducing or repressing expression or the study of expression in *E. coli*.

It is clearly understood, on the one hand, that, in the present invention, the nucleotide 20 sequences (ORF) and the amino acid sequences (SEQ ID No. 2 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6848) which are listed by functional group, are not exhaustive within the group considered. Moreover, it is also clearly understood that, in the present invention, a nucleotide sequence (ORF) or an amino acid sequence mentioned within a given functional group may also be part of another group taking into account, for example, the interrelationship between the groups listed. 25 Accordingly, and as an example of this interrelationship, an exported and/or secreted polypeptide as well as its coding nucleotide sequence may also be involved in the *Chlamydia pneumoniae* virulence process by modifying the defense mechanism of the infected host cell, or a transmembrane polypeptide or its coding nucleotide sequence is also part of the polypeptides or coding nucleotide sequences of the cellular envelope.

30 The subject of the present invention is also the nucleotide and/or polypeptide sequences according to the invention, characterized in that the said sequences are recorded on a medium, called recording medium, whose type and nature facilitate the reading, the analysis and the exploitation of the said sequences. These media may of course also contain other information extracted from the present invention, such as in particular the analogies with already known sequences, such as those 35 mentioned in Table 1 of the present description, and/or may contain, in addition, information relating to the nucleotide and/or polypeptide sequences of other microorganisms so as to facilitate the comparative analysis and the exploitation of the results obtained.

Among these recording media, computer-readable media, such as magnetic, optical, electrical and hybrid media such as, for example, floppy disks, CD-ROMs or recording cassettes, are preferred in particular.

The invention also relates to nucleotide sequences which can be used as primer or probe,  
5 characterized in that the said sequences are chosen from the nucleotide sequences according to the invention.

The invention relates, in addition, to the use of a nucleotide sequence according to the invention, as primer or probe, for the detection and/or amplification of nucleic acid sequences.

The nucleotide sequences according to the invention may thus be used to amplify  
10 nucleotide sequences, in particular by the PCR technique (polymerase chain reaction) (Erich, 1989; Innis et al., 1990; Rolfs et al., 1991, and White et al., 1997).

These oligodeoxyribonucleotide or oligoribonucleotide primers correspond to representative nucleotide fragments, and are advantageously at least 8 nucleotides, preferably at least 12 nucleotides, 15 nucleotides and still more preferably at least 20 nucleotides long.

15 Other techniques for amplifying the target nucleic acid may be advantageously used as alternatives to PCR.

The nucleotide sequences of the invention, in particular the primers according to the invention, may also be used in other methods for amplifying a target nucleic acid, such as:

- the TAS (Transcription-based Amplification System) technique described by Kwok et al. in 1989;
- 20 - the 3SR (Self-Sustained Sequence Replication) technique described by Guatelli et al. in 1990;
- the NASBA (Nucleic Acid Sequence Based Amplification) technique described by Kievitis et al. in 1991;
- the SDA (Strand Displacement Amplification) technique (Walker et al., 1992);
- the TMA (Transcription Mediated Amplification) technique.

25 The polynucleotides of the invention may also be used in techniques for amplifying or for modifying the nucleic acid serving as probe, such as:

- the LCR (Ligase Chain Reaction) technique described by Landegren et al. in 1988 and perfected by Barany et al. in 1991, which uses a thermostable ligase;
- the RCR (Repair Chain Reaction) technique described by Segev in 1992;
- 30 - the CPR (Cycling Probe Reaction) technique described by Duck et al. in 1990;
- the Q-beta-replicase amplification technique described by Miele et al. in 1983 and perfected in particular by Chu et al. in 1986, Lizardi et al. in 1988, and then by Burg et al. as well as by Stone et al. in 1996.

The invention also relates to the nucleotide sequences of fragments which can be  
35 obtained by amplification with the aid of at least one primer according to the invention. The present invention encompasses both hybridization probes and primers. In general, the complementary probes should be of a length sufficient to form a stable hybrid complex with the target sequences. Primers,

while complementary to the target sequences need not form stable hybridization complexes with the target sequences alone. Rather, primers form stable complexes with the target sequences in the presence of polymerase to permit extension of the primer.

In the case where the target polynucleotide to be detected is possibly an RNA, for example an mRNA, it will be possible to use, prior to the use of an amplification reaction with the aid of at least one primer according to the invention or to the use of a method of detection with the aid of at least one probe of the invention, a reverse transcriptase-type enzyme so as to obtain a cDNA from the RNA contained in the biological sample. The cDNA obtained will then serve as target for the primer(s) or the probe(s) used in the amplification or detection method according to the invention.

10 The detection probe will be chosen so that it hybridizes with the target sequence or the amplicon generated from the target sequence. Such a detection probe will advantageously have as sequence a sequence of at least 12 nucleotides, in particular of at least 20 nucleotides, and preferably at least 100 nucleotides.

The invention also comprises the nucleotide sequences which can be used as probe or primer according to the invention, characterized in that they are labelled with a radioactive compound or with a nonradioactive compound.

The nonlabelled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labelled with a radioactive element ( $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{125}\text{I}$ ) or with a nonradioactive molecule (biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, fluorescein) so as to obtain probes which can be used in numerous applications.

20 Examples of nonradioactive labelling of nucleotide sequences are described, for example, in French patent No. 78,10975 or by Urdea et al. or by Sanchez-Pescador et al. in 1988.

In the latter case, one of the labelling methods described in patents FR-2 422 956 and FR-2 518 755 may also be used.

25 The invention also relates to the nucleotide sequences of fragments which can be obtained by hybridization with the aid of at least one probe according to the invention.

The hybridization technique may be performed in various ways (Matthews et al., 1988). The most common method consists in immobilizing the nucleic acid extracted from *Chlamydia pneumoniae* cells on a support (such as nitrocellulose, nylon, polystyrene) and in incubating, under well-defined conditions, the target nucleic acid immobilized with the probe. After hybridization, the excess probe is removed and the hybrid molecules formed are detected by the appropriate method (measurement of the radioactivity, of the fluorescence or of the enzymatic activity linked to the probe).

35 The invention also comprises the nucleotide sequences according to the invention, characterized in that they are covalently or noncovalently immobilized on a support.

According to another advantageous embodiment of the nucleic sequences according to the invention, the latter may be used immobilized on a support and may thus serve to capture, through

specific hybridization, the target nucleic acid obtained from the biological sample to be tested. If necessary, the solid support is separated from the sample and the hybridization complex formed between the so-called capture probe and the target nucleic acid is then detected by means of a second probe, called detection probe, labelled with an easily detectable element.

5           The nucleotide sequences according to the invention may also be used in new analytical systems, DNA chips, which allow sequencing, the study of mutations and of the expression of genes, and which are currently of interest given their very small size and their high capacity in terms of number of analyses.

10           The principle of the operation of these chips is based on molecular probes, most often oligonucleotides, which are attached onto a miniaturized surface, generally of the order of a few square centimetres. During an analysis, a sample containing fragments of a target nucleic acid to be analysed, for example DNA or RNA labelled, for example, after amplification, is deposited onto the DNA chip in which the support has been coated beforehand with probes. Bringing the labelled target sequences into contact with the probes leads to the formation, through hybridization, of a duplex  
15 according to the rule of pairing defined by J.D. Watson and F. Crick. After a washing step, analysis of the surface of the chip allows the effective hybridizations to be located by means of the signals emitted by the labels tagging the target. A hybridization fingerprint results from this analysis which, by appropriate computer processing, will make it possible to determine information such as the presence of specific fragments in the sample, the determination of sequences and the presence of mutations.

20           The chip consists of a multitude of molecular probes, precisely organized or arrayed on a solid support whose surface is miniaturized. It is at the centre of a system where other elements (imaging system, microcomputer) allow the acquisition and interpretation of a hybridization fingerprint.

25           The hybridization supports are provided in the form of flat or porous surfaces (pierced with wells) composed of various materials. The choice of a support is determined by its physicochemical properties, or more precisely, by the relationship between the latter and the conditions under which the support will be placed during the synthesis or the attachment of the probes or during the use of the chip. It is therefore necessary, before considering the use of a particular support (R.S. Matson et al., 1994), to consider characteristics such as its stability to pH, its physical  
30 strength, its reactivity and its chemical stability as well as its capacity to nonspecifically bind nucleic acids. Materials such as glass, silicon and polymers are commonly used. Their surface is, in a first step, called "functionalization", made reactive towards the groups which it is desired to attach thereon. After the functionalization, so-called spacer molecules are grafted onto the activated surface. Used as intermediates between the surface and the probe, these molecules of variable size render unimportant  
35 the surface properties of the supports, which often prove to be problematic for the synthesis or the attachment of the probes and for the hybridization.

Among the hybridization supports, there may be mentioned glass which is used, for



example, in the method of in situ synthesis of oligonucleotides by photochemical addressing developed by the company Affymetrix (E.L. Sheldon, 1993), the glass surface being activated by silane. Genosensor Consortium (P. Mérel, 1994) also uses glass slides carrying wells 3 mm apart, this support being activated with epoxysilane.

5           Polymers or silicon may also be mentioned among these hybridization supports. For example, the Andrein Mirzabekov team has developed a chip consisting of polyacrylamide squares polymerized on a silanized glass surface (G. Yershov et al., 1996). Several teams use silicon, in particular the IFOS laboratory of Ecole Centrale of Lyon which uses a silicon semiconductor substrate which is p-doped by introducing it into its crystalline structure atoms whose valency is different from  
10 that of silicon. Various types of metals, in particular gold and platinum, may also be used as support (Genosensor Consortium (K. Beattie et al., 1993)).

          The probes according to the invention may be synthesized directly in situ on the supports of the DNA chips. This in situ synthesis may be carried out by photochemical addressing (developed by the company Affymax (Amsterdam, Holland) and exploited industrially by its subsidiary  
15 Affymetrix (United States)) or based on the VLSIPS (very large scale immobilized polymer synthesis) technology (S.P.A. Fodor et al., 1991) which is based on a method of photochemically directed combinatorial synthesis and the principle of which combines solid-phase chemistry, the use of photolabile protecting groups and photolithography.

          The probes according to the invention may be attached to the DNA chips in various ways  
20 such as electrochemical addressing, automated addressing or the use of probe printers (T. Livache et al., 1994; G. Yershov et al., 1996; J. Derisi et al., 1996, and S. Borman, 1996).

          The revealing of the hybridization between the probes of the invention, deposited or synthesized in situ on the supports of the DNA chips, and the sample to be analysed, may be determined, for example, by measurement of fluorescent signals, by radioactive counting or by  
25 electronic detection.

          The use of fluorescent molecules such as fluorescein constitutes the most common method of labelling the samples. It allows direct or indirect revealing of the hybridization and allows the use of various fluorochromes.

          Affymetrix currently provides an apparatus or a scanner designed to read its Gene Chip™  
30 chips. It makes it possible to detect the hybridizations by scanning the surface of the chip in confocal microscopy (R.J. Lipshutz et al., 1995). Other methods of detecting fluorescent signals have been tested: coupling of an epifluorescence microscope and a CCD camera (G. Yershov et al., 1996), the use of an optical fibre collecting system (E.L. Sheldon, 1993). A conventional method consists in carrying out an end labelling, with phosphorus 32, of the target sequences, by means of an appropriate  
35 apparatus, the Phosphorimager (marketed by Molecular Dynamics). The electronic detection is based on the principle that the hybridization of two nucleic acid molecules is accompanied by physical phenomena which can be quantified under certain conditions (system developed by Ecole Centrale of

Lyon and called GEN-FET (GEN field effect transistor)). Genosensor Consortium and the company Beckman Instruments who are developing an electronic chip or Permittivity Chips™ may also be mentioned (K. Beattie et al., 1993).

The nucleotide sequences according to the invention may thus be used in DNA chips to  
5 carry out the analysis of mutations. This analysis is based on the production of chips capable of analysing each base of a nucleotide sequence according to the invention.

The nucleotide sequences according to the invention may also be used in DNA chips to carry out the analysis of the expression of the *Chlamydia pneumoniae* genes. This analysis of the expression of *Chlamydia pneumoniae* genes is based on the use of chips where probes of the  
10 invention, chosen for their specificity to characterize a given gene, are present (D.J. Lockhart et al., 1996; D.D. Shoemaker et al., 1996). For the methods of analysis of gene expression using the DNA chips, reference may, for example, be made to the methods described by D.J. Lockhart et al. (1996) and Sosnowsky et al. (1997) for the synthesis of probes in situ or for the addressing and the attachment of previously synthesized probes. The target sequences to be analysed are labelled and in general  
15 fragmented into sequences of about 50 to 100 nucleotides before being hybridized onto the chip. After washing as described, for example, by D.J. Lockhart et al. (1996) and application of different electric fields (Sosnowsky et al., 1997), the labelled compounds are detected and quantified, the hybridizations being carried out at least in duplicate. Comparative analyses of the signal intensities obtained with respect to the same probe for different samples and/or for different probes with the same sample,  
20 determine the differential expression of RNA or of DNA derived from the sample.

The nucleotide sequences according to the invention may, in addition, be used in DNA chips where other nucleotide probes specific for other microorganisms are also present, and may allow the carrying out of a serial test allowing rapid identification of the presence of a microorganism in a sample.

25 Accordingly, the subject of the invention is also the nucleotide sequences according to the invention, characterized in that they are immobilized on a support of a DNA chip.

The DNA chips, characterized in that they contain at least one nucleotide sequence according to the invention, immobilized on the support of the said chip, also form part of the invention.

30 The said chips will preferably contain several probes or nucleotide sequences of the invention of different length and/or corresponding to different genes so as to identify, with greater certainty, the specificity of the target sequences or the desired mutation in the sample to be analysed.

Accordingly, the analyses carried out by means of primers and/or probes according to the invention, immobilized on supports such as DNA chips, will make it possible, for example, to identify,  
35 in samples, mutations linked to variations such as intraspecies variations. These variations may be correlated or associated with pathologies specific to the variant identified and will make it possible to select the appropriate treatment.

The invention thus comprises a DNA chip according to the invention, characterized in that it contains, in addition, at least one nucleotide sequence of a microorganism different from *Chlamydia pneumoniae*, immobilized on the support of the said chip; preferably, the different microorganism will be chosen from an associated microorganism, a bacterium of the *Chlamydia* family, and a variant of the species *Chlamydia pneumoniae*.

Another subject of the present invention is a vector for the cloning and/or the expression of a sequence, characterized in that it contains a nucleotide sequence according to the invention. Among the said vectors according to the invention, the vectors containing a nucleotide sequence encoding a polypeptide of the cellular, preferably outer, envelope of *Chlamydia pneumoniae* or one of its representative fragments, are preferred. In a specific embodiment, the vectors contain a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide (LPS) biosynthesis, a Type III and non-Type III secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*.

According to the invention, the vectors comprise the elements necessary to allow the expression and/or the secretion of the said nucleotide sequences in a given host cell, and form part of the invention. The vector should, in this case, comprise a promoter, signals for initiation and for termination of translation, as well as appropriate regions for regulation of transcription. It should be capable of being stably maintained in the host cell and may optionally possess particular signals specifying the secretion of the translated protein. These different elements are chosen according to the host cell used. To this effect, the nucleotide sequences according to the invention may be inserted into autonomously-replicating vectors within the chosen host, or integrative vectors in the chosen host.

Any of the standard methods known to those skilled in the art for the insertion of DNA fragments into a vector may be used to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinants (genetic recombination).

Expression of a polypeptide, peptide or derivative, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1 or ORFs contained within SEQ ID No. 1 may be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host transformed

with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, *Nature* 296:39-42); prokaryotic expression vectors such as the  $\beta$ -lactamase promoter (Villa-Kamaroff, *et al.*, 1978, *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25); see also "Useful proteins from recombinant bacteria" in *Scientific American*, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella *et al.*, 1983, *Nature* 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, *et al.*, 1981, *Nucl. Acids Res.* 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella *et al.*, 1984, *Nature* 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, *Cell* 38:639-646; Ornitz *et al.*, 1986, *Cold Spring Harbor Symp. Quant. Biol.* 50:399-409; MacDonald, 1987, *Hepatology* 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, *Nature* 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, *Cell* 38:647-658; Adames *et al.*, 1985, *Nature* 318:533-538; Alexander *et al.*, 1987, *Mol. Cell. Biol.* 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, *Cell* 45:485-495), albumin gene control region which is active in liver (Pinkert *et al.*, 1987, *Genes and Devel.* 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, *Mol. Cell. Biol.* 5:1639-1648; Hammer *et al.*, 1987, *Science* 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey *et al.*, 1987, *Genes and Devel.* 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram *et al.*, 1985, *Nature* 315:338-340; Kollias *et al.*, 1986, *Cell* 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, *Cell* 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, *Nature* 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, *Science* 234:1372-1378).

The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a protein or peptide-encoding a nucleic acid sequence in SEQ ID No. 1, or ORFs contained within SEQ ID No. 1, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an

antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Preferred vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen). Furthermore, the vectors according to the invention are useful for transforming  
5 host cells so as to clone or express the nucleotide sequences of the invention.

Expression can also be achieved using targeted homologous recombination to activate *Chlamydia pneumoniae* genes present in the cloned genomic DNA. A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous *Chlamydia pneumoniae* gene present in the cloned genome, using  
10 techniques, such as targeted homologous recombination, which are well known to those of skill in the art (See, e.g., Chappel, U.S. Patent No. 4,215,051 and Skoultchi, WO 91/06667 each of which is incorporated herein in its entirety).

Expression vector/host cell systems containing inserts of polynucleotide sequences in SEQ ID No. 1 or ORFs within SEQ ID No. 1, which encode polypeptides, peptides or derivatives, or  
15 analogs thereof, can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a polynucleotide sequence inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted polynucleotide sequence. In the second approach, the recombinant vector/host system can be  
20 identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a polynucleotide sequence in the vector. For example, if the polynucleotide sequence in SEQ ID No. 1 or ORFs within SEQ ID No. 1 is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified by  
25 the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying the product of the polynucleotide sequence expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the expressed polypeptide in *in vitro* assay systems, e.g., binding with antibody, promotion of cell proliferation.

Once a particular recombinant DNA molecule is identified and isolated, several methods  
30 known in the art may be used to propagate it. The clones identified may be introduced into an appropriate host cell by standard methods, such as for example lipofection, electroporation, and heat shock. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity.

The invention also encompasses the host cells transformed by a vector according to the  
35 invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or the expression of the transfected nucleotide sequence.

The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells (Olins and Lee, 1993), but also yeast cells (Buckholz, 1993), as well as animal cells, in particular cultures of mammalian cells (Edwards and Aruffo, 1993), and in particular Chinese hamster ovary (CHO) cells, but also insect cells in which methods using baculoviruses for example  
5 may be used (Luckow, 1993).

Furthermore, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host  
10 cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in  
15 mammalian cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

A preferred host cell for the expression of the proteins of the invention consists of prokaryotic cells, such as Gram<sup>-</sup> bacteria. A further preferred host cell according to the invention is a bacterium belonging to the *Chlamydia* family, more preferably belonging to the species *Chlamydia*  
20 *pneumoniae* or chosen from a microorganism associated with the species *Chlamydia pneumoniae*.

In other specific embodiments, the polypeptides, peptides or derivatives, or analogs thereof may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences  
25 encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

Genomic sequences can be cloned and expressed as translational gene products (*i.e.*,  
30 peptides, polypeptides, and proteins) or transcriptional gene products (*i.e.*, antisense and ribozymes).

The invention further relates to the intracellular production of an antisense nucleic acid sequence of SEQ ID No. 1 by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would  
35 contain a sequence encoding an antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art.

Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the an antisense RNA can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the CMV promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 5 3N long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42), etc.

In a specific embodiment, the antisense oligonucleotide comprises catalytic RNA, or a ribozyme (see, *e.g.*, PCT International Publication WO 90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2N-0-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

In another embodiment, the antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a polynucleotide sequence in SEQ ID No. 1. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acid sequence, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA transcribed from SEQ ID No. 1 may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The invention also relates to the animals, except humans, comprising one of the above-described transformed cells according to the invention.

The production of transgenic animals according to the invention overexpressing one or more of the *Chlamydia pneumoniae* genes will be preferably carried out on rats, mice or rabbits according to methods well known to persons skilled in the art such as viral or nonviral transfections. The transgenic animals overexpressing one or more of the said genes may be obtained by transfection of multiple copies of the said genes under the control of a powerful promoter of a ubiquitous nature, or which is selective for one type of tissue. The transgenic animals may also be obtained by homologous recombination on embryonic stem cells, transfer of these stem cells to embryos, selection of the chimeras affected at the level of the reproductive lines, and growth of the said chimeras.

The transformed cells as well as the transgenic animals according to the invention can be used in methods of preparing the recombinant polypeptide.

It is now possible to produce recombinant polypeptides in a relatively large quantity by genetic engineering using the cells transformed with expression vectors according to the invention or using transgenic animals according to the invention.

The methods of preparing a polypeptide of the invention in recombinant form, characterized in that they use a vector and/or a cell transformed with a vector according to the invention and/or a transgenic animal comprising one of the said transformed cells according to the invention, are themselves included in the present invention.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a polypeptide of the cellular envelope of *Chlamydia pneumoniae* or one of its representative fragments, more preferably encoding a polypeptide of the outer cellular envelope of *Chlamydia pneumoniae* or one of its fragment, are preferred.

Among the said methods of preparing a polypeptide of the invention in recombinant form, the methods of preparation using a vector, and/or a cell transformed with the said vector and/or a transgenic animal comprising one of the said transformed cells, containing a nucleotide sequence encoding a *Chlamydia pneumoniae* secreted polypeptide or one of its representative fragments or encoding a transport polypeptide, a surface exposed polypeptide, a lipoprotein or one of its representative fragments, a polypeptide involved in lipopolysaccharide biosynthesis, a Type III or other secreted polypeptide, a polypeptide containing RGD attachment sites, a cell wall anchored surface polypeptide, a polypeptide not found in *Chlamydia trachomatis*, a ribosomal polypeptide or a polypeptide involved in secretion, transcription, translation, maturation of proteins, a polypeptide involved in the synthesis of the wall, a polypeptide involved in the virulence, a polypeptide involved in the intermediate metabolism, in particular in the metabolism of sugars and/or of cofactors, a polypeptide involved in the metabolism of nucleotides, of amino acids, of nucleic acids or of fatty acids of *Chlamydia pneumoniae* or one of their representative fragments, or a polypeptide specific to *Chlamydia pneumoniae*, are also preferred.

The recombinant polypeptides obtained as indicated above may be provided either in glycosylated or non-glycosylated form and may or may not have the natural tertiary structure.

A preferred variant consists in producing a recombinant polypeptide fused to a "carrier" protein (chimeric protein). The advantage of this system is that it allows a stabilization and a reduction in proteolysis of the recombinant product, an increase in solubility during renaturation in vitro and/or a simplification of purification when the fusion partner has affinity for a specific ligand.

More particularly, the invention relates to a method of preparing a polypeptide of the

invention comprising the following steps:

a) culture of the transformed cells under conditions allowing the expression of a recombinant polypeptide having a nucleic acid sequence according to the invention;



b) where appropriate, recovery of the said recombinant polypeptide.

When the method of preparing a polypeptide of the invention uses a transgenic animal according to the invention, the recombinant polypeptide is then extracted from the said animal.

The subject of the invention is also a polypeptide capable of being obtained by a method  
5 of the invention as described above.

The invention also comprises a method of preparing a synthetic polypeptide, characterized in that it uses an amino acid sequence of polypeptides according to the invention.

The invention also relates to a synthetic polypeptide obtained by a method according to the invention.

10 Polypeptides according to the invention may also be prepared by conventional techniques in the field of peptide synthesis under conditions suitable to produce the polypeptides encoded by the polynucleotide of the invention. This synthesis may be carried out in and recovered from a homogeneous solution or on a solid phase.

For example, the synthesis technique in a homogeneous solution described by  
15 Houbenweyl in 1974 may be used.

This method of synthesis consists in successively condensing, in pairs, the successive amino acids in the required order, or in condensing amino acids and fragments previously formed and already containing several amino acids in the appropriate order, or alternatively several fragments thus previously prepared, it being understood that care will have been taken to protect beforehand all the  
20 reactive functional groups carried by these amino acids or fragments, with the exception of the amine functional groups of one and the carboxyl functional groups of the other or vice versa, which should normally take part in the formation of the peptide bonds, in particular after activation of the carboxyl functional group, according to methods well known in peptide synthesis.

According to another preferred technique of the invention, the one described by  
25 Merrifield is used.

To manufacture a peptide chain according to the Merrifield method, a highly porous polymer resin is used, onto which the first C-terminal amino acid of the chain is attached. This amino acid is attached onto a resin via its carboxyl group and its amine functional group is protected. The amino acids which will constitute the peptide chain are thus attached, one after another, onto the amine  
30 group, each time deprotected beforehand, of the portion of the peptide chain already formed, and which is attached to the resin. When the entire peptide chain desired is formed, the protecting groups are removed from the various amino acids constituting the peptide chain and the peptide is detached from the resin with the aid of an acid.

The invention relates, in addition, to hybrid (fusion) polypeptides having at least one  
35 polypeptide or one of its representative fragments according to the invention, and a sequence of a polypeptide capable of eliciting an immune response in humans or animals.

Advantageously, the antigenic determinant is such that it is capable of eliciting a humoral

and/or cellular response. An antigenic determinant may be identified by screening expression libraries of the *Chlamydia pneumoniae* genome with antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*. An antigenic determinant may comprise a polypeptide or one of its representative fragments according to the invention, in glycosylated form, used in order to obtain immunogenic compositions capable of inducing the synthesis of antibodies directed against multiple epitopes. The said polypeptides or their glycosylated fragments also form part of the invention.

These hybrid molecules may consist, in part, of a carrier molecule for polypeptides or for their representative fragments according to the invention, combined with a portion which may be immunogenic, in particular an epitope of the diphtheria toxin, the tetanus toxin, a hepatitis B virus surface antigen (patent FR 79 21811), the poliomyelitis virus VP1 antigen or any other viral or bacterial toxin or antigen.

The methods of synthesizing the hybrid molecules include the methods used in genetic engineering to construct hybrid nucleotide sequences encoding the desired polypeptide sequences. Reference may be advantageously made, for example, to the technique for producing genes encoding fusion proteins described by Minton in 1984.

The said hybrid nucleotide sequences encoding a hybrid polypeptide as well as the hybrid polypeptides according to the invention, characterized in that they are recombinant polypeptides obtained by the expression of the said hybrid nucleotide sequences, also form part of the invention.

The invention also comprises the vectors characterized in that they contain one of the said hybrid nucleotide sequences. The host cells transformed by the said vectors, the transgenic animals comprising one of the said transformed cells as well as the methods of preparing recombinant polypeptides using the said vectors, the said transformed cells and/or the said transgenic animals of course also form part of the invention.

The polypeptides according to the invention, the antibodies according to the invention described below and the nucleotide sequences according to the invention may advantageously be used in *in vitro* and/or *in vivo* methods for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, in a biological sample (biological tissue or fluid) which is likely to contain them. These methods, depending on the specificity of the polypeptides, of the antibodies and of the nucleotide sequences according to the invention which will be used, may in particular detect and/or identify the bacterial variants belonging to the species *Chlamydia pneumoniae* as well as the associated microorganisms capable of being detected by the polypeptides, the antibodies and the nucleotide sequences according to the invention which will be chosen. It may, for example, be advantageous to choose a polypeptide, an antibody or a nucleotide sequence according to the invention, which is capable of detecting any bacterium of the *Chlamydia* family by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the family or, on the contrary, it will be most particularly advantageous to target a variant of the

species *Chlamydia pneumoniae*, which is responsible, for example, for the induction or the worsening of pathologies specific to the targeted variant, by choosing a polypeptide, an antibody and/or a nucleotide sequence according to the invention which is specific to the said variant.

The polypeptides according to the invention may advantageously be used in a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, in a biological sample (biological tissue or fluid) which is likely to contain them, characterized in that it comprises the following steps:

- a) bringing this biological sample into contact with a polypeptide or one of its representative fragments according to the invention (under conditions allowing an immunological reaction between the said polypeptide and the antibodies which may be present in the biological sample);
- b) detecting the antigen-antibody complexes which may be formed.

Preferably, the biological sample consists of a fluid, for example a human or animal serum, blood or biopsies.

Any conventional procedure may be used to carry out such a detection of the antigen-antibody complexes which may be formed.

By way of example, a preferred method uses immunoenzymatic procedures based on the ELISA technique, immunofluorescence procedures or radioimmunological procedures (RIA), and the like.

Accordingly, the invention also relates to the polypeptides according to the invention, labelled with the aid of a suitable label such as a label of the enzymatic, fluorescent or radioactive type.

Such methods comprise, for example, the following steps:

- deposition of defined quantities of a polypeptide composition according to the invention into the wells of a microtitre plate,
- introduction, into the said wells, of increasing dilutions of serum, or of a different biological sample as defined above, which has to be analysed,
- incubation of the microplate,
- introduction, into the wells of the microtitre plate, of labelled antibodies directed against human or animal immunoglobulins, these antibodies having been labelled with the aid of an enzyme selected from those which are capable of hydrolyzing a substrate, thereby modifying the absorption of the radiation of the latter, at least at a defined wavelength, for example at 550 nm,
- detection, by comparison with a control, of the quantity of substrate hydrolyzed.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polypeptide according to the invention,

- where appropriate, the reagents for constituting the medium appropriate for the immunological or specific reaction,
- the reagents allowing the detection of the antigen-antibody complexes produced by the immunological reaction between the polypeptide(s) of the invention and the antibodies which may be present in the biological sample, it being possible for these reagents also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the polypeptide according to the invention is not labelled,
- where appropriate, a reference biological sample (negative control) free of antibodies recognized by a polypeptide according to the invention,
- 10 - where appropriate, a reference biological sample (positive control) containing a predetermined quantity of antibodies recognized by a polypeptide according to the invention.

According to the invention, the polypeptides, peptides, fusion proteins or other derivatives, or analogs thereof encoded by a polynucleotide sequence in SEQ ID No. 1, may be used as an immunogen to generate antibodies which immunospecifically bind such an immunogen. Such antibodies may include, but are not limited to, polyclonal and monoclonal antibodies, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')<sub>2</sub> fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. In a specific embodiment, the antibody to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1 is a bispecific antibody (see generally, *e.g.* Fanger and Drakeman, 1995, *Drug News and Perspectives* 8: 133-137). Such a bispecific antibody is genetically engineered to recognize both (1) an epitope and (2) one of a variety of "trigger" molecules, *e.g.* Fc receptors on myeloid cells, and CD3 and CD2 on T cells, that have been identified as being able to cause a cytotoxic T-cell to destroy a particular target. Such bispecific antibodies can be prepared either by chemical conjugation, hybridoma, or recombinant molecular biology techniques known to the skilled artisan.

Various procedures known in the art may be used for the production of polyclonal antibodies to a polypeptide, peptide or other derivative, or analog thereof encoded by a polynucleotide sequence in SEQ ID No. 1. For the production of antibody, various host animals can be immunized by injection with a polypeptide, or peptide or other derivative, or analog thereof, including but not limited to rabbits, mice, rats, etc. Various adjuvants, depending on the host species, may be used to increase the immunological response, including but not limited to Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA), Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, BCG (bacille Calmette-Guerin), and corynebacterium parvum. Alternatively, polyclonal antibodies may be prepared by purifying, on an affinity column

onto which a polypeptide according to the invention has been previously attached, the antibodies contained in the serum of patients infected with a bacterium belonging to the species *Chlamydia pneumoniae*.

For preparation of monoclonal antibodies directed toward a polypeptide, peptide or other derivative, or analog, any technique which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, *Immunology Today* 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing technology described in PCT/US90/02545. In another embodiment of the invention, transgenic non-human animals can be used for the production of human antibodies utilizing technology described in WO 98/24893 and WO 96/33735. According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole *et al.*, 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, *PROC. NATL. ACAD. SCI. U.S.A.* 81:6851-6855; Neuberger *et al.*, 1984, *Nature* 312:604-608; Takeda *et al.*, 1985, *Nature* 314:452-454) by splicing the genes from a mouse antibody molecule specific for a polypeptide, peptide or other derivative, or analog together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce polypeptide or peptide-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, *Science* 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for polypeptides, derivatives, or analogs.

Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')<sub>2</sub> fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragment, the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent, and Fv fragments.

In addition, techniques have been developed for the production of chimerized (*See, e.g.*, Boss, M. *et al.*, U.S. Patent No. 4,816,397; and Cabilly, S. *et al.*, U.S. Patent No. 5,585,089 each of which is incorporated herein by reference in its entirety) humanized antibodies (*See, e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin

light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined ( See, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983).

- 5 Briefly, humanized antibodies are antibody molecules from non-human species having one or more CDRs from the non-human species and a framework from a human immunoglobulin molecule.

The antibodies of the invention may also be labelled in the same manner as described above for the nucleic probes of the invention such as an enzymatic, fluorescent or radioactive type labelling.

- 10 The invention relates, in addition, to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

- a) bringing the biological sample (biological tissue or fluid) into contact with a mono- or polyclonal antibody according to the invention (under conditions allowing an immunological reaction  
15 between the said antibodies and the polypeptides of the bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism which may be present in the biological sample, that is, under conditions suitable for the formation of immune complexes);
- b) detecting the antigen-antibody complex which may be formed.

- 20 Also falling within the scope of the invention is a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a polyclonal or monoclonal antibody according to the invention, labeled where appropriate;
- where appropriate, a reagent for constituting the medium appropriate for carrying out the  
25 immunological reaction;
- a reagent allowing the detection of the antigen-antibody complexes produced by the immunological reaction, it being possible for this reagent also to carry a label, or to be capable of being recognized in turn by a labelled reagent, more particularly in the case where the said monoclonal or polyclonal antibody is not labelled;
- 30 - where appropriate, reagents for carrying out the lysis of the cells in the sample tested.

- The principle of the DNA chip which was explained above may also be used to produce protein "chips" on which the support has been coated with a polypeptide or an antibody according to the invention, or arrays thereof, in place of the DNA. These protein "chips" make it possible, for example, to analyze the biomolecular interactions (BIA) induced by the affinity capture of target  
35 analytes onto a support coated, for example, with proteins, by surface plasma resonance (SPR). Reference may be made, for example, to the techniques for coupling proteins onto a solid support which are described in EP 524 800 or to the methods describing the use of biosensor-type protein

chips such as the BIAcore-type technique (Pharmacia) (Arlinghaus et al., 1997, Krone et al., 1997, Chatelier et al., 1995). These polypeptides or antibodies according to the invention, capable of specifically binding antibodies or polypeptides derived from the sample to be analysed, may thus be used in protein chips for the detection and/or the identification of proteins in samples. The said protein  
5 chips may in particular be used for infectious diagnosis and may preferably contain, per chip, several polypeptides and/or antibodies of the invention of different specificity, and/or polypeptides and/or antibodies capable of recognizing microorganisms different from *Chlamydia pneumoniae*.

Accordingly, the subject of the present invention is also the polypeptides and the antibodies according to the invention, characterized in that they are immobilized on a support, in  
10 particular of a protein chip.

The protein chips, characterized in that they contain at least one polypeptide or one antibody according to the invention immobilized on the support of the said chip, also form part of the invention.

The invention comprises, in addition, a protein chip according to the invention,  
15 characterized in that it contains, in addition, at least one polypeptide of a microorganism different from *Chlamydia pneumoniae* or at least one antibody directed against a compound of a microorganism different from *Chlamydia pneumoniae*, immobilized on the support of the said chip.

The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the  
20 detection and/or the identification of a microorganism characterized in that it comprises a protein chip according to the invention.

The subject of the present invention is also a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it uses a nucleotide sequence according to  
25 the invention.

More particularly, the invention relates to a method for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism in a biological sample, characterized in that it comprises the following steps:

- a) where appropriate, isolation of the DNA from the biological sample to be analysed, or optionally  
30 production of a cDNA from the RNA in the biological sample;
- b) specific amplification of the DNA of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism with the aid of at least one primer according to the invention;
- c) detection of the amplification products.

35 These may be detected, for example, by the molecular hybridization technique using a nucleic probe according to the invention. This probe will be advantageously labelled with a nonradioactive (cold probe) or radioactive element.

For the purposes of the present invention, "DNA in the biological sample" or "DNA contained in the biological sample" will be understood to mean either the DNA present in the biological sample considered, or optionally the cDNA obtained after the action of a reverse transcriptase-type enzyme on the RNA present in the said biological sample.

5 Another aim of the present invention consists in a method according to the invention, characterized in that it comprises the following steps:

- a) bringing a nucleotide probe according to the invention into contact with a biological sample, the DNA contained in the biological sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to complementary base pairs of the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated microorganism;
- 10 b) detecting the hybridization complex formed between the nucleotide probe and the DNA in the biological sample.

The present invention also relates to a method according to the invention, characterized in  
15 that it comprises the following steps:

- a) bringing a nucleotide probe immobilized on a support according to the invention into contact with a biological sample, the DNA in the sample having, where appropriate, been previously made accessible to hybridization, under conditions allowing the hybridization of the probe to the DNA of a bacterium belonging to the species *Chlamydia pneumoniae* or to an associated  
20 microorganism;
- b) bringing the hybrid formed between the nucleotide probe immobilized on a support and the DNA contained in the biological sample, where appropriate after removal of the DNA in the biological sample which has not hybridized with the probe, into contact with a labelled nucleotide probe according to the invention;
- 25 c) detecting the new hybrid formed in step b).

According to an advantageous embodiment of the method for the detection and/or the identification defined above, it is characterized in that, prior to step a), the DNA in the biological sample is primer-extended and/or amplified beforehand with the aid of at least one primer according to the invention.

30 The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) a nucleotide probe according to the invention;
- b) where appropriate, the reagents necessary for carrying out a hybridization reaction;
- 35 c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.



The invention also relates to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) a nucleotide probe, called capture probe, according to the invention;
- 5 b) an oligonucleotide probe, called detection probe, according to the invention;
- c) where appropriate, at least one primer according to the invention as well as the reagents (e.g., polymerase and/or deoxynucleotide triphosphates) necessary for a DNA amplification reaction.

The invention also relates to a kit or set for the detection and/or the identification of  
10 bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, characterized in that it comprises the following components:

- a) at least one primer according to the invention;
- b) where appropriate, the reagents necessary for carrying out a DNA amplification reaction;
- c) where appropriate, a component which makes it possible to check the sequence of the amplified  
15 fragment, more particularly an oligonucleotide probe according to the invention.

The invention relates, in addition, to a kit or set for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* or to an associated microorganism, or for the detection and/or the identification of a microorganism characterized in that it comprises a DNA chip according to the invention.

20 The invention also relates to a method or to a kit or set according to the invention for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae*, characterized in that the said primer and/or the said probe according to the invention are chosen from the nucleotide sequences specific to the species *Chlamydia pneumoniae*, in that the said polypeptides according to the invention are chosen from the polypeptides specific to the species *Chlamydia*  
25 *pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides specific to the species *Chlamydia pneumoniae*.

Preferably, the said method or the said kit or set above according to the invention, for the detection and/or the identification of bacteria belonging to the species *Chlamydia pneumoniae* is  
30 characterized in that the said primer and/or the said probe or the said polypeptides are chosen from the nucleotide sequences or polypeptides according to the invention which have been identified as being specific to the species *Chlamydia pneumoniae* and in that the said antibodies according to the invention are chosen from the antibodies directed against the polypeptides according to the invention chosen from the polypeptides identified as being specific to the species *Chlamydia pneumoniae*.

35 The invention relates, in addition, to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of a condition caused by, cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by a *Chlamydia pneumoniae*

infection.

The invention also relates to a method or a kit or set according to the invention for the diagnosis of predispositions to, or of conditions caused by, respiratory diseases induced or worsened by a *Chlamydia pneumoniae* infection; preferably, the said respiratory disease is asthma.

5 According to another aspect, the subject of the invention is the use of polypeptides according to the invention, of cells transformed with a vector according to the invention and/or of transformed animals according to the invention, for the biosynthesis or the biodegradation of organic or inorganic compounds.

10 As has been mentioned above, the nucleotide sequences of the invention were identified by homology with sequences known to encode, for example, polypeptides or fragments of enzymatic polypeptides involved in the biosynthesis or the biodegradation of organic or inorganic molecules.

It is thus possible to use the said polypeptides of the invention in a similar manner for the biosynthesis or the biodegradation of organic or inorganic compounds of industrial or therapeutic interest (called compounds of interest).

15 Among these polypeptides, there may be mentioned in particular the enzymes involved in metabolism, such as the proteolytic enzymes, amino transferases, glucose metabolism, or the enzymes which may be used in the biosynthesis of sugars, amino acids, fatty acids, polypeptides, nucleotides, nucleic acids or any other organic or inorganic compound or in the biodegradation of organic or inorganic compounds.

20 Among these polypeptides, there may be mentioned, in addition, the mutated or modified enzymes corresponding to mutated or modified polypeptides according to the invention which may also be used for the biosynthesis or the biodegradation of organic or inorganic compounds at the industrial level, such as, for example, the production of compounds of interest, the reprocessing of manufacturing residues applied to the food industries, to the papermaking industry or to the chemical  
25 and pharmaceutical industries.

The methods of biosynthesis or biodegradation of organic or inorganic compounds, characterized in that they use a polypeptide or one of its representative fragments according to the invention, transformed cells according to the invention and/or a transformed animal according to the invention, also form part of the invention.

30 The invention relates, in addition, to the use of a nucleotide sequence according to the invention, of a polypeptide according to the invention, of an antibody according to the invention, of a cell according to the invention, and/or of a transformed animal according to the invention, for the selection of an organic or inorganic compound capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the cellular replication of eukaryotic or  
35 prokaryotic cells or capable of inducing, inhibiting or worsening the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The invention also comprises screening assays that comprise methods of selecting

compounds capable of binding to a polypeptide, fusion polypeptide or one of its representative fragments according to the invention, capable of binding to a nucleotide sequence according to the invention, or capable of recognizing an antibody according to the invention, and/or capable of modulating, regulating, inducing or inhibiting the expression of genes, and/or of modifying the growth  
5 or the cellular replication of eukaryotic or prokaryotic cells, or capable of inducing, inhibiting or worsening, in an animal or human organism, the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms, characterized in that it comprises the following steps:

a) bringing the said compound into contact with the said polypeptide, the said nucleotide  
10 sequence, with a transformed cell according to the invention and/or administering the said compound to a transformed animal according to the invention;

b) determining the capacity of the said compound to bind with the said polypeptide or the said nucleotide sequence, or to modulate, regulate, induce or inhibit the expression of genes, or to modulate growth or cellular replication, or to induce, inhibit or worsen in the said transformed animal,  
15 the pathologies linked to an infection by *Chlamydia pneumoniae* or one of its associated microorganisms.

The transformed cells and/or animals according to the invention may advantageously serve as a model and may be used in methods for studying, identifying and/or selecting compounds capable of being responsible for pathologies induced or worsened by *Chlamydia pneumoniae*, or  
20 capable of preventing and/or of treating these pathologies such as, for example, cardiovascular or respiratory diseases. In particular, the transformed host cells, in particular bacteria of the *Chlamydia* family whose transformation with a vector according to the invention may, for example, increase or inhibit its infectivity, or modulate the pathologies usually induced or worsened by the infection, may be used to infect animals in which the onset of pathologies will be monitored. These nontransformed  
25 animals, infected for example with transformed *Chlamydia* bacteria, may serve as a study model. In the same manner, the transformed animals according to the invention may, for example, exhibit predispositions to cardiovascular and/or respiratory diseases and thus be used in methods for selecting compounds capable of preventing and/or of treating the said diseases. The said methods using the said transformed cells and/or transformed animals form part of the invention.

30 The compounds capable of being selected may be organic compounds such as polypeptides or carbohydrates or any other organic or inorganic compounds already known, or new organic compounds produced using molecular modeling techniques and obtained by chemical or biochemical synthesis, these techniques being known to persons skilled in the art.

The said selected compounds may be used to modulate the growth and/or the cellular  
35 replication of *Chlamydia pneumoniae* or any other associated microorganism and thus to control infection by these microorganisms. The said compounds according to the invention may also be used to modulate the growth and/or the cellular replication of all eukaryotic or prokaryotic cells, in

particular tumour cells and infectious microorganisms, for which the said compounds will prove active, the methods which make it possible to determine the said modulations being well known to persons skilled in the art.

Compound capable of modulating the growth of a microorganism is understood to  
5 designate any compound which makes it possible to act, to modify, to limit and/or to reduce the development, the growth, the rate of proliferation and/or the viability of the said microorganism.

This modulation may be achieved, for example, by an agent capable of binding to a protein and thus of inhibiting or of potentiating its biological activity, or capable of binding to a membrane protein of the outer surface of a microorganism and of blocking the penetration of the said  
10 microorganism into the host cell or of promoting the action of the immune system of the infected organism directed against the said microorganism. This modulation may also be achieved by an agent capable of binding to a nucleotide sequence of a DNA or RNA of a microorganism and of blocking, for example, the expression of a polypeptide whose biological or structural activity is necessary for the growth or for the reproduction of the said microorganism.

15 Associated microorganism is understood to designate in the present invention any microorganism whose gene expression may be modulated, regulated, induced or inhibited, or whose growth or cellular replication may also be modulated by a compound of the invention. Associated microorganism is also understood to designate in the present invention any microorganism containing nucleotide sequences or polypeptides according to the invention. These microorganisms may, in some  
20 cases, contain polypeptides or nucleotide sequences identical or homologous to those of the invention may also be detected and/or identified by the detection and/or identification methods or kit according to the invention and may also serve as a target for the compounds of the invention.

The invention relates to the compounds capable of being selected by a method of selection according to the invention.

25 The invention also relates to a pharmaceutical composition comprising a compound chosen from the following compounds:

a nucleotide sequence according to the invention;

a polypeptide according to the invention;

a vector according to the invention;

30 an antibody according to the invention; and

a compound capable of being selected by a method of selection according to the invention, optionally in combination with a pharmaceutically acceptable vehicle.

An effective quantity is understood to designate a sufficient quantity of the said compound or antibody, or of a polypeptide of the invention, which makes it possible to modulate the  
35 growth of *Chlamydia pneumoniae* or of an associated microorganism.

The invention also relates to a pharmaceutical composition comprising one or more polypeptides according to the invention and/or one or more fusion polypeptides according to the

invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Pharmaceutical compositions include compositions that comprise a polypeptide or fusion polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*. In one embodiment, a pharmaceutical composition according to the invention can be utilized for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention relates, in addition, to an immunogenic composition or a vaccine composition, characterized in that it comprises one or more polypeptides according to the invention and/or one or more hybrid (fusion) polypeptides according to the invention. Such compositions further comprise a pharmaceutically acceptable carrier or vehicle. Immunogenic compositions or fusion polypeptide include compositions that comprise a polypeptide that immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

Immunogenic or vaccine compositions can also comprise DNA immunogenic or vaccine compositions comprising polynucleotide sequences of the invention operatively associated with a regulatory sequence that controls gene expression. Such compositions can include compositions that direct expression of a neutralizing epitope of *Chlamydia pneumoniae*.

The invention also comprises the use of a transformed cell according to the invention, for the preparation of a vaccine composition.

The invention also relates to a vaccine composition, characterized in that it contains a nucleotide sequence according to the invention, a vector according to the invention and/or a transformed cell according to the invention.

The invention also relates to the vaccine compositions according to the invention, for the prevention or the treatment of an infection by a bacterium belonging to the species *Chlamydia pneumoniae* or by an associated microorganism.

The invention also relates to the use of DNA encoding polypeptides of *Chlamydia pneumoniae*, in particular antigenic determinants, to be formulated as vaccine compositions. In accordance with this aspect of the invention, the DNA of interest is engineered into an expression vector under the control of regulatory elements, which will promote expression of the DNA, i.e., promoter or enhancer elements. In one preferred embodiment, the promoter element may be cell-specific and permit substantial transcription of the DNA only in predetermined cells. The DNA may be introduced directly into the host either as naked DNA (U.S. Patent No. 5,679,647 incorporated herein by reference in their entirety) or formulated in compositions with other agents which may facilitate uptake of the DNA including viral vectors, i.e., adenovirus vectors, or agents which facilitate immunization, such as bupivacaine and other local anesthetics (U.S. Patent 5,593,972 incorporated herein by reference in their entirety), saponins (U.S. Patent 5,739,118 incorporated herein by reference in their entirety) and cationic polyamines (published international application WO 96/10038 incorporated herein by reference in their entirety).

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by  
5 reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is  
10 incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of  
15 its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are  
20 those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to  
25 persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of  
30 the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

35 Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough),

recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of vaccination with naked DNA.

The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae* or *Chlamydia trachomatis*.

Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* ( $10^4$  IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37EC for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37E for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C. trachomatis*, etc. IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumoniae* infection described by Moazed et al. (1997). Briefly, male homozygous apoE deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately  $3 \times 10^7$  IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated  
5 intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately  $3 \times 10^7$  IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and  
10 immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention  
15 may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention,  
20 the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with  
25 liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector  
30 according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen ® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in  
35 addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, e.g., a human host, an



immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetylmuramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition, tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

#### Legend to the figures :

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

Figure 2 : Analysis of the sequences and assembling

Figure 3 : Finishing techniques

Figure 3a) : Assembly map

Figure 3b) : Determination and use of the orphan ends of the contigs

5

## EXAMPLES

### Experimental procedures

10

#### Cells

The *Chlamydia pneumoniae* strain (CM1) used by the inventors is obtained from ATCC (American Culture Type Collection) where it has the reference number ATCC 1360-VR.

15 It is cultured on HeLa 229 cells, obtained from the American Type Culture Collection, under the reference ATCC CCL-2.1.

#### Culture of the cells

20 The HeLa ATCC CCL-2.1 cells are cultured in 75-ml cell culture flasks (Corning). The culture medium is Dulbecco's modified cell culture medium (Gibco BRL No. 04101965) supplemented with MEM amino acids (Gibco BRL - No. 04301140) L (5 ml per 500 ml of medium) and 5% foetal calf serum (Gibco BRL No. 10270 batch 40G8260K) without antibiotics or antifungals.

25 The cell culture stock is maintained in the following manner. The cell cultures are examined under an inverted microscope. 24 hours after confluence, each cellular lawn is washed with PBS (Gibco BRL No. 04114190), rinsed and then placed for 5 min in an oven in the presence of 3 ml of trypsin (Gibco BRL No. 25200056). The cellular lawn is then detached and then resuspended in 120 ml of culture medium, the whole is stirred in order to make the cellular suspension homogeneous. 30 30 ml of this suspension are then distributed per cell culture flask. The flasks are kept in a CO<sub>2</sub> oven (5%) for 48 hours at a temperature of 37°C. The cell stock is maintained so as to have available daily 16 flasks of subconfluent cells. It is these subconfluent cells which will be used so as to be infected with *Chlamydia*. 25-ml cell culture flasks are also used, these flasks are prepared in a similar manner but the volumes used for maintaining the cells are the following: 1 ml of trypsin, 28 ml of culture medium to resuspend the cells, 7 ml of culture medium are used per 25-ml flask.

#### Infection of the cells with *Chlamydia*

35 Initially, the *Chlamydiae* are obtained frozen from ATCC (-70°C), in suspension in a volume of 1 ml. This preparation is slowly thawed, 500 µl are collected and brought into contact with subconfluent cells, which are obtained as indicated above, in a 25-ml cell culture flask, containing 1 ml of medium, so as to cover the cells. The flask is then centrifuged at 2000 rpm in a "swing" rotor for microtitre plates, the centrifuge being maintained at a temperature of 35°C. After centrifugation,

the two flasks are placed in an oven at 35°C for three hours. 6 ml of culture medium containing cycloheximide (1 µg/ml) are then added and the flask is stored at 35°C. After 72 hours, the level of infection is evaluated by direct immunofluorescence and by the cytopathogenic effect caused to the cells.

5        Direct immunofluorescence

Starting with infected cells, which were obtained as indicated above, a cellular smear is deposited with a Pasteur pipette on a microscope slide. The cellular smear is fixed with acetone for 10 minutes; after draining the acetone, the smear is covered with 30 µl of murine monoclonal antibodies directed against MOMP (major outer membrane protein) of Chlamydia (Syva, Biomérieux) labelled with fluorescein isothiocyanate. The whole is then incubated in a humid chamber at a temperature of 37°C. The slides are then rinsed with water, slightly dried, and then after depositing a drop of mounting medium, a coverslip is mounted before reading. The reading is carried out with the aid of a fluorescence microscope equipped with the required filters (excitation at 490 nm, emission at 520 nm).

15       Harvesting of the *Chlamydia pneumoniae*

After checking the infection by direct immunofluorescence, carried out as indicated above, the culture flasks are opened under a sterile cabinet, sterile glass beads with a diameter of the order of a millimeter are placed in the flask. The flask is closed and then vigorously stirred while being maintained horizontally, the cellular lawn at the bottom, so that the glass beads can have a mechanical action on the cellular lawn. Most of the cells are thus detached or broken; the effect of the stirring is observed under an optical microscope so as to ensure proper release of Chlamydiae.

20       Large-scale infection of the cell cultures

The product of the Chlamydiae harvest (culture medium and cellular debris) is collected with a pipette, and distributed into three cell culture flasks containing subconfluent HeLa ATCC CCL-2.1 cells, obtained as indicated above. The cells thus inoculated are placed under gentle stirring (swing) in an oven at 35°C. After one hour, the flasks are kept horizontally in an oven so that the culture medium covers the cells for 3 hours. 30 ml of culture medium containing actydione (1 µg/ml) are then added to each of the flasks. The culture flasks are then stored at 35°C for 72 hours. The cells thus infected are examined under an optical microscope after 24 hours, the cytopathogenic effect is evaluated by the appearance of cytoplasmic inclusions which are visible under an inverted optical microscope. After 72 hours, the vacuoles containing the Chlamydiae occupy the cytoplasm of the cell and push the cell nucleus sideways. At this stage, numerous cells are spontaneously destroyed and have left free elementary bodies in the culture medium. The Chlamydiae are harvested as described above and are either frozen at -80°C or used for another propagation.

35       Purification of the Chlamydiae

The product of the Chlamydia harvests is stored at -80°C and thawed on a water bath at

room temperature. After thawing, each tube is vigorously stirred for one minute and immersed for one minute in an ultrasound tank (BRANSON 1200); the tubes are then stirred by inverting before being centrifuged for 5 min at 2000 rpm. The supernatant is carefully removed and kept at cold temperature (ice). The supernatant is vigorously stirred and then filtered on nylon filters having pores of 5 microns in diameter on a support (Nalgene) allowing a delicate vacuum to be established under the nylon filter. For each filtration, three nylon filters are superposed; these filters are replaced after every 40 ml of filtrate. Two hundred milliliters of filtration product are kept at cold temperature, and then after stirring by inverting, are centrifuged at 10,000 rpm for 90 min, the supernatant is removed and the pellet is taken up in 10 ml of 10 mM Tris, vigorously vortexed and then centrifuged at 10,000 rpm for 90 min. The supernatant is removed and the pellet is taken up in a buffer (20 mM Tris pH 8.0, 50 mM KCl, 5 mM MgCl<sub>2</sub>) to which 800 units of DNase I (Boehringer) are added. The whole is kept at 37°C for one hour. One ml of 0.5 M EDTA is then added, the whole is vortexed and frozen at -20°C.

#### Preparation of the DNA

The Chlamydiae purified above are thawed and subjected to a proteinase K (Boehringer) digestion in a final volume of 10 ml. The digestion conditions are the following: 0.1 mg/ml proteinase K, 0.1 × SDS at 55°C, stirring every 10 min. The product of digestion is then subjected to a double extraction with phenol-chloroform, two volumes of ethanol are added and the DNA is directly recovered with a Pasteur pipette having one end in the form of a hook. The DNA is dried on the edge of the tube and then resuspended in 500 µl of 2 mM Tris pH 7.5. The DNA is stored at 4°C for at least 24 hours before being used for the cloning.

#### Cloning of the DNA

After precipitation, the DNA is quantified by measuring the optical density at 260 nm. Thirty µg of Chlamydia DNA are distributed into 10 tubes of 1.5 ml and diluted in 300 µl of water. Each of the tubes is subjected to 10 applications of ultrasound lasting for 0.5 sec in a sonicator (unisonix XL2020). The contents of the 10 tubes are then grouped and concentrated by successive extractions with butanol (Sigma B1888) in the following manner: two volumes of butanol are added to the dilute DNA mixture. After stirring, the whole is centrifuged for five minutes at 2500 rpm and the butanol is removed. This operation is repeated until the volume of the aqueous phase is less than 1 ml. The DNA is then precipitated in the presence of ethanol and of 0.5 M sodium acetate pH 5.4, and then centrifuged for thirty minutes at 15,000 rpm at cold temperature (4°C). The pellet is washed with 75% ethanol, centrifuged for five minutes at 15,000 rpm and dried at room temperature. A tenth of the preparation is analysed on a 0.8% agarose gel. Typically, the size of the DNA fragments thus prepared is between 200 and 8000 base pairs.

To allow the cloning of the DNA obtained, the ends are repaired. The DNA is distributed in an amount of 10 µg/tube, in the following reaction medium: 100 µl final volume, 1 × buffer

(Biolabs 201L), 0.5 µl BSA 0.05 mg/ml, 0.1 mM dATP, 0.1 mM each of dGTP, dCTP or dTTP, 60,000 IU T4 DNA polymerase. The reaction is incubated for thirty minutes at 16°C. The contents of each of the tubes are then grouped before carrying out an extraction with phenol-chloroform and then precipitating the aqueous phase as described above. After this step, the DNA thus prepared is phosphorylated. For that, the DNA is distributed into tubes in an amount of 10 µg per tube, and then in a final volume of 50 µl, the reaction is prepared in the following manner: 1 mM ATP, 1 × kinase buffer, 10 IU T4 polynucleotide kinase (Biolabs 201L). The preparation is incubated for thirty minutes at 37°C. The contents of the tubes are combined and a phenol-chloroform extraction and then a precipitation are carried out in order to precipitate the DNA. The latter is then suspended in 1 µl of water and then the DNA fragments are separated according to their size on a 0.8% agarose gel (1 × TAE). The DNA is subjected to an electric field of 5 V/cm and then visualized on a UV table. The fragments whose size varies between 1200 and 2000 base pairs are selected by cutting out the gel. The gel fragment thus isolated is placed in a tube and then the DNA is purified with the Qiaex kit (20021 Qiagen), according to the procedure provided by the manufacturer.

#### 15      Preparation of the vector

14 µg of the cloning vector pGEM-5Zf (Proméga P2241) are diluted in a final volume of 150 µl and are subjected to digestion with the restriction enzyme EcoRV 300 IU (Biolabs 195S) according to the protocol and with the reagents provided by the manufacturer. The whole is placed at 37°C for 150 min and then distributed in the wells of a 0.8% agarose gel subjected to an electric field of 5 V/cm. The linearized vector is visualized on a UV table, isolated by cutting out the gel and then purified by the Qiaex kit (Qiagen 20021) according to the manufacturer's recommendations. The purification products are grouped in a tube, the volume is measured and then half the volume of phenol is added and the whole is vigorously stirred for 1 min. Half the volume of chloroform-isoamyl alcohol 24:1 is added and vigorously stirred for 1 min. The whole is centrifuged at 15,000 rpm for 5 min at 4°C, the aqueous phase is recovered and transferred into a tube. The DNA is precipitated in the presence of 0.3 M sodium acetate, pH 5.4 and 3 volumes of ethanol and placed at -20°C for 1 hour. The DNA is then centrifuged at 15,000 rpm for 30 min at 4°C, the supernatant is removed while preserving the pellet, washed twice with 70% ethanol. After drying at room temperature, the DNA is suspended in 25 µl of water.

#### 30      Phosphorylation of the vector

25 µl of the vector prepared in the preceding step are diluted in a final volume of 500 µl of the following reaction mixture:

After repair, the DNA is subjected to a phenol-chloroform extraction and a precipitation, the pellet is then taken up in 10 µl of water, the DNA is quantified by measuring the optical density at 260 nm. The quantified DNA is ligated into the vector pGEM-5Zf(+) prepared by the restriction

enzyme EcoRV and dephosphorylated (see preparation of the vector). The ligation is carried out under three conditions which vary in the ratio between the number of vector molecules and the number of insert molecules. Typically, an equimolar ratio, a ratio of 1:3 and a ratio of 3:1 are used for the ligations which are, moreover, carried out under the following conditions: vector PGE<sub>m</sub>-5Zf(+)  
5 25 ng, cut DNA, ligation buffer in a final volume of 20 µl with T4 DNA ligase (Amersham E70042X); the whole is then placed in a refrigerator overnight and then a phenol-chloroform extraction and a precipitation are carried out in a conventional manner. The pellet is taken up in 5 µl of water.

#### Transformation of the bacteria

##### Plating of the bacteria

10 Petri dishes containing LB Agar medium containing ampicillin (50 µg/ml), Xgal (280 µg/ml) [5-bromo-4-chloro-indolyl-beta-D-galactopyranoside (Sigma B-4252)], IPTG (140 µg/ml) [isopropyl-beta-D-thiogalactoside (Sigma I-6758)] are used, 50 and 100 µl of bacteria are plated for each of the ligations. The Petri dishes are placed upside down at 37°C for 15 to 16 hours in an oven. The number of "recombinant" positive clones is evaluated by counting the white colonies and  
15 the blue colonies which are thought to contain the vector alone.

##### Evaluation of the "recombinant" positive clones

Ninety-four white colonies and two blue colonies are collected with the aid of sterile cones and are deposited at the bottom of the wells of plates designed for carrying out the amplification techniques. 30 µl of the following reaction mixture are added to each well: 1.7 mM MgCl<sub>2</sub>, 0.2 mM  
20 each of dATP, dCTP, dGTP and dTTP, two synthetic oligonucleotides corresponding to sequences flanking the cloning site on either side and orienting the synthesis of the DNA in a convergent manner (0.5 µM RP and PU primers, 1 U TAQ polymerase (GibcoBRL 18038-026)).

The colonies thus prepared are subjected to a temperature of 94°C for 5 min and then to 30 thermal cycles composed of the following steps: 94°C for 40 s, 50°C for 30 s, 72°C for 180 s. The  
25 reaction is then kept for 7 min at 72°C and then kept at 4°C.

The amplification products are deposited on an agarose gel (0.8%), stained with ethidium bromide, subjected to electrophoresis, and then analysed on an ultraviolet table. The presence of an amplification fragment having a size greater than 500 base pairs indicates the presence of an insert. The bacterial clones are then prepared so as to study the sequence of their insert.

##### Sequencing

30 To sequence the inserts of the clones obtained as above, these were amplified by PCR on bacteria cultures carried out overnight using the primers for the vectors flanking the inserts. The sequence of the ends of these inserts (on average 500 bases on each side) was determined by automated fluorescent sequencing on an ABI 377 sequencer, equipped with the ABI Prism DNA  
35 Sequencing Analysis software (version 2.1.2).

##### Analysis of the sequences

The sequences obtained by sequencing in a high-yield line (Figure 1) are stored in a database; this part of the production is independent of any treatment of the sequences. The sequences are extracted from the database, avoiding all the regions of inadequate quality, that is to say the regions for which uncertainties are observed on the sequence at more than 95%. After extraction, the sequences are introduced into a processing line, the diagram of which is described in Figure 2. In a first path of this processing line, the sequences are assembled by the Gap4 software from R. Staden (Bonfield et al., 1995) (OS UNIX/SUN Solaris); the results obtained by this software are kept in the form of two files which will be used for a subsequent processing. The first of these files provides information on the sequence of each of the contigs obtained. The second file represents all the clones participating in the composition of all the contigs as well as their positions on the respective contigs.

The second processing path uses a sequence assembler (TIGR-Asmg assembler UNIX/SUN Solaris); the results of this second processing path are kept in the form of a file in the TIGR-Asmg format which provides information on the relationship existing between the sequences selected for the assembly. This assembler is sometimes incapable of linking contigs whose ends overlap over several hundreds of base pairs.

The results obtained from these two assemblers are compared with the aid of the BLAST program, each of the contigs derived from one assembly path being compared with the contigs derived from the other path.

For the two processing paths, the strict assembly parameters are fixed (95% homology, 30 superposition nucleotides). These parameters avoid 3 to 5% of the clones derived from eukaryotic cells being confused with sequences obtained from the clones derived from *Chlamydia pneumoniae*. The eukaryotic sequences are however preserved during the course of this project; the strategy introduced, which is described below, will be designed, inter alia, not to be impeded by these sequences derived from contaminating clones.

The results of these two assemblers are processed in a software developed for this project. This software operates on a Windows NT platform and receives, as data, the results derived from the STADEN software and/or the results derived from the TIGR-Asmg assembler, the software, results, after processing of the data, in the determination of an assembly map which gives the proximity relationship and the orientation of the contigs in relation to one another (Figure 3a). Using this assembly map, the software determines all the primers necessary for finishing the project. This treatment, which will be detailed below, has the advantage of distinguishing the isolated sequences derived from the contaminations, by the DNA eukaryotic cells, of the small-sized sequences clearly integrated into the project by the relationships which they establish with contigs. In order to allow, without any risk of error, the arrangement and the orientation of the contigs in relation to one another, a statistical evaluation of the accuracy of the names (naming) "naming" of sequence is made from the results of "contigation". This evaluation makes it possible to give each of the clone plates, as well as each of the subsets of plates, a weight which is inversely proportional to probable error rate existing in

the "naming" of the sequences obtained from this plate or from a subset of this plate. In spite of a low error rate, errors may occur throughout the steps of production of the clones and of the sequences. These steps are numerous, repetitive and although most of them are automated, others, like the deposition in the sequencers, are manual; it is then possible for the operator to make mistakes such as the inversion of two sequences. This type of error has a repercussion on the subsequent processing of the data, by resulting in relationships (between the contigs) which do not exist in reality, then in attempts at directed sequencing between the contigs which will end in failure. It is because of this that the evaluation of the naming errors is of particular importance since it allows the establishment of a probabilistic assembly map from which it becomes possible to determine all the clones which will serve as template to obtain sequences separating two adjacent contigs. Table 2 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the clones and the sequences of the primers initially used during the initial operations.

To avoid the step which consists in ordering and then preparing the clones by conventional microbiological means, outer and inner primers oriented towards the regions not yet sequenced are defined by the software. The primers thus determined make it possible to prepare, by PCR, a template covering the nonsequenced region. It is the so-called outer primers (the ones most distant from the region to be sequenced) which are used to prepare this template. The template is then purified and a sequence is obtained on each of the two strands during 2 sequencing reactions which each use one of the 2 inner primers. In order to facilitate the use of this approach, the two outer primers and the two inner primers are prepared and then stored on the same position of 4 different 96-well plates. The two plates containing the outer primers are used to perform the PCRs which will serve to prepare the templates. These templates will be purified on purification columns preserving the topography of the plates. Each of the sequences will be obtained using primers situated on one and then on the other of the plates containing the inner primers. This distribution allows a very extensive automation of the process and results in a method which is simple to use for finishing the regions not yet sequenced. Table 3 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997, each of which is incorporated by reference herein in its entirety, gives the names and the sequences of the primers used for finishing *Chlamydia pneumoniae*.

Finally, a number of contigs exist in a configuration where one of their ends is not linked to any other contig end (Figure 3b) by a connecting clone relationship (a connecting clone is defined as a clone having one sequence end on a contig and the other end of its sequence on another contig; furthermore, this clone must be derived from a plate or a subset of plates with adequate naming quality). For the *Chlamydia pneumoniae* project, this particular case occurred 24 times. Two adjacent PCR primers orienting the synthesis of the DNA towards the end of the consensus sequence are defined for each of the orphan ends of the consensus sequence. The primer which is closest to the end



of the sequence is called the inner primer whereas the primer which is more distant from the end of the sequence is called the outer primer. The outer primers are used to explore the mutual relationship between the orphan ends of the different contigs. The presence of a single PCR product and the possibility of amplifying this product unambiguously using the inner primers evokes the probable relationship between the contigs on which the primers which allowed the amplification are situated. This relationship will be confirmed by sequencing and will allow the connection between the orphan ends of the consensus sequences. This strategy has made it possible to obtain a complete map of the *Chlamydia pneumoniae* chromosome and then to finish the project.

#### Quality control

All the bases not determined with certainty in the chromosomal sequence were noted and the density of uncertainties was measured on the entire chromosome. The regions with a high density of uncertainties were noted and the PCR primers spanning these regions were drawn and are represented in Table 4 of parent U.S. application serial No. 60/107078 filed November 4, 1998 and French application 97-14673 filed November 21, 1997 each of which is incorporated by reference herein in its entirety.

The sequence of each of the PCR products was obtained with two operational primers different from the amplification primers. The sequences were obtained in both directions for all the PCRs (100% success).

#### Data banks

Local reorganizations of major public banks were used. The protein bank used consists of the nonredundant fusion of the Genpept bank (automated translation of GenBank, NCBI; Benson et al., 1996).

The entire BLAST software (public domain, Altschul et al., 1990) for searching for homologies between a sequence and protein or nucleic data banks was used. The significance levels used depend on the length and the complexity of the region tested as well as the size of the reference bank. They were adjusted and adapted to each analysis.

The results of the search for homologies between a sequence according to the invention and protein or nucleic data banks are presented and summarized in Table 1 below.

Table 1: List of coding chromosome regions and homologies between these regions and the sequence banks.

Legend to Table 1: Open reading frames are identified with the GenMark software version 2.3A (GenePro), the template used is *Chlamydia pneumoniae* of order 4 on a length of 196 nucleotides with a window of 12 nucleotides and a minimum signal of 0.5. The reading frames ORF2 to ORF 1137 are numbered in order of appearance on the chromosome, starting with ORF2 (ORF column). The positions of the beginning and of the end are then given in column 2 (position). When the position of the beginning is greater than the position of the end, this means that the region is

encoded by the strand complementary to the sequence which was given in the sequence SEQ ID No. 1.

All the putative products were subjected to a search for homology on GENPEPT (release 102 for SEQ ID No. 2 to SEQ ID No. 1137, and release 108 for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849) with the BLASTP software (Altschul et al. 1990). With, as parameters, the default parameters with the exception of the expected value E set at  $10^{-5}$  (for SEQ ID No. 2 to SEQ ID No. 1137) and P value set at  $e^{-10}$  (for SEQ ID No. 1138 to SEQ ID No. 1291 and SEQ ID No. 6844 to SEQ ID No. 6849). Subsequently, only the identities greater than 30% (1% column) were taken into account. The description of the most homologous sequence is given in the Homology column; the identifier for the latter sequence is given in the ID column and the animal species to which this sequence belongs is given in the Species column. The Homology score is evaluated by the sum of the blast scores for each region of homology and reported in the Score column.

#### Materials and Methods for transmembrane domains:

The DAS software was used as recommended by the authors (Cserzo et al., 1997).

This method uses, to predict the transmembrane domains, templates derived from a sampling of selected proteins. All the regions for which a "Cutoff" greater than 1.5 was found by the program were taken into account.

#### Additional ORF Finder Programs

For this analysis, two additional ORF finder programs were used to predict potential open reading frames of a minimum length of 74 amino acids; Glimmer (Salzberg, S.L., Delcher, A., Kasif, S., and W. White. 1998. Microbial gene identification using interpolated Markov models. Nucleic Acids Res. 26:544-548.), and an in-house written program. The in-house program used a very simple search algorithm. The analysis required that the genomic DNA sequence text be in the 5' to 3' direction, the genome is circular, and that TAA, TAG, and TGA are stop codons. The search parameters were as follows:

- (1) A search for an ORF that started with a GTG codon was performed. If no GTG codons were found, then a search for an ATG codon was performed. However, if a GTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.
- (2) A search for an ORF that started with a TTG codon was performed. If no TTG codons were found, then a search for a ATG codon was performed. However, if a TTG codon was found, then a search downstream for a ATG codon was performed. All start and stop nucleotide positions were recorded.
- (3) The analysis described in steps 1 and 2 were repeated for the opposite strand of DNA sequence.

- (4) A search for ORFs that determined all ORF lengths using start and stop positions in the same reading frames was performed.
- (5) All ORFs whose DNA length was less than 225 nucleotides were eliminated from the search.

#### 5 Surface Exposed Protein Search Criteria

Potential cell surface vaccine targets are outer membrane proteins such as porins, lipoproteins, adhesions and other non-integral proteins. In *Chlamydia psittaci*, the major immunogens is a group of putative outer membrane proteins (POMPs) and no homologs have been found in *Chlamydia pneumoniae* and *Chlamydia trachomatis* by traditional analysis (Longbottom, D., Russell, 10 M., Dunbar, S.M., Jones, G.E., and A.J. Herring. 1998. Molecular Cloning and Characterization of the Genes Coding for the Highly Immunogenic Cluster of 90-Kilodalton Envelope Proteins from *Chlamydia psittaci* Subtype That Causes Abortion in Sheep. Infect Immun 66:1317-1324.) Several putative outer membrane proteins have been identified in *Chlamydia pneumoniae*, all of which may represent vaccine candidates. The major outer membrane protein (MOMP) gene (omp1) has been 15 found in various isolates of *Chlamydia pneumoniae* (Jantos, CA., Heck, S., Roggendorf, R., Sen-Gupta, M., and Hegemann, JH. 1997. Antigenic and molecular analyses of different chlamydia pneumoniae strains. J. Clin Microbiology 35(3):620-623.) Various criteria, as listed below, were used to identify putative surface exposed ORFs from the genomic DNA sequence of *Chlamydia pneumoniae* (French application 97-14673 filed 21 November 1997). Any ORF which met any one or 20 more of the individual criteria were listed in this category.

Protein homology searches were done using the Blastp 2.0 tool (Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and D.J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402. ) An ORF product was labeled surface exposed if there was homology to a known, or 25 hypothetical, or putative surface exposed protein with a P score better than  $e^{-10}$ .

Most, if not all, proteins that are localized to the membrane of bacteria, via a secretory pathway, contain a signal peptide. A software program, SignalP, analyzes the amino acid sequence of an ORF for such a signal peptide (Nielsen, H., Engelbrecht, J., Brunak, S., and G. von Heijne. 1997. Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. 30 Protein Engineering 10:1-6.) The first 60 N-terminal amino acids of each ORF were analyzed by SignalP using the Gram-Negative software database. The output generates four separate values, maximum C, maximum Y, maximum S, and mean S. The S-score, or signal region, is the probability of the position belonging to the signal peptide. The C-score, or cleavage site, is the probability of the position being the first in the mature protein. The Y-score is the geometric average of the C-score and 35 a smoothed derivative of the S-score. A conclusion of either a Yes or No is given next to each score. If all four conclusions are Yes and the C-terminal amino acid is either a phenylalanine (F) or a tyrosine (Y), the ORF product was labelled outer membrane (Struyve, M., Moons, M., and J. Tommassen.

1991. Carboxy-terminal Phenylalanine is Essential for the Correct Assembly of a Bacterial Outer Membrane Protein. J. Mol. Biol. 218:141-148.)

The program called Psort, determines the localization of a protein based on its signal sequence, recognition of transmembrane segments, and analysis of its amino acid composition (Nakai, K., and M. Kanehisa. 1991. Expert system for predicting protein localization sites in gram-negative bacteria. Proteins 11:95-110.) An ORF product is considered to be an outer membrane protein if the output data predicts the protein as outer membrane with a certainty value of 0.5 or better and whose value is at least twice as large as the next predicted localized certainty value.

Finally, ORF products that were not predicted to be outer membrane or surface exposed, based on the above criteria, were further analyzed. The blastp output data for these ORFs were searched using various general and specific keywords, suggestive of known cell surface exposed proteins. An ORF was labeled surface exposed if the keywords matched had a Blastp hit, had a P score better than  $e^{-10}$ , and that there was no better data indicating otherwise. The following is a list of the searched keywords:

15

	Adhesion	Adhesin	Invasin	Invasion	Extensin	
	Omp	Outer Surface	Porin	Outer Membrane		
	Cell Surface	Cell Wall	Pilus	Pilin	Flagellar sheath	BtuB
	Cir	ChuA	CopB	ExeD	FadL	FecA
20	FepA	FhuA	FmdC	FomA	FrpB	GspD
	HemR	HgbA	Hgp	HmbR	HmuR	HMW
	HrcC	Hrp	InvG	LamB	LbpA	LcrQ
	Lmp1	MxiD	MOMP	PilE	HpaA	NolW
	NspA	OpcP	OpnP	Opr	OspA	PhoE
25	PldA	Por	PscC	PulD	PupA	QuiX
	RafY	ScrY	SepC	ShuA	SomA	SpiA
	Tbp1	Yop	YscC	mip	Tol	

Those ORFs that did not meet the minimum requirement for being an outer membrane protein based on the above search criteria but which were homologous to identified outer membrane ORFs in *Chlamydia trachomatis* were included. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of outer membrane ORFs were identified. These *Chlamydia trachomatis* ORFs were then tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value better than  $e^{-10}$  against a *Chlamydia trachomatis* outer membrane was included in this section, if there was no better data

indicating otherwise. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative surface exposed proteins is set forth above in the specification.

Identification of Putative Lipoproteins in the Genome of *Chlamydia pneumoniae*

5 Lipoproteins are the most abundant post-translationally modified bacterial secretory proteins (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The characteristic features of lipoproteins are a thiol-linked diacylglyceride and an amine-linked monoacyl group on the cysteine that becomes the amino-terminal residue after signal peptide cleavage by Signal Peptidase II.

10 (Pugsley, A. P.. 1993. The complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108). The identification of putative lipoproteins from the genomic sequencing of *Chlamydia pneumoniae* was done by examining the deduced amino acid sequence of identified ORFs for the presence of a signal peptide with a Signal Peptidase II cleavage site analogous to the consensus sequence for prolipoprotein modification and

15 processing reactions (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. In N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.).

20 *Chlamydia pneumoniae* ORFs were initially screened for the most basic of lipoprotein characteristics, a cysteine in the first 30 amino acids of the deduced protein. ORFs with a standard start codon (ATG, GTG, or TTG) and having one or more of the following characteristics were selected for direct analysis of their first 30 amino acids:

(a) Significant Signal P value (at least two out of the four values are Yes)

25

(b) PSORT value indicating membrane passage (IM-inner membrane, Peri-periplasm, or OM-outer membrane)

(c) Identification of the word lipoprotein among the ORF blastp data set.

30 (d) A Blastp value of  $<e^{-10}$  with a putative lipoprotein from *Chlamydia trachomatis* (French applications 97-15041 filed 28 November 1997 and 97-16034 filed 17 December 1997).

The first 30 amino acids of each ORF in this set were analyzed for the characteristics commonly found in lipoprotein signal peptides (Pugsley, A. P.. 1993. The complete general secretory

35 pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108; Hayashi, S., and H. C. Wu. 1992.

Identification and characterization of lipid- modified proteins in bacteria, p. 261-285. In N. M. Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York; Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128.) Putative lipoprotein signal peptides were required to have a  
 5 cysteine between amino acid 10 and 30 and reach a minimum score of three based on the following criteria for lipoprotein signal peptides:

- (a) Identification of specific amino acids in specific positions around the cysteine which are part of the consensus Signal Peptidase II cleavage site (Hayashi, S., and H. C. Wu. 1992. Identification and characterization of lipid-modified proteins in bacteria, p. 261-285. In N. M.  
 10 Hooper and A. J. Turner (ed.) Lipid modification of proteins: A practical approach. Oxford University Press, New York); Sutcliffe, I. C. and R. R. B. Russell. 1995. Lipoproteins of Gram-positive bacteria. J. Bacteriol. 177:1123-1128). Since the identification of the cleavage site is the most important factor in identifying putative lipoproteins, each correctly positioned amino acid contributed toward reaching the minimum score of three.
- (b) A hydrophobic region rich in alanine and leucine prior to the cleavage site (Pugsley, A. P.. 1993. The  
 15 complete general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.
- (c) A short stretch of hydrophilic amino acids greater than or equal to 1 usually lysine or arginine following the N-terminal methionine (Pugsley, A. P.. 1993. The complete  
 20 general secretory pathway in Gram-negative bacteria. Microbiol. Rev. 57:50-108) contributed toward reaching the minimum score of three.

A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative lipoproteins is set forth above in the specification.

## 25 LPS-Related ORFs of *Chlamydia pneumoniae*

Lipopolysaccharide (LPS) is an important major surface antigen of *Chlamydia* cells. Monoclonal antibodies (Mab) directed against LPS of *Chlamydia pneumoniae* have been identified that can neutralize the infectivity of *Chlamydia pneumoniae* both in vitro and in vivo (Peterson, E.M., de la Maza, L.M., Brade, L., Brade, H. 1998. Characterization of a Neutralizing Monoclonal  
 30 Antibody Directed at the Lipopolysaccharide of *Chlamydia pneumoniae*. Infect. Immun. Aug. 66(8):3848-3855.) Chlamydial LPS is composed of lipid A and a core oligosaccharide portion and is phenotypically of the rough type (R-LPS) (Lukacova, M., Baumann, M., Brade, L., Mamat, U., Brade, H. 1994. Lipopolysaccharide Smooth-Rough Phase Variation in Bacteria of the Genus *Chlamydia*. Infect. Immun. June 62(6):2270-2276.) The lipid A component is composed of fatty acids  
 35 which serve to anchor LPS in the outer membrane. The core component contains sugars and sugar derivatives such as a trisaccharide of 3-deoxy-D-manno-octulosonic acid (KDO) (Reeves, P.R., Hobbs, M., Valvano, M.A., Skurnik, M., Whitfield, C., Coplin, D., Kido, N., Klena, J., Maskell, D.,

- Raetz, C.R.H., Rick, P.D. 1996. *Bacterial Polysaccharide Synthesis and Gene Nomenclature* pp. 10071-10078, Elsevier Science Ltd.). The KDO gene product is a multifunctional glycosyltransferase and represents a shared epitope among the Chlamydia. For a review of LPS biosynthesis see, e.g., Schnaitman, C.A., Klena, J.D. 1993. Genetics of Lipopolysaccharide
- 5 Biosynthesis in Enteric Bacteria. Microbiol. Rev. 57:655-682.

A text search of the ORF blastp results identified several genes that are involved in Chlamydial LPS production with a P score better than  $e^{-10}$ . The following key-terms were used in the text search: KDO, CPS (Capsular Polysaccharide Biosynthesis), capsule, LPS, rfa, rfb, rfc, rfe, rha, rhl, core, epimerase, isomerase, transferase, pyrophosphorylase, phosphatase, aldolase, heptose,

10 manno, glucose, lpxB, fibronectin, fibrinogen, fucosyltransferase, lic, lgt, pgm, tolC, rol, ChoP, phosphorylcholine, waaF, PGL-Tb1. A list of ORFs in the *Chlamydia pneumoniae* genome encoding putative polypeptides involved in LPS biosynthesis is set forth above in the specification.

#### Type-III And Other Secreted Products

- 15 Type III secretion enables gram-negative bacteria to secrete and inject pathogenicity proteins into the cytosol of eukaryotic host cells (Hueck, C. J., 1998. Type III Protein Secretion Systems in Bacterial Pathogens of Animals and Plants. In Microbiology and Molecular Biology Reviews. 62:379-433.) These secreted factors often resemble eukaryotic signal transduction factors, thus enabling the bacterium to redirect host cell functions (Lee, C.A., 1997. Type III secretion
- 20 systems: machines to deliver bacterial proteins into eukaryotic cells? Trends Microbiol. 5:148-156.) In an attempt to corrupt normal cellular functions, Chlamydial pathogenicity factors injected into the host cytosol will nonetheless, as cytoplasmic constituents be processed and presented in the context of the Major Histocompatibility Complex (MHC class I). As such, these pathogenicity proteins represent MHC class I antigens and will play an important role in cellular immunity. Also included in this set
- 25 are secreted non-type III products that may play a role as vaccine components.

A text search of the ORF blastp results identified genes that are involved in *Chlamydia pneumoniae* protein secretion with a P score better than  $e^{-10}$ . The following key-terms were used in the text search in an effort to identify surface localized or secreted products: Yop, Lcr, Ypk, Exo, Pcr, Pop, Ipa, Vir, Ssp, Spt, Esp, Tir, Hrp, Mxi, hemolysin, toxin, IgA protease, cytolysin, tox, hap,

30 secreted and Mip.

*Chlamydia pneumoniae* ORFs that did not meet the above keyword search criteria, but have homologs in *Chlamydia trachomatis* that do meet the search criteria are included herein. The *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) was analyzed using the above search criteria and a number of

35 ORFs were identified. These *Chlamydia trachomatis* ORFs were tested against the *Chlamydia pneumoniae* genome using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value  $< e^{-10}$  against a *Chlamydia trachomatis* homolog, identified using the above search criteria, was included. A

list of ORFs in the *Chlamydia pneumoniae* genome encoding putative secreted proteins is in the specification.

*Chlamydia pneumoniae*: RGD Recognition Sequence

5 Proteins that contain Arg-Gly-Asp (RGD) attachment site, together with integrins that serve as their receptor constitute a major recognition system for cell adhesion. The RGD sequence is the cell attachment site of a large number of adhesive extracellular matrix, blood, and cell surface proteins and nearly half of the known integrins recognize this sequence in their adhesion protein ligands. There are many RGD containing microbial proteins such as the penton protein of adenovirus,  
10 the coxsackie virus, the foot and mouth virus and pertactin, a 69 kDa (kilodalton) surface protein of *Bordetella pertussis*, that serve as ligands through which these microbes bind to integrins on the cell surfaces and gain entry into the cell. The following provides evidence supporting the importance of RGD in microbial adhesion:

15 a) The adenovirus penton base protein has a cell rounding activity and when penton base was expressed in *E. coli*, it caused cell rounding and cells adhered to polystyrene wells coated with the protein. Mutant analysis showed that both these properties required an RGD sequence. Virus mutants with amino acid substitutions in the RGD sequence, showed much less adherence to HeLa S3 cells, and also were delayed in virus reproduction (Bai, M., Harfe, B., and Freimuth, P. 1993. Mutations That Alter an RGD Sequence in the Adenovirus Type 2  
20 Penton Base Protein Abolish Its Cell-Rounding Activity and Delay Virus Reproduction in Flat Cells. *J. Virol.* 67:5198-5205).

25 b) It has been shown that attachment and entry of coxsackie virus A9 to GMK cells were dependent on an RGD motif in the capsid protein VP1. VP1 has also been shown to bind  $\alpha_v\beta_3$  integrin, which is a vitronectin receptor (Roivainen, M., Piirainen, L., Hovi, T., Virtanen, I., Riikonen, T., Heino, J., and Hyypia, T. 1994. Entry of Coxsackievirus A9 into Host Cells: Specific Interactions with  $\alpha_v\beta_3$  Integrin, the Vitronectin Receptor *Virology*, 203:357-65).

30 c) During the course of whooping cough, *Bordetella pertussis* interacts with alveolar macrophages and other leukocytes on the respiratory epithelium. Whole bacteria adheres by means of two proteins, filamentous hemagglutinin (FHA) and pertussis toxin. FHA interacts with two classes of molecules on macrophages, galactose containing glycoconjugates and the integrin CR3. The interaction between CR3 and FHA involves recognition of RGD sequence at the positions 1097-1099 in FHA (Relman, D., Tuomanen, E., Falkow, S., Golenbock, D. T.,  
35 Saukkonen, K., and Wright, S. D. "Recognition of a Bacterial Adhesin by an Integrin: Macrophage CR3 Binds Filamentous Hemagglutinin of *Bordetella Pertussis*." *Cell*, 61:1375-1382 (1990)).



d) Pertactin, a 69 kDa outer membrane protein of *Bordetella pertussis*, has been shown to promote attachment of Chinese hamster ovary cells (CHO). This attachment is mediated by recognition of RGD sequence in pertactin by integrins on CHO cells and can be inhibited by synthetic RGD containing peptide homologous to the one present in pertactin (Leininger, E., Roberts, M., Kenimer, J. G., Charles, I. G., Fairweather, N., Novotny, P., and Brennan, M. J. 1991. Pertactin, an Arg-Gly-Asp containing *Bordetella pertussis* surface protein that promotes adherence of mammalian cells Proc. Natl. Acad. Sci. USA, 88:345-349).

e) The RGD sequence is highly conserved in the VP1 protein of foot and mouth disease virus (FMDV). Attachment of FMDV to baby hamster kidney cells (BHK) has been shown to be mediated by VP1 protein via the RGD sequence. Antibodies against the RGD sequence of VP1 blocked attachment of virus to BHK cells (Fox, G., Parry, N. R., Barnett, P. V., McGinn, B., Rowland, D. J., and Brown, F. 1989. The Cell Attachment Site on Foot-and-Mouth Disease Virus Includes the Amino Acid Sequence RGD (Arginine-Glycine-Aspartic Acid) J. Gen. Virol., 70:625-637).

It has been demonstrated that bacterial adherence can be based on interaction of a bacterial adhesin RGD sequence with an integrin and that bacterial adhesins can have multiple binding site characteristic of eukaryotic extracellular matrix proteins. RGD recognition is one of the important mechanisms used by microbes to gain entry into eukaryotic cells.

The complete deduced protein sequence of the *Chlamydia pneumoniae* genome was searched for the presence of RGD sequence. There were a total of 54 ORFs that had one or more RGD sequences. Not all RGD containing proteins mediate cell attachment. It has been shown that RGD containing peptides that have proline immediately following the RGD sequence are inactive in cell attachment assays (Pierschbacher & Ruoslahti. 1987. Influence of stereochemistry of the sequence Arg-Gly-Asp-Xaa on binding specificity in cell adhesion. J. Biol. Chem. 262:17294-98). ORFs that had RGD, with proline as the amino acid following the RGD sequence were excluded from the list. Also, RGD sequence may not be available at the surface of the protein or may be present in a context that is not compatible with integrin binding. Since not all RGD- containing proteins are involved in cell attachment, several other criteria were used to refine the list of RGD- containing proteins. A list of ORFs in the *Chlamydia pneumoniae* genome encoding polypeptides with RGD recognition sequence(s) is in the specification.

#### Non-*Chlamydia trachomatis* ORFs

*Chlamydia pneumoniae* ORFs were compared to the ORFs in the *Chlamydia trachomatis* genome (French patent applications FR97-15041, filed 28 November 1997 and 97-16034 filed 17 December 1997) using Blastp. Any *Chlamydia pneumoniae* ORF with a Blastp P value worse than e

<sup>10</sup> (i.e.  $>e^{-10}$ ) against *Chlamydia trachomatis* ORFs are included in this section. A list of ORFs in the *Chlamydia pneumoniae* genome which are not found in *Chlamydia trachomatis* is set forth above in the specification.

#### 5                    Cell Wall Anchor Surface ORFs

Many surface proteins are anchored to the cell wall of Gram-positive bacteria via the conserved LPXTG motif (Schneewind, O., Fowler, A., and Faull, K.F. 1995. Structure of the Cell Wall Anchor of Surface Proteins in *Staphylococcus aureus*. Science 268:103-106). A search of the *Chlamydia pneumoniae* ORFs was done using the motif LPXTG. A list of ORFs in the *Chlamydia*  
 10 *pneumoniae* genome encoding polypeptides anchored to the cell wall is in the specification.

#### ATCC Deposits

Samples of *Chlamydia pneumoniae* were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the accession  
 15 number ---. Cells can be grown, harvested and purified, and DNA can be prepared as discussed above. In order to enable recovery of specific fragments of the chromosome, one can run targeted PCR reactions, whose amplification products can then be sequenced and/or cloned into any suitable vector, according to standard procedures known to those skilled in the art.

In addition, a sample of three pools of clones covering chromosomal regions of interest  
 20 were deposited with the American Type Culture Collection (ATCC), Rockville, Maryland, on November 19, 1998 and assigned the indicated accession number: —. Each pool of clones contains a series of clones. When taken together, the three pools in the sample cover a portion of the chromosome, with a redundancy of slightly more than two. The total number of clones in the sample is 196.

25                    The clones cover the following three regions of interest:

- (i) position 30,000 to 40,000 of SEQ ID No. 1, referred to as region A;
- (ii) position 501,500 to 557,000 of SEQ ID No. 1, referred to as region B; and
- (iii) position 815,000 to 830,000 of SEQ ID No. 1, referred to as region C.

Table 4 lists groups of oligonucleotides to be used to amplify each of ORFs 2-1291  
 30 according to standard procedures known to those skilled in the art. Such oligonucleotides are listed as SEQ ID Nos. 1292 to 6451. For each ORF, the following is listed: one forward primer positioned 2,000 bp upstream of the beginning of the ORF; one forward primer positioned 200 bp upstream of the beginning of the ORF; one reverse primer positioned 2,000 bp downstream at the end of ORF, which is 2,000 bp upstream of the end site of the ORF on the complementary strand;  
 35 and one reverse primer 200 bp downstream at the end of ORF, which is 200 bp upstream of the end site of the ORF on the complementary strand. The corresponding SEQ ID Nos. for the primers are listed in Table 4, where Fp is the proximal forward primer; Fd is the distal forward

primer; Bp is the proximal reverse primer; and Bd is the distal reverse primer. The positions of the 5' ends of each of these primers on the nucleotide sequence of SEQ ID No. 1 are shown in Table 5.

5 Table 6 lists oligonucleotides (SEQ ID Nos. 6452-6843) to be used to amplify the inserts of each of the 196 clones present in the pooled sample according to standard procedures well known to those of skill in the art. These primers can also be utilized to amplify the chromosomal region corresponding to the region A, B or C within which the particular insert lies. Their positions are indicated in Table 7.

10 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

15 All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

TABLE 1							Score	I%
ORF	Begin	End	Homology	ID	Species			
ORF2	42	794	triosephosphate isomerase	L27492	<i>Thermotoga maritima</i>		567	54
ORF3	1258	1614	putative					
ORF4	1807	2418	polypeptide deformylase	D90906	<i>Synechocystis</i> sp.		316	40
ORF5	3393	2491	hypothetical protein	Z75208	<i>Bacillus subtilis</i>		338	42
ORF6	3639	4067	unknown	U87792	<i>Bacillus subtilis</i>		117	38
ORF7	5649	4270	putative					
ORF8	7463	6012	putative					
ORF9	8051	8962	putative					
ORF10	9129	9959	putative					
ORF11	10687	10361	putative					
ORF12	10927	11232	putative					
ORF13	11246	12727	amidase	U49269	<i>Moraxella catarrhalis</i>		1108	42
ORF14	12691	14190	PET112	D90913	<i>Synechocystis</i> sp.		1044	46
ORF15	14484	17249	POMP91A	U65942	<i>Chlamydia psittaci</i>		1074	43
ORF16	16039	15770	putative					
ORF17	17845	20853	putative					
ORF18	21137	22042	putative					
ORF19	22046	23476	putative					
ORF20	23681	26110	putative					
ORF21	26109	25861	putative					
ORF22	26241	26978	putative					
ORF23	26960	27754	putative					
ORF24	27747	28577	putative					
ORF25	28887	29492	POMP91A	U65942	<i>Chlamydia psittaci</i>		180	39
ORF26	29432	30028	POMP91A	U65942	<i>Chlamydia psittaci</i>		361	51
ORF27	30024	31472	POMP91A	U65942	<i>Chlamydia psittaci</i>		879	54
ORF28	31758	32288	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		144	43
ORF29	32201	33991	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		1126	48
ORF30	33852	34541	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		589	62
ORF31	34783	36063	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>		469	46
ORF32	36009	37529	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		1338	51
ORF33	37881	39362	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>		671	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF34	39418	39161	putative				
ORF35	39366	40715	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	904	47
ORF36	43076	41094	putative				
ORF37	43800	43066	putative				
ORF38	44828	43785	putative				
ORF39	45340	44753	homologous to unidentified <i>E. coli</i> protein o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES HAEIN SW: P44808	M96343 AE000184	<i>Bacillus subtilis</i> <i>Escherichia coli</i>	136 269	44 43
ORF40	45752	45372					
ORF41	46996	45701	ABC transporter, ATP-binding protein (yheS)	AE000596	<i>Helicobacter pylori</i>	878	39
ORF42	47961	47569	putative				
ORF43	48960	48040	hypothetical protein	D64001	<i>Synechocystis sp.</i>	404	37
ORF44	51452	50133	Lon protease-like protein	X74215	<i>Homo sapiens</i>	1232	54
ORF45	52606	51335	unknown	Z54285	<i>Schizosaccharomyces pombe</i>	781	47
ORF46	53684	53319	putative				
ORF47	54195	53746	putative				
ORF48	55278	56453	heat-shock protein	U15010	<i>Legionella pneumophila</i>	975	45
ORF49	56493	57266	branched chain alpha-keto acid dehydrogenase E1-alpha	M97391	<i>Bacillus subtilis</i>	329	36
ORF50	57297	58526	branched chain alpha-keto acid dehydrogenase E1-beta	M97391	<i>Bacillus subtilis</i>	707	50
ORF51	59851	58565	putative				
ORF52	61495	59924	ComE	D90903	<i>Synechocystis sp.</i>	134	55
ORF53	61324	62151	putative				
ORF54	62132	62470	Hpr protein	X12832	<i>Bacillus subtilis</i>	136	36
ORF55	62474	63733	enzyme I (ptsI)	U32844	<i>Haemophilus influenzae</i>	381	35
ORF56	63881	64186	f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A ECOLI SW: P32670	AE000326	<i>Escherichia coli</i>	123	34
ORF57	64611	64318	ORF107	X17014	<i>Bacillus subtilis</i>	128	33
ORF58	65485	64673	putative				
ORF59	65999	65301	dnaX-like ORF put. DNA polymerase III	X06803	<i>Bacillus subtilis</i>	596	52

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF60	66244	67281	putative				
ORF61	67265	67699	putative				
ORF62	67703	68539	putative				
ORF63	68805	70736	putative				
ORF64	69172	68831	putative				
ORF65	70642	71142	putative				
ORF66	71325	72029	putative				
ORF67	72060	73637	putative	D84432	<i>Bacillus subtilis</i>	542	44
ORF68	74061	76175	YqfF	D28503	<i>Clostridium josui</i>	262	42
ORF69	78351	77680	porphobilinogen deaminase	D90914	<i>Synechocystis</i> sp.	736	52
ORF70	79356	78355	sms protein	AE000579	<i>Helicobacter pylori</i>	98	33
ORF71	79983	79693	ribonuclease III (mc)	D64116	<i>Bacillus subtilis</i>	268	44
ORF72	80441	79938	ORF3				
ORF73	80475	80969	putative				
ORF74	81296	83080	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	893	38
ORF75	83291	83932	manganese superoxide dismutase	X77021	<i>Caenorhabditis elegans</i>	622	58
ORF76	84005	84769	acetyl-CoA carboxylase beta subunit (accD)	AE000604	<i>Helicobacter pylori</i>	602	50
ORF77	84975	85244	deoxyuridinetriphosphatase (dut)	U32776	<i>Haemophilus influenzae</i>	110	41
ORF78	85123	85425	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	AE000596	<i>Helicobacter pylori</i>	265	68
ORF79	85397	85903	ORF2	L26916	<i>Pseudomonas aeruginosa</i>	173	34
ORF80	85909	86583	enzyme IIANtr	U18997	<i>Escherichia coli</i>	170	42
ORF81	86626	88065	putative				
ORF82	89257	91026	putative				
ORF83	91291	93030	putative				
ORF84	93295	94086	putative				
ORF85	95285	94707	putative				
ORF86	95667	96557	putative				
ORF87	96317	97456	putative				
ORF88	98435	97968	putative				
ORF89	99460	98426	putative				
ORF90	100144	101325	elongation factor Tu	L22216	<i>Chlamydia trachomatis</i>	1917	95

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF91	101457	101720	putative				
ORF92	101704	102273	transcription factor	L10348	<i>Thermus aquaticus thermophilus</i>	376	49
ORF93	102356	102805	ribosomal protein L11	D13303	<i>Bacillus subtilis</i>	458	63
ORF94	102835	103530	ribosomal protein L1	Z11839	<i>Thermotoga maritima</i>	642	51
ORF95	103549	104058	ribosomal protein L10	M89911	<i>Streptomyces antibioticus</i>	82	31
ORF96	104096	104491	rpl12 (AA 1-128)	X53178	<i>Synechocystis PCC6803</i>	325	47
ORF97	104601	108386	DNA-directed RNA polymerase beta chain	X64172	<i>Staphylococcus aureus</i>	2740	52
ORF98	108401	112054	rpoC	V00339	<i>Escherichia coli</i>	2947	54
ORF99	112033	112590	acetylornithine deacetylase (EC 5.1.1.16)	M22622	<i>Leptospira biflexa</i>	514	62
ORF100	112672	113682	transaldolase	L19437	<i>Homo sapiens</i>	755	49
ORF101	113726	114121	putative				
ORF102	114711	114136	putative				
ORF103	115267	115755	putative				
ORF104	115911	116543	putative				
ORF105	116736	118055	ATPase alpha-subunit	X63855	<i>Thermus aquaticus thermophilus</i>	934	50
ORF106	117968	118522	adenosine triphosphatase A subunit	D50528	<i>Acetabularia acetabulum</i>	147	32
ORF107	118530	119843	V-ATPase B subunit	U96487	<i>Desulfurococcus sp. SY</i>	751	48
ORF108	119816	120457	putative				
ORF109	120451	122430	v-type Na-ATPase	X76913	<i>Enterococcus hirae</i>	264	35
ORF110	122504	122950	ATP synthase, subunit K	U67478	<i>Methanococcus jannaschii</i>	184	31
ORF111	123528	126347	valyl-tRNA synthetase	X05891	<i>Escherichia coli</i>	1679	49
ORF112	126332	129166	protein kinase-like protein	U19250	<i>Streptomyces coelicolor</i>	427	37
ORF113	134690	129213	UvrA	D49911	<i>Thermus thermophilus</i>	3107	41
ORF114	134925	136382	pyruvate kinase	U83196	<i>Chlamydia trachomatis</i>	1748	71
ORF115	137870	136482	HtrB protein	X61000	<i>Escherichia coli</i>	147	38
ORF116	137899	138240	putative				
ORF117	138239	137928	putative				
ORF118	139558	138257	putative				
ORF119	140352	139516	YbbP	AB002150	<i>Bacillus subtilis</i>	231	46
ORF120	140498	141841	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	538	50
ORF121	141855	142658	cyanide insensitive terminal oxidase	Y10528	<i>Pseudomonas aeruginosa</i>	310	40
ORF122	144258	143050	putative				
ORF123	145258	144494	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF124	145454	146749	product similar to E. coli PhoH protein	Z97025	<i>Bacillus subtilis</i>	836	47
ORF125	147318	146767	putative				
ORF126	148261	147677	putative				
ORF127	149029	152157	isoleucyl-tRNA synthetase	U04953	<i>Homo sapiens</i>	2361	52
ORF128	154108	152201	leader peptidase I	D90904	<i>Synechocystis sp.</i>	225	47
ORF129	155135	154308	putative				
ORF130	155141	155467	YtiA	AF008220	<i>Bacillus subtilis</i>	201	43
ORF131	155703	156779	orf 361; ranslated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of <i>Salmonella typhimurium</i>	X78969	<i>Coxiella burnetii</i>	863	59
ORF132	156748	157635	product similar to E.coli PRFA2 protein	Z49782	<i>Bacillus subtilis</i>	144	37
ORF133	157653	158996	Ffh	U82109	<i>Thermus aquaticus</i>	797	45
ORF134	159363	159986	tRNA (guanine-N1)-methyltransferase (trmD)	U32705	<i>Haemophilus influenzae</i>	545	49
ORF135	159880	160446	putative				
ORF136	160477	160839	ribosomal protein L19	X72627	<i>Synechocystis sp.</i>	319	50
ORF137	160898	161539	putative protein highly homologous to E. coli RNase HII.	D32253	<i>Magnetospirillum sp.</i>	427	49
ORF138	161527	162153	5'guanylate kinase (gmk)	U32848	<i>Haemophilus influenzae</i>	385	43
ORF139	162144	162443	putative				
ORF140	162437	164098	methionyl-tRNA synthetase	AB004537	<i>Schizosaccharomyces pombe</i>	861	54
ORF141	165451	164228	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	432	32
ORF142	166349	165411	putative				
ORF143	166949	168442	putative				
ORF144	169416	171029	putative				
ORF145	170857	171459	putative				
ORF146	172652	173428	putative biotin-protein ligase	Z97992	<i>Schizosaccharomyces pombe</i>	292	44
ORF147	174626	173439	putative				
ORF148	174816	175613	putative				
ORF149	175598	175954	putative				
ORF150	175958	176935	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF151	17708	176938	orf 3' of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Peptide Partial, 98 aa]	S40172	<i>Chlamydia psittaci</i>	376	74
ORF152	177128	177376	putative				
ORF153	179472	177841	putative	M69217	<i>Chlamydia pneumoniae</i>	2678	100
ORF154	179822	179517	putative	M69217	<i>Chlamydia pneumoniae</i>	498	99
ORF155	181793	179943	Pz-peptidase	D88209	<i>Bacillus licheniformis</i>	1088	38
ORF156	182628	181876	o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7 CHRVI SW: P45371	AE000174	<i>Escherichia coli</i>	401	42
ORF157	184420	183074	glutamate-1-semialdehyde 2,1- aminomutase	X53696	<i>Escherichia coli</i>	823	41
ORF158	184988	184467	ORF o211	U28377	<i>Escherichia coli</i>	87	54
ORF159	185483	185112	hypothetical protein	D90906	<i>Synechocystis sp.</i>	91	33
ORF160	185902	185483	ribose 5-phosphate isomerase	U28377	<i>Escherichia coli</i>	111	41
ORF161	186174	185839	ribose 5-phosphate isomerase A (SP:P27252)	U32729	<i>Haemophilus influenzae</i>	190	46
ORF162	187720	186587	hypothetical	D83026	<i>Bacillus subtilis</i>	536	42
ORF163	188318	190933	ATP-dependent protease binding subunit	M29364	<i>Escherichia coli</i>	2010	53
ORF164	191090	191635	putative				
ORF165	191547	192743	putative				
ORF166	192969	193469	putative				
ORF167	194044	193610	putative				
ORF168	194196	195809	unknown	Z84395	<i>Mycobacterium tuberculosis</i>	242	52
ORF169	196088	198073	DNA ligase (EC 6.5.1.2)	M24278	<i>Escherichia coli</i>	1317	46
ORF170	198132	199454	putative				
ORF171	199351	202818	putative				
ORF172	204552	202999	PcpB	U60175	<i>Sphingomonas chlorophenolica</i>	80	41
ORF173	205648	204692	putative				
ORF174	205807	207327	leucine tRNA synthetase	AF008220	<i>Bacillus subtilis</i>	1595	57
ORF175	207182	207775	leucyl-tRNA synthetase	X06331	<i>Escherichia coli</i>	363	51
ORF176	207779	208267	transfer RNA-Leu synthetase	M88581	<i>Bacillus subtilis</i>	285	43
ORF177	208267	209577	KDO transferase	Z31593	<i>Chlamydia pneumoniae</i>	2262	100

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF178	211807	211271	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	105	38
ORF179	212188	211844	putative				
ORF180	214079	212448	pyrophosphate-dependent phosphofructokinase beta subunit	Z32850	<i>Ricinus communis</i>	1003	45
ORF181	214907	214083	CinI	U44893	<i>Butyrivibrio fibrisolvens</i>	111	41
ORF182	216154	215429	putative				
ORF183	216115	216678	putative				
ORF184	216728	217282	putative				
ORF185	217267	217866	putative				
ORF186	218593	218261	putative				
ORF187	219821	218994	putative				
ORF188	221382	220309	putative				
ORF189	222719	221433	GMP synthetase	M10101	<i>Escherichia coli</i>	1151	48
ORF190	223521	222724	IMP dehydrogenase	X66859	<i>Acinetobacter calcoaceticus</i>	778	58
ORF191	224499	225008	putative				
ORF192	225140	225559	putative				
ORF193	225555	226802	putative				
ORF194	227800	226892	putative				
ORF195	228335	228072	putative				
ORF196	229251	228643	putative				
ORF197	230983	229622	YqhX	D84432	<i>Bacillus subtilis</i>	1386	56
ORF198	231483	230983	acetyl-CoA carboxylase biotin carboxyl carrier protein	U38804	<i>Porphyra purpurea</i>	199	52
ORF199	232063	231509	elongation factor P	D64001	<i>Synechocystis sp.</i>	282	32
ORF200	232739	232053	pentose-5-phosphate-3-epimerase	D90911	<i>Synechocystis sp.</i>	463	43
ORF201	233166	234356	putative				
ORF202	233518	233165	putative				
ORF203	234536	235186	ORF2	L35036	<i>Chlamydia psittaci</i>	570	60
ORF204	235379	236689	putative				
ORF205	236680	237618	putative				
ORF206	237521	238345	putative				
ORF207	238281	238973	putative				
ORF208	238871	240115	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF209	240191	241564	putative				
ORF210	242281	241604	YqiZ	D84432	<i>Bacillus subtilis</i>	379	39
ORF211	242933	242274	f222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA BACSU SW: P42399	AE000284	<i>Escherichia coli</i>	382	45
ORF212	243416	242976	arginine repressor protein (argR)	U32800	<i>Haemophilus influenzae</i>	229	46
ORF213	243500	244531	sialoglycoprotease	U15958	<i>Pasteurella haemolytica</i>	565	53
ORF214	244480	246021	oligopeptide permease homolog AII	AF000366	<i>Borrelia burgdorferi</i>	457	34
ORF215	246330	247811	OppAIV	AF000948	<i>Borrelia burgdorferi</i>	453	35
ORF216	247831	249174	OppA gene product	X56347	<i>Bacillus subtilis</i>	255	37
ORF217	249437	251038	dcIAE	X56678	<i>Bacillus subtilis</i>	469	37
ORF218	251325	252212	OppB gene product	X56347	<i>Bacillus subtilis</i>	652	42
ORF219	253156	254007	oligopeptidase	X89237	<i>Streptococcus pyogenes</i>	574	48
ORF220	253974	254852	ATP binding protein	L18760	<i>Lactococcus lactis</i>	433	40
ORF221	255258	256094	KDO-transferase	X80061	<i>Chlamydia psittaci</i>	106	46
ORF222	256640	257455	putative				
ORF223	257502	258239	2-OXOGLUTARAT	A47930	<i>Spinacia oleracea</i>	636	52
ORF224	257869	257501	putative				
ORF225	259248	260897	pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit	M55191	<i>Solanum tuberosum</i>	1055	44
ORF226	262753	261788	putative				
ORF227	263059	262757	putative				
ORF228	264375	263182	putative				
ORF229	265985	264747	putative				
ORF230	266637	266059	putative				
ORF231	267338	266538	putative				
ORF232	267922	267473	putative				
ORF233	269647	270771	tRNA guanine transglycosylase	L33777	<i>Zymomonas mobilis</i>	628	44
ORF234	272777	273145	ORF 4	D00624	<i>Bacteriophage chpl</i>	100	41
ORF235	273253	273636	putative				
ORF236	273705	273977	putative				
ORF237	276016	275717	putative				
ORF238	276439	276020	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF239	276792	277253	putative				
ORF240	277318	277599	putative				
ORF241	278578	277877	putative				
ORF242	279258	278554	FbpC	U33937	<i>Neisseria gonorrhoeae</i>	312	39
ORF243	280435	279533	putative				
ORF244	281547	280849	putative				
ORF245	281696	282325	CMP-2-keto-3-deoxyoctulosonic acid synthetase	U15192	<i>Chlamydia trachomatis</i>	637	63
ORF246	282459	284069	CTP synthetase	U15192	<i>Chlamydia trachomatis</i>	2000	68
ORF247	284056	284517	ORF3	U15192	<i>Chlamydia trachomatis</i>	453	65
ORF248	284606	285775	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	1263	77
ORF249	285592	285987	glucose 6-phosphate dehydrogenase	U83195	<i>Chlamydia trachomatis</i>	519	79
ORF250	286179	286976	glucose-6-phosphate dehydrogenase isozyme	D88189	<i>Actinobacillus actinomycetemcomitans</i>	216	40
ORF251	287583	287002	putative				
ORF252	287951	287451	putative				
ORF253	288499	288816	putative				
ORF254	289674	288505	putative				
ORF255	288839	289213	putative				
ORF256	289970	290254	putative				
ORF257	291931	292803	gamma-D-glutamyl-L-diamino acid endopeptidase II	X64809	<i>Bacillus sphaericus</i>	95	39
ORF258	293258	292755	Scs9	U43429	<i>Streptomyces coelicolor</i>	233	45
ORF259	293718	293272	ribosomal protein L13 (rpL13)	U32823	<i>Haemophilus influenzae</i>	364	47
ORF260	294630	293953	glutamine transport ATP-binding protein Q	U67524	<i>Methanococcus jannaschii</i>	387	46
ORF261	296153	294636	putative				
ORF262	294817	295068	putative				
ORF263	296354	297862	conserved hypothetical protein	AE000586	<i>Helicobacter pylori</i>	641	46
ORF264	298415	297879	putative				
ORF265	298777	298253	putative				
ORF266	299572	298781	putative				
ORF267	300487	299633	putative				
ORF268	301586	300702	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF269	302440	301571	putative				
ORF270	302838	302437	putative				
ORF271	303335	302745	putative				
ORF272	304394	303852	putative				
ORF273	304606	305223	f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyu1 of D21139	AE000232	<i>Escherichia coli</i>	250	38
ORF274	305394	306236	survival protein surE	U81296	<i>Sinorhizobium meliloti</i>	156	42
ORF275	306501	307439	YqfU	D84432	<i>Bacillus subtilis</i>	547	42
ORF276	308033	307458	3-octaprenyl-4-hydroxybenzoate carboxylase	U61168	<i>Bacillus firmus</i>	403	42
ORF277	308924	308037	4-hydroxybenzoate octaprenyltransferase	U61168	<i>Bacillus firmus</i>	152	40
ORF278	309485	310180	putative				
ORF279	310426	311214	putative				
ORF280	311597	311253	putative				
ORF281	312772	311780	putative				
ORF282	313425	312772	putative				
ORF283	313646	313377	putative				
ORF284	313937	314665	lysophospholipase homolog	AF006678	<i>Schistosoma mansoni</i>	141	44
ORF285	315576	314755	dnaZX	X17014	<i>Bacillus subtilis</i>	154	39
ORF286	316157	315531	unknown	D26185	<i>Bacillus subtilis</i>	284	31
ORF287	318657	316156	DNA gyrase	L47978	<i>Aeromonas salmonicida</i>	1785	48
ORF288	321042	318676	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	1838	59
ORF289	321445	321098	putative				
ORF290	322309	321710	putative				
ORF291	323190	322366	outer membrane protein	AE000654	<i>Helicobacter pylori</i>	376	43
ORF292	323843	323181	hypothetical	U70214	<i>Escherichia coli</i>	356	37
ORF293	324878	323856	ATP-binding protein (abc)	U32744	<i>Haemophilus influenzae</i>	545	44
ORF294	325340	326410	f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLJC SALMU SW: P06177	AE000299	<i>Escherichia coli</i>	1194	62
ORF295	326433	327836	Xas A	AE000246	<i>Escherichia coli</i>	479	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF296	328465	327839	putative				
ORF297	329360	328857	putative				
ORF298	330907	329357	putative				
ORF299	332455	330956	MgtE	U18744	<i>Bacillus firmus</i>	203	36
ORF300	334536	332395	putative				
ORF301	336091	334877	putative				
ORF302	336103	337302	putative				
ORF303	338129	338830	putative				
ORF304	338965	339501	putative				
ORF305	339508	340143	putative				
ORF306	340247	342967	putative				
ORF307	343385	343810	cAMP-dependent protein kinase type I regulatory subunit	U75932	<i>Rattus norvegicus</i>	102	37
ORF308	344171	343935	acyl carrier protein (acpP)	AE000570	<i>Helicobacter pylori</i>	198	55
ORF309	345082	344330	3-ketoacyl-ACP reductase	U39441	<i>Vibrio harveyi</i>	598	48
ORF310	346005	345082	malonyl-CoA:Acyl carrier protein transacylase	U59433	<i>Bacillus subtilis</i>	538	45
ORF311	346784	346437	beta-ketoacyl-acyl carrier protein synthase III (fabH)	AE000540	<i>Helicobacter pylori</i>	273	50
ORF312	347029	346715	beta-ketoacyl-acyl carrier protein synthase III	M77744	<i>Escherichia coli</i>	265	63
ORF313	347034	347723	recombination protein	D90916	<i>Synechocystis sp.</i>	363	42
ORF314	348075	350459	putative				
ORF315	350598	351071	putative				
ORF316	351075	352175	rifampicin resistance protein	L22690	<i>Rickettsia rickettsii</i>	495	46
ORF317	353291	352230	putative				
ORF318	353442	354467	pyruvate dehydrogenase E1 component, alpha subunit	D90915	<i>Synechocystis sp.</i>	571	44
ORF319	354451	354933	pyruvate dehydrogenase E1 beta subunit	U09137	<i>Arabidopsis thaliana</i>	495	59
ORF320	355000	355449	pyruvate dehydrogenase E1 component, beta subunit	U38804	<i>Porphyra purpurea</i>	336	47
ORF321	355448	356743	F23B12.5	Z77659	<i>Caenorhabditis elegans</i>	759	46
ORF322	355953	355642	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF323	359310	356827	glycogen phosphorylase B	U47025	<i>Homo sapiens</i>	2193	57
ORF324	359120	359377	putative				
ORF325	359525	359908	putative				
ORF326	361290	359947	DnaA	D89066	<i>Staphylococcus aureus</i>	375	46
ORF327	363785	361362	hypothetical	U32781	<i>Haemophilus influenzae</i>	394	44
ORF328	364496	363888	putative				
ORF329	364832	365290	putative				
ORF330	365304	365669	dpi	M76470	<i>Escherichia coli</i>	160	45
ORF331	366599	365667	NADPH thioredoxin reductase	AC002329	<i>Arabidopsis thaliana</i>	975	60
ORF332	367291	369030	ribosomal protein S1 (rpS1)	U32801	<i>Haemophilus influenzae</i>	1209	41
ORF333	369134	369808	NusA	U74759	<i>Chlamydia trachomatis</i>	995	87
ORF334	369917	370438	NusA	U74759	<i>Chlamydia trachomatis</i>	760	87
ORF335	370365	372647		U74759	<i>Chlamydia trachomatis</i>	2173	61
ORF336	372557	373066	initiation factor IF2-beta (infB; gtg start codon)	X00513	<i>Escherichia coli</i>	333	39
ORF337	373020	373442	ORF6 gene product	Z18631	<i>Bacillus subtilis</i>	192	34
ORF338	373467	374195	tRNA pseudouridine 55 synthase	D90917	<i>Synechocystis sp.</i>	358	47
ORF339	374176	375099	hypothetical 34.6 kD protein in rpsT-ileS intergenic region	AE000113	<i>Escherichia coli</i>	395	39
ORF340	375676	375083	hypothetical GTP-binding protein in pth 3' region	AE000219	<i>Escherichia coli</i>	507	53
ORF341	376173	375634	hypothetical	U32723	<i>Haemophilus influenzae</i>	480	59
ORF342	376564	377643	YscU	U08019	<i>Yersinia enterocolitica</i>	538	37
ORF343	377956	379773	IcrD gene product	X67771	<i>Yersinia enterocolitica</i>	1302	47
ORF344	379781	380425	putative				
ORF345	380281	381000	putative				
ORF346	381008	381460	putative				
ORF347	381460	383037	4-alpha-glucanotransferase	L37874	<i>Clostridium butyricum</i>	302	38
ORF348	383257	383523	ribosomal protein L28 (rpL28)	U32776	<i>Haemophilus influenzae</i>	175	55
ORF349	383553	385304	hypothetical protein	D90901	<i>Synechocystis sp.</i>	565	38
ORF350	385397	386458	comE ORF1	D64002	<i>Synechocystis sp.</i>	187	10
ORF351	387242	386514	putative				
ORF352	388764	387013	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF353	390120	390932	methylenetetrahydrofolate dehydrogenase	D64000	<i>Synechocystis</i> sp.	588	53
ORF354	390919	391818	f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943	AE000310	<i>Escherichia coli</i>	186	39
ORF355	392379	391885	small protein	D90914	<i>Synechocystis</i> sp.	387	46
ORF356	392582	392986	putative				
ORF357	392776	393684	putative				
ORF358	394151	394804	RecF protein	D90907	<i>Synechocystis</i> sp.	232	34
ORF359	394928	395308	putative				
ORF360	395259	395990	putative				
ORF361	397815	395953	hypothetical	U32773	<i>Haemophilus influenzae</i>	391	36
ORF362	398850	397831	H. influenzae predicted coding region HI0807	U32763	<i>Haemophilus influenzae</i>	580	39
ORF363	400085	399099	putative				
ORF364	401245	400073	YtgC	AF008220	<i>Bacillus subtilis</i>	244	30
ORF365	401474	401136	putative				
ORF366	402199	401423	unknown	U52850	<i>Erysipelothrix rhusiopathiae</i>	534	46
ORF367	403193	402186	putative				
ORF368	403650	404165	putative				
ORF369	404343	405914	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	1280	55
ORF370	405984	407327	putative				
ORF371	407712	408806	putative				
ORF372	410439	409075	putative				
ORF373	411826	410954	putative				
ORF374	412482	414302	lepA gene product	X91655	<i>Bacillus subtilis</i>	1827	59
ORF375	415402	414407	6-phosphogluconate dehydrogenase, decarboxylating (gnd)	U32737	<i>Haemophilus influenzae</i>	687	51
ORF376	415848	415237	6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa]	S67873	<i>Ceratitis capitata</i>	695	64
ORF377	417131	415866	tyrosyl-tRNA synthetase (tyrS)	J01719	<i>Escherichia coli</i>	821	45
ORF378	417258	417566	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF379	418326	417454	whiG-Stv gene product	X68709	<i>Streptovercillium griseocarneum</i>	464	41
ORF380	420057	418426	FLHA gene product	X63698	<i>Bacillus subtilis</i>	455	49
ORF381	420448	420720	ferredoxin IV	M59855	<i>Rhodobacter capsulatus</i>	174	63
ORF382	420980	421552	putative				
ORF383	421556	422029	putative				
ORF384	422461	422925	putative				
ORF385	423562	424320	putative				
ORF386	424250	424591	putative				
ORF387	424830	426047	putative				
ORF388	426240	427397	putative				
ORF389	428841	430703	GcpE	D90908	<i>Synechocystis sp.</i>	877	47
ORF390	430694	431446	YfiH	U50134	<i>Escherichia coli</i>	136	35
ORF391	431597	432100	putative				
ORF392	432165	432779	putative				
ORF393	433272	432832	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	475	64
ORF394	433925	433227	dihydrolipoamide succinyltransferase (sucB)	U32839	<i>Haemophilus influenzae</i>	332	45
ORF395	436678	433934	alpha-ketoglutarate dehydrogenase	U41762	<i>Rhodobacter capsulatus</i>	1530	44
ORF396	437176	438357	oxygen-independent coproporphyrinogen III oxidase (hemN)	AE000628	<i>Helicobacter pylori</i>	442	42
ORF397	440317	438518	putative				
ORF398	440001	440345	putative				
ORF399	441233	440517	ORF f286	U18997	<i>Escherichia coli</i>	168	45
ORF400	440719	441012	putative				
ORF401	442192	441230	putative				
ORF402	442888	442343	putative				
ORF403	442371	442961	putative				
ORF404	443578	443003	[karp] gene products	M86605	<i>Chlamydia trachomatis</i>	505	78
ORF405	444500	443526	aminopeptidase	D17450	<i>Mycoplasma salivarium</i>	273	39
ORF406	444842	444528	putative				
ORF407	445009	444743	putative	L39923	<i>Mycobacterium leprae</i>	133	33

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF408	445718	445182	putative				
ORF409	445807	447804	Sulp	U18908	<i>Zea mays</i>	1307	52
ORF410	448738	447803	putative				
ORF411	449628	448618	RuvB protein	U38840	<i>Thermotoga maritima</i>	845	53
ORF412	450298	450867	deoxycytidine triphosphate deaminase (dcd)	AE000554	<i>Helicobacter pylori</i>	573	58
ORF413	450713	451207	putative				
ORF414	451211	452452	hemolysin	D90914	<i>Synechocystis sp.</i>	227	39
ORF415	452448	453659	similar to [SwissProt Accession Number P37908]	D90888	<i>Escherichia coli</i>	96	33
ORF416	454843	453725	NifS gene product	L34879	<i>Anabaena azollae</i>	533	38
ORF417	455608	454865	hypothetical protein	D90908	<i>Synechocystis sp.</i>	371	36
ORF418	456243	457007	putative				
ORF419	457016	457708	putative				
ORF420	458368	457979	unknown	D26185	<i>Bacillus subtilis</i>	152	36
ORF421	459496	458372	mutY homolog	U63329	<i>Homo sapiens</i>	466	46
ORF422	459493	460194	hypothetical protein	D90914	<i>Synechocystis sp.</i>	98	38
ORF423	461446	460355	putative				
ORF424	462298	461450	putative				
ORF425	462444	463349	enoyl-ACP reductase	Y13861	<i>Nicotiana tabacum</i>	1008	69
ORF426	464241	463342	putative				
ORF427	464574	465065	putative				
ORF428	465129	465611	putative				
ORF429	465571	466317	putative				
ORF430	466317	467093	H. pylori predicted coding region HP0152	AE000536	<i>Helicobacter pylori</i>	246	36
ORF431	466999	467502	putative				
ORF432	469691	467715	unidentified transporter-ATP binding	Z82044	<i>Bacillus subtilis</i>	496	45
ORF433	470691	469660	acetyl-CoA carboxylase subunit	AF008220	<i>Bacillus subtilis</i>	781	52
ORF434	472010	470709	putative				
ORF435	471545	471799	putative				
ORF436	472359	472045	putative				
ORF437	473523	472732	orf1	X75413	<i>Escherichia coli</i>	313	42
ORF438	474889	473441	murE gene product	Z15056	<i>Bacillus subtilis</i>	679	37
ORF439	477323	475365	penicillin-binding protein 2	X59630	<i>Neisseria meningitidis</i>	451	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF440	478496	477597	hypothetical protein	D90906	<i>Synechocystis sp.</i>	534	52
ORF441	478722	479273	putative				
ORF442	479277	479705	putative				
ORF443	480050	481450	chromosomal replication initiator protein	D90909	<i>Synechocystis sp.</i>	793	40
			DnaA				
ORF444	481469	482053	OrfH	U35673	<i>Borrelia burgdorferi</i>	157	37
ORF445	482600	482025	putative				
ORF446	482654	484204	NADH:ubiquinone oxidoreductase subunit	Z37111	<i>Vibrio alginolyticus</i>	801	49
			B				
ORF447	484211	485170	NADH:ubiquinone oxidoreductase	U32702	<i>Haemophilus influenzae</i>	258	48
			(GP:Z37111 4)				
ORF448	485170	485838	NADH:ubiquinone oxidoreductase	Z37111	<i>Vibrio alginolyticus</i>	543	55
ORF449	485813	486580	unidentified protein of Na <sup>+</sup> -translocating	D49364	<i>Vibrio alginolyticus</i>	488	48
			NADH-quinone reductase				
ORF450	486976	486638	putative				
ORF451	489071	487764	putative				
ORF452	489341	489090	putative				
ORF453	489958	489152	putative				
ORF454	490549	489962	putative				
ORF455	491163	490522	putative				
ORF456	491396	491112	putative				
ORF457	492121	491390	putative				
ORF458	492304	494838	ClpC adenosine triphosphatase	U02604	<i>Bacillus subtilis</i>	2370	46
ORF459	495943	494822	hypothetical protein in purB 5' region	AE000213	<i>Escherichia coli</i>	927	53
ORF460	496011	496565	putative				
ORF461	496569	497228	putative				
ORF462	497358	497834	putative				
ORF463	497770	498327	putative				
ORF464	499209	499589	putative				
ORF465	499520	499792	putative				
ORF466	500774	504169	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1215	45
ORF467	504139	504600	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	319	47
ORF468	504865	506877	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	992	42

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF469	506790	507671	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	739	46
ORF470	507718	510507	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1813	42
ORF471	508325	507912	putative				
ORF472	510660	513440	POMP90A precursor	U65942	<i>Chlamydia psittaci</i>	1830	46
ORF473	514965	513787	hypothetical	D83026	<i>Bacillus subtilis</i>	482	48
ORF474	517347	515419	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1554	51
ORF475	517058	517363	putative				
ORF476	517798	517277	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	222	41
ORF477	518200	517847	POMP91B precursor	U65943	<i>Chlamydia psittaci</i>	162	42
ORF478	518300	521146	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	1900	45
ORF479	521392	522948	POMP91A	U65942	<i>Chlamydia psittaci</i>	490	39
ORF480	523244	524809	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	507	35
ORF481	524379	524125	putative				
ORF482	524649	526238	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	969	41
ORF483	526265	527104	putative				
ORF484	526947	526702	putative				
ORF485	526975	528450	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	197	48
ORF486	528408	529199	putative outer membrane protein	U72499	<i>Chlamydia psittaci</i>	154	37
ORF487	530612	529542	putative				
ORF488	531656	530616	putative				
ORF489	533974	532067	putative				
ORF490	536432	534324	putative				
ORF491	537150	536707	putative				
ORF492	537928	537080	putative				
ORF493	538438	537932	putative				
ORF494	538737	538333	putative				
ORF495	539594	539127	putative				
ORF496	541215	539590	putative				
ORF497	542571	541282	putative				
ORF498	543014	542457	putative				
ORF499	543369	542962	putative				
ORF500	543809	546628	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	506	89
ORF501	546619	549525	POMP91A	U65942	<i>Chlamydia psittaci</i>	128	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF502	547293	546994	putative				
ORF503	549699	550523	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	96	32
ORF504	550490	551551	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	223	33
ORF505	551448	552623	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	139	46
ORF506	552652	555117	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	487	48
ORF507	555029	555493	putative				
ORF508	558006	555673	putative				
ORF509	559694	558162	putative				
ORF510	558208	558573	putative				
ORF511	561692	559899	putative				
ORF512	561412	561708	putative				
ORF513	563942	561777	1,4-alpha-glucan branching enzyme	X73903	<i>Streptomyces coelicolor</i>	1743	45
ORF514	564969	563950	putative				
ORF515	566204	564936	Yqe V	D84432	<i>Bacillus subtilis</i>	639	38
ORF516	567717	566302	putative GTPase required for high frequency lysogenization by bacteriophage lambda	U00005	<i>Escherichia coli</i>	686	41
ORF517	568526	567708	putative				
ORF518	569467	568742	putative				
ORF519	571065	569431	putative				
ORF520	571828	571118	arginine-binding periplasmic protein 1 precursor	AE000188	<i>Escherichia coli</i>	197	45
ORF521	572202	573308	putative				
ORF522	573146	575056	putative				
ORF523	575023	575916	carboxysome formation protein	D90901	<i>Synechocystis sp.</i>	557	59
ORF524	577891	576497	putative				
ORF525	578914	578204	putative				
ORF526	579924	578857	putative				
ORF527	580187	579858	protein kinase C inhibitor	D90906	<i>Synechocystis sp.</i>	260	49
ORF528	580017	580406	putative				
ORF529	581086	580187	Yer156cp	U18917	<i>Saccharomyces cerevisiae</i>	176	34
ORF530	581367	581828	putative				
ORF531	581678	582367	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF532	582361	583428	putative				
ORF533	584690	583431	putative				
ORF534	585237	584950	putative				
ORF535	585626	586888	hypothetical protein	D64004	<i>Synechocystis</i> sp.	805	45
ORF536	586846	587907	putative				
ORF537	589049	588180	putative				
ORF538	590500	589301	putative				
ORF539	590755	592458	aminoacyl-tRNA synthetase	L25105	<i>Chlamydia trachomatis</i>	2125	71
ORF540	592526	592903	has homology to putative heat shock proteins of <i>Bacillus subtilis</i> and <i>Clostridium acetobutylicum</i> ; ORF A; putative	L25105	<i>Chlamydia trachomatis</i>	324	59
ORF541	592836	593747	Possible negative regulator of CIRCE element; Homologs in <i>B. subtilis</i> and <i>Clostridia</i> spp. referred to as <i>hrcA</i> or <i>orfA</i>	U52216	<i>Chlamydia trachomatis</i>	960	65
ORF542	593747	594298	grpE	M62819	<i>Chlamydia trachomatis</i>	661	71
ORF543	594331	595947	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	2619	100
ORF544	595905	596309	DnaK protein homolog; 71,550 Da; putative	M69227	<i>Chlamydia pneumoniae</i>	674	100
ORF545	596514	597215	putative				
ORF546	597184	597957	vacB gene product	U14003	<i>Escherichia coli</i>	306	48
ORF547	597755	598612	ORF-2	D11024	<i>Shigella flexneri</i>	168	46
ORF548	598602	599204	homologous to DNA glycosylases; hypothetical	D83026	<i>Bacillus subtilis</i>	374	47
ORF549	599373	599939	putative				
ORF550	600903	602072	hemolysin	X73141	<i>Serpulina hyodysenteriae</i>	362	36
ORF551	602240	602587	hypothetical protein	D90908	<i>Synechocystis</i> sp.	182	35
ORF552	602637	603272	putative				
ORF553	603142	604512	putative				
ORF554	604627	605853	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	423	40
ORF555	605790	606620	putative				
ORF556	606571	607281	putative	L14679	<i>Lactococcus lactis</i>	384	45
ORF557	609004	607355	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF558	610906	609932	putative				
ORF559	611786	611004	diaminopimelate epimerase	D90917	<i>Synechocystis</i> sp.	207	55
ORF560	612333	611746	ATP-dependent Clp protease proteolytic subunit	D90915	<i>Synechocystis</i> sp.	389	44
ORF561	613897	612341	serine hydroxymethyltransferase	D90903	<i>Synechocystis</i> sp.	909	52
ORF562	615179	616279	putative				
ORF563	616610	617383	putative				
ORF564	618796	617810	ORF o328	U18997	<i>Escherichia coli</i>	413	45
ORF565	620004	618826	branched chain alpha-keto acid dehydrogenase E2	M97391	<i>Bacillus subtilis</i>	688	41
ORF566	619649	619918	putative				
ORF567	621265	620021	Hypothetical protein	Y14083	<i>Bacillus subtilis</i>	727	37
ORF568	622359	621265	hypothetical	U32691	<i>Haemophilus influenzae</i>	294	52
ORF569	623420	622560	rRNA methylase	D90913	<i>Synechocystis</i> sp.	244	38
ORF570	624297	623335	hypothetical protein (SP:P39587)	U67605	<i>Methanococcus jannaschii</i>	147	35
ORF571	624773	624174	riboflavin synthase alpha chain	AE000261	<i>Escherichia coli</i>	424	50
ORF572	625029	625484	ORF 168	D28752	<i>Synechococcus</i> sp.	323	43
ORF573	625488	625883	YteA	AF008220	<i>Bacillus subtilis</i>	172	35
ORF574	625892	626395	signal peptidase II	X78084	<i>Staphylococcus carnosus</i>	204	38
ORF575	626444	627790	D-alanine permease (dagA)	U32770	<i>Haemophilus influenzae</i>	566	33
ORF576	627912	628607	putative				
ORF577	628774	629697	putative				
ORF578	629660	631639	POMP91A	U65942	<i>Chlamydia psittaci</i>	579	44
ORF579	631725	633551	putative				
ORF580	633520	636957	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	266	45
ORF581	637232	638098	adhesion protein	D90903	<i>Synechocystis</i> sp.	267	38
ORF582	640648	639593	GTP-binding protein	D90901	<i>Synechocystis</i> sp.	759	45
ORF583	640979	640728	50S ribosomal protein L27	U38804	<i>Porphyra purpurea</i>	265	65
ORF584	641327	641007	50S ribosomal subunit protein L21	U18997	<i>Escherichia coli</i>	210	41
ORF585	641687	642283	hypothetical protein	D90906	<i>Synechocystis</i> sp.	76	39
ORF586	643023	642286	assimilatory sulfite reductase	L26503	<i>Saccharomyces cerevisiae</i>	284	42
ORF587	643330	643076	putative				
ORF588	643704	643351	ribosomal protein S10 (rpS10)	U32761	<i>Haemophilus influenzae</i>	349	69

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF589	645628	643676	translation elongation factor EF-G (fusA)	AE000625	<i>Helicobacter pylori</i>	1991	58
ORF590	645783	645538	elongation factor G (AA 1-691)	X16278	<i>Thermus aquaticus thermophilus</i>	170	80
ORF591	646269	645793	ribosomal protein S7	Z11567	<i>Chlamydia trachomatis</i>	730	88
ORF592	646751	646314	ribosomal protein S12 (AA 1-123)	X52912	<i>Cryptomonas phi</i>	485	67
ORF593	647848	647045	putative				
ORF594	648393	650336	ORF of prc gene (alt.)	D00674	<i>Escherichia coli</i>	554	42
ORF595	651016	650420	hypothetical sulfur-rich protein	U41759	<i>Chlamydia psittaci</i>	301	50
ORF596	652956	651289	60kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	2951	100
ORF597	653395	653126	9kDa CrP	X53511	<i>Chlamydia pneumoniae</i>	502	99
ORF598	655740	654193	glutamyl-tRNA synthetase homolog	U41759	<i>Chlamydia psittaci</i>	2259	82
ORF599	656508	655966	early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO)	L13598	<i>Chlamydia psittaci</i>	666	62
ORF600	658140	657022	unknown	U41759	<i>Chlamydia psittaci</i>	950	44
ORF601	660216	658525	RecJ recombination protein	U41759	<i>Chlamydia psittaci</i>	807	73
ORF602	663238	660248	protein-export membrane protein SecD	D64000	<i>Synechocystis sp.</i>	413	41
ORF603	664461	663157	putative				
ORF604	665735	664635	putative				
ORF605	666212	666994	hypothetical protein	D64006	<i>Synechocystis sp.</i>	538	58
ORF606	666998	667921	o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA ECOLI SW: P06466	AE000238	<i>Escherichia coli</i>	253	45
ORF607	667909	668568	cytidylate kinase	AE000193	<i>Escherichia coli</i>	400	48
ORF608	668502	669203	hypothetical protein	D90915	<i>Synechocystis sp.</i>	225	33
ORF609	669154	670893	arginyl-tRNA-synthetase	D64006	<i>Synechocystis sp.</i>	1365	49
ORF610	672226	670853	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	U32788	<i>Haemophilus influenzae</i>	642	40
ORF611	671137	671424	putative				
ORF612	672453	673001	putative				
ORF613	673072	674721	putative				
ORF614	674549	674262	putative				
ORF615	675518	674796	ORF246 gene product	X59551	<i>Escherichia coli</i>	520	43
ORF616	676083	675499	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF617	676630	676067	putative				
ORF618	677016	676600	ORF3	D10279	<i>Bacillus subtilis</i>	361	63
ORF619	677647	677015	peptide release factor 2	X99401	<i>Bacillus firmus</i>	427	43
ORF620	677990	678259	unknown	Z49939	<i>Saccharomyces cerevisiae</i>	175	48
ORF621	679444	680097	unknown	D26185	<i>Bacillus subtilis</i>	263	38
ORF622	680097	680897	unknown	D64126	<i>Bacillus subtilis</i>	506	45
ORF623	681637	680849	putative				
ORF624	681409	682281	putative				
ORF625	682453	682821	putative				
ORF626	682763	683902	sensor protein	L39904	<i>Myxococcus xanthus</i>	190	48
ORF627	684616	683969	putative				
ORF628	685169	684534	putative				
ORF629	685986	685117	putative				
ORF630	686278	687288	NtrC/NifA-like protein regulator	U17902	<i>Escherichia coli</i>	820	45
ORF631	687483	688151	putative				
ORF632	688740	689501	putative				
ORF633	690242	689622	putative				
ORF634	690470	691126	unknown	Z48008	<i>Saccharomyces cerevisiae</i>	380	46
ORF635	692600	691497	putative				
ORF636	692674	695064	phenylalanyl-tRNA synthetase beta-subunit (pheT)	U32810	<i>Haemophilus influenzae</i>	593	45
ORF637	695049	696032	putative				
ORF638	697964	696585	OppC-like protein	D85103	<i>Synechococcus sp.</i>	371	37
ORF639	699803	698274	OppB gene product	X56347	<i>Bacillus subtilis</i>	197	40
ORF640	701926	699788	AppA	U20909	<i>Bacillus subtilis</i>	324	43
ORF641	703196	702567	putative				
ORF642	704221	703208	putative				
ORF643	704240	705289	ferrochelatase	X73417	<i>Arabidopsis thaliana</i>	266	42
ORF644	706070	705300	histidine periplasmic binding protein P29	U58045	<i>Campylobacter jejuni</i>	128	31
ORF645	706841	706254	conserved hypothetical protein	AE000592	<i>Helicobacter pylori</i>	155	37
ORF646	707596	706811	putative				
ORF647	708666	707677	ADP-glucose pyrophosphorylase	X55650	<i>Solanum tuberosum</i>	595	43
ORF648	709793	709119	pyrE-F gene product	X71842	<i>Arabidopsis thaliana</i>	400	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF649	711523	710132	transcription termination factor	J01673	<i>Escherichia coli</i>	1251	60
ORF650	712236	711523	putative				
ORF651	714734	712125	DNA polymerase I	J04479	<i>Streptococcus pneumoniae</i>	1334	43
ORF652	715759	714761	protease IV	U67512	<i>Methanococcus jannaschii</i>	101	55
ORF653	717538	715886	adenine nucleotide translocase	Z49227	<i>Arabidopsis thaliana</i>	832	39
ORF654	719113	720243	replicative DNA helicase	D26185	<i>Bacillus subtilis</i>	776	44
ORF655	720590	722422	homologous to E.coli gidA	X62540	<i>Pseudomonas putida</i>	1575	52
ORF656	722406	723056	putative				
ORF657	723551	723120	nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6)	J05207	<i>Myxococcus xanthus</i>	451	62
ORF658	724246	723626	Holliday junction DNA helicase (ruvA)	U32716	<i>Haemophilus influenzae</i>	293	43
ORF659	724754	724251	crossover junction endodeoxyribonuclease (ruvC)	U32717	<i>Haemophilus influenzae</i>	296	53
ORF660	725868	724900	putative				
ORF661	727115	726270	putative				
ORF662	728126	727119	glyceraldehyde-3-phosphate dehydrogenase	U83198	<i>Chlamydia trachomatis</i>	1340	75
ORF663	728594	728208	ribosomal protein L17	L33834	<i>Chlamydia trachomatis</i>	439	82
ORF664	729614	728604	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	1356	89
ORF665	729778	729533	RNA polymerase alpha-subunit	L33834	<i>Chlamydia trachomatis</i>	273	82
ORF666	730149	729751	ribosomal protein S11	L33834	<i>Chlamydia trachomatis</i>	562	90
ORF667	730539	730174	ribosomal protein S13	L33834	<i>Chlamydia trachomatis</i>	544	89
ORF668	731983	730598	homolog	L25077	<i>Chlamydia trachomatis</i>	1956	83
ORF669	732427	731996	ribosomal protein CtrL15e	M80325	<i>Chlamydia trachomatis</i>	563	77
ORF670	732917	732423	ribosomal protein CtrS5e	M80325	<i>Chlamydia trachomatis</i>	702	84
ORF671	733598	733320	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	316	87
ORF672	733869	733492	ribosomal protein L6	M60652	<i>Chlamydia trachomatis</i>	469	77
ORF673	734298	733900	ribosomal protein CtrS8e	M80325	<i>Chlamydia trachomatis</i>	572	82
ORF674	734858	734319	ribosomal protein CtrL5e	M80325	<i>Chlamydia trachomatis</i>	730	90
ORF675	735195	734863	ribosomal protein CtrL24e	M80325	<i>Chlamydia trachomatis</i>	420	70
ORF676	735578	735342	ribosomal protein CtrL14e	M80325	<i>Chlamydia trachomatis</i>	270	95
ORF677	735861	735604	ribosomal protein S17e	M80325	<i>Chlamydia trachomatis</i>	322	77
ORF678	736492	736079	50S ribosomal protein L16	D90905	<i>Synechocystis sp.</i>	439	60

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF679	737192	736524	ribosomal protein S3	D64071	<i>Actinobacillus actinomycetecomitans</i>	612	58
ORF680	737555	737211	ribosomal protein L22	Z21677	<i>Thermotoga maritima</i>	228	48
ORF681	738688	737837	50S ribosomal subunit protein L2	U18997	<i>Escherichia coli</i>	769	62
ORF682	739048	738713	putative				
ORF683	739736	739065	ribosomal protein L4	X67014	<i>Bacillus stearothermophilus</i>	308	46
ORF684	740477	739773	ribosomal protein L3	Z46265	<i>Thermus aquaticus thermophilus</i>	463	50
ORF685	740659	740958	putative				
ORF686	741722	740721	putative				
ORF687	742789	741827	methionyl-tRNA formyltransferase	D64001	<i>Synechocystis sp.</i>	511	48
ORF688	743618	742782	UDP-N-acetylglucosamine acyltransferase	L22690	<i>Rickettsia rickettsii</i>	542	43
ORF689	744092	743634	(3R)-hydroxymyristol acyl carrier protein dehydrase	D90910	<i>Synechocystis sp.</i>	339	55
ORF690	744604	744107	UDP-3-0-acyl N-acetylglucosamine deacetylase	D90902	<i>Synechocystis sp.</i>	287	45
ORF691	744953	744498	UDP-3-O-acyl-GlcNAc deacetylase	U67855	<i>Pseudomonas aeruginosa</i>	262	51
ORF692	746608	744986	apolipoprotein N-acyltransferase (cute)	U32716	<i>Haemophilus influenzae</i>	194	50
ORF693	747085	746621	low homology to P14 protein of <i>Haemophilus influenzae</i> and 14.2 kDa protein of <i>Escherichia coli</i>	D78189	<i>Bacillus subtilis</i>	235	37
ORF694	747974	747219	polymerase III	M22996	<i>Bacillus subtilis</i>	180	34
ORF695	748594	748169	hypothetical protein	D90914	<i>Synechocystis sp.</i>	160	43
ORF696	749145	748573	putative				
ORF697	749652	749957	trxA	L39892	<i>Chlamydia psittaci</i>	393	72
ORF698	750446	749979	spoU	L39892	<i>Chlamydia psittaci</i>	559	72
ORF699	751219	750446	mip	L39892	<i>Chlamydia psittaci</i>	948	60
ORF700	753042	751291	aspartyl-tRNA synthetase	D90910	<i>Synechocystis sp.</i>	1347	47
ORF701	754309	753020	histidine--tRNA ligase	Z17214	<i>Sireptococcus equisimilis</i>	757	44
ORF702	755120	756175	hexosephosphate transport protein	M89480	<i>Salmonella typhimurium</i>	870	49
ORF703	756120	756485	hexosephosphate transport protein	M89479	<i>Escherichia coli</i>	321	45
ORF704	756499	760227	DNA polymerase III alpha-subunit (dnaE)	AE000646	<i>Helicobacter pylori</i>	1977	42
ORF705	761217	760297	putative				
ORF706	761297	761809	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF707	761782	762282	putative				
ORF708	762260	762895	putative				
ORF709	762867	763316	hypothetical protein	D90908	<i>Synechocystis</i> sp.	177	43
ORF710	763780	763325	putative				
ORF711	763861	765168	DD-carboxypeptidase	M85047	<i>Bacillus subtilis</i>	292	37
ORF712	766809	765697	fmu and fmv protein	D90902	<i>Synechocystis</i> sp.	130	36
ORF713	768051	766888	putative				
ORF714	768566	768321	putative				
ORF715	769342	768551	putative				
ORF716	770532	769378	putative				
ORF717	771451	770804	putative				
ORF718	773058	771847	3-phosphoglycerate kinase	U83197	<i>Chlamydia trachomatis</i>	1540	72
ORF719	773094	773456	putative				
ORF720	774376	773093	putative phosphate permease	U84890	<i>Mesembryanthemum crystallinum</i>	870	45
ORF721	775123	774380	putative				
ORF722	775398	774916	putative				
ORF723	775046	776077	sporulation protein	M57689	<i>Bacillus subtilis</i>	698	43
ORF724	776070	777041	was dppE	U00039	<i>Escherichia coli</i>	565	56
ORF725	777964	777536	orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of <i>Pseudomonas putida</i>	Y10436	<i>Coxiella burnetii</i>	256	46
ORF726	778176	777904	B. subtilis genes rpmH, mpA, 50kd, gidA and gidB	X62539	<i>Bacillus subtilis</i>	112	37
ORF727	778621	779334	putative				
ORF728	781173	780307	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	603	40
ORF729	781526	781116	f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089	AE000263	<i>Escherichia coli</i>	258	45
ORF730	782784	781555	f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24 CYAPA SW: P48260	AE000263	<i>Escherichia coli</i>	197	44

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF731	783572	782805	hypothetical chloroplast ORF 16	U38804	<i>Porphyrha purpurea</i>	597	52
ORF732	785032	783581	ABC transporter subunit	D64004	<i>Synechocystis sp.</i>	1720	62
ORF733	786412	785360	putative				
ORF734	788429	786450	pbp	Y14206	<i>Streptomyces coelicolor</i>	148	55
ORF735	788944	788528	penicillin-binding protein 3	X84053	<i>Pseudomonas aeruginosa</i>	148	38
ORF736	789758	788901	putative				
ORF737	790332	791504	major outer membrane protein	M64064	<i>Chlamydia pneumoniae</i>	2028	99
ORF738	791846	792721	ribosomal protein S2	U60196	<i>Chlamydia trachomatis</i>	904	70
ORF739	792724	793569	elongation factor Ts	U60196	<i>Chlamydia trachomatis</i>	1023	71
ORF740	793580	794323	UMP kinase	U60196	<i>Chlamydia trachomatis</i>	891	72
ORF741	794304	794843	ribosome-releasing factor	U60196	<i>Chlamydia trachomatis</i>	673	73
ORF742	795217	795732	unknown	D26185	<i>Bacillus subtilis</i>	105	42
ORF743	795722	796795	unknown	D26185	<i>Bacillus subtilis</i>	208	33
ORF744	798735	797053	putative	L33796	<i>Vibrio cholerae</i>	386	34
ORF745	799823	798681	putative				
ORF746	799297	799578	putative				
ORF747	801313	799808	Pkn5	U40656	<i>Myxococcus xanthus</i>	345	33
ORF748	802453	801332	putative				
ORF749	803299	802457	putative				
ORF750	803811	803290	putative				
ORF751	805151	803826	YscN	U02499	<i>Yersinia enterocolitica</i>	1185	53
ORF752	805860	805156	putative				
ORF753	806604	806332	putative				
ORF754	806913	806608	putative				
ORF755	808222	806903	putative				
ORF756	808751	808146	putative				
ORF757	809437	808673	putative				
ORF758	809939	809454	putative				
ORF759	811235	810213	delta-aminolevulinatase synthase (EC 2.3.1.37)	M30785	<i>Escherichia coli</i>	172	40
ORF760	811779	813056	DNA gyrase subunit B	U35453	<i>Clostridium acetobutylicum</i>	584	38
ORF761	812890	812516	putative				
ORF762	812954	813583	DNA gyrase subunit B	Z19108	<i>Spiroplasma citri</i>	371	39

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF763	813587	815023	gyrA	X92503	<i>Mycobacterium smegmatis</i>	414	55
ORF764	815420	815746	putative				
ORF765	816036	817010	orf-X; hypothetical protein; Method: conceptual translation supplied by author	U48870	<i>Bacillus subtilis</i>	569	47
ORF766	817111	817356	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	114	34
ORF767	817791	818609	3-deoxy-d-manno-octulosonic acid 8- phosphate synthetase	Z50747	<i>Chlamydia psittaci</i>	1112	78
ORF768	818609	819094	protein of unknown function	Z50747	<i>Chlamydia psittaci</i>	545	65
ORF769	819104	819823	ATP binding protein	U72493	<i>Chlamydia trachomatis</i>	1099	88
ORF770	820722	819826	putative				
ORF771	822313	821000	putative				
ORF772	823503	822238	putative				
ORF773	823678	825612	putative				
ORF774	825461	826312	putative				
ORF775	827280	826645	putative				
ORF776	828604	827171	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	2179	100
ORF777	830026	828713	76 kDa protein	L23921	<i>Chlamydia pneumoniae</i>	1162	100
ORF778	831047	830085	mviB homolog	U50732	<i>Chlamydia trachomatis</i>	982	58
ORF779	831725	831051	mviB homolog	U50732	<i>Chlamydia trachomatis</i>	740	65
ORF780	832220	833098	T05H10.2	Z47812	<i>Caenorhabditis elegans</i>	407	34
ORF781	833851	833396	ribosomal protein S4 (rps4)	AE000633	<i>Helicobacter pylori</i>	372	53
ORF782	834068	835039	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from <i>E. coli</i> . Accession Number X61000	L22217	<i>Mycoplasma-like organism</i>	377	49
ORF783	835792	835127	uridine kinase	L31783	<i>Mus musculus</i>	436	43
ORF784	837624	836116	ORF f397	U29581	<i>Escherichia coli</i>	92	38
ORF785	838951	840882	putative				
ORF786	840869	842185	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	409	40
ORF787	841989	843455	DNA helicase II	U39703	<i>Mycoplasma genitalium</i>	110	46
ORF788	843242	844021	exodeoxyribonuclease V (recB)	U32811	<i>Haemophilus influenzae</i>	196	40
ORF789	845018	843987	MreC protein	M31792	<i>Escherichia coli</i>	76	53
ORF790	846174	844990	aspartate aminotransferase (aspC)	X03629	<i>Escherichia coli</i>	754	40
ORF791	848509	846311	GreA	U02878	<i>Rickettsia prowazekii</i>	190	35

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF792	848568	849014	putative				
ORF793	849082	850488	NADH:ubiquinone oxidoreductase subunit A (GP:Z37111 2)	U32702	<i>Haemophilus influenzae</i>	445	37
ORF794	851512	850574	porphobilinogen synthase	U38348	<i>Chlorobium vibrioforme</i>	769	45
ORF795	852064	852447	putative				
ORF796	852398	853690	putative				
ORF797	855118	854243	geranylgeranyl pyrophosphate synthase	D85029	<i>Arabidopsis thaliana</i>	408	41
ORF798	855751	855128	f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE RABIT SW: P47823	AE000143	<i>Escherichia coli</i>	187	36
ORF799	856551	855829	membrane associated regulatory protein	M28368	<i>Salmonella typhimurium</i>	172	36
ORF800	856730	858556	unknown function	Z32530	<i>Chlamydia trachomatis</i>	842	35
ORF801	858717	859601	exodeoxyribonuclease V (recD)	U32811	<i>Haemophilus influenzae</i>	182	51
ORF802	859591	860205	exonuclease V alpha subunit (AA 1-608)	X04582	<i>Escherichia coli</i>	235	45
ORF803	861132	860284	putative				
ORF804	861426	861163	30S ribosomal protein S20	Z67753	<i>Odontella sinensis</i>	153	41
ORF805	861701	862921	putative				
ORF806	863026	864798	major sigma factor	U04442	<i>Chlamydia psittaci</i>	2661	94
ORF807	864831	865256	putative				
ORF808	865226	866581	dihydropterin pyrophosphokinase /dihydropteroate synthase	Y08611	<i>Pisum sativum</i>	455	48
ORF809	866562	867119	dehydrofolate reductase, type I (folA)	U32772	<i>Haemophilus influenzae</i>	213	49
ORF810	867025	867816	M. jannaschii predicted coding region MJ0768	U67522	<i>Methanococcus jannaschii</i>	207	36
ORF811	867820	868497	putative				
ORF812	869743	868661	RecA	U16739	<i>Chlamydia trachomatis</i>	1512	87
ORF813	870633	870094	unknown function	Z32530	<i>Chlamydia trachomatis</i>	308	45
ORF814	871929	870646	unknown function	Z32530	<i>Chlamydia trachomatis</i>	1410	63
ORF815	872538	872086	putative				
ORF816	873908	872517	putative				
ORF817	874281	874670	mifR3-like gene product	Z37984	<i>Azospirillum brasilense</i>	181	32
ORF818	874582	875286	ORF1 gene product	X62399	<i>Escherichia coli</i>	307	42
ORF819	877857	875377	DNA topoisomerase I	L27797	<i>Bacillus subtilis</i>	1488	50

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF820	878446	879255	putative				
ORF821	880635	879268	sigma factor (ntrA) (AA 1-502)	X05888	<i>Azotobacter vinelandii</i>	257	47
ORF822	882524	880593	DNA helicase II	D90906	<i>Synechocystis sp.</i>	1140	50
ORF823	882612	883319	ipa-57d gene product	X73124	<i>Bacillus subtilis</i>	601	51
ORF824	884155	883538	hypothetical protein	D90915	<i>Synechocystis sp.</i>	344	39
ORF825	884340	885611	19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned <i>B. subtilis</i> gene.; putative	L19954	<i>Bacillus subtilis</i>	456	37
ORF826	885722	887302	heat shock protein	L12004	<i>Chlamydia trachomatis</i>	915	39
ORF827	887587	888153	bas1 protein	Z34917	<i>Hordeum vulgare</i>	474	50
ORF828	888627	888220	putative				
ORF829	889330	888716	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	223	55
ORF830	889898	889323	peptidoglycan-associated lipoprotein	X65796	<i>Escherichia coli</i>	222	50
ORF831	891190	889898	TolB	U32470	<i>Haemophilus influenzae</i>	280	35
ORF832	891828	891247	putative				
ORF833	892421	892017	exbD peptide	M28819	<i>Escherichia coli</i>	77	48
ORF834	893116	892421	inner membrane protein (tolQ)	U32722	<i>Haemophilus influenzae</i>	157	54
ORF835	892521	892925	putative				
ORF836	893392	895419	inner membrane copper tolerance protein	Z36905	<i>Escherichia coli</i>	120	35
ORF837	895745	896527	unknown	D26185	<i>Bacillus subtilis</i>	381	41
ORF838	896668	897558	succinate dehydrogenase subunit C	Y08563	<i>Paenibacillus macerans</i>	253	40
ORF839	897565	899442	succinate dehydrogenase subunit A	Y08563	<i>Paenibacillus macerans</i>	1667	57
ORF840	899420	900229	succinate dehydrogenase subunit B	Y08563	<i>Paenibacillus macerans</i>	656	54
ORF841	903230	900237	putative				
ORF842	905081	903234	putative				
ORF843	906931	905045	sigma factor SibG regulation protein RsbU	D90905	<i>Synechocystis sp.</i>	117	35
ORF844	907248	907832	putative				
ORF845	907784	908128	putative				
ORF846	908132	908677	putative				
ORF847	908589	909320	putative				
ORF848	909405	911465	putative				
ORF849	911677	912360	putative				



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF850	912303	912821	putative				
ORF851	912937	913983	putative				
ORF852	915128	914067	putative				
ORF853	916658	915303	enolase	L29475	<i>Bacillus subtilis</i>	1036	60
ORF854	915627	915376	enolase	U43738	<i>Mycoplasma pneumoniae</i>	226	65
ORF855	917707	916853	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	724	46
ORF856	918837	917722	excinuclease ABC subunit B (uvrB)	U32804	<i>Haemophilus influenzae</i>	1029	54
ORF857	919868	918837	tryptophanyl-tRNA synthetase (trpS)	U32746	<i>Haemophilus influenzae</i>	376	40
ORF858	920434	919880	putative				
ORF859	921187	920438	ORF8	X82078	<i>Chlamydia sp.</i>	164	50
ORF860	921959	921195	hypothetical protein	X62475	<i>Chlamydia psittaci</i>	511	44
ORF861	923773	921995	Threonyl tRNA Synthetase	Z80360	<i>Bacillus subtilis</i>	1476	44
ORF862	922146	922415	putative				
ORF863	923943	923674	putative				
ORF864	924077	925006	putative				
ORF865	925436	925083	putative				
ORF866	926524	925349	putative				
ORF867	927920	926433	putative				
ORF868	928319	927951	putative				
ORF869	928963	928334	putative				
ORF870	929248	930987	DNA mismatch repair protein (mutL)	U32692	<i>Haemophilus influenzae</i>	585	40
ORF871	930995	932059	YqhT	D84432	<i>Bacillus subtilis</i>	445	39
ORF872	932121	933515	putative				
ORF873	932881	932513	putative				
ORF874	933485	935746	puID (tfg start codon)	M32613	<i>Klebsiella pneumoniae</i>	210	33
ORF875	935724	937082	epsE	M96172	<i>Vibrio cholerae</i>	890	55
ORF876	937229	938410	PilG	U32588	<i>Neisseria gonorrhoeae</i>	280	38
ORF877	938281	938805	putative				
ORF878	938809	939255	putative				
ORF879	939165	939782	putative				
ORF880	939760	940791	putative				
ORF881	940822	941106	putative				
ORF882	940977	941351	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF883	942537	941623	yscT	L25667	<i>Yersinia pseudotuberculosis</i>	169	44
ORF884	942784	942500	yscS	L25667	<i>Yersinia pseudotuberculosis</i>	173	42
ORF885	943149	942799	HrcR	AE000107	<i>Rhizobium sp. NGR234</i>	265	52
ORF886	943799	943029	pathogenicity protein	M64094	<i>Xanthomonas campestris</i>	252	41
ORF887	944055	943732	putative	M74011	<i>Yersinia enterocolitica</i>	112	33
ORF888	944413	943994	putative				
ORF889	945395	944556	putative				
ORF890	945853	945389	putative				
ORF891	946392	945751	HrcJ	U56662	<i>Erwinia amylovora</i>	229	44
ORF892	947410	948081	putative				
ORF893	949871	948915	ORF YOR196c	Z75104	<i>Saccharomyces cerevisiae</i>	702	44
ORF894	951058	949868	dihydrolipoamide dehydrogenase E3 subunit	M57435	<i>Bacillus subtilis</i>	745	39
ORF895	951249	950959	dihydrolipoamide acetyltransferase E3 subunit	M73535	<i>Staphylococcus aureus</i>	166	49
ORF896	951664	952134	putative				
ORF897	952674	952165	SNF	X98455	<i>Bacillus cereus</i>	229	47
ORF898	953491	952589	helicase	U39680	<i>Mycoplasma genitalium</i>	307	42
ORF899	955324	953495	F01G4.1	Z68341	<i>Caenorhabditis elegans</i>	133	57
ORF900	955823	955281	putative				
ORF901	957082	955847	branched-chain amino acid carrier	Z48676	<i>Lactobacillus delbrueckii</i>	297	40
ORF902	957902	957270	endonuclease III	U11289	<i>Bacillus subtilis</i>	317	37
ORF903	959231	957906	homologous to E.coli 50K	X62539	<i>Bacillus subtilis</i>	805	45
ORF904	959376	960284	phosphatidylserine decarboxylase	U72715	<i>Chlamydia trachomatis</i>	776	51
ORF905	960266	961669	putative				
ORF906	961856	964765	secretory component	U06928	<i>Caulobacter crescentus</i>	1812	55
ORF907	966855	965395	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative	L47648	<i>Bacillus subtilis</i>	778	41
ORF908	968204	966975	poly(A) polymerase	L47709	<i>Bacillus subtilis</i>	383	41
ORF909	968791	968237	ClpX-like protein	U18229	<i>Bacillus subtilis</i>	340	39
ORF910	969498	968731	ATP-dependent protease ATPase subunit	D64006	<i>Synechocystis sp.</i>	846	66
ORF911	969858	969511	ClpP	U16135	<i>Synechococcus sp.</i>	257	54

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF912	970118	969762	ATP-dependent clp protease proteolytic component (clpP)	AE000591	<i>Helicobacter pylori</i>	362	63
ORF913	970593	970300	putative				
ORF914	971261	970542	putative				
ORF915	971680	971123	putative				
ORF916	971876	975100	SNF	X98455	<i>Bacillus cereus</i>	778	49
ORF917	975419	976516	MreB protein	M96343	<i>Bacillus subtilis</i>	960	55
ORF918	976584	978320	phospho enol pyruvate carboxykinase	S56812	<i>Chlorobium limicola</i>	1667	64
ORF919	977680	977231	putative				
ORF920	978399	980738	putative				
ORF921	980756	981928	putative				
ORF922	982974	981931	precursor protein (AA -22 to 371)	X52557	<i>Chlamydia trachomatis</i>	97	50
ORF923	984120	983119	NAD+ dependent glycerol-3-phosphate dehydrogenase	L47648	<i>Bacillus subtilis</i>	618	43
ORF924	985502	984120	AgX-1 antigen [human, infertile patient, testis. Peptide, 505 aa]	S73498	<i>Homo sapiens</i>	254	34
ORF925	987180	985882	ORF 4	M72718	<i>Bacillus subtilis</i>	697	38
ORF926	987172	987444	putative				
ORF927	989846	989049	nifU-like protein	AE000542	<i>Helicobacter pylori</i>	302	31
ORF928	991048	989846	putative				
ORF929	991638	990955	phosphoglyceromutase	L09651	<i>Zymomonas mobilis</i>	471	53
ORF930	991794	992498	ORFX13	L09228	<i>Bacillus subtilis</i>	403	39
ORF931	993619	993041	biotin [acetyl-CoA-carboxylase] ligase	L47709	<i>Bacillus subtilis</i>	136	38
ORF932	993530	994792	rod-shape-determining protein	M22857	<i>Escherichia coli</i>	312	44
ORF933	995970	994795	cadmium-transporting ATPase	D64005	<i>Synechocystis sp.</i>	358	47
ORF934	996857	995739	ATPase	L28104	<i>Transposon Tn5422</i>	449	39
ORF935	997603	996782	putative				
ORF936	998969	997572	seryl-trna synthetase	Y09924	<i>Staphylococcus aureus</i>	851	42
ORF937	998896	1000023	orf2, homologue to B.subtilis ribG	X64395	<i>Escherichia coli</i>	596	40
ORF938	1000087	1001340	GTP cyclohydrolase II	D90912	<i>Synechocystis sp.</i>	1078	52
ORF939	1001357	1001818	riboflavin synthase beta subunit	U27202	<i>Actinobacillus pleuropneumoniae</i>	278	36
ORF940	1003288	1001873	putative				
ORF941	1003487	1004146	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF942	1004485	1005639	D-alanine glycine permease (dagA)	AE000603	<i>Helicobacter pylori</i>	394	33
ORF943	1005643	1005972	hypothetical protein MTCY180.08	Z97193	<i>Mycobacterium tuberculosis</i>	274	58
ORF944	1006784	1006116	similar to trithorax protein in final three exons	U13875	<i>Caenorhabditis elegans</i>	155	46
ORF945	1007563	1006769	YycJ	D78193	<i>Bacillus subtilis</i>	406	38
ORF946	1009226	1007568	YtpT	AF008220	<i>Bacillus subtilis</i>	992	47
ORF947	1009989	1009336	putative				
ORF948	1015852	1016337	putative				
ORF949	1016561	1016181	putative				
ORF950	1016297	1017532	putative				
ORF951	1016802	1016452	putative				
ORF952	1018993	1017701	phenolhydroxylase component	U32702	<i>Haemophilus influenzae</i>	909	47
ORF953	1019454	1019137	ORF	M63939	<i>Escherichia coli</i>	96	45
ORF954	1020764	1019562	pCTHm1 gene product	M94254	<i>Chlamydia trachomatis</i>	1185	65
ORF955	1021405	1021037	histone H1-like protein	M80324	<i>Chlamydia psittaci</i>	319	62
ORF956	1021821	1024286	phosphoprotein	L25078	<i>Chlamydia trachomatis</i>	739	41
ORF957	1024697	1024248	putative				
ORF958	1025569	1024508	protoporphyrinogen oxidase	U25114	<i>Mus musculus</i>	86	38
ORF959	1026969	1025590	oxygen independent coprophorphyrinogen III oxidase	D90912	<i>Synechocystis sp.</i>	880	42
ORF960	1027789	1026947	uroporphyrinogen decarboxylase	M97208	<i>Bacillus subtilis</i>	372	38
ORF961	1031199	1027945	transcription-repair coupling factor (trcF) (mfd)	U32805	<i>Haemophilus influenzae</i>	1584	42
ORF962	1031717	1031172	alanyl-tRNA synthetase	X95571	<i>Thiobacillus ferrooxidans</i>	76	31
ORF963	1033057	1031612	alanyl-tRNA synthetase	AE000353	<i>Escherichia coli</i>	889	40
ORF964	1033425	1033039	alanyl-tRNA synthetase (alaS)	AE000629	<i>Helicobacter pylori</i>	327	51
ORF965	1033784	1033200	alanyl-tRNA synthetase	X59956	<i>Rhizobium leguminosarum</i>	416	47
ORF966	1033963	1036038	transketolase	Z73234	<i>Bacillus subtilis</i>	1398	44
ORF967	1036945	1036010	AMP nucleosidase	AE000290	<i>Escherichia coli</i>	265	42
ORF968	1037110	1037679	elongation factor P	U14003	<i>Escherichia coli</i>	458	51
ORF969	1037696	1037944	putative				
ORF970	1038916	1037975	putative				
ORF971	1040582	1039026	HSP60 chaperonin	X62914	<i>Clostridium perfringens</i>	284	31

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF972	1040997	1042337	PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15)	AB001488	<i>Bacillus subtilis</i>	446	39
ORF973	1042357	1043403	ORF-Y (AA 1-360)	X51584	<i>Escherichia coli</i>	582	45
ORF974	1043367	1044623	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	U32793	<i>Haemophilus influenzae</i>	348	42
ORF975	1044607	1045362	hypothetical protein	Y14079	<i>Bacillus subtilis</i>	115	38
ORF976	1045384	1046538	spoVE gene product (AA 1-366)	X51419	<i>Bacillus subtilis</i>	479	35
ORF977	1046447	1047517	mur	Y13922	<i>Enterococcus hirae</i>	256	45
ORF978	1047521	1049956	UDP-N-acetylmuramate-alanine ligase (murC)	U32794	<i>Haemophilus influenzae</i>	756	38
ORF979	1050611	1050036	unknown	Z74024	<i>Mycobacterium tuberculosis</i>	78	44
ORF980	1050925	1050566	cycY gene product	U14003	<i>Escherichia coli</i>	179	34
ORF981	1051728	1051090	putative				
ORF982	1051743	1052063	hypothetical protein	D90908	<i>Synechocystis sp.</i>	135	33
ORF983	1052101	1053126	tma delta(2)-isopentenylpyrophosphate transferase	Z98209	<i>Mycobacterium tuberculosis</i>	441	37
ORF984	1054201	1053107	conserved hypothetical protein	AE000579	<i>Helicobacter pylori</i>	826	44
ORF985	1054242	1055555	putative				
ORF986	1055483	1055908	putative				
ORF987	1056609	1056965	YqeL	D84432	<i>Bacillus subtilis</i>	202	38
ORF988	1056961	1058232	beta-ketoacyl-ACP synthase	L13242	<i>Ricinus communis</i>	1266	55
ORF989	1058238	1058687	diadenosine tetraphosphatase	U30313	<i>Homo sapiens</i>	122	42
ORF990	1059371	1058727	inorganic pyrophosphatase (ppa)	AE000576	<i>Helicobacter pylori</i>	209	39
ORF991	1059526	1060578	leucine dehydrogenase LeuD	U51099	<i>Bacillus cereus</i>	680	45
ORF992	1061553	1060579	3'(2'), 5'-bispophosphate nucleotidase	U40433	<i>Arabidopsis thaliana</i>	335	43
ORF993	1061674	1062411	putative				
ORF994	1062377	1064077	2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase	U29581	<i>Escherichia coli</i>	383	44
ORF995	1064116	1065243	7-keto-8-aminopelargonic acid synthetase (bioF)	M29291	<i>Bacillus sphaericus</i>	200	35
ORF996	1067451	1065178	priA	Y10304	<i>Bacillus subtilis</i>	1009	43

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF997	1068065	1067376	putative				
ORF998	1068209	1068706	putative				
ORF999	1069958	1068819	unknown	U41759	<i>Chlamydia psittaci</i>	777	41
ORF1000	1071163	1070033	unknown	U41759	<i>Chlamydia psittaci</i>	381	36
ORF1001	1072438	1071332	unknown	U41759	<i>Chlamydia psittaci</i>	254	37
ORF1002	1072997	1073476	putative				
ORF1003	1074239	1075864	lysyl-tRNA synthetase	D90906	<i>Synechocystis</i> sp.	1007	48
ORF1004	1076790	1075867	cysteinyI-tRNA synthetase	L14580	<i>Bacillus subtilis</i>	395	52
ORF1005	1077268	1076573	cys-tRNA synthetase (cysS)	U32693	<i>Haemophilus influenzae</i>	431	56
ORF1006	1077999	1078724	putative				
ORF1007	1079088	1078672	ribonuclease P protein component (gtg start codon)	M11056	<i>Escherichia coli</i>	78	46
ORF1008	1079642	1079944	30S ribosomal subunit protein S14	U18997	<i>Escherichia coli</i>	260	50
ORF1009	1080501	1079995	F18C12.2	Z75536	<i>Caenorhabditis elegans</i>	118	38
ORF1010	1080775	1081341	putative				
ORF1011	1083158	1081350	deoxyribodipyrimidine photolyase	J03294	<i>Bacillus subtilis</i>	687	44
ORF1012	1084677	1083235	DNA mismatch repair protein	U71154	<i>Aquifex pyrophilus</i>	735	48
ORF1013	1085648	1084632	DNA mismatch repair protein	D90909	<i>Synechocystis</i> sp.	565	39
ORF1014	1086117	1086737	DNA primase (dnaG)	U32735	<i>Haemophilus influenzae</i>	303	40
ORF1015	1086692	1087897	DnaG	Z83860	<i>Mycobacterium tuberculosis</i>	222	37
ORF1016	1088646	1089005	putative				
ORF1017	1089146	1089805	putative				
ORF1018	1092931	1089890	glycyl-tRNA synthetase	U20547	<i>Chlamydia trachomatis</i>	2569	48
ORF1019	1093179	1092889	putative				
ORF1020	1093584	1094204	phosphatidylglycerophosphate synthase	U87792	<i>Bacillus subtilis</i>	163	55
ORF1021	1095619	1094192	glycogen (starch) synthase	D90899	<i>Synechocystis</i> sp.	574	40
ORF1022	1096074	1096628	partial ctc gene product (AA 1-186)	X16518	<i>Bacillus subtilis</i>	86	37
ORF1023	1096633	1097082	peptidyl-tRNA hydrolase	U31570	<i>Chlamydia trachomatis</i>	378	53
ORF1024	1097266	1097601	ribosomal protein S6 (rps6)	AE000630	<i>Helicobacter pylori</i>	179	39
ORF1025	1097622	1097867	ribosomal protein S18 homolog; putative	M62820	<i>Chlamydia trachomatis</i>	324	86
ORF1026	1097886	1098392	putative heat shock protein ORF; putative	M62820	<i>Chlamydia trachomatis</i>	190	79
ORF1027	1099521	1099279	putative				
ORF1028	1099689	1101053	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1029	1102192	1101107	putative				
ORF1030	1104950	1102116	glycerol-3-phosphate acyltransferase	M80571	<i>Cucumis sativus</i>	574	43
ORF1031	1106508	1104946	ORF_f495; orfF of ECMRED, uses 2nd start	U18997	<i>Escherichia coli</i>	855	38
ORF1032	1106722	1107249	putative				
ORF1033	1107463	1108101	PlsX	U59433	<i>Bacillus subtilis</i>	282	45
ORF1034	1108041	1108421	fatty acid/phospholipid synthesis protein (plsX)	AE000540	<i>Helicobacter pylori</i>	205	35
ORF1035	1108520	1113370	putative 98 kDa outer membrane protein	U72499	<i>Chlamydia psittaci</i>	352	44
ORF1036	1114958	1113447	putative				
ORF1037	1116915	1115071	lipid A disaccharide synthetase (lpxB)	U32786	<i>Haemophilus influenzae</i>	477	42
ORF1038	1118183	1116894	poly(A) polymerase	AE000123	<i>Escherichia coli</i>	555	46
ORF1039	1118846	1120030	putative	L12968	<i>Escherichia coli</i>	880	50
ORF1040	1120040	1120522	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	AE000651	<i>Helicobacter pylori</i>	396	52
ORF1041	1120510	1121430	glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase	AE000450	<i>Escherichia coli</i>	494	44
ORF1042	1121321	1121866	L-glutamine:D-fructose-6-P amidotransferase precursor	U17352	<i>Thermus aquaticus thermophilus</i>	374	50
ORF1043	1122123	1122899	tyrosine-specific transport protein	AE000284	<i>Escherichia coli</i>	281	41
ORF1044	1124842	1125564	putative				
ORF1045	1126526	1125579	cell division protein (ftsY)	U32760	<i>Haemophilus influenzae</i>	497	41
ORF1046	1126519	1127676	succinyl-CoA synthetase beta-subunit	J01619	<i>Escherichia coli</i>	784	43
ORF1047	1127672	1128571	succinyl coenzyme A synthetase alpha subunit	U23408	<i>Dictyostelium discoideum</i>	978	63
ORF1048	1130230	1131336	putative				
ORF1049	1131480	1132553	putative				
ORF1050	1132830	1133843	putative				
ORF1051	1134121	1134855	serine protease HtrA	D90905	<i>Synechocystis sp.</i>	307	51
ORF1052	1134642	1135592	GsrA protein	D78376	<i>Yersinia enterocolitica</i>	497	41
ORF1053	1135964	1135653	putative				
ORF1054	1137132	1135954	R11H6.1	Z93386	<i>Caenorhabditis elegans</i>	445	37
ORF1055	1137169	1140102	Ydr430cp; CAI: 0.15	U33007	<i>Saccharomyces cerevisiae</i>	559	40

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1056	1141365	1140112	hypothetical 54.7 kD protein in udp 3' region precursor (o475)	AE000459	<i>Escherichia coli</i>	222	34
ORF1057	1142150	1141356	phosphatidylserine synthase (pssA)	AE000614	<i>Helicobacter pylori</i>	307	41
ORF1058	1142520	1145660	ribonucleotide reductase subunit M1	K02927	<i>Mus musculus</i>	1433	45
ORF1059	1145627	1146721	ribonucleoside diphosphate reductase, beta subunit (nrdB)	AE000553	<i>Helicobacter pylori</i>	443	32
ORF1060	1146862	1147545	unknown	Z95398	<i>Mycobacterium leprae</i>	191	35
ORF1061	1147666	1148190	YtaB	AF008220	<i>Bacillus subtilis</i>	262	44
ORF1062	1148514	1148224	ORF2	U01958	<i>Bacillus licheniformis</i>	135	54
ORF1063	1149136	1148348	ORF2	M31827	<i>Bacillus subtilis</i>	268	40
ORF1064	1149702	1149166	putative				
ORF1065	1150031	1150591	unknown	Z85982	<i>Mycobacterium tuberculosis</i>	445	49
ORF1066	1150785	1151147	ribosomal protein L20 (AA 1-119)	X16188	<i>Bacillus stearothermophilus</i>	273	44
ORF1067	1151165	1152181	phenylalanyl-tRNA synthetase beta subunit	Z75208	<i>Bacillus subtilis</i>	777	40
ORF1068	1152522	1154591	putative				
ORF1069	1155666	1154566	putative				
ORF1070	1156743	1155670	putative				
ORF1071	1156859	1157815	hypothetical				
ORF1072	1157982	1160735	ATP-binding protein	U32723	<i>Haemophilus influenzae</i>	252	42
ORF1073	1162620	1160917	polynucleotide phosphorylase	U01376	<i>Escherichia coli</i>	1314	56
ORF1074	1162970	1162590	polynucleotide phosphorylase	AF010578	<i>Pisum sativum</i>	1416	52
ORF1075	1163532	1164020	orf150 gene product	U52048	<i>Spinacia oleracea</i>	312	53
ORF1076	1163995	1164294	putative	X95938	<i>Porphyromonas gingivalis</i>	335	43
ORF1077	1165569	1165030	putative				
ORF1078	1166108	1165566	putative				
ORF1079	1166644	1166141	putative				
ORF1080	1167055	1168374	putative				
ORF1081	1169218	1168337	methionine aminopeptidase	D64003	<i>Synechocystis sp.</i>	488	54
ORF1082	1169823	1169218	ORF o197	U18997	<i>Escherichia coli</i>	281	30
ORF1083	1171324	1170572	putative				
ORF1084	1172085	1171177	hypothetical	U32720	<i>Haemophilus influenzae</i>	162	44
ORF1085	1172394	1173773	fumarase	D64000	<i>Synechocystis sp.</i>	1292	57
ORF1086	1175209	1173881	prs-associated putative membrane protein	U02424	<i>Escherichia coli</i>	570	39



ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1087	117555	1175127	hypothetical protein in pth-prs intergenic region	AE000219	<i>Escherichia coli</i>	278	46
ORF1088	1175778	1177043	hypothetical protein	Z96072	<i>Mycobacterium tuberculosis</i>	109	43
ORF1089	1177177	1179048	putative				
ORF1090	1179156	1180085	penicillin tolerance protein (lytB)	U32781	<i>Haemophilus influenzae</i>	731	54
ORF1091	1180045	1180779	putative				
ORF1092	1181942	1180788	putative				
ORF1093	1182296	1181961	putative				
ORF1094	1183844	1182300	putative				
ORF1095	1184420	1183848	putative				
ORF1096	1185382	1184366	putative				
ORF1097	1185858	1185226	putative				
ORF1098	1186164	1186481	putative				
ORF1099	1187386	1186484	site-specific recombinase	U92524	<i>Salmonella typhimurium</i>	401	48
ORF1100	1187370	1189028	phosphoglucosomerase-like protein	L40822	<i>Chlamydia trachomatis</i>	1154	63
ORF1101	1189321	1190889	putative				
ORF1102	1191142	1192146	NADP-malate dehydrogenase	L40958	<i>Flavaria bidentis</i>	775	46
ORF1103	1191974	1191729	putative				
ORF1104	1193815	1192991	putative				
ORF1105	1195702	1194248	o460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD PSEAE SW: P18275	AE000256	<i>Escherichia coli</i>	1022	44
ORF1106	1196303	1195716	putative				
ORF1107	1196831	1196337	putative				
ORF1108	1197807	1196746	putative				
ORF1109	1198740	1197883	putative				
ORF1110	1200232	1198721	shikimate 5-dehydrogenase	U67551	<i>Methanococcus jannaschii</i>	245	37
ORF1111	1201286	1200135	3-dehydroquinase synthase (aroB)	U32705	<i>Haemophilus influenzae</i>	478	45
ORF1112	1202386	1201259	2,3-dihydroxybenzoic acid	L29562	<i>Vibrio anguillarum</i>	780	50
ORF1113	1202901	1202350	putative				
ORF1114	1204162	1202816	5-enolpyruvylshikimate 3-phosphate synthase	U67500	<i>Methanococcus jannaschii</i>	520	40
ORF1115	1203177	1203464	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1116	1205028	1204180	putative				
ORF1117	1206392	1204878	bioA gene product	A02587	unidentified	834	48
ORF1118	1206742	1206086	dethiobiotin synthase (bioD)	U32830	<i>Haemophilus influenzae</i>	243	37
ORF1119	1207872	1206724	L-alanine - pimelyl CoA ligase	U51868	<i>Bacillus subtilis</i>	601	41
ORF1120	1208852	1207851	biotin synthase	U24147	<i>Arabidopsis thaliana</i>	892	52
ORF1121	1210518	1209742	tryptophan hydroxylase	U26428	<i>Gallus gallus</i>	237	34
ORF1122	1210703	1211494	dihydrodipicolinate reductase	U47017	<i>Pseudomonas syringae pv. tabaci</i>	345	37
ORF1123	1211870	1212754	aspartate-semialdehyde dehydrogenase	U67476	<i>Methanococcus jannaschii</i>	444	43
ORF1124	1212742	1214064	aspartokinase III	U00006	<i>Escherichia coli</i>	473	47
ORF1125	1214046	1214858	dihydrodipicolinate synthase	D64006	<i>Synechocystis sp.</i>	238	40
ORF1126	1215551	1216318	putative				
ORF1127	1216493	1216849	putative				
ORF1128	1217183	1219612	putative				
ORF1129	1220068	1219673	putative				
ORF1130	1219710	1220669	putative				
ORF1131	1220630	1221376	putative				
ORF1132	1221645	1223681	unknown	D26185	<i>Bacillus subtilis</i>	621	43
ORF1133	1223894	1224988	putative				
ORF1134	1225000	1225830	high level kasamycin resistance	D26185	<i>Bacillus subtilis</i>	422	41
ORF1135	1227810	1225879	hypothetical protein	D90903	<i>Synechocystis sp.</i>	1129	43
ORF1136	1226528	1226908	putative				
ORF1137	1229972	1228311	exonuclease VII, large subunit (xseA)	U32723	<i>Haemophilus influenzae</i>	666	46
ORF1138	47569	47018	Integrase/recombinase	AE001308	<i>Chlamydia trachomatis</i>	716	72
ORF1139	49980	49117	putative				
ORF1140	53356	52898	putative				
ORF1141	54477	54884	O-Sialoglycoprotein Endopeptidase	AE001307	<i>Chlamydia trachomatis</i>	311	51
ORF1142	63753	63998	PTS PEP Phosphotransferase	AE001306	<i>Chlamydia trachomatis</i>	198	61
ORF1143	77164	77487	putative				
ORF1144	79724	79302	Sms Protein	AE001302	<i>Chlamydia trachomatis</i>	458	57
ORF1145	88721	88951	putative				
ORF1146	94067	94429	putative				
ORF1147	122832	123341	hypothetical protein	AE001303	<i>Chlamydia trachomatis</i>	398	61
ORF1148	147536	147234	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1149	158990	159346	S16 Ribosomal Protein	AE001277	<i>Chlamydia trachomatis</i>	467	78
ORF1150	168470	168979	putative				
ORF1151	169183	169452	putative				
ORF1152	171785	171504	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	262	68
ORF1153	172518	171775	Cationic Amino Acid Transporter	AE001278	<i>Chlamydia trachomatis</i>	533	48
ORF1154	193599	194045	putative				
ORF1155	195704	196075	S/T Protein Kinase	AE001288	<i>Chlamydia trachomatis</i>	536	82
ORF1156	210687	210145	KDO-transferase	X80061	<i>Chlamydia pneumoniae</i>	856	96
ORF1157	211100	210708	putative				
ORF1158	215420	215088	putative				
ORF1159	217914	218246	putative				
ORF1160	218925	218701	putative				
ORF1161	223785	223525	IMP dehydrogenase	U13372	<i>Borrelia burgdorferi</i>	270	63
ORF1162	224271	223999	putative				
ORF1163	228691	228407	putative				
ORF1164	235050	235334	(Methylase)	AE001287	<i>Chlamydia trachomatis</i>	331	66
ORF1165	252308	253021	Oligopeptide Permease	AE001293	<i>Chlamydia trachomatis</i>	838	72
ORF1166	258280	258912	Dicarboxylate Translocator	AE001294	<i>Chlamydia trachomatis</i>	909	80
ORF1167	261325	261567	putative				
ORF1168	268195	268878	hypothetical protein	AE001287	<i>Chlamydia trachomatis</i>	556	52
ORF1169	269447	268881	putative				
ORF1170	271263	271538	putative				
ORF1171	271957	272346	putative				
ORF1172	274176	274550	putative				
ORF1173	275736	275314	Disulfide bond Oxidoreductase	AE001291	<i>Chlamydia trachomatis</i>	519	73
ORF1174	276490	276927	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	249	53
ORF1175	277577	277861	hypothetical protein	AE001291	<i>Chlamydia trachomatis</i>	256	52
ORF1176	288163	287909	putative				
ORF1177	290130	289789	putative				
ORF1178	290989	291225	putative				
ORF1179	291372	291860	adenylate cyclase	AE001286	<i>Chlamydia trachomatis</i>	388	48
ORF1180	311239	311622	putative				
ORF1181	328665	328384	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1182	337348	338289	sodium-dependent transporter	AF017105	<i>Chlamydia psittaci</i>	1112	72
ORF1183	364764	364369	Prolipoprotein Diacylglycerol Transferase	AE001298	<i>Chlamydia trachomatis</i>	300	54
ORF1184	389623	390135	hypothetical protein	AE001282	<i>Chlamydia trachomatis</i>	75	33
ORF1185	393729	394343	ABC superfamily ATPase	AE001282	<i>Chlamydia trachomatis</i>	473	52
ORF1186	407379	407621	putative				
ORF1187	410944	410708	putative				
ORF1188	427632	427988	putative				
ORF1189	428172	428486	putative				
ORF1190	436761	437246	hypothetical protein	AE001279	<i>Chlamydia trachomatis</i>	661	81
ORF1191	460911	461159	putative				
ORF1192	477597	477313	hypothetical protein	AE001300	<i>Chlamydia trachomatis</i>	309	62
ORF1193	487303	487001	putative				
ORF1194	487764	487534	Glycine Cleavage System H Protein	AE001300	<i>Chlamydia trachomatis</i>	221	67
ORF1195	498502	499017	hypothetical protein	AE001275	<i>Chlamydia trachomatis</i>	206	32
ORF1196	499795	500466	putative				
ORF1197	571928	572344	putative				
ORF1198	572367	572131	putative				
ORF1199	588184	587915	hypothetical protein	AE001312	<i>Chlamydia trachomatis</i>	256	62
ORF1200	600587	600907	(Metalloenzyme)	AE001316	<i>Chlamydia trachomatis</i>	314	61
ORF1201	609731	608895	putative				
ORF1202	614039	614755	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	475	46
ORF1203	614823	615152	putative				
ORF1204	638244	638831	ABC Transporter ATPase	AE001315	<i>Chlamydia trachomatis</i>	614	61
ORF1205	638819	639094	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	265	63
ORF1206	639073	639636	(Metal Transport Protein)	AE001315	<i>Chlamydia trachomatis</i>	687	69
ORF1207	647901	648236	hypothetical protein	AE001317	<i>Chlamydia trachomatis</i>	139	38
ORF1208	678510	679469	phosphohydrolase	AE001320	<i>Chlamydia trachomatis</i>	995	63
ORF1209	688178	688732	hypothetical protein	AE001320	<i>Chlamydia trachomatis</i>	366	43
ORF1210	696045	696563	methyltransferase	AE001321	<i>Chlamydia trachomatis</i>	369	49
ORF1211	708998	708588	Glucose-1-P Adenylyltransferase	AE001322	<i>Chlamydia trachomatis</i>	507	83
ORF1212	709808	710089	putative				
ORF1213	718240	717737	Glycerol-3-P Phosphatidyltransferase	AE001323	<i>Chlamydia trachomatis</i>	573	66
ORF1214	737828	737565	S19 Ribosomal Protein	AE001323	<i>Chlamydia trachomatis</i>	439	94

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1215	779502	780257	hypothetical protein	AE001322	<i>Chlamydia trachomatis</i>	476	48
ORF1216	806310	805864	hypothetical protein	AE001337	<i>Chlamydia trachomatis</i>	512	67
ORF1217	820931	820707	putative				
ORF1218	837696	839096	Exodeoxyribonuclease V, Gamma	AE001334	<i>Chlamydia trachomatis</i>	967	49
ORF1219	883307	883549	putative				
ORF1220	892010	891726	putative				
ORF1221	893277	893564	putative				
ORF1222	936998	937225	Gen. Secretion Protein E	AE001327	<i>Chlamydia trachomatis</i>	256	67
ORF1223	946865	947419	putative				
ORF1224	975187	975411	SWF/SNF family helicase	AE001341	<i>Chlamydia trachomatis</i>	363	96
ORF1225	985882	985517	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	166	33
ORF1226	987713	987180	hypothetical protein	AE001342	<i>Chlamydia trachomatis</i>	447	59
ORF1227	988215	987733	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	304	44
ORF1228	988754	988530	Flagellar M-Ring Protein	AE001342	<i>Chlamydia trachomatis</i>	92	36
ORF1229	992542	992841	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	112	39
ORF1230	992759	993067	hypothetical protein	AE001343	<i>Chlamydia trachomatis</i>	100	32
ORF1231	1004247	1004528	D-Ala/Gly Permease	AE001344	<i>Chlamydia trachomatis</i>	283	64
ORF1232	1015013	1014294	235aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	104	54
ORF1233	1056147	1056545	putative				
ORF1234	1077682	1078035	predicted disulfide bond isomerase	AE001351	<i>Chlamydia trachomatis</i>	233	46
ORF1235	1088121	1088381	putative				
ORF1236	1098430	1098852	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	384	59
ORF1237	1098798	1099319	Predicted Kinase	AE001352	<i>Chlamydia trachomatis</i>	322	45
ORF1238	1123198	1123515	Transport Permease	AE001354	<i>Chlamydia trachomatis</i>	313	72
ORF1239	1123606	1124256	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	577	58
ORF1240	1124453	1124797	Tyrosine Transport	AE001354	<i>Chlamydia trachomatis</i>	323	50
ORF1241	1129253	1129567	putative				
ORF1242	1164947	1164474	hypothetical protein	AE001357	<i>Chlamydia trachomatis</i>	412	56
ORF1243	1170457	1170053	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	283	59
ORF1244	1172342	1171863	ABC transporter permease	AE001358	<i>Chlamydia trachomatis</i>	457	55
ORF1245	1192155	1192835	putative				
ORF1246	1192759	1192992	putative				
ORF1247	1193861	1194142	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1248	1194036	1193779	(D-Amino Acid Dehydrogenase)	AE001311	<i>Chlamydia trachomatis</i>	269	79
ORF1249	1209748	1209053	conserved hypothetical protein	AE000958	<i>Archaeoglobus fulgidus</i>	121	38
ORF1250	1215111	1215419	putative				
ORF1251	1216302	1216538	putative				
ORF1252	1228072	1227818	hypothetical protein	AE001306	<i>Chlamydia trachomatis</i>	134	39
ORF1253	1228304	1228080	xseB	AL021897	<i>Mycobacterium tuberculosis</i>	89	33
ORF1254	26599	26222	putative				
ORF1255	27609	27367	putative				
ORF1256	67206	66967	putative				
ORF1257	70612	70352	putative				
ORF1258	132703	132945	putative				
ORF1259	178073	178393	putative				
ORF1260	208576	208349	putative				
ORF1261	209156	208929	putative				
ORF1262	209263	209024	putative				
ORF1263	210304	210639	putative				
ORF1264	299009	299452	putative				
ORF1265	352106	351717	putative				
ORF1266	420182	419949	Flagellar Secretion Protein	AE001280	<i>Chlamydia trachomatis</i>	115	43
ORF1267	553602	553381	putative				
ORF1268	556538	556807	putative				
ORF1269	594348	593797	putative				
ORF1270	595169	594876	putative				
ORF1271	662148	662381	putative				
ORF1272	706528	706893	putative				
ORF1273	803315	803650	putative				
ORF1274	849551	849306	putative				
ORF1275	913676	913275	putative				
ORF1276	927087	926836	putative				
ORF1277	930587	930360	putative				
ORF1278	986531	986764	ORF 12	M72718	<i>Bacillus subtilis</i>	106	48
ORF1279	996229	996486	putative				
ORF1280	1000373	1000002	putative				

ORF	Begin	End	Homology	ID	Species	Score	I%
ORF1281	1010291	1010037	putative				
ORF1282	1011128	1010793	106aa long hypothetical protein	AB009472	<i>Pyrococcus horikoshii</i>	159	50
ORF1283	1012924	1012694	putative				
ORF1284	1028659	1028913	putative				
ORF1285	1086481	1086762	putative				
ORF1286	1118658	1118879	Phosphoglucomutase	AE001354	<i>Chlamydia trachomatis</i>	291	84
ORF1287	1170098	1169835	hypothetical protein	AE001358	<i>Chlamydia trachomatis</i>	187	53
ORF1288	1180828	1181184	putative				
ORF1289	1182658	1183035	putative				
ORF1290	1195076	1194795	putative				
ORF1291	1195890	1196183	putative				

Table 2

ORF Nos	begin	end	potential start
2	42	794	42
3	1258	1614	1261
4	1807	2418	1807
5	3393	2491	3393
6	3639	4067	3639
7	5649	4270	5649
8	7463	6012	7463
9	8051	8962	8051
10	9129	9959	9138
11	10687	10361	10639
12	10927	11232	10927
13	11246	12727	11246
14	12691	14190	12691
15	14484	17249	14484
16	16039	15770	16036
17	17845	20853	17845
18	21137	22042	21137
19	22046	23476	22046
20	23681	26110	23681
21	26109	25861	26109
22	26241	26978	26241
23	26960	27754	26960
24	27747	28577	27747
25	28887	29492	28950
26	29432	30028	29432
27	30024	31472	30024
28	31758	32288	31758
29	32201	33991	32201
30	33852	34541	33852
31	34783	36063	34783
32	36009	37529	36009
33	37881	39362	37881
34	39418	39161	39418



ORF Nos	begin	end	potential start
35	39366	40715	39366
36	43076	41094	43076
37	43800	43066	43800
38	44828	43785	44768
39	45340	44753	45340
40	45752	45372	45752
41	46996	45701	46996
42	47961	47569	47961
43	48960	48040	48960
44	51452	50133	51452
45	52606	51335	52606
46	53684	53319	53684
47	54195	53746	54195
48	55278	56453	55278
49	56493	57266	56493
50	57297	58526	57297
51	59851	58565	59851
52	61495	59924	61495
53	61324	62151	61324
54	62132	62470	62132
55	62474	63733	62474
56	63881	64186	63881
57	64611	64318	64611
58	65485	64673	65485
59	65999	65301	65999
60	66244	67281	66244
61	67265	67699	67265
62	67703	68539	67760
63	68805	70736	68805
64	69172	68831	69172
65	70642	71142	70642
66	71325	72029	71325
67	72060	73637	72060
68	74061	76175	74061

ORF Nos	begin	end	potential start
69	78351	77680	78351
70	79356	78355	79356
71	79983	79693	79983
72	80441	79938	80441
73	80475	80969	80475
74	81296	83080	81332
75	83291	83932	83291
76	84005	84769	84005
77	84975	85244	84975
78	85123	85425	85123
79	85397	85903	85397
80	85909	86583	85909
81	86626	88065	86626
82	89257	91026	89257
83	91291	93030	91291
84	93295	94086	93295
85	95285	94707	95279
86	95667	96557	95667
87	96317	97456	96317
88	98435	97968	98435
89	99460	98426	99460
90	100144	101325	100144
91	101457	101720	101457
92	101704	102273	101704
93	102356	102805	102356
94	102835	103530	102835
95	103549	104058	103549
96	104096	104491	104096
97	104601	108386	104601
98	108401	112054	108401
99	112033	112590	112033
100	112672	113682	112672
101	113726	114121	113726
102	114711	114136	114711

ORF Nos	begin	end	potential start
103	115267	115755	115267
104	115911	116543	115911
105	116736	118055	116778
106	117968	118522	117968
107	118530	119843	118530
108	119816	120457	119816
109	120451	122430	120451
110	122504	122950	122504
111	123528	126347	123528
112	126332	129166	126332
113	134690	129213	134690
114	134925	136382	134931
115	137870	136482	137867
116	137899	138240	137899
117	138239	137928	138239
118	139558	138257	139558
119	140352	139516	140352
120	140498	141841	140498
121	141855	142658	141855
122	144258	143050	144258
123	145258	144494	145258
124	145454	146749	145454
125	147318	146767	147318
126	148261	147677	148261
127	149029	152157	149029
128	154108	152201	154108
129	155135	154308	155135
130	155141	155467	155141
131	155703	156779	155703
132	156748	157635	156748
133	157653	158996	157653
134	159363	159986	159363
135	159880	160446	159880
136	160477	160839	160477

ORF Nos	begin	end	potential start
137	160898	161539	160898
138	161527	162153	161527
139	162144	162443	162144
140	162437	164098	162437
141	165451	164228	165451
142	166349	165411	166349
143	166949	168442	166949
144	169416	171029	169416
145	170857	171459	170857
146	172652	173428	172652
147	174626	173439	174626
148	174816	175613	174816
149	175598	175954	175598
150	175958	176935	175958
151	177708	176938	177708
152	177128	177376	177128
153	179472	177841	179472
154	179822	179517	179822
155	181793	179943	181793
156	182628	181876	182628
157	184420	183074	184420
158	184988	184467	184988
159	185483	185112	185483
160	185902	185483	185902
161	186174	185839	186174
162	187720	186587	187720
163	188318	190933	188318
164	191090	191635	191090
165	191547	192743	191547
166	192969	193469	192969
167	194044	193610	194044
168	194196	195809	194196
169	196088	198073	196088
170	198132	199454	198132

ORF Nos	begin	end	potential start
171	199351	202818	199351
172	204552	202999	204552
173	205648	204692	205639
174	205807	207327	205807
175	207182	207775	207182
176	207779	208267	207779
177	208267	209577	208267
178	211807	211271	211807
179	212188	211844	212188
180	214079	212448	214079
181	214907	214083	214907
182	216154	215429	216154
183	216115	216678	216115
184	216728	217282	216728
185	217267	217866	217267
186	218593	218261	218590
187	219821	218994	219821
188	221382	220309	221382
189	222719	221433	222719
190	223521	222724	223521
191	224499	225008	224499
192	225140	225559	225140
193	225555	226802	225555
194	227800	226892	227743
195	228335	228072	228335
196	229251	228643	229251
197	230983	229622	230983
198	231483	230983	231483
199	232063	231509	232063
200	232739	232053	232739
201	233166	234356	233166
202	233518	233165	233518
203	234536	235186	234536
204	235379	236689	235379

ORF Nos	begin	end	potential start
205	236680	237618	236689
206	237521	238345	237521
207	238281	238973	238281
208	238871	240115	238871
209	240191	241564	240191
210	242281	241604	242281
211	242933	242274	242933
212	243416	242976	243416
213	243500	244531	243500
214	244480	246021	244480
215	246330	247811	246330
216	247831	249174	247870
217	249437	251038	249455
218	251325	252212	251325
219	253156	254007	253156
220	253974	254852	253974
221	255258	256094	255258
222	256640	257455	256640
223	257502	258239	257502
224	257869	257501	257869
225	259248	260897	259248
226	262753	261788	262753
227	263059	262757	263059
228	264375	263182	264375
229	265985	264747	265985
230	266637	266059	266637
231	267338	266538	267338
232	267922	267473	267922
233	269647	270771	269647
234	272777	273145	272777
235	273253	273636	273253
236	273705	273977	273705
237	276016	275717	276016
238	276439	276020	276418

ORF Nos	begin	end	potential start
239	276792	277253	276792
240	277318	277599	277318
241	278578	277877	278578
242	279258	278554	279258
243	280435	279533	280435
244	281547	280849	281547
245	281696	282325	281717
246	282459	284069	282459
247	284056	284517	284056
248	284606	285775	284606
249	285592	285987	285592
250	286179	286976	286179
251	287583	287002	287583
252	287951	287451	287951
253	288499	288816	288499
254	289674	288505	289674
255	288839	289213	288839
256	289970	290254	289970
257	291931	292803	291931
258	293258	292755	293258
259	293718	293272	293718
260	294630	293953	294630
261	296153	294636	296153
262	294817	295068	294817
263	296354	297862	296354
264	298415	297879	298415
265	298777	298253	298777
266	299572	298781	299572
267	300487	299633	300487
268	301586	300702	301568
269	302440	301571	302440
270	302838	302437	302838
271	303335	302745	303335
272	304394	303852	304394

ORF Nos	begin	end	potential start
273	304606	305223	304606
274	305394	306236	305394
275	306501	307439	306501
276	308033	307458	308033
277	308924	308037	308924
278	309485	310180	309485
279	310426	311214	310426
280	311597	311253	311504
281	312772	311780	312772
282	313425	312772	313425
283	313646	313377	313646
284	313937	314665	313937
285	315576	314755	315576
286	316157	315531	316157
287	318657	316156	318657
288	321042	318676	321042
289	321445	321098	321445
290	322309	321710	322309
291	323190	322366	323181
292	323843	323181	323843
293	324878	323856	324878
294	325340	326410	325340
295	326433	327836	326433
296	328465	327839	328465
297	329360	328857	329360
298	330907	329357	330907
299	332455	330956	332455
300	334536	332395	334536
301	336091	334877	336091
302	336103	337302	336103
303	338129	338830	338129
304	338965	339501	338965
305	339508	340143	339508
306	340247	342967	340247



ORF Nos	begin	end	potential start
307	343385	343810	343385
308	344171	343935	344171
309	345082	344330	345073
310	346005	345082	346005
311	346784	346437	346784
312	347029	346715	347029
313	347034	347723	347034
314	348075	350459	348075
315	350598	351071	350598
316	351075	352175	351096
317	353291	352230	353267
318	353442	354467	353442
319	354451	354933	354451
320	355000	355449	355000
321	355448	356743	355448
322	355953	355642	355953
323	359310	356827	359310
324	359120	359377	359120
325	359525	359908	359525
326	361290	359947	361290
327	363785	361362	363746
328	364496	363888	364496
329	364832	365290	364832
330	365304	365669	365304
331	366599	365667	366599
332	367291	369030	367291
333	369134	369808	369134
334	369917	370438	369917
335	370365	372647	370365
336	372557	373066	372557
337	373020	373442	373020
338	373467	374195	373467
339	374176	375099	374176
340	375676	375083	375676

ORF Nos	begin	end	potential start
341	376173	375634	376173
342	376564	377643	376564
343	377956	379773	377956
344	379781	380425	379805
345	380281	381000	380281
346	381008	381460	381008
347	381460	383037	381460
348	383257	383523	383257
349	383553	385304	383553
350	385397	386458	385400
351	387242	386514	387242
352	388764	387013	388764
353	390120	390932	390120
354	390919	391818	390961
355	392379	391885	392379
356	392582	392986	392582
357	392776	393684	392776
358	394151	394804	394151
359	394928	395308	394928
360	395259	395990	395259
361	397815	395953	397815
362	398850	397831	398850
363	400085	399099	400085
364	401245	400073	401236
365	401474	401136	401474
366	402199	401423	402199
367	403193	402186	403166
368	403650	404165	403650
369	404343	405914	404343
370	405984	407327	405984
371	407712	408806	407712
372	410439	409075	410439
373	411826	410954	411826
374	412482	414302	412482

ORF Nos	begin	end	potential start
375	415402	414407	415402
376	415848	415237	415848
377	417131	415866	417131
378	417258	417566	417258
379	418326	417454	418326
380	420057	418426	420057
381	420448	420720	420448
382	420980	421552	420980
383	421556	422029	421556
384	422461	422925	422461
385	423562	424320	423562
386	424250	424591	424250
387	424830	426047	424830
388	426240	427397	426240
389	428841	430703	428841
390	430694	431446	430694
391	431597	432100	431597
392	432165	432779	432165
393	433272	432832	433272
394	433925	433227	433922
395	436678	433934	436678
396	437176	438357	437176
397	440317	438518	440317
398	440001	440345	440001
399	441233	440517	441233
400	440719	441012	440719
401	442192	441230	442192
402	442888	442343	442888
403	442371	442961	442371
404	443578	443003	443578
405	444500	443526	444500
406	444842	444528	444842
407	445009	444743	445009
408	445718	445182	445718

ORF Nos	begin	end	potential start
409	445807	447804	445807
410	448738	447803	448738
411	449628	448618	449628
412	450298	450867	450298
413	450713	451207	450713
414	451211	452452	451211
415	452448	453659	452448
416	454843	453725	454843
417	455608	454865	455608
418	456243	457007	456243
419	457016	457708	457016
420	458368	457979	458368
421	459496	458372	459496
422	459493	460194	459493
423	461446	460355	461446
424	462298	461450	462298
425	462444	463349	462444
426	464241	463342	464241
427	464574	465065	464574
428	465129	465611	465129
429	465571	466317	465571
430	466317	467093	466317
431	466999	467502	466999
432	469691	467715	469691
433	470691	469660	470691
434	472010	470709	472010
435	471545	471799	471545
436	472359	472045	472359
437	473523	472732	473523
438	474889	473441	474889
439	477323	475365	477323
440	478496	477597	478496
441	478722	479273	478722
442	479277	479705	479277

ORF Nos	begin	end	potential start
443	480050	481450	480050
444	481469	482053	481469
445	482600	482025	482600
446	482654	484204	482654
447	484211	485170	484211
448	485170	485838	485170
449	485813	486580	485813
450	486976	486638	486976
451	489071	487764	489071
452	489341	489090	489341
453	489958	489152	489958
454	490549	489962	490549
455	491163	490522	491163
456	491396	491112	491396
457	492121	491390	492121
458	492304	494838	492304
459	495943	494822	495943
460	496011	496565	496170
461	496569	497228	496569
462	497358	497834	497358
463	497770	498327	497770
464	499209	499589	499209
465	499520	499792	499520
466	500774	504169	500774
467	504139	504600	504139
468	504865	506877	504865
469	506790	507671	506790
470	507718	510507	507718
471	508325	507912	508325
472	510660	513440	510660
473	514965	513787	514920
474	517347	515419	517347
475	517058	517363	517058
476	517798	517277	517798

ORF Nos	begin	end	potential start
477	518200	517847	518200
478	518300	521146	518363
479	521392	522948	521407
480	523244	524809	523322
481	524379	524125	524379
482	524649	526238	524649
483	526265	527104	526268
484	526947	526702	526947
485	526975	528450	526975
486	528408	529199	528408
487	530612	529542	530612
488	531656	530616	531656
489	533974	532067	533974
490	536432	534324	536432
491	537150	536707	537150
492	537928	537080	537928
493	538438	537932	538438
494	538737	538333	538737
495	539594	539127	539594
496	541215	539590	541215
497	542571	541282	542571
498	543014	542457	543014
499	543369	542962	543369
500	543809	546628	543815
501	546619	549525	546619
502	547293	546994	547293
503	549699	550523	549699
504	550490	551551	550490
505	551448	552623	551448
506	552652	555117	552652
507	555029	555493	555029
508	558006	555673	558006
509	559694	558162	559694
510	558208	558573	558208

ORF Nos	begin	end	potential start
511	561692	559899	561692
512	561412	561708	561412
513	563942	561777	563942
514	564969	563950	564969
515	566204	564936	566198
516	567717	566302	567717
517	568526	567708	568526
518	569467	568742	569467
519	571065	569431	571065
520	571828	571118	571783
521	572202	573308	572202
522	573146	575056	573146
523	575023	575916	575023
524	577891	576497	577891
525	578914	578204	578914
526	579924	578857	579924
527	580187	579858	580187
528	580017	580406	580017
529	581086	580187	581086
530	581367	581828	581367
531	581678	582367	581678
532	582361	583428	582361
533	584690	583431	584690
534	585237	584950	585237
535	585626	586888	585626
536	586846	587907	586888
537	589049	588180	589049
538	590500	589301	590455
539	590755	592458	590755
540	592526	592903	592526
541	592836	593747	592836
542	593747	594298	593747
543	594331	595947	594331
544	595905	596309	595905

ORF Nos	begin	end	potential start
545	596514	597215	596514
546	597184	597957	597184
547	597755	598612	597755
548	598602	599204	598602
549	599373	599939	599373
550	600903	602072	600903
551	602240	602587	602240
552	602637	603272	602637
553	603142	604512	603142
554	604627	605853	604627
555	605790	606620	605790
556	606571	607281	606571
557	609004	607355	609004
558	610906	609932	610906
559	611786	611004	611786
560	612333	611746	612333
561	613897	612341	613897
562	615179	616279	615179
563	616610	617383	616610
564	618796	617810	618796
565	620004	618826	620004
566	619649	619918	619649
567	621265	620021	621265
568	622359	621265	622359
569	623420	622560	623420
570	624297	623335	624297
571	624773	624174	624773
572	625029	625484	625029
573	625488	625883	625488
574	625892	626395	625892
575	626444	627790	626444
576	627912	628607	627930
577	628774	629697	628774
578	629660	631639	629660



ORF Nos	begin	end	potential start
579	631725	633551	631725
580	633520	636957	633520
581	637232	638098	637232
582	640648	639593	640648
583	640979	640728	640979
584	641327	641007	641327
585	641687	642283	641687
586	643023	642286	643023
587	643330	643076	643330
588	643704	643351	643704
589	645628	643676	645628
590	645783	645538	645756
591	646269	645793	646269
592	646751	646314	646751
593	647848	647045	647848
594	648393	650336	648393
595	651016	650420	651007
596	652956	651289	652956
597	653395	653126	653395
598	655740	654193	655740
599	656508	655966	656508
600	658140	657022	658140
601	660216	658525	660216
602	663238	660248	663238
603	664461	663157	664452
604	665735	664635	665735
605	666212	666994	666212
606	666998	667921	666998
607	667909	668568	667909
608	668502	669203	668502
609	669154	670893	669175
610	672226	670853	672226
611	671137	671424	671137
612	672453	673001	672453

ORF Nos	begin	end	potential start
613	673072	674721	673072
614	674549	674262	674549
615	675518	674796	675518
616	676083	675499	676083
617	676630	676067	676630
618	677016	676600	677016
619	677647	677015	677647
620	677990	678259	677990
621	679444	680097	679444
622	680097	680897	680097
623	681637	680849	681637
624	681409	682281	681409
625	682453	682821	682453
626	682763	683902	682763
627	684616	683969	684616
628	685169	684534	685169
629	685986	685117	685986
630	686278	687288	686278
631	687483	688151	687483
632	688740	689501	688740
633	690242	689622	690242
634	690470	691126	690470
635	692600	691497	692600
636	692674	695064	692674
637	695049	696032	695064
638	697964	696585	697964
639	699803	698274	699803
640	701926	699788	701926
641	703196	702567	703196
642	704221	703208	704221
643	704240	705289	704240
644	706070	705300	706070
645	706841	706254	706838
646	707596	706811	707596

ORF Nos	begin	end	potential start
647	708666	707677	708666
648	709793	709119	709793
649	711523	710132	711523
650	712236	711523	712236
651	714734	712125	714734
652	715759	714761	715759
653	717538	715886	717538
654	719113	720243	719113
655	720590	722422	720590
656	722406	723056	722406
657	723551	723120	723551
658	724246	723626	724246
659	724754	724251	724754
660	725868	724900	725868
661	727115	726270	727115
662	728126	727119	728126
663	728594	728208	728594
664	729614	728604	729614
665	729778	729533	729778
666	730149	729751	730149
667	730539	730174	730539
668	731983	730598	731983
669	732427	731996	732427
670	732917	732423	732917
671	733598	733320	733598
672	733869	733492	733869
673	734298	733900	734298
674	734858	734319	734858
675	735195	734863	735195
676	735578	735342	735578
677	735861	735604	735861
678	736492	736079	736492
679	737192	736524	737192
680	737555	737211	737555

ORF Nos	begin	end	potential start
681	738688	737837	738688
682	739048	738713	739048
683	739736	739065	739736
684	740477	739773	740477
685	740659	740958	740659
686	741722	740721	741722
687	742789	741827	742789
688	743618	742782	743618
689	744092	743634	744092
690	744604	744107	744604
691	744953	744498	744953
692	746608	744986	746608
693	747085	746621	747085
694	747974	747219	747974
695	748594	748169	748594
696	749145	748573	749145
697	749652	749957	749652
698	750446	749979	750446
699	751219	750446	751219
700	753042	751291	753042
701	754309	753020	754309
702	755120	756175	755120
703	756120	756485	756120
704	756499	760227	756499
705	761217	760297	761178
706	761297	761809	761330
707	761782	762282	761782
708	762260	762895	762299
709	762867	763316	762867
710	763780	763325	763780
711	763861	765168	763861
712	766809	765697	766809
713	768051	766888	768051
714	768566	768321	768566

ORF Nos	begin	end	potential start
715	769342	768551	769342
716	770532	769378	770532
717	771451	770804	771451
718	773058	771847	773058
719	773094	773456	773094
720	774376	773093	774376
721	775123	774380	775123
722	775398	774916	775398
723	775046	776077	775046
724	776070	777041	776070
725	777964	777536	777964
726	778176	777904	778176
727	778621	779334	778684
728	781173	780307	781173
729	781526	781116	781526
730	782784	781555	782784
731	783572	782805	783572
732	785032	783581	785032
733	786412	785360	786412
734	788429	786450	788429
735	788944	788528	788944
736	789758	788901	789758
737	790332	791504	790338
738	791846	792721	791846
739	792724	793569	792724
740	793580	794323	793580
741	794304	794843	794304
742	795217	795732	795217
743	795722	796795	795722
744	798735	797053	798735
745	799823	798681	799823
746	799297	799578	799297
747	801313	799808	801313
748	802453	801332	802453

ORF Nos	begin	end	potential start
749	803299	802457	803299
750	803811	803290	803811
751	805151	803826	805151
752	805860	805156	805860
753	806604	806332	806604
754	806913	806608	806913
755	808222	806903	808222
756	808751	808146	808751
757	809437	808673	809437
758	809939	809454	809939
759	811235	810213	811235
760	811779	813056	811779
761	812890	812516	812890
762	812954	813583	812954
763	813587	815023	813587
764	815420	815746	815420
765	816036	817010	816036
766	817111	817356	817111
767	817791	818609	817797
768	818609	819094	818609
769	819104	819823	819104
770	820722	819826	820722
771	822313	821000	822313
772	823503	822238	823503
773	823678	825612	823678
774	825461	826312	825461
775	827280	826645	827280
776	828604	827171	828604
777	830026	828713	830026
778	831047	830085	831047
779	831725	831051	831725
780	832220	833098	832220
781	833851	833396	833851
782	834068	835039	834068

ORF Nos	begin	end	potential start
783	835792	835127	835792
784	837624	836116	837624
785	838951	840882	838951
786	840869	842185	840869
787	841989	843455	841989
788	843242	844021	843242
789	845018	843987	844997
790	846174	844990	846174
791	848509	846311	848509
792	848568	849014	848568
793	849082	850488	849088
794	851512	850574	851512
795	852064	852447	852064
796	852398	853690	852398
797	855118	854243	855118
798	855751	855128	855751
799	856551	855829	856551
800	856730	858556	856730
801	858717	859601	858717
802	859591	860205	859591
803	861132	860284	861132
804	861426	861163	861426
805	861701	862921	861701
806	863026	864798	863026
807	864831	865256	864831
808	865226	866581	865226
809	866562	867119	866562
810	867025	867816	867025
811	867820	868497	867820
812	869743	868661	869743
813	870633	870094	870633
814	871929	870646	871929
815	872538	872086	872538
816	873908	872517	873908

ORF Nos	begin	end	potential start
817	874281	874670	874281
818	874582	875286	874582
819	877857	875377	877857
820	878446	879255	878446
821	880635	879268	880635
822	882524	880593	882524
823	882612	883319	882612
824	884155	883538	884155
825	884340	885611	884343
826	885722	887302	885722
827	887587	888153	887587
828	888627	888220	888627
829	889330	888716	889330
830	889898	889323	889898
831	891190	889898	891190
832	891828	891247	891828
833	892421	892017	892421
834	893116	892421	893116
835	892521	892925	892521
836	893392	895419	893392
837	895745	896527	895745
838	896668	897558	896668
839	897565	899442	897565
840	899420	900229	899420
841	903230	900237	903230
842	905081	903234	905081
843	906931	905045	906931
844	907248	907832	907299
845	907784	908128	907784
846	908132	908677	908132
847	908589	909320	908589
848	909405	911465	909405
849	911677	912360	911725
850	912303	912821	912303



ORF Nos	begin	end	potential start
851	912937	913983	912937
852	915128	914067	915128
853	916658	915303	916658
854	915627	915376	915627
855	917707	916853	917707
856	918837	917722	918837
857	919868	918837	919868
858	920434	919880	920434
859	921187	920438	921187
860	921959	921195	921959
861	923773	921995	923773
862	922146	922415	922146
863	923943	923674	923943
864	924077	925006	924077
865	925436	925083	925436
866	926524	925349	926524
867	927920	926433	927920
868	928319	927951	928319
869	928963	928334	928963
870	929248	930987	929248
871	930995	932059	930995
872	932121	933515	932175
873	932881	932513	932881
874	933485	935746	933485
875	935724	937082	935724
876	937229	938410	937229
877	938281	938805	938281
878	938809	939255	938824
879	939165	939782	939165
880	939760	940791	939790
881	940822	941106	940822
882	940977	941351	940977
883	942537	941623	942429
884	942784	942500	942763

ORF Nos	begin	end	potential start
885	943149	942799	943149
886	943799	943029	943799
887	944055	943732	944055
888	944413	943994	944404
889	945395	944556	945395
890	945853	945389	945853
891	946392	945751	946392
892	947410	948081	947431
893	949871	948915	949871
894	951058	949868	951058
895	951249	950959	951249
896	951664	952134	951664
897	952674	952165	952674
898	953491	952589	953491
899	955324	953495	955324
900	955823	955281	955823
901	957082	955847	957082
902	957902	957270	957902
903	959231	957906	959231
904	959376	960284	959376
905	960266	961669	960347
906	961856	964765	961856
907	966855	965395	966855
908	968204	966975	968204
909	968791	968237	968791
910	969498	968731	969498
911	969858	969511	969858
912	970118	969762	970118
913	970593	970300	970593
914	971261	970542	971261
915	971680	971123	971680
916	971876	975100	971876
917	975419	976516	975419
918	976584	978320	976584

ORF Nos	begin	end	potential start
919	977680	977231	977680
920	978399	980738	978399
921	980756	981928	980756
922	982974	981931	982962
923	984120	983119	984120
924	985502	984120	985502
925	987180	985882	987180
926	987172	987444	987172
927	989846	989049	989846
928	991048	989846	991048
929	991638	990955	991638
930	991794	992498	991794
931	993619	993041	993619
932	993530	994792	993548
933	995970	994795	995970
934	996857	995739	996857
935	997603	996782	997603
936	998969	997572	998969
937	998896	1000023	998896
938	1000087	1001340	1000087
939	1001357	1001818	1001357
940	1003288	1001873	1003288
941	1003487	1004146	1003496
942	1004485	1005639	1004689
943	1005643	1005972	1005643
944	1006784	1006116	1006784
945	1007563	1006769	1007563
946	1009226	1007568	1009226
947	1009989	1009336	1009989
948	1015852	1016337	1015852
949	1016561	1016181	1016561
950	1016297	1017532	1016297
951	1016802	1016452	1016802
952	1018993	1017701	1018993

ORF Nos	begin	end	potential start
953	1019454	1019137	1019454
954	1020764	1019562	1020764
955	1021405	1021037	1021405
956	1021821	1024286	1021821
957	1024697	1024248	1024697
958	1025569	1024508	1025551
959	1026969	1025590	1026969
960	1027789	1026947	1027789
961	1031199	1027945	1031199
962	1031717	1031172	1031717
963	1033057	1031612	1033057
964	1033425	1033039	1033425
965	1033784	1033200	1033784
966	1033963	1036038	1033963
967	1036945	1036010	1036945
968	1037110	1037679	1037110
969	1037696	1037944	1037696
970	1038916	1037975	1038916
971	1040582	1039026	1040582
972	1040997	1042337	1040997
973	1042357	1043403	1042357
974	1043367	1044623	1043367
975	1044607	1045362	1044607
976	1045384	1046538	1045384
977	1046447	1047517	1046447
978	1047521	1049956	1047521
979	1050611	1050036	1050611
980	1050925	1050566	1050925
981	1051728	1051090	1051728
982	1051743	1052063	1051743
983	1052101	1053126	1052101
984	1054201	1053107	1054201
985	1054242	1055555	1054242
986	1055483	1055908	1055483

ORF Nos	begin	end	potential start
987	1056609	1056965	1056609
988	1056961	1058232	1056985
989	1058238	1058687	1058238
990	1059371	1058727	1059371
991	1059526	1060578	1059526
992	1061553	1060579	1061553
993	1061674	1062411	1061674
994	1062377	1064077	1062377
995	1064116	1065243	1064116
996	1067451	1065178	1067451
997	1068065	1067376	1068065
998	1068209	1068706	1068230
999	1069958	1068819	1069958
1000	1071163	1070033	1071163
1001	1072438	1071332	1072438
1002	1072997	1073476	1072997
1003	1074239	1075864	1074239
1004	1076790	1075867	1076790
1005	1077268	1076573	1077268
1006	1077999	1078724	1077999
1007	1079088	1078672	1079088
1008	1079642	1079944	1079642
1009	1080501	1079995	1080468
1010	1080775	1081341	1080775
1011	1083158	1081350	1083158
1012	1084677	1083235	1084677
1013	1085648	1084632	1085648
1014	1086117	1086737	1086117
1015	1086692	1087897	1086692
1016	1088646	1089005	1088646
1017	1089146	1089805	1089146
1018	1092931	1089890	1092931
1019	1093179	1092889	1093179
1020	1093584	1094204	1093584

ORF Nos	begin	end	potential start
1021	1095619	1094192	1095619
1022	1096074	1096628	1096074
1023	1096633	1097082	1096633
1024	1097266	1097601	1097266
1025	1097622	1097867	1097622
1026	1097886	1098392	1097886
1027	1099521	1099279	1099521
1028	1099689	1101053	1099704
1029	1102192	1101107	1102192
1030	1104950	1102116	1104950
1031	1106508	1104946	1106508
1032	1106722	1107249	1106722
1033	1107463	1108101	1107463
1034	1108041	1108421	1108041
1035	1108520	1113370	1108520
1036	1114958	1113447	1114958
1037	1116915	1115071	1116915
1038	1118183	1116894	1118183
1039	1118846	1120030	1118846
1040	1120040	1120522	1120040
1041	1120510	1121430	1120510
1042	1121321	1121866	1121321
1043	1122123	1122899	1122123
1044	1124842	1125564	1124842
1045	1126526	1125579	1126526
1046	1126519	1127676	1126519
1047	1127672	1128571	1127672
1048	1130230	1131336	1130230
1049	1131480	1132553	1131480
1050	1132830	1133843	1132830
1051	1134121	1134855	1134121
1052	1134642	1135592	1134642
1053	1135964	1135653	1135964
1054	1137132	1135954	1137132

ORF Nos	begin	end	potential start
1055	1137169	1140102	1137169
1056	1141365	1140112	1141344
1057	1142150	1141356	1142150
1058	1142520	1145660	1142520
1059	1145627	1146721	1145627
1060	1146862	1147545	1146862
1061	1147666	1148190	1147666
1062	1148514	1148224	1148514
1063	1149136	1148348	1149136
1064	1149702	1149166	1149702
1065	1150031	1150591	1150031
1066	1150785	1151147	1150785
1067	1151165	1152181	1151165
1068	1152522	1154591	1152522
1069	1155666	1154566	1155666
1070	1156743	1155670	1156740
1071	1156859	1157815	1156859
1072	1157982	1160735	1157982
1073	1162620	1160917	1162620
1074	1162970	1162590	1162970
1075	1163532	1164020	1163532
1076	1163995	1164294	1163995
1077	1165569	1165030	1165569
1078	1166108	1165566	1166108
1079	1166644	1166141	1166644
1080	1167055	1168374	1167055
1081	1169218	1168337	1169218
1082	1169823	1169218	1169823
1083	1171324	1170572	1171324
1084	1172085	1171177	1172085
1085	1172394	1173773	1172394
1086	1175209	1173881	1175209
1087	1175555	1175127	1175360
1088	1175778	1177043	1175778

ORF Nos	begin	end	potential start
1089	1177177	1179048	1177177
1090	1179156	1180085	1179156
1091	1180045	1180779	1180045
1092	1181942	1180788	1181942
1093	1182296	1181961	1182296
1094	1183844	1182300	1183844
1095	1184420	1183848	1184420
1096	1185382	1184366	1185382
1097	1185858	1185226	1185858
1098	1186164	1186481	1186185
1099	1187386	1186484	1187386
1100	1187370	1189028	1187370
1101	1189321	1190889	1189321
1102	1191142	1192146	1191142
1103	1191974	1191729	1191974
1104	1193815	1192991	1193815
1105	1195702	1194248	1195702
1106	1196303	1195716	1196303
1107	1196831	1196337	1196831
1108	1197807	1196746	1197651
1109	1198740	1197883	1198668
1110	1200232	1198721	1200232
1111	1201286	1200135	1201286
1112	1202386	1201259	1202350
1113	1202901	1202350	1202901
1114	1204162	1202816	1204162
1115	1203177	1203464	1203177
1116	1205028	1204180	1205028
1117	1206392	1204878	1206392
1118	1206742	1206086	1206742
1119	1207872	1206724	1207872
1120	1208852	1207851	1208852
1121	1210518	1209742	1210518
1122	1210703	1211494	1210703



ORF Nos	begin	end	potential start
1123	1211870	1212754	1211870
1124	1212742	1214064	1212742
1125	1214046	1214858	1214046
1126	1215551	1216318	1215551
1127	1216493	1216849	1216493
1128	1217183	1219612	1217183
1129	1220068	1219673	1220068
1130	1219710	1220669	1219710
1131	1220630	1221376	1220630
1132	1221645	1223681	1221645
1133	1223894	1224988	1223900
1134	1225000	1225830	1225000
1135	1227810	1225879	1227810
1136	1226528	1226908	1226528
1137	1229972	1228311	1229972
1138	47569	47018	47569
1139	49980	49117	49980
1140	53356	52898	53356
1141	54477	54884	54477
1142	63753	63998	63753
1143	77164	77487	77164
1144	79724	79302	79724
1145	88721	88951	88721
1146	94067	94429	94067
1147	122832	123341	122832
1148	147536	147234	147536
1149	158990	159346	158990
1150	168470	168979	168470
1151	169183	169452	169204
1152	171785	171504	171785
1153	172518	171775	172518
1154	193599	194045	193599
1155	195704	196075	195704
1156	210687	210145	210684

ORF Nos	begin	end	potential start
1157	211100	210708	211100
1158	215420	215088	215420
1159	217914	218246	217914
1160	218925	218701	218925
1161	223785	223525	223785
1162	224271	223999	224271
1163	228691	228407	228691
1164	235050	235334	235050
1165	252308	253021	252308
1166	258280	258912	258280
1167	261325	261567	261325
1168	268195	268878	268195
1169	269447	268881	269447
1170	271263	271538	271263
1171	271957	272346	271957
1172	274176	274550	274176
1173	275736	275314	275736
1174	276490	276927	276490
1175	277577	277861	277577
1176	288163	287909	288163
1177	290130	289789	290130
1178	290989	291225	290989
1179	291372	291860	291372
1180	311239	311622	311239
1181	328665	328384	328665
1182	337348	338289	337348
1183	364764	364369	364764
1184	389623	390135	389623
1185	393729	394343	393729
1186	407379	407621	407379
1187	410944	410708	410944
1188	427632	427988	427632
1189	428172	428486	428172
1190	436761	437246	436761

ORF Nos	begin	end	potential start
1191	460911	461159	460911
1192	477597	477313	477597
1193	487303	487001	487303
1194	487764	487534	487764
1195	498502	499017	498502
1196	499795	500466	499795
1197	571928	572344	571928
1198	572367	572131	572367
1199	588184	587915	588184
1200	600587	600907	600587
1201	609731	608895	609731
1202	614039	614755	614039
1203	614823	615152	614823
1204	638244	638831	638244
1205	638819	639094	638819
1206	639073	639636	639073
1207	647901	648236	647901
1208	678510	679469	678510
1209	688178	688732	688178
1210	696045	696563	696045
1211	708998	708588	708998
1212	709808	710089	709808
1213	718240	717737	718240
1214	737828	737565	737828
1215	779502	780257	779502
1216	806310	805864	806310
1217	820931	820707	820931
1218	837696	839096	837696
1219	883307	883549	883307
1220	892010	891726	892010
1221	893277	893564	893277
1222	936998	937225	936998
1223	946865	947419	946865
1224	975187	975411	975187

ORF Nos	begin	end	potential start
1225	985882	985517	985882
1226	987713	987180	987713
1227	988215	987733	988215
1228	988754	988530	988754
1229	992542	992841	992542
1230	992759	993067	992759
1231	1004247	1004528	1004268
1232	1015013	1014294	1015013
1233	1056147	1056545	1056147
1234	1077682	1078035	1077682
1235	1088121	1088381	1088121
1236	1098430	1098852	1098430
1237	1098798	1099319	1098798
1238	1123198	1123515	1123198
1239	1123606	1124256	1123606
1240	1124453	1124797	1124453
1241	1129253	1129567	1129253
1242	1164947	1164474	1164947
1243	1170457	1170053	1170457
1244	1172342	1171863	1172342
1245	1192155	1192835	1192155
1246	1192759	1192992	1192759
1247	1193861	1194142	1193861
1248	1194036	1193779	1194036
1249	1209748	1209053	1209748
1250	1215111	1215419	1215111
1251	1216302	1216538	1216302
1252	1228072	1227818	1228072
1253	1228304	1228080	1228304
1254	26599	26222	26599
1255	27609	27367	27609
1256	67206	66967	67197
1257	70612	70352	70588
1258	132703	132945	132703

ORF Nos	begin	end	potential start
1259	178073	178393	178073
1260	208576	208349	208576
1261	209156	208929	209156
1262	209263	209024	209263
1263	210304	210639	210304
1264	299009	299452	299030
1265	352106	351717	352061
1266	420182	419949	420170
1267	553602	553381	553602
1268	556538	556807	556538
1269	594348	593797	594342
1270	595169	594876	595160
1271	662148	662381	662160
1272	706528	706893	706528
1273	803315	803650	803339
1274	849551	849306	849551
1275	913676	913275	913676
1276	927087	926836	927087
1277	930587	930360	930587
1278	986531	986764	986531
1279	996229	996486	996229
1280	1000373	1000002	1000334
1281	1010291	1010037	1010273
1282	1011128	1010793	1011128
1283	1012924	1012694	1012924
1284	1028659	1028913	1028659
1285	1086481	1086762	1086481
1286	1118658	1118879	1118658
1287	1170098	1169835	1170098
1288	1180828	1181184	1180828
1289	1182658	1183035	1182658
1290	1195076	1194795	1195055
1291	1195890	1196183	1195890
1292	189042	188809	189030

ORF Nos	begin	end	potential start
1293	691250	691567	691250
1294	914544	914780	914556
1295	928525	928833	928579
1296	1040685	1040948	1040712
1297	377646	378068	377646

**Table 4**

<i>SEQ ID NO (ORF)</i>	<i>Fp</i>	<i>Fd</i>	<i>Bp</i>	<i>Bd</i>
2	1292	1293	3796	3797
3	1294	1295	3798	3799
4	1296	1297	3800	3801
5	1298	1299	3802	3803
6	1300	1301	3804	3805
7	1302	1303	3806	3807
8	1304	1305	3808	3809
9	1306	1307	3810	3811
10	1308	1309	3812	3813
11	1310	1311	3814	3815
12	1312	1313	3816	3817
13	1314	1315	3818	3819
14	1316	1317	3820	3821
15	1318	1319	3822	3823
16	1320	1321	3824	3825
17	1322	1323	3826	3827
18	1324	1325	3828	3829
19	1326	1327	3830	3831
20	1328	1329	3832	3833
21	1330	1331	3834	3835
22	1332	1333	3836	3837
23	1334	1335	3838	3839
24	1336	1337	3840	3841
25	1338	1339	3842	3843
26	1340	1341	3844	3845
27	1342	1343	3846	3847
28	1344	1345	3848	3849
29	1346	1347	3850	3851
30	1348	1349	3852	3853
31	1350	1351	3854	3855
32	1352	1353	3856	3857
33	1354	1355	3858	3859
34	1358	1359	3862	3863

35	1356	1357	3860	3861
36	1360	1361	3864	3865
37	1362	1363	3866	3867
38	1364	1365	3868	3869
39	1366	1367	3870	3871
40	1368	1369	3872	3873
41	1370	1371	3874	3875
42	1374	1375	3878	3879
43	1376	1377	3880	3881
44	1380	1381	3884	3885
45	1382	1383	3886	3887
46	1386	1387	3890	3891
47	1388	1389	3892	3893
48	1392	1393	3896	3897
49	1394	1395	3898	3899
50	1396	1397	3900	3901
51	1398	1399	3902	3903
52	1402	1403	3906	3907
53	1400	1401	3904	3905
54	1404	1405	3908	3909
55	1406	1407	3910	3911
56	1410	1411	3914	3915
57	1412	1413	3916	3917
58	1414	1415	3918	3919
59	1416	1417	3920	3921
60	1418	1419	3922	3923
61	1420	1421	3924	3925
62	1422	1423	3926	3927
63	1424	1425	3928	3929
64	1426	1427	3930	3931
65	1428	1429	3932	3933
66	1430	1431	3934	3935
67	1432	1433	3936	3937
68	1434	1435	3938	3939
69	1438	1439	3942	3943



70	1440	1441	3944	3945
71	1444	1445	3948	3949
72	1446	1447	3950	3951
73	1448	1449	3952	3953
74	1450	1451	3954	3955
75	1452	1453	3956	3957
76	1454	1455	3958	3959
77	1456	1457	3960	3961
78	1458	1459	3962	3963
79	1460	1461	3964	3965
80	1462	1463	3966	3967
81	1464	1465	3968	3969
82	1468	1469	3972	3973
83	1470	1471	3974	3975
84	1472	1473	3976	3977
85	1476	1477	3980	3981
86	1478	1479	3982	3983
87	1480	1481	3984	3985
88	1482	1483	3986	3987
89	1484	1485	3988	3989
90	1486	1487	3990	3991
91	1488	1489	3992	3993
92	1490	1491	3994	3995
93	1492	1493	3996	3997
94	1494	1495	3998	3999
95	1496	1497	4000	4001
96	1498	1499	4002	4003
97	1500	1501	4004	4005
98	1502	1503	4006	4007
99	1504	1505	4008	4009
100	1506	1507	4010	4011
101	1508	1509	4012	4013
102	1510	1511	4014	4015
103	1512	1513	4016	4017
104	1514	1515	4018	4019

105	1516	1517	4020	4021
106	1518	1519	4022	4023
107	1520	1521	4024	4025
108	1522	1523	4026	4027
109	1524	1525	4028	4029
110	1526	1527	4030	4031
111	1530	1531	4034	4035
112	1532	1533	4036	4037
113	1534	1535	4038	4039
114	1536	1537	4040	4041
115	1538	1539	4042	4043
116	1540	1541	4044	4045
117	1542	1543	4046	4047
118	1544	1545	4048	4049
119	1546	1547	4050	4051
120	1548	1549	4052	4053
121	1550	1551	4054	4055
122	1552	1553	4056	4057
123	1554	1555	4058	4059
124	1556	1557	4060	4061
125	1558	1559	4062	4063
126	1562	1563	4066	4067
127	1564	1565	4068	4069
128	1566	1567	4070	4071
129	1568	1569	4072	4073
130	1570	1571	4074	4075
131	1572	1573	4076	4077
132	1574	1575	4078	4079
133	1576	1577	4080	4081
134	1580	1581	4084	4085
135	1582	1583	4086	4087
136	1584	1585	4088	4089
137	1586	1587	4090	4091
138	1588	1589	4092	4093
139	1590	1591	4094	4095

140	1592	1593	4096	4097
141	1594	1595	4098	4099
142	1596	1597	4100	4101
143	1598	1599	4102	4103
144	1604	1605	4108	4109
145	1606	1607	4110	4111
146	1612	1613	4116	4117
147	1614	1615	4118	4119
148	1616	1617	4120	4121
149	1618	1619	4122	4123
150	1620	1621	4124	4125
151	1624	1625	4128	4129
152	1622	1623	4126	4127
153	1626	1627	4130	4131
154	1628	1629	4132	4133
155	1630	1631	4134	4135
156	1632	1633	4136	4137
157	1634	1635	4138	4139
158	1636	1637	4140	4141
159	1638	1639	4142	4143
160	1640	1641	4144	4145
161	1642	1643	4146	4147
162	1644	1645	4148	4149
163	1646	1647	4150	4151
164	1648	1649	4152	4153
165	1650	1651	4154	4155
166	1652	1653	4156	4157
167	1656	1657	4160	4161
168	1658	1659	4162	4163
169	1662	1663	4166	4167
170	1664	1665	4168	4169
171	1666	1667	4170	4171
172	1668	1669	4172	4173
173	1670	1671	4174	4175
174	1672	1673	4176	4177

175	1674	1675	4178	4179
176	1676	1677	4180	4181
177	1678	1679	4182	4183
178	1684	1685	4188	4189
179	1686	1687	4190	4191
180	1688	1689	4192	4193
181	1690	1691	4194	4195
182	1694	1695	4198	4199
183	1696	1697	4200	4201
184	1698	1699	4202	4203
185	1700	1701	4204	4205
186	1704	1705	4208	4209
187	1708	1709	4212	4213
188	1710	1711	4214	4215
189	1712	1713	4216	4217
190	1714	1715	4218	4219
191	1720	1721	4224	4225
192	1722	1723	4226	4227
193	1724	1725	4228	4229
194	1726	1727	4230	4231
195	1728	1729	4232	4233
196	1732	1733	4236	4237
197	1734	1735	4238	4239
198	1736	1737	4240	4241
199	1738	1739	4242	4243
200	1740	1741	4244	4245
201	1742	1743	4246	4247
202	1744	1745	4248	4249
203	1746	1747	4250	4251
204	1750	1751	4254	4255
205	1752	1753	4256	4257
206	1754	1755	4258	4259
207	1756	1757	4260	4261
208	1758	1759	4262	4263
209	1760	1761	4264	4265

210	1762	1763	4266	4267
211	1764	1765	4268	4269
212	1766	1767	4270	4271
213	1768	1769	4272	4273
214	1770	1771	4274	4275
215	1772	1773	4276	4277
216	1774	1775	4278	4279
217	1776	1777	4280	4281
218	1778	1779	4282	4283
219	1782	1783	4286	4287
220	1784	1785	4288	4289
221	1786	1787	4290	4291
222	1788	1789	4292	4293
223	1790	1791	4294	4295
224	1792	1793	4296	4297
225	1796	1797	4300	4301
226	1800	1801	4304	4305
227	1802	1803	4306	4307
228	1804	1805	4308	4309
229	1806	1807	4310	4311
230	1808	1809	4312	4313
231	1810	1811	4314	4315
232	1812	1813	4316	4317
233	1818	1819	4322	4323
234	1824	1825	4328	4329
235	1826	1827	4330	4331
236	1828	1829	4332	4333
237	1834	1835	4338	4339
238	1836	1837	4340	4341
239	1840	1841	4344	4345
240	1842	1843	4346	4347
241	1846	1847	4350	4351
242	1848	1849	4352	4353
243	1850	1851	4354	4355
244	1852	1853	4356	4357

245	1854	1855	4358	4359
246	1856	1857	4360	4361
247	1858	1859	4362	4363
248	1860	1861	4364	4365
249	1862	1863	4366	4367
250	1864	1865	4368	4369
251	1866	1867	4370	4371
252	1868	1869	4372	4373
253	1872	1873	4376	4377
254	1876	1877	4380	4381
255	1874	1875	4378	4379
256	1878	1879	4382	4383
257	1886	1887	4390	4391
258	1888	1889	4392	4393
259	1890	1891	4394	4395
260	1892	1893	4396	4397
261	1896	1897	4400	4401
262	1894	1895	4398	4399
263	1898	1899	4402	4403
264	1900	1901	4404	4405
265	1902	1903	4406	4407
266	1904	1905	4408	4409
267	1906	1907	4410	4411
268	1908	1909	4412	4413
269	1910	1911	4414	4415
270	1912	1913	4416	4417
271	1914	1915	4418	4419
272	1916	1917	4420	4421
273	1918	1919	4422	4423
274	1920	1921	4424	4425
275	1922	1923	4426	4427
276	1924	1925	4428	4429
277	1926	1927	4430	4431
278	1928	1929	4432	4433
279	1930	1931	4434	4435

280	1934	1935	4438	4439
281	1936	1937	4440	4441
282	1938	1939	4442	4443
283	1940	1941	4444	4445
284	1942	1943	4446	4447
285	1944	1945	4448	4449
286	1946	1947	4450	4451
287	1948	1949	4452	4453
288	1950	1951	4454	4455
289	1952	1953	4456	4457
290	1954	1955	4458	4459
291	1956	1957	4460	4461
292	1958	1959	4462	4463
293	1960	1961	4464	4465
294	1962	1963	4466	4467
295	1964	1965	4468	4469
296	1966	1967	4470	4471
297	1970	1971	4474	4475
298	1972	1973	4476	4477
299	1974	1975	4478	4479
300	1976	1977	4480	4481
301	1978	1979	4482	4483
302	1980	1981	4484	4485
303	1984	1985	4488	4489
304	1986	1987	4490	4491
305	1988	1989	4492	4493
306	1990	1991	4494	4495
307	1992	1993	4496	4497
308	1994	1995	4498	4499
309	1996	1997	4500	4501
310	1998	1999	4502	4503
311	2000	2001	4504	4505
312	2002	2003	4506	4507
313	2004	2005	4508	4509
314	2006	2007	4510	4511

315	2008	2009	4512	4513
316	2010	2011	4514	4515
317	2012	2013	4516	4517
318	2014	2015	4518	4519
319	2016	2017	4520	4521
320	2018	2019	4522	4523
321	2020	2021	4524	4525
322	2022	2023	4526	4527
323	2026	2027	4530	4531
324	2024	2025	4528	4529
325	2028	2029	4532	4533
326	2030	2031	4534	4535
327	2032	2033	4536	4537
328	2034	2035	4538	4539
329	2038	2039	4542	4543
330	2040	2041	4544	4545
331	2042	2043	4546	4547
332	2044	2045	4548	4549
333	2046	2047	4550	4551
334	2048	2049	4552	4553
335	2050	2051	4554	4555
336	2052	2053	4556	4557
337	2054	2055	4558	4559
338	2056	2057	4560	4561
339	2058	2059	4562	4563
340	2060	2061	4564	4565
341	2062	2063	4566	4567
342	2064	2065	4568	4569
343	2066	2067	4570	4571
344	2068	2069	4572	4573
345	2070	2071	4574	4575
346	2072	2073	4576	4577
347	2074	2075	4578	4579
348	2076	2077	4580	4581
349	2078	2079	4582	4583



350	2080	2081	4584	4585
351	2082	2083	4586	4587
352	2084	2085	4588	4589
353	2088	2089	4592	4593
354	2090	2091	4594	4595
355	2092	2093	4596	4597
356	2094	2095	4598	4599
357	2096	2097	4600	4601
358	2100	2101	4604	4605
359	2102	2103	4606	4607
360	2104	2105	4608	4609
361	2106	2107	4610	4611
362	2108	2109	4612	4613
363	2110	2111	4614	4615
364	2112	2113	4616	4617
365	2114	2115	4618	4619
366	2116	2117	4620	4621
367	2118	2119	4622	4623
368	2120	2121	4624	4625
369	2122	2123	4626	4627
370	2124	2125	4628	4629
371	2128	2129	4632	4633
372	2130	2131	4634	4635
373	2134	2135	4638	4639
374	2136	2137	4640	4641
375	2138	2139	4642	4643
376	2140	2141	4644	4645
377	2142	2143	4646	4647
378	2144	2145	4648	4649
379	2146	2147	4650	4651
380	2148	2149	4652	4653
381	2150	2151	4654	4655
382	2152	2153	4656	4657
383	2154	2155	4658	4659
384	2156	2157	4660	4661

385	2158	2159	4662	4663
386	2160	2161	4664	4665
387	2162	2163	4666	4667
388	2164	2165	4668	4669
389	2170	2171	4674	4675
390	2172	2173	4676	4677
391	2174	2175	4678	4679
392	2176	2177	4680	4681
393	2178	2179	4682	4683
394	2180	2181	4684	4685
395	2182	2183	4686	4687
396	2186	2187	4690	4691
397	2190	2191	4694	4695
398	2188	2189	4692	4693
399	2194	2195	4698	4699
400	2192	2193	4696	4697
401	2196	2197	4700	4701
402	2200	2201	4704	4705
403	2198	2199	4702	4703
404	2202	2203	4706	4707
405	2204	2205	4708	4709
406	2206	2207	4710	4711
407	2208	2209	4712	4713
408	2210	2211	4714	4715
409	2212	2213	4716	4717
410	2214	2215	4718	4719
411	2216	2217	4720	4721
412	2218	2219	4722	4723
413	2220	2221	4724	4725
414	2222	2223	4726	4727
415	2224	2225	4728	4729
416	2226	2227	4730	4731
417	2228	2229	4732	4733
418	2230	2231	4734	4735
419	2232	2233	4736	4737

420	2234	2235	4738	4739
421	2236	2237	4740	4741
422	2238	2239	4742	4743
423	2242	2243	4746	4747
424	2244	2245	4748	4749
425	2246	2247	4750	4751
426	2248	2249	4752	4753
427	2250	2251	4754	4755
428	2252	2253	4756	4757
429	2254	2255	4758	4759
430	2256	2257	4760	4761
431	2258	2259	4762	4763
432	2260	2261	4764	4765
433	2262	2263	4766	4767
434	2266	2267	4770	4771
435	2264	2265	4768	4769
436	2268	2269	4772	4773
437	2270	2271	4774	4775
438	2272	2273	4776	4777
439	2274	2275	4778	4779
440	2278	2279	4782	4783
441	2280	2281	4784	4785
442	2282	2283	4786	4787
443	2284	2285	4788	4789
444	2286	2287	4790	4791
445	2288	2289	4792	4793
446	2290	2291	4794	4795
447	2292	2293	4796	4797
448	2294	2295	4798	4799
449	2296	2297	4800	4801
450	2298	2299	4802	4803
451	2304	2305	4808	4809
452	2306	2307	4810	4811
453	2308	2309	4812	4813
454	2310	2311	4814	4815

455	2312	2313	4816	4817
456	2314	2315	4818	4819
457	2316	2317	4820	4821
458	2318	2319	4822	4823
459	2320	2321	4824	4825
460	2322	2323	4826	4827
461	2324	2325	4828	4829
462	2326	2327	4830	4831
463	2328	2329	4832	4833
464	2332	2333	4836	4837
465	2334	2335	4838	4839
466	2338	2339	4842	4843
467	2340	2341	4844	4845
468	2342	2343	4846	4847
469	2344	2345	4848	4849
470	2346	2347	4850	4851
471	2348	2349	4852	4853
472	2350	2351	4854	4855
473	2352	2353	4856	4857
474	2356	2357	4860	4861
475	2354	2355	4858	4859
476	2358	2359	4862	4863
477	2360	2361	4864	4865
478	2362	2363	4866	4867
479	2364	2365	4868	4869
480	2366	2367	4870	4871
481	2368	2369	4872	4873
482	2370	2371	4874	4875
483	2372	2373	4876	4877
484	2374	2375	4878	4879
485	2376	2377	4880	4881
486	2378	2379	4882	4883
487	2380	2381	4884	4885
488	2382	2383	4886	4887
489	2384	2385	4888	4889

490	2386	2387	4890	4891
491	2388	2389	4892	4893
492	2390	2391	4894	4895
493	2392	2393	4896	4897
494	2394	2395	4898	4899
495	2396	2397	4900	4901
496	2398	2399	4902	4903
497	2400	2401	4904	4905
498	2402	2403	4906	4907
499	2404	2405	4908	4909
500	2406	2407	4910	4911
501	2408	2409	4912	4913
502	2410	2411	4914	4915
503	2412	2413	4916	4917
504	2414	2415	4918	4919
505	2416	2417	4920	4921
506	2418	2419	4922	4923
507	2420	2421	4924	4925
508	2422	2423	4926	4927
509	2426	2427	4930	4931
510	2424	2425	4928	4929
511	2430	2431	4934	4935
512	2428	2429	4932	4933
513	2432	2433	4936	4937
514	2434	2435	4938	4939
515	2436	2437	4940	4941
516	2438	2439	4942	4943
517	2440	2441	4944	4945
518	2442	2443	4946	4947
519	2444	2445	4948	4949
520	2446	2447	4950	4951
521	2450	2451	4954	4955
522	2454	2455	4958	4959
523	2456	2457	4960	4961
524	2458	2459	4962	4963

525	2460	2461	4964	4965
526	2462	2463	4966	4967
527	2466	2467	4970	4971
528	2464	2465	4968	4969
529	2468	2469	4972	4973
530	2470	2471	4974	4975
531	2472	2473	4976	4977
532	2474	2475	4978	4979
533	2476	2477	4980	4981
534	2478	2479	4982	4983
535	2480	2481	4984	4985
536	2482	2483	4986	4987
537	2486	2487	4990	4991
538	2488	2489	4992	4993
539	2490	2491	4994	4995
540	2492	2493	4996	4997
541	2494	2495	4998	4999
542	2496	2497	5000	5001
543	2498	2499	5002	5003
544	2500	2501	5004	5005
545	2502	2503	5006	5007
546	2504	2505	5008	5009
547	2506	2507	5010	5011
548	2508	2509	5012	5013
549	2510	2511	5014	5015
550	2514	2515	5018	5019
551	2516	2517	5020	5021
552	2518	2519	5022	5023
553	2520	2521	5024	5025
554	2522	2523	5026	5027
555	2524	2525	5028	5029
556	2526	2527	5030	5031
557	2528	2529	5032	5033
558	2532	2533	5036	5037
559	2534	2535	5038	5039

560	2536	2537	5040	5041
561	2538	2539	5042	5043
562	2544	2545	5048	5049
563	2546	2547	5050	5051
564	2548	2549	5052	5053
565	2552	2553	5056	5057
566	2550	2551	5054	5055
567	2554	2555	5058	5059
568	2556	2557	5060	5061
569	2558	2559	5062	5063
570	2560	2561	5064	5065
571	2562	2563	5066	5067
572	2564	2565	5068	5069
573	2566	2567	5070	5071
574	2568	2569	5072	5073
575	2570	2571	5074	5075
576	2572	2573	5076	5077
577	2574	2575	5078	5079
578	2576	2577	5080	5081
579	2578	2579	5082	5083
580	2580	2581	5084	5085
581	2582	2583	5086	5087
582	2590	2591	5094	5095
583	2592	2593	5096	5097
584	2594	2595	5098	5099
585	2596	2597	5100	5101
586	2598	2599	5102	5103
587	2600	2601	5104	5105
588	2602	2603	5106	5107
589	2604	2605	5108	5109
590	2606	2607	5110	5111
591	2608	2609	5112	5113
592	2610	2611	5114	5115
593	2612	2613	5116	5117
594	2616	2617	5120	5121

595	2618	2619	5122	5123
596	2620	2621	5124	5125
597	2622	2623	5126	5127
598	2624	2625	5128	5129
599	2626	2627	5130	5131
600	2628	2629	5132	5133
601	2630	2631	5134	5135
602	2632	2633	5136	5137
603	2634	2635	5138	5139
604	2636	2637	5140	5141
605	2638	2639	5142	5143
606	2640	2641	5144	5145
607	2642	2643	5146	5147
608	2644	2645	5148	5149
609	2646	2647	5150	5151
610	2650	2651	5154	5155
611	2648	2649	5152	5153
612	2652	2653	5156	5157
613	2654	2655	5158	5159
614	2656	2657	5160	5161
615	2658	2659	5162	5163
616	2660	2661	5164	5165
617	2662	2663	5166	5167
618	2664	2665	5168	5169
619	2666	2667	5170	5171
620	2668	2669	5172	5173
621	2672	2673	5176	5177
622	2674	2675	5178	5179
623	2678	2679	5182	5183
624	2676	2677	5180	5181
625	2680	2681	5184	5185
626	2682	2683	5186	5187
627	2684	2685	5188	5189
628	2686	2687	5190	5191
629	2688	2689	5192	5193



630	2690	2691	5194	5195
631	2692	2693	5196	5197
632	2696	2697	5200	5201
633	2698	2699	5202	5203
634	2700	2701	5204	5205
635	2702	2703	5206	5207
636	2704	2705	5208	5209
637	2706	2707	5210	5211
638	2710	2711	5214	5215
639	2712	2713	5216	5217
640	2714	2715	5218	5219
641	2716	2717	5220	5221
642	2718	2719	5222	5223
643	2720	2721	5224	5225
644	2722	2723	5226	5227
645	2724	2725	5228	5229
646	2726	2727	5230	5231
647	2728	2729	5232	5233
648	2732	2733	5236	5237
649	2736	2737	5240	5241
650	2738	2739	5242	5243
651	2740	2741	5244	5245
652	2742	2743	5246	5247
653	2744	2745	5248	5249
654	2748	2749	5252	5253
655	2750	2751	5254	5255
656	2752	2753	5256	5257
657	2754	2755	5258	5259
658	2756	2757	5260	5261
659	2758	2759	5262	5263
660	2760	2761	5264	5265
661	2762	2763	5266	5267
662	2764	2765	5268	5269
663	2766	2767	5270	5271
664	2768	2769	5272	5273

665	2770	2771	5274	5275
666	2772	2773	5276	5277
667	2774	2775	5278	5279
668	2776	2777	5280	5281
669	2778	2779	5282	5283
670	2780	2781	5284	5285
671	2782	2783	5286	5287
672	2784	2785	5288	5289
673	2786	2787	5290	5291
674	2788	2789	5292	5293
675	2790	2791	5294	5295
676	2792	2793	5296	5297
677	2794	2795	5298	5299
678	2796	2797	5300	5301
679	2798	2799	5302	5303
680	2800	2801	5304	5305
681	2804	2805	5308	5309
682	2806	2807	5310	5311
683	2808	2809	5312	5313
684	2810	2811	5314	5315
685	2812	2813	5316	5317
686	2814	2815	5318	5319
687	2816	2817	5320	5321
688	2818	2819	5322	5323
689	2820	2821	5324	5325
690	2822	2823	5326	5327
691	2824	2825	5328	5329
692	2826	2827	5330	5331
693	2828	2829	5332	5333
694	2830	2831	5334	5335
695	2832	2833	5336	5337
696	2834	2835	5338	5339
697	2836	2837	5340	5341
698	2838	2839	5342	5343
699	2840	2841	5344	5345

700	2842	2843	5346	5347
701	2844	2845	5348	5349
702	2846	2847	5350	5351
703	2848	2849	5352	5353
704	2850	2851	5354	5355
705	2852	2853	5356	5357
706	2854	2855	5358	5359
707	2856	2857	5360	5361
708	2858	2859	5362	5363
709	2860	2861	5364	5365
710	2862	2863	5366	5367
711	2864	2865	5368	5369
712	2866	2867	5370	5371
713	2868	2869	5372	5373
714	2870	2871	5374	5375
715	2872	2873	5376	5377
716	2874	2875	5378	5379
717	2876	2877	5380	5381
718	2878	2879	5382	5383
719	2880	2881	5384	5385
720	2882	2883	5386	5387
721	2886	2887	5390	5391
722	2888	2889	5392	5393
723	2884	2885	5388	5389
724	2890	2891	5394	5395
725	2892	2893	5396	5397
726	2894	2895	5398	5399
727	2896	2897	5400	5401
728	2900	2901	5404	5405
729	2902	2903	5406	5407
730	2904	2905	5408	5409
731	2906	2907	5410	5411
732	2908	2909	5412	5413
733	2910	2911	5414	5415
734	2912	2913	5416	5417

735	2914	2915	5418	5419
736	2916	2917	5420	5421
737	2918	2919	5422	5423
738	2920	2921	5424	5425
739	2922	2923	5426	5427
740	2924	2925	5428	5429
741	2926	2927	5430	5431
742	2928	2929	5432	5433
743	2930	2931	5434	5435
744	2932	2933	5436	5437
745	2934	2935	5438	5439
746	2936	2937	5440	5441
747	2938	2939	5442	5443
748	2940	2941	5444	5445
749	2942	2943	5446	5447
750	2944	2945	5448	5449
751	2946	2947	5450	5451
752	2948	2949	5452	5453
753	2952	2953	5456	5457
754	2954	2955	5458	5459
755	2956	2957	5460	5461
756	2958	2959	5462	5463
757	2960	2961	5464	5465
758	2962	2963	5466	5467
759	2964	2965	5468	5469
760	2966	2967	5470	5471
761	2968	2969	5472	5473
762	2970	2971	5474	5475
763	2972	2973	5476	5477
764	2974	2975	5478	5479
765	2976	2977	5480	5481
766	2978	2979	5482	5483
767	2980	2981	5484	5485
768	2982	2983	5486	5487
769	2984	2985	5488	5489

770	2986	2987	5490	5491
771	2990	2991	5494	5495
772	2992	2993	5496	5497
773	2994	2995	5498	5499
774	2996	2997	5500	5501
775	2998	2999	5502	5503
776	3000	3001	5504	5505
777	3002	3003	5506	5507
778	3004	3005	5508	5509
779	3006	3007	5510	5511
780	3008	3009	5512	5513
781	3010	3011	5514	5515
782	3012	3013	5516	5517
783	3014	3015	5518	5519
784	3016	3017	5520	5521
785	3020	3021	5524	5525
786	3022	3023	5526	5527
787	3024	3025	5528	5529
788	3026	3027	5530	5531
789	3028	3029	5532	5533
790	3030	3031	5534	5535
791	3032	3033	5536	5537
792	3034	3035	5538	5539
793	3036	3037	5540	5541
794	3038	3039	5542	5543
795	3040	3041	5544	5545
796	3042	3043	5546	5547
797	3044	3045	5548	5549
798	3046	3047	5550	5551
799	3048	3049	5552	5553
800	3050	3051	5554	5555
801	3052	3053	5556	5557
802	3054	3055	5558	5559
803	3056	3057	5560	5561
804	3058	3059	5562	5563

805	3060	3061	5564	5565
806	3062	3063	5566	5567
807	3064	3065	5568	5569
808	3066	3067	5570	5571
809	3068	3069	5572	5573
810	3070	3071	5574	5575
811	3072	3073	5576	5577
812	3074	3075	5578	5579
813	3076	3077	5580	5581
814	3078	3079	5582	5583
815	3080	3081	5584	5585
816	3082	3083	5586	5587
817	3084	3085	5588	5589
818	3086	3087	5590	5591
819	3088	3089	5592	5593
820	3090	3091	5594	5595
821	3092	3093	5596	5597
822	3094	3095	5598	5599
823	3096	3097	5600	5601
824	3100	3101	5604	5605
825	3102	3103	5606	5607
826	3104	3105	5608	5609
827	3106	3107	5610	5611
828	3108	3109	5612	5613
829	3110	3111	5614	5615
830	3112	3113	5616	5617
831	3114	3115	5618	5619
832	3116	3117	5620	5621
833	3120	3121	5624	5625
834	3124	3125	5628	5629
835	3122	3123	5626	5627
836	3128	3129	5632	5633
837	3130	3131	5634	5635
838	3132	3133	5636	5637
839	3134	3135	5638	5639

840	3136	3137	5640	5641
841	3138	3139	5642	5643
842	3140	3141	5644	5645
843	3142	3143	5646	5647
844	3144	3145	5648	5649
845	3146	3147	5650	5651
846	3148	3149	5652	5653
847	3150	3151	5654	5655
848	3152	3153	5656	5657
849	3154	3155	5658	5659
850	3156	3157	5660	5661
851	3158	3159	5662	5663
852	3160	3161	5664	5665
853	3164	3165	5668	5669
854	3162	3163	5666	5667
855	3166	3167	5670	5671
856	3168	3169	5672	5673
857	3170	3171	5674	5675
858	3172	3173	5676	5677
859	3174	3175	5678	5679
860	3176	3177	5680	5681
861	3180	3181	5684	5685
862	3178	3179	5682	5683
863	3182	3183	5686	5687
864	3184	3185	5688	5689
865	3186	3187	5690	5691
866	3188	3189	5692	5693
867	3190	3191	5694	5695
868	3192	3193	5696	5697
869	3194	3195	5698	5699
870	3196	3197	5700	5701
871	3198	3199	5702	5703
872	3200	3201	5704	5705
873	3202	3203	5706	5707
874	3204	3205	5708	5709

875	3206	3207	5710	5711
876	3210	3211	5714	5715
877	3212	3213	5716	5717
878	3214	3215	5718	5719
879	3216	3217	5720	5721
880	3218	3219	5722	5723
881	3220	3221	5724	5725
882	3222	3223	5726	5727
883	3224	3225	5728	5729
884	3226	3227	5730	5731
885	3228	3229	5732	5733
886	3230	3231	5734	5735
887	3232	3233	5736	5737
888	3234	3235	5738	5739
889	3236	3237	5740	5741
890	3238	3239	5742	5743
891	3240	3241	5744	5745
892	3244	3245	5748	5749
893	3246	3247	5750	5751
894	3248	3249	5752	5753
895	3250	3251	5754	5755
896	3252	3253	5756	5757
897	3254	3255	5758	5759
898	3256	3257	5760	5761
899	3258	3259	5762	5763
900	3260	3261	5764	5765
901	3262	3263	5766	5767
902	3264	3265	5768	5769
903	3266	3267	5770	5771
904	3268	3269	5772	5773
905	3270	3271	5774	5775
906	3272	3273	5776	5777
907	3274	3275	5778	5779
908	3276	3277	5780	5781
909	3278	3279	5782	5783



910	3280	3281	5784	5785
911	3282	3283	5786	5787
912	3284	3285	5788	5789
913	3286	3287	5790	5791
914	3288	3289	5792	5793
915	3290	3291	5794	5795
916	3292	3293	5796	5797
917	3296	3297	5800	5801
918	3298	3299	5802	5803
919	3300	3301	5804	5805
920	3302	3303	5806	5807
921	3304	3305	5808	5809
922	3306	3307	5810	5811
923	3308	3309	5812	5813
924	3310	3311	5814	5815
925	3316	3317	5820	5821
926	3314	3315	5818	5819
927	3324	3325	5828	5829
928	3326	3327	5830	5831
929	3328	3329	5832	5833
930	3330	3331	5834	5835
931	3338	3339	5842	5843
932	3336	3337	5840	5841
933	3340	3341	5844	5845
934	3342	3343	5846	5847
935	3344	3345	5848	5849
936	3346	3347	5850	5851
937	3348	3349	5852	5853
938	3350	3351	5854	5855
939	3352	3353	5856	5857
940	3354	3355	5858	5859
941	3356	3357	5860	5861
942	3360	3361	5864	5865
943	3362	3363	5866	5867
944	3364	3365	5868	5869

945	3366	3367	5870	5871
946	3368	3369	5872	5873
947	3370	3371	5874	5875
948	3374	3375	5878	5879
949	3378	3379	5882	5883
950	3376	3377	5880	5881
951	3380	3381	5884	5885
952	3382	3383	5886	5887
953	3384	3385	5888	5889
954	3386	3387	5890	5891
955	3388	3389	5892	5893
956	3390	3391	5894	5895
957	3392	3393	5896	5897
958	3394	3395	5898	5899
959	3396	3397	5900	5901
960	3398	3399	5902	5903
961	3400	3401	5904	5905
962	3402	3403	5906	5907
963	3404	3405	5908	5909
964	3406	3407	5910	5911
965	3408	3409	5912	5913
966	3410	3411	5914	5915
967	3412	3413	5916	5917
968	3414	3415	5918	5919
969	3416	3417	5920	5921
970	3418	3419	5922	5923
971	3420	3421	5924	5925
972	3422	3423	5926	5927
973	3424	3425	5928	5929
974	3426	3427	5930	5931
975	3428	3429	5932	5933
976	3430	3431	5934	5935
977	3432	3433	5936	5937
978	3434	3435	5938	5939
979	3436	3437	5940	5941

980	3438	3439	5942	5943
981	3440	3441	5944	5945
982	3442	3443	5946	5947
983	3444	3445	5948	5949
984	3446	3447	5950	5951
985	3448	3449	5952	5953
986	3450	3451	5954	5955
987	3454	3455	5958	5959
988	3456	3457	5960	5961
989	3458	3459	5962	5963
990	3460	3461	5964	5965
991	3462	3463	5966	5967
992	3464	3465	5968	5969
993	3466	3467	5970	5971
994	3468	3469	5972	5973
995	3470	3471	5974	5975
996	3472	3473	5976	5977
997	3474	3475	5978	5979
998	3476	3477	5980	5981
999	3478	3479	5982	5983
1000	3480	3481	5984	5985
1001	3482	3483	5986	5987
1002	3484	3485	5988	5989
1003	3486	3487	5990	5991
1004	3488	3489	5992	5993
1005	3490	3491	5994	5995
1006	3494	3495	5998	5999
1007	3496	3497	6000	6001
1008	3498	3499	6002	6003
1009	3500	3501	6004	6005
1010	3502	3503	6006	6007
1011	3504	3505	6008	6009
1012	3506	3507	6010	6011
1013	3508	3509	6012	6013
1014	3510	3511	6014	6015

1015	3512	3513	6016	6017
1016	3516	3517	6020	6021
1017	3518	3519	6022	6023
1018	3520	3521	6024	6025
1019	3522	3523	6026	6027
1020	3524	3525	6028	6029
1021	3526	3527	6030	6031
1022	3528	3529	6032	6033
1023	3530	3531	6034	6035
1024	3532	3533	6036	6037
1025	3534	3535	6038	6039
1026	3536	3537	6040	6041
1027	3542	3543	6046	6047
1028	3544	3545	6048	6049
1029	3546	3547	6050	6051
1030	3548	3549	6052	6053
1031	3550	3551	6054	6055
1032	3552	3553	6056	6057
1033	3554	3555	6058	6059
1034	3556	3557	6060	6061
1035	3558	3559	6062	6063
1036	3560	3561	6064	6065
1037	3562	3563	6066	6067
1038	3564	3565	6068	6069
1039	3566	3567	6070	6071
1040	3568	3569	6072	6073
1041	3570	3571	6074	6075
1042	3572	3573	6076	6077
1043	3574	3575	6078	6079
1044	3582	3583	6086	6087
1045	3584	3585	6088	6089
1046	3586	3587	6090	6091
1047	3588	3589	6092	6093
1048	3592	3593	6096	6097
1049	3594	3595	6098	6099

1050	3596	3597	6100	6101
1051	3598	3599	6102	6103
1052	3600	3601	6104	6105
1053	3602	3603	6106	6107
1054	3604	3605	6108	6109
1055	3606	3607	6110	6111
1056	3608	3609	6112	6113
1057	3610	3611	6114	6115
1058	3612	3613	6116	6117
1059	3614	3615	6118	6119
1060	3616	3617	6120	6121
1061	3618	3619	6122	6123
1062	3620	3621	6124	6125
1063	3622	3623	6126	6127
1064	3624	3625	6128	6129
1065	3626	3627	6130	6131
1066	3628	3629	6132	6133
1067	3630	3631	6134	6135
1068	3632	3633	6136	6137
1069	3634	3635	6138	6139
1070	3636	3637	6140	6141
1071	3638	3639	6142	6143
1072	3640	3641	6144	6145
1073	3642	3643	6146	6147
1074	3644	3645	6148	6149
1075	3646	3647	6150	6151
1076	3648	3649	6152	6153
1077	3652	3653	6156	6157
1078	3654	3655	6158	6159
1079	3656	3657	6160	6161
1080	3658	3659	6162	6163
1081	3660	3661	6164	6165
1082	3662	3663	6166	6167
1083	3666	3667	6170	6171
1084	3668	3669	6172	6173

1085	3672	3673	6176	6177
1086	3674	3675	6178	6179
1087	3676	3677	6180	6181
1088	3678	3679	6182	6183
1089	3680	3681	6184	6185
1090	3682	3683	6186	6187
1091	3684	3685	6188	6189
1092	3686	3687	6190	6191
1093	3688	3689	6192	6193
1094	3690	3691	6194	6195
1095	3692	3693	6196	6197
1096	3694	3695	6198	6199
1097	3696	3697	6200	6201
1098	3698	3699	6202	6203
1099	3702	3703	6206	6207
1100	3700	3701	6204	6205
1101	3704	3705	6208	6209
1102	3706	3707	6210	6211
1103	3708	3709	6212	6213
1104	3714	3715	6218	6219
1105	3720	3721	6224	6225
1106	3722	3723	6226	6227
1107	3724	3725	6228	6229
1108	3726	3727	6230	6231
1109	3728	3729	6232	6233
1110	3730	3731	6234	6235
1111	3732	3733	6236	6237
1112	3734	3735	6238	6239
1113	3736	3737	6240	6241
1114	3740	3741	6244	6245
1115	3738	3739	6242	6243
1116	3742	3743	6246	6247
1117	3744	3745	6248	6249
1118	3746	3747	6250	6251
1119	3748	3749	6252	6253

1120	3750	3751	6254	6255
1121	3754	3755	6258	6259
1122	3756	3757	6260	6261
1123	3758	3759	6262	6263
1124	3760	3761	6264	6265
1125	3762	3763	6266	6267
1126	3766	3767	6270	6271
1127	3770	3771	6274	6275
1128	3772	3773	6276	6277
1129	3776	3777	6280	6281
1130	3774	3775	6278	6279
1131	3778	3779	6282	6283
1132	3780	3781	6284	6285
1133	3782	3783	6286	6287
1134	3784	3785	6288	6289
1135	3788	3789	6292	6293
1136	3786	3787	6290	6291
1137	3794	3795	6298	6299
1138	1372	1373	3876	3877
1139	1378	1379	3882	3883
1140	1384	1385	3888	3889
1141	1390	1391	3894	3895
1142	1408	1409	3912	3913
1143	1436	1437	3940	3941
1144	1442	1443	3946	3947
1145	1466	1467	3970	3971
1146	1474	1475	3978	3979
1147	1528	1529	4032	4033
1148	1560	1561	4064	4065
1149	1578	1579	4082	4083
1150	1600	1601	4104	4105
1151	1602	1603	4106	4107
1152	1608	1609	4112	4113
1153	1610	1611	4114	4115
1154	1654	1655	4158	4159

1155	1660	1661	4164	4165
1156	1680	1681	4184	4185
1157	1682	1683	4186	4187
1158	1692	1693	4196	4197
1159	1702	1703	4206	4207
1160	1706	1707	4210	4211
1161	1716	1717	4220	4221
1162	1718	1719	4222	4223
1163	1730	1731	4234	4235
1164	1748	1749	4252	4253
1165	1780	1781	4284	4285
1166	1794	1795	4298	4299
1167	1798	1799	4302	4303
1168	1814	1815	4318	4319
1169	1816	1817	4320	4321
1170	1820	1821	4324	4325
1171	1822	1823	4326	4327
1172	1830	1831	4334	4335
1173	1832	1833	4336	4337
1174	1838	1839	4342	4343
1175	1844	1845	4348	4349
1176	1870	1871	4374	4375
1177	1880	1881	4384	4385
1178	1882	1883	4386	4387
1179	1884	1885	4388	4389
1180	1932	1933	4436	4437
1181	1968	1969	4472	4473
1182	1982	1983	4486	4487
1183	2036	2037	4540	4541
1184	2086	2087	4590	4591
1185	2098	2099	4602	4603
1186	2126	2127	4630	4631
1187	2132	2133	4636	4637
1188	2166	2167	4670	4671
1189	2168	2169	4672	4673



1190	2184	2185	4688	4689
1191	2240	2241	4744	4745
1192	2276	2277	4780	4781
1193	2300	2301	4804	4805
1194	2302	2303	4806	4807
1195	2330	2331	4834	4835
1196	2336	2337	4840	4841
1197	2448	2449	4952	4953
1198	2452	2453	4956	4957
1199	2484	2485	4988	4989
1200	2512	2513	5016	5017
1201	2530	2531	5034	5035
1202	2540	2541	5044	5045
1203	2542	2543	5046	5047
1204	2584	2585	5088	5089
1205	2586	2587	5090	5091
1206	2588	2589	5092	5093
1207	2614	2615	5118	5119
1208	2670	2671	5174	5175
1209	2694	2695	5198	5199
1210	2708	2709	5212	5213
1211	2730	2731	5234	5235
1212	2734	2735	5238	5239
1213	2746	2747	5250	5251
1214	2802	2803	5306	5307
1215	2898	2899	5402	5403
1216	2950	2951	5454	5455
1217	2988	2989	5492	5493
1218	3018	3019	5522	5523
1219	3098	3099	5602	5603
1220	3118	3119	5622	5623
1221	3126	3127	5630	5631
1222	3208	3209	5712	5713
1223	3242	3243	5746	5747
1224	3294	3295	5798	5799

1225	3312	3313	5816	5817
1226	3318	3319	5822	5823
1227	3320	3321	5824	5825
1228	3322	3323	5826	5827
1229	3332	3333	5836	5837
1230	3334	3335	5838	5839
1231	3358	3359	5862	5863
1232	3372	3373	5876	5877
1233	3452	3453	5956	5957
1234	3492	3493	5996	5997
1235	3514	3515	6018	6019
1236	3538	3539	6042	6043
1237	3540	3541	6044	6045
1238	3576	3577	6080	6081
1239	3578	3579	6082	6083
1240	3580	3581	6084	6085
1241	3590	3591	6094	6095
1242	3650	3651	6154	6155
1243	3664	3665	6168	6169
1244	3670	3671	6174	6175
1245	3710	3711	6214	6215
1246	3712	3713	6216	6217
1247	3716	3717	6220	6221
1248	3718	3719	6222	6223
1249	3752	3753	6256	6257
1250	3764	3765	6268	6269
1251	3768	3769	6272	6273
1252	3790	3791	6294	6295
1253	3792	3793	6296	6297
1254	6300	6301	6376	6377
1255	6302	6303	6378	6379
1256	6304	6305	6380	6381
1257	6306	6307	6382	6383
1258	6308	6309	6384	6385
1259	6310	6311	6386	6387

1260	6312	6313	6388	6389
1261	6314	6315	6390	6391
1262	6316	6317	6392	6393
1263	6318	6319	6394	6395
1264	6320	6321	6396	6397
1265	6322	6323	6398	6399
1266	6324	6325	6400	6401
1267	6326	6327	6402	6403
1268	6328	6329	6404	6405
1269	6330	6331	6406	6407
1270	6332	6333	6408	6409
1271	6334	6335	6410	6411
1272	6336	6337	6412	6413
1273	6338	6339	6414	6415
1274	6340	6341	6416	6417
1275	6342	6343	6418	6419
1276	6344	6345	6420	6421
1277	6346	6347	6422	6423
1278	6348	6349	6424	6425
1279	6350	6351	6426	6427
1280	6352	6353	6428	6429
1281	6354	6355	6430	6431
1282	6356	6357	6432	6433
1283	6358	6359	6434	6435
1284	6360	6361	6436	6437
1285	6362	6363	6438	6439
1286	6364	6365	6440	6441
1287	6366	6367	6442	6443
1288	6368	6369	6444	6445
1289	6370	6371	6446	6447
1290	6372	6373	6448	6449
1291	6374	6375	6450	6451

TABLE 5

<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>
1292	F	1229848	3012	F	833844	4732	B	455875
1293	F	1227874	3013	F	831936	4733	B	457736
1294	F	1018	3014	F	834905	4734	B	457231
1295	F	1229162	3015	F	832943	4735	B	459146
1296	F	1588	3016	F	835834	4736	B	458008
1297	F	1229711	3017	F	833938	4737	B	459836
1298	F	2253	3018	F	837457	4738	B	458598
1299	F	369	3019	F	835536	4739	B	460488
1300	F	3381	3020	F	838723	4740	B	459717
1301	F	1508	3021	F	836826	4741	B	461652
1302	F	4042	3022	F	840649	4742	B	460417
1303	F	2126	3023	F	838723	4743	B	462365
1304	F	5735	3024	F	841751	4744	B	461391
1305	F	3843	3025	F	839825	4745	B	463286
1306	F	7832	3026	F	842960	4746	B	461680
1307	F	5909	3027	F	841123	4747	B	463584
1308	F	8887	3028	F	843765	4748	B	462520
1309	F	7010	3029	F	841844	4749	B	464418
1310	F	10139	3030	F	844768	4750	B	463584
1311	F	8175	3031	F	842852	4751	B	465539
1312	F	10640	3032	F	846089	4752	B	464547
1313	F	8799	3033	F	844175	4753	B	466398
1314	F	10997	3034	F	848293	4754	B	465288
1315	F	9037	3035	F	846449	4755	B	467243
1316	F	12458	3036	F	848867	4756	B	465835
1317	F	10572	3037	F	846964	4757	B	467738
1318	F	14187	3038	F	850351	4758	B	466558
1319	F	12365	3039	F	848426	4759	B	468474
1320	F	15529	3040	F	851788	4760	B	467322
1321	F	13629	3041	F	849899	4761	B	469217
1322	F	17626	3042	F	852166	4762	B	467738
1323	F	15699	3043	F	850278	4763	B	469637
1324	F	20909	3044	F	853976	4764	B	469912

1325	F	19006
1326	F	21800
1327	F	19927
1328	F	23462
1329	F	21557
1330	F	25637
1331	F	23729
1332	F	25997
1333	F	24071
1334	F	26727
1335	F	24828
1336	F	27528
1337	F	25628
1338	F	28643
1339	F	26765
1340	F	29202
1341	F	27313
1342	F	29793
1343	F	27835
1344	F	31488
1345	F	29639
1346	F	31957
1347	F	30050
1348	F	33570
1349	F	31666
1350	F	34564
1351	F	32664
1352	F	35783
1353	F	33875
1354	F	37597
1355	F	35741
1356	F	39135
1357	F	37236
1358	F	38939
1359	F	37038

3045	F	852069
3046	F	854899
3047	F	853006
3048	F	855595
3049	F	853679
3050	F	856479
3051	F	854582
3052	F	858498
3053	F	856492
3054	F	859372
3055	F	857424
3056	F	860050
3057	F	858116
3058	F	860941
3059	F	859023
3060	F	861464
3061	F	859572
3062	F	862749
3063	F	860895
3064	F	864599
3065	F	862683
3066	F	865003
3067	F	863040
3068	F	866331
3069	F	864443
3070	F	866799
3071	F	864889
3072	F	867574
3073	F	865664
3074	F	868402
3075	F	866513
3076	F	869823
3077	F	867898
3078	F	870414
3079	F	868478

4765	B	471814
4766	B	470920
4767	B	472826
4768	B	472075
4769	B	473922
4770	B	472231
4771	B	474144
4772	B	472579
4773	B	474501
4774	B	473751
4775	B	475664
4776	B	475116
4777	B	477009
4778	B	477566
4779	B	479490
4780	B	477851
4781	B	479753
4782	B	478728
4783	B	480616
4784	B	479496
4785	B	481418
4786	B	479928
4787	B	481844
4788	B	481674
4789	B	483578
4790	B	482281
4791	B	484243
4792	B	482820
4793	B	484721
4794	B	484449
4795	B	486360
4796	B	485499
4797	B	487293
4798	B	486116
4799	B	487980

1360	F	40872
1361	F	38972
1362	F	42825
1363	F	40923
1364	F	43563
1365	F	41652
1366	F	44531
1367	F	42623
1368	F	45150
1369	F	43250
1370	F	45478
1371	F	43579
1372	F	46755
1373	F	44874
1374	F	47347
1375	F	45386
1376	F	47818
1377	F	45897
1378	F	48893
1379	F	46995
1380	F	49907
1381	F	48000
1382	F	51088
1383	F	49169
1384	F	52651
1385	F	50721
1386	F	53065
1387	F	51176
1388	F	53516
1389	F	51611
1390	F	54242
1391	F	52351
1392	F	55058
1393	F	53159
1394	F	56274

3080	F	871862
3081	F	869956
3082	F	872261
3083	F	870367
3084	F	874062
3085	F	872141
3086	F	874363
3087	F	872439
3088	F	875155
3089	F	873244
3090	F	878156
3091	F	876291
3092	F	879046
3093	F	877133
3094	F	880361
3095	F	878450
3096	F	882361
3097	F	880493
3098	F	883067
3099	F	881185
3100	F	883310
3101	F	881416
3102	F	884035
3103	F	882152
3104	F	885495
3105	F	883599
3106	F	887340
3107	F	885448
3108	F	887996
3109	F	886093
3110	F	888494
3111	F	886570
3112	F	889100
3113	F	887201
3114	F	889655

4800	B	486811
4801	B	488721
4802	B	487217
4803	B	489101
4804	B	487567
4805	B	489423
4806	B	487984
4807	B	489909
4808	B	489291
4809	B	491191
4810	B	489561
4811	B	491461
4812	B	490221
4813	B	492078
4814	B	490773
4815	B	492672
4816	B	491383
4817	B	493293
4818	B	491616
4819	B	493537
4820	B	492362
4821	B	494246
4822	B	495083
4823	B	497027
4824	B	496168
4825	B	498063
4826	B	496789
4827	B	498688
4828	B	497500
4829	B	499390
4830	B	498057
4831	B	499966
4832	B	498552
4833	B	500508
4834	B	499240

1395	F	54348
1396	F	57078
1397	F	55156
1398	F	58343
1399	F	56392
1400	F	61103
1401	F	59177
1402	F	59701
1403	F	57802
1404	F	61887
1405	F	59971
1406	F	62255
1407	F	60348
1408	F	63515
1409	F	61557
1410	F	63657
1411	F	61761
1412	F	64088
1413	F	62196
1414	F	64422
1415	F	62537
1416	F	65072
1417	F	63140
1418	F	65978
1419	F	64088
1420	F	67046
1421	F	65146
1422	F	67466
1423	F	65580
1424	F	68569
1425	F	66686
1426	F	68609
1427	F	66688
1428	F	70423
1429	F	68479

3115	F	887776
3116	F	891025
3117	F	889105
3118	F	891504
3119	F	889593
3120	F	891795
3121	F	889841
3122	F	892279
3123	F	890400
3124	F	892182
3125	F	890288
3126	F	893010
3127	F	891139
3128	F	893101
3129	F	891211
3130	F	895494
3131	F	893599
3132	F	896448
3133	F	894511
3134	F	897341
3135	F	895442
3136	F	899197
3137	F	897279
3138	F	899999
3139	F	898075
3140	F	903008
3141	F	901103
3142	F	904798
3143	F	902923
3144	F	906993
3145	F	905129
3146	F	907564
3147	F	905665
3148	F	907913
3149	F	905998

4835	B	501145
4836	B	499812
4837	B	501762
4838	B	500020
4839	B	501915
4840	B	500716
4841	B	502628
4842	B	504395
4843	B	506292
4844	B	504885
4845	B	506772
4846	B	507107
4847	B	509003
4848	B	507933
4849	B	509795
4850	B	510741
4851	B	512656
4852	B	508573
4853	B	510445
4854	B	513663
4855	B	515585
4856	B	515276
4857	B	517040
4858	B	517602
4859	B	519510
4860	B	517602
4861	B	519510
4862	B	518075
4863	B	519947
4864	B	518429
4865	B	520326
4866	B	521416
4867	B	523319
4868	B	523196
4869	B	525096

1430	F	71099
1431	F	69206
1432	F	71829
1433	F	69935
1434	F	73745
1435	F	71931
1436	F	76942
1437	F	75022
1438	F	77404
1439	F	75556
1440	F	78133
1441	F	76192
1442	F	79079
1443	F	77122
1444	F	79471
1445	F	77481
1446	F	79670
1447	F	77816
1448	F	80236
1449	F	78356
1450	F	81108
1451	F	79182
1452	F	83024
1453	F	81158
1454	F	83786
1455	F	81886
1456	F	84739
1457	F	82821
1458	F	84866
1459	F	82967
1460	F	85175
1461	F	83240
1462	F	85690
1463	F	83790
1464	F	86397

3150	F	908349
3151	F	906425
3152	F	909186
3153	F	907286
3154	F	911413
3155	F	909481
3156	F	912084
3157	F	910176
3158	F	912718
3159	F	910814
3160	F	913813
3161	F	911941
3162	F	915106
3163	F	913211
3164	F	915053
3165	F	913141
3166	F	916630
3167	F	914731
3168	F	917500
3169	F	915594
3170	F	918615
3171	F	916715
3172	F	919639
3173	F	917732
3174	F	920216
3175	F	918312
3176	F	920971
3177	F	919057
3178	F	921889
3179	F	920015
3180	F	921773
3181	F	919871
3182	F	923428
3183	F	921546
3184	F	923841

4870	B	525033
4871	B	526939
4872	B	524599
4873	B	526501
4874	B	526494
4875	B	528361
4876	B	527330
4877	B	529238
4878	B	527167
4879	B	529067
4880	B	528673
4881	B	530573
4882	B	529456
4883	B	531376
4884	B	530864
4885	B	532745
4886	B	531906
4887	B	533776
4888	B	534199
4889	B	536103
4890	B	536674
4891	B	538552
4892	B	537422
4893	B	539270
4894	B	538165
4895	B	540048
4896	B	538658
4897	B	540578
4898	B	538970
4899	B	540857
4900	B	539859
4901	B	541736
4902	B	541474
4903	B	543411
4904	B	542791



1465	F	84507
1466	F	88470
1467	F	86563
1468	F	89038
1469	F	87121
1470	F	91017
1471	F	89146
1472	F	93075
1473	F	91147
1474	F	93846
1475	F	91948
1476	F	94410
1477	F	92561
1478	F	95447
1479	F	93541
1480	F	96074
1481	F	94197
1482	F	97706
1483	F	95841
1484	F	98142
1485	F	96292
1486	F	99925
1487	F	98011
1488	F	101229
1489	F	99338
1490	F	101429
1491	F	99552
1492	F	102137
1493	F	100237
1494	F	102600
1495	F	100657
1496	F	103330
1497	F	101429
1498	F	103877
1499	F	101966

3185	F	921936
3186	F	924795
3187	F	922945
3188	F	925102
3189	F	923188
3190	F	926130
3191	F	924248
3192	F	927729
3193	F	925829
3194	F	928112
3195	F	926130
3196	F	929014
3197	F	927129
3198	F	930776
3199	F	928876
3200	F	931898
3201	F	929987
3202	F	932291
3203	F	930323
3204	F	933264
3205	F	931339
3206	F	935505
3207	F	933605
3208	F	936779
3209	F	934873
3210	F	937000
3211	F	935108
3212	F	938062
3213	F	936162
3214	F	938536
3215	F	936689
3216	F	938934
3217	F	937000
3218	F	939541
3219	F	937640

4905	B	544691
4906	B	543234
4907	B	545134
4908	B	543608
4909	B	545513
4910	B	546851
4911	B	548762
4912	B	549793
4913	B	551652
4914	B	547523
4915	B	549430
4916	B	550754
4917	B	552702
4918	B	551775
4919	B	553674
4920	B	552876
4921	B	554756
4922	B	555340
4923	B	557240
4924	B	555736
4925	B	557619
4926	B	558229
4927	B	560135
4928	B	558821
4929	B	560696
4930	B	559955
4931	B	561816
4932	B	561979
4933	B	563858
4934	B	561979
4935	B	563812
4936	B	564167
4937	B	566081
4938	B	565229
4939	B	567096

1500	F	104336
1501	F	102469
1502	F	108182
1503	F	106280
1504	F	111814
1505	F	109911
1506	F	112412
1507	F	110553
1508	F	113442
1509	F	111571
1510	F	113891
1511	F	112010
1512	F	114990
1513	F	113112
1514	F	115684
1515	F	113776
1516	F	116526
1517	F	114656
1518	F	117731
1519	F	115825
1520	F	118292
1521	F	116389
1522	F	119593
1523	F	117685
1524	F	120231
1525	F	118292
1526	F	122278
1527	F	120382
1528	F	122610
1529	F	120682
1530	F	123309
1531	F	121390
1532	F	126113
1533	F	124213
1534	F	128975

3220	F	940603
3221	F	938681
3222	F	940758
3223	F	938826
3224	F	941387
3225	F	939470
3226	F	942261
3227	F	940373
3228	F	942563
3229	F	940654
3230	F	942807
3231	F	940907
3232	F	943510
3233	F	941608
3234	F	943771
3235	F	941872
3236	F	944330
3237	F	942413
3238	F	945147
3239	F	943262
3240	F	945527
3241	F	943620
3242	F	946627
3243	F	944741
3244	F	947165
3245	F	945278
3246	F	948674
3247	F	946774
3248	F	949646
3249	F	947716
3250	F	950731
3251	F	948837
3252	F	951418
3253	F	949545
3254	F	951940

4940	B	566419
4941	B	568318
4942	B	567974
4943	B	569872
4944	B	568753
4945	B	570655
4946	B	569707
4947	B	571605
4948	B	571285
4949	B	573207
4950	B	572080
4951	B	573948
4952	B	572628
4953	B	574524
4954	B	573563
4955	B	575436
4956	B	572628
4957	B	574524
4958	B	575279
4959	B	577202
4960	B	576190
4961	B	578039
4962	B	578174
4963	B	580011
4964	B	579148
4965	B	581040
4966	B	580227
4967	B	582047
4968	B	580656
4969	B	582542
4970	B	580420
4971	B	582322
4972	B	581322
4973	B	583212
4974	B	582051

1535	F	127091
1536	F	134603
1537	F	132806
1538	F	136249
1539	F	134352
1540	F	137680
1541	F	135756
1542	F	137680
1543	F	135799
1544	F	138035
1545	F	136135
1546	F	139266
1547	F	137363
1548	F	140208
1549	F	138351
1550	F	141636
1551	F	139735
1552	F	142808
1553	F	140900
1554	F	144272
1555	F	142372
1556	F	145217
1557	F	143335
1558	F	146527
1559	F	144645
1560	F	146965
1561	F	145086
1562	F	147455
1563	F	145501
1564	F	148810
1565	F	146904
1566	F	151964
1567	F	150062
1568	F	154064
1569	F	152113

3255	F	950034
3256	F	952365
3257	F	950461
3258	F	953230
3259	F	951316
3260	F	954978
3261	F	953125
3262	F	955613
3263	F	953697
3264	F	956989
3265	F	955136
3266	F	957684
3267	F	955778
3268	F	959156
3269	F	957187
3270	F	960035
3271	F	958117
3272	F	961584
3273	F	959727
3274	F	965172
3275	F	963269
3276	F	966747
3277	F	964843
3278	F	968015
3279	F	966111
3280	F	968508
3281	F	966609
3282	F	969289
3283	F	967389
3284	F	969537
3285	F	967640
3286	F	970078
3287	F	968137
3288	F	970317
3289	F	968394

4975	B	583973
4976	B	582592
4977	B	584513
4978	B	583651
4979	B	585588
4980	B	584932
4981	B	586813
4982	B	585457
4983	B	587360
4984	B	587145
4985	B	589063
4986	B	588150
4987	B	590044
4988	B	588404
4989	B	590304
4990	B	589320
4991	B	591193
4992	B	590733
4993	B	592677
4994	B	592682
4995	B	594583
4996	B	593126
4997	B	595026
4998	B	594005
4999	B	595882
5000	B	594521
5001	B	596421
5002	B	596170
5003	B	598096
5004	B	596532
5005	B	598451
5006	B	597438
5007	B	599365
5008	B	598191
5009	B	600088

1570	F	154888	3290	F	970857	5010	B	598836
1571	F	152963	3291	F	968969	5011	B	600749
1572	F	155418	3292	F	971657	5012	B	599476
1573	F	153558	3293	F	969757	5013	B	601327
1574	F	156528	3294	F	974954	5014	B	600192
1575	F	154606	3295	F	973067	5015	B	602103
1576	F	157433	3296	F	975200	5016	B	601131
1577	F	155516	3297	F	973300	5017	B	603030
1578	F	158771	3298	F	976362	5018	B	602307
1579	F	156842	3299	F	974418	5019	B	604209
1580	F	159105	3300	F	977009	5020	B	602810
1581	F	157219	3301	F	975050	5021	B	604759
1582	F	159657	3302	F	978153	5022	B	603529
1583	F	157761	3303	F	976255	5023	B	605402
1584	F	160240	3304	F	980532	5024	B	604759
1585	F	158316	3305	F	978632	5025	B	606662
1586	F	160675	3306	F	981701	5026	B	606076
1587	F	158778	3307	F	979785	5027	B	608046
1588	F	161289	3308	F	982885	5028	B	606843
1589	F	159402	3309	F	980983	5029	B	608746
1590	F	161918	3310	F	983878	5030	B	607504
1591	F	159979	3311	F	981973	5031	B	609404
1592	F	162214	3312	F	985264	5032	B	609224
1593	F	160297	3313	F	983395	5033	B	611138
1594	F	163996	3314	F	986953	5034	B	609952
1595	F	162045	3315	F	985049	5035	B	611865
1596	F	165189	3316	F	985623	5036	B	611138
1597	F	163288	3317	F	983760	5037	B	613033
1598	F	166730	3318	F	986956	5038	B	612012
1599	F	164828	3319	F	985049	5039	B	613917
1600	F	168243	3320	F	987506	5040	B	612554
1601	F	166327	3321	F	985592	5041	B	614453
1602	F	168907	3322	F	988307	5042	B	614136
1603	F	167064	3323	F	986404	5043	B	616017
1604	F	169129	3324	F	988783	5044	B	614978

1605	F	167294
1606	F	170632
1607	F	168692
1608	F	171229
1609	F	169381
1610	F	171553
1611	F	169614
1612	F	172433
1613	F	170533
1614	F	173217
1615	F	171316
1616	F	174567
1617	F	172680
1618	F	175342
1619	F	173479
1620	F	175709
1621	F	173752
1622	F	176909
1623	F	175009
1624	F	176704
1625	F	174761
1626	F	177608
1627	F	175709
1628	F	179259
1629	F	177384
1630	F	179719
1631	F	177800
1632	F	181629
1633	F	179743
1634	F	182851
1635	F	180952
1636	F	184230
1637	F	182335
1638	F	184870
1639	F	182962

3325	F	986927
3326	F	989593
3327	F	987694
3328	F	990733
3329	F	988783
3330	F	991559
3331	F	989675
3332	F	992323
3333	F	990421
3334	F	992522
3335	F	990640
3336	F	993308
3337	F	991361
3338	F	992795
3339	F	990919
3340	F	994573
3341	F	992673
3342	F	995517
3343	F	993570
3344	F	996518
3345	F	994660
3346	F	997317
3347	F	995450
3348	F	998653
3349	F	996762
3350	F	999865
3351	F	997908
3352	F	1001112
3353	F	999238
3354	F	1001651
3355	F	999731
3356	F	1003237
3357	F	1001317
3358	F	1004049
3359	F	1002132

5045	B	616936
5046	B	615399
5047	B	617342
5048	B	616565
5049	B	618402
5050	B	617618
5051	B	619515
5052	B	619027
5053	B	620937
5054	B	620142
5055	B	622052
5056	B	620230
5057	B	622124
5058	B	621498
5059	B	623385
5060	B	622583
5061	B	624479
5062	B	623718
5063	B	625598
5064	B	624533
5065	B	626462
5066	B	625020
5067	B	626893
5068	B	625774
5069	B	627660
5070	B	626146
5071	B	628010
5072	B	626646
5073	B	628522
5074	B	628020
5075	B	629982
5076	B	628882
5077	B	630730
5078	B	629982
5079	B	631822

1640	F	185241	3360	F	1004252	5080	B	631862
1641	F	183348	3361	F	1002307	5081	B	633762
1642	F	185611	3362	F	1005400	5082	B	633774
1643	F	183685	3363	F	1003518	5083	B	635675
1644	F	186336	3364	F	1005892	5084	B	637192
1645	F	184445	3365	F	1003958	5085	B	639082
1646	F	188059	3366	F	1006516	5086	B	638321
1647	F	186171	3367	F	1004599	5087	B	640221
1648	F	190828	3368	F	1007332	5088	B	639082
1649	F	188956	3369	F	1005446	5089	B	640954
1650	F	191294	3370	F	1009066	5090	B	639317
1651	F	189428	3371	F	1007190	5091	B	641243
1652	F	192686	3372	F	1014072	5092	B	639860
1653	F	190788	3373	F	1012172	5093	B	641780
1654	F	193380	3374	F	1015614	5094	B	640868
1655	F	191474	3375	F	1013733	5095	B	642770
1656	F	193388	3376	F	1016078	5096	B	641243
1657	F	191474	3377	F	1014172	5097	B	643106
1658	F	193977	3378	F	1015924	5098	B	641605
1659	F	192059	3379	F	1014059	5099	B	643503
1660	F	195480	3380	F	1016230	5100	B	642538
1661	F	193585	3381	F	1014330	5101	B	644407
1662	F	195868	3382	F	1017479	5102	B	643243
1663	F	193969	3383	F	1015558	5103	B	645145
1664	F	197913	3384	F	1018915	5104	B	643550
1665	F	196013	3385	F	1017003	5105	B	645450
1666	F	199088	3386	F	1019328	5106	B	643925
1667	F	197213	3387	F	1017440	5107	B	645837
1668	F	202776	3388	F	1020813	5108	B	645848
1669	F	200876	3389	F	1018915	5109	B	647759
1670	F	204467	3390	F	1021621	5110	B	645987
1671	F	202497	3391	F	1019671	5111	B	647969
1672	F	205584	3392	F	1023996	5112	B	646490
1673	F	203664	3393	F	1022107	5113	B	648429
1674	F	206940	3394	F	1024277	5114	B	646973

1675	F	205063	3395	F	1022385	5115	B	648871
1676	F	207560	3396	F	1025368	5116	B	648115
1677	F	205587	3397	F	1023468	5117	B	650007
1678	F	208048	3398	F	1026671	5118	B	648516
1679	F	206139	3399	F	1024821	5119	B	650374
1680	F	209923	3400	F	1027688	5120	B	650567
1681	F	208023	3401	F	1025823	5121	B	652472
1682	F	210455	3402	F	1030916	5122	B	651251
1683	F	208569	3403	F	1029047	5123	B	653140
1684	F	211049	3404	F	1031342	5124	B	653186
1685	F	209147	3405	F	1029430	5125	B	655076
1686	F	211596	3406	F	1032795	5126	B	653628
1687	F	209705	3407	F	1030916	5127	B	655515
1688	F	212226	3408	F	1032978	5128	B	656010
1689	F	210311	3409	F	1031078	5129	B	657870
1690	F	213832	3410	F	1033730	5130	B	656761
1691	F	211960	3411	F	1031839	5131	B	658636
1692	F	214866	3412	F	1035774	5132	B	658389
1693	F	212921	3413	F	1033821	5133	B	660295
1694	F	215173	3414	F	1036884	5134	B	660436
1695	F	213307	3415	F	1034954	5135	B	662352
1696	F	215800	3416	F	1037476	5136	B	663483
1697	F	213957	3417	F	1035577	5137	B	665358
1698	F	216489	3418	F	1037714	5138	B	664701
1699	F	214549	3419	F	1035847	5139	B	666607
1700	F	216980	3420	F	1038782	5140	B	665978
1701	F	215100	3421	F	1036884	5141	B	667856
1702	F	217665	3422	F	1040777	5142	B	667238
1703	F	215793	3423	F	1038856	5143	B	669172
1704	F	218039	3424	F	1042132	5144	B	668195
1705	F	216071	3425	F	1040216	5145	B	670046
1706	F	218476	3426	F	1043148	5146	B	668791
1707	F	216560	3427	F	1041215	5147	B	670691
1708	F	218769	3428	F	1044388	5148	B	669426
1709	F	216809	3429	F	1042445	5149	B	671326

1710	F	220020
1711	F	218128
1712	F	221210
1713	F	219275
1714	F	222497
1715	F	220601
1716	F	223292
1717	F	221403
1718	F	223775
1719	F	221877
1720	F	224250
1721	F	222377
1722	F	224906
1723	F	223008
1724	F	225283
1725	F	223418
1726	F	226670
1727	F	224770
1728	F	227849
1729	F	225937
1730	F	228185
1731	F	226269
1732	F	228393
1733	F	226512
1734	F	229334
1735	F	227499
1736	F	230761
1737	F	228846
1738	F	231287
1739	F	229334
1740	F	231731
1741	F	229927
1742	F	232865
1743	F	231027
1744	F	232865

3430	F	1045164
3431	F	1043224
3432	F	1046223
3433	F	1044324
3434	F	1047299
3435	F	1045364
3436	F	1049803
3437	F	1047914
3438	F	1050341
3439	F	1048431
3440	F	1050862
3441	F	1048907
3442	F	1051515
3443	F	1049572
3444	F	1051828
3445	F	1049917
3446	F	1052885
3447	F	1050957
3448	F	1053963
3449	F	1052057
3450	F	1055238
3451	F	1053362
3452	F	1055849
3453	F	1053963
3454	F	1056332
3455	F	1054465
3456	F	1056738
3457	F	1054830
3458	F	1058019
3459	F	1056110
3460	F	1058504
3461	F	1056587
3462	F	1059300
3463	F	1057406
3464	F	1060356

5150	B	671116
5151	B	673055
5152	B	671659
5153	B	673547
5154	B	672474
5155	B	674347
5156	B	673238
5157	B	675140
5158	B	674944
5159	B	676911
5160	B	674797
5161	B	676669
5162	B	675741
5163	B	677643
5164	B	676340
5165	B	678204
5166	B	676911
5167	B	678770
5168	B	677240
5169	B	679136
5170	B	677873
5171	B	679767
5172	B	678549
5173	B	680420
5174	B	679692
5175	B	681628
5176	B	680320
5177	B	682220
5178	B	681126
5179	B	683046
5180	B	682558
5181	B	684404
5182	B	681857
5183	B	683768
5184	B	683046



1745	F	231027
1746	F	234315
1747	F	232394
1748	F	234823
1749	F	232865
1750	F	235154
1751	F	233245
1752	F	236429
1753	F	234520
1754	F	237268
1755	F	235271
1756	F	238047
1757	F	236162
1758	F	238636
1759	F	236736
1760	F	239957
1761	F	238047
1762	F	241373
1763	F	239482
1764	F	242017
1765	F	240072
1766	F	242740
1767	F	240829
1768	F	243281
1769	F	241373
1770	F	244244
1771	F	242345
1772	F	246052
1773	F	244179
1774	F	247581
1775	F	245697
1776	F	249216
1777	F	247244
1778	F	251003
1779	F	249137

3465	F	1058400
3466	F	1061455
3467	F	1059456
3468	F	1062092
3469	F	1060243
3470	F	1063884
3471	F	1061983
3472	F	1064928
3473	F	1063056
3474	F	1067125
3475	F	1065240
3476	F	1067963
3477	F	1066075
3478	F	1068596
3479	F	1066668
3480	F	1069752
3481	F	1067890
3482	F	1071068
3483	F	1069210
3484	F	1072701
3485	F	1070806
3486	F	1073987
3487	F	1072090
3488	F	1075643
3489	F	1073742
3490	F	1076350
3491	F	1074450
3492	F	1077354
3493	F	1075555
3494	F	1077778
3495	F	1075880
3496	F	1078445
3497	F	1076529
3498	F	1079373
3499	F	1077523

5185	B	684944
5186	B	684128
5187	B	686124
5188	B	684893
5189	B	686740
5190	B	685389
5191	B	687290
5192	B	686207
5193	B	688106
5194	B	687534
5195	B	689424
5196	B	688416
5197	B	690275
5198	B	688955
5199	B	690855
5200	B	689727
5201	B	691626
5202	B	690496
5203	B	692386
5204	B	691349
5205	B	693249
5206	B	692864
5207	B	694724
5208	B	695287
5209	B	697187
5210	B	696275
5211	B	698172
5212	B	696786
5213	B	698696
5214	B	698185
5215	B	700090
5216	B	700037
5217	B	701923
5218	B	702172
5219	B	704050

1780	F	252064	3500	F	1079715	5220	B	703443
1781	F	250189	3501	F	1077850	5221	B	705316
1782	F	252900	3502	F	1080538	5222	B	704441
1783	F	251000	3503	F	1078655	5223	B	706351
1784	F	253718	3504	F	1081108	5224	B	705516
1785	F	251855	3505	F	1079228	5225	B	707413
1786	F	254993	3506	F	1083006	5226	B	706312
1787	F	253138	3507	F	1081108	5227	B	708190
1788	F	256414	3508	F	1084404	5228	B	707058
1789	F	254509	3509	F	1082465	5229	B	708979
1790	F	257283	3510	F	1085896	5230	B	707856
1791	F	255383	3511	F	1083990	5231	B	709719
1792	F	257279	3512	F	1086468	5232	B	708906
1793	F	255379	3513	F	1084563	5233	B	710811
1794	F	258061	3514	F	1087889	5234	B	709258
1795	F	256107	3515	F	1085985	5235	B	711132
1796	F	259005	3516	F	1088427	5236	B	710074
1797	F	257128	3517	F	1086527	5237	B	711924
1798	F	261075	3518	F	1088927	5238	B	710328
1799	F	259195	3519	F	1087027	5239	B	712212
1800	F	261551	3520	F	1089668	5240	B	711748
1801	F	259650	3521	F	1087768	5241	B	713690
1802	F	262535	3522	F	1092655	5242	B	712456
1803	F	260611	3523	F	1090767	5243	B	714407
1804	F	262960	3524	F	1093357	5244	B	715001
1805	F	261060	3525	F	1091465	5245	B	716854
1806	F	264509	3526	F	1093957	5246	B	715983
1807	F	262614	3527	F	1092070	5247	B	717887
1808	F	265837	3528	F	1095818	5248	B	717800
1809	F	263925	3529	F	1093955	5249	B	719668
1810	F	266239	3530	F	1096359	5250	B	718468
1811	F	264367	3531	F	1094509	5251	B	720383
1812	F	267185	3532	F	1097047	5252	B	720469
1813	F	265286	3533	F	1095114	5253	B	722367
1814	F	267909	3534	F	1097365	5254	B	722645

1815	F	266037
1816	F	268594
1817	F	266756
1818	F	269299
1819	F	267505
1820	F	271044
1821	F	269121
1822	F	271737
1823	F	269838
1824	F	272558
1825	F	270645
1826	F	273007
1827	F	271098
1828	F	273463
1829	F	271500
1830	F	273922
1831	F	272057
1832	F	275083
1833	F	273094
1834	F	275495
1835	F	273554
1836	F	275739
1837	F	273878
1838	F	276229
1839	F	274371
1840	F	276548
1841	F	274638
1842	F	277098
1843	F	275178
1844	F	277358
1845	F	275448
1846	F	277609
1847	F	275739
1848	F	278314
1849	F	276386

3535	F	1095498
3536	F	1097646
3537	F	1095767
3538	F	1098161
3539	F	1096242
3540	F	1098560
3541	F	1096663
3542	F	1099044
3543	F	1097150
3544	F	1099454
3545	F	1097547
3546	F	1100878
3547	F	1098942
3548	F	1101839
3549	F	1099956
3550	F	1104621
3551	F	1102789
3552	F	1106487
3553	F	1104562
3554	F	1107225
3555	F	1105318
3556	F	1107814
3557	F	1105922
3558	F	1108282
3559	F	1106374
3560	F	1113162
3561	F	1111308
3562	F	1114813
3563	F	1112949
3564	F	1116611
3565	F	1114766
3566	F	1118605
3567	F	1116725
3568	F	1119754
3569	F	1117874

5255	B	724559
5256	B	723280
5257	B	725273
5258	B	723775
5259	B	725691
5260	B	724469
5261	B	726387
5262	B	725016
5263	B	726902
5264	B	726088
5265	B	727988
5266	B	727397
5267	B	729236
5268	B	728347
5269	B	730278
5270	B	728816
5271	B	730718
5272	B	729846
5273	B	731740
5274	B	730005
5275	B	731898
5276	B	730377
5277	B	732272
5278	B	730759
5279	B	732659
5280	B	732249
5281	B	734124
5282	B	732647
5283	B	734590
5284	B	733144
5285	B	735088
5286	B	733858
5287	B	735787
5288	B	734124
5289	B	736028

1850	F	279310
1851	F	277385
1852	F	280627
1853	F	278702
1854	F	281471
1855	F	279559
1856	F	282239
1857	F	280288
1858	F	283832
1859	F	281933
1860	F	284384
1861	F	282486
1862	F	285373
1863	F	283473
1864	F	285919
1865	F	284059
1866	F	286742
1867	F	284879
1868	F	287216
1869	F	285329
1870	F	287671
1871	F	285751
1872	F	288273
1873	F	286323
1874	F	288618
1875	F	286685
1876	F	288273
1877	F	286323
1878	F	289723
1879	F	287836
1880	F	289508
1881	F	287667
1882	F	290750
1883	F	288858
1884	F	291142

3570	F	1120291
3571	F	1118385
3572	F	1121099
3573	F	1119202
3574	F	1121886
3575	F	1119982
3576	F	1122979
3577	F	1121038
3578	F	1123376
3579	F	1121486
3580	F	1124136
3581	F	1122333
3582	F	1124623
3583	F	1122723
3584	F	1125306
3585	F	1123423
3586	F	1126300
3587	F	1124399
3588	F	1127440
3589	F	1125545
3590	F	1128968
3591	F	1127134
3592	F	1129916
3593	F	1128111
3594	F	1131255
3595	F	1129330
3596	F	1132598
3597	F	1130684
3598	F	1133896
3599	F	1132002
3600	F	1134373
3601	F	1132510
3602	F	1135431
3603	F	1133531
3604	F	1135730

5290	B	734523
5291	B	736441
5292	B	735088
5293	B	736978
5294	B	735416
5295	B	737315
5296	B	735822
5297	B	737700
5298	B	736099
5299	B	737981
5300	B	736714
5301	B	738612
5302	B	737448
5303	B	739321
5304	B	737802
5305	B	739693
5306	B	738048
5307	B	739948
5308	B	738964
5309	B	740808
5310	B	739282
5311	B	741190
5312	B	739956
5313	B	741906
5314	B	740743
5315	B	742597
5316	B	741190
5317	B	743081
5318	B	741942
5319	B	743875
5320	B	743009
5321	B	744914
5322	B	743875
5323	B	745738
5324	B	744325

1885	F	289253
1886	F	291702
1887	F	289812
1888	F	292522
1889	F	290633
1890	F	293035
1891	F	291142
1892	F	293731
1893	F	291786
1894	F	294530
1895	F	292670
1896	F	294367
1897	F	292513
1898	F	296092
1899	F	294209
1900	F	297611
1901	F	295757
1902	F	298027
1903	F	296092
1904	F	298555
1905	F	296582
1906	F	299403
1907	F	297511
1908	F	300409
1909	F	298579
1910	F	301332
1911	F	299433
1912	F	302215
1913	F	300282
1914	F	302492
1915	F	300618
1916	F	303627
1917	F	301730
1918	F	304350
1919	F	302487

3605	F	1133823
3606	F	1136932
3607	F	1135040
3608	F	1139875
3609	F	1137942
3610	F	1141133
3611	F	1139231
3612	F	1142301
3613	F	1140366
3614	F	1145346
3615	F	1143505
3616	F	1146637
3617	F	1144743
3618	F	1147417
3619	F	1145547
3620	F	1147981
3621	F	1146086
3622	F	1148126
3623	F	1146211
3624	F	1148913
3625	F	1147044
3626	F	1149702
3627	F	1147890
3628	F	1150561
3629	F	1148660
3630	F	1150946
3631	F	1149046
3632	F	1152302
3633	F	1150392
3634	F	1154344
3635	F	1152371
3636	F	1155448
3637	F	1153548
3638	F	1156630
3639	F	1154729

5325	B	746234
5326	B	744824
5327	B	746724
5328	B	745207
5329	B	747073
5330	B	746828
5331	B	748738
5332	B	747344
5333	B	749206
5334	B	748253
5335	B	750094
5336	B	748856
5337	B	750717
5338	B	749376
5339	B	751265
5340	B	750180
5341	B	752086
5342	B	750667
5343	B	752569
5344	B	751458
5345	B	753343
5346	B	753262
5347	B	755162
5348	B	754535
5349	B	756429
5350	B	756398
5351	B	758298
5352	B	756708
5353	B	758611
5354	B	760465
5355	B	762358
5356	B	761441
5357	B	763356
5358	B	762077
5359	B	763945

1920	F	305173
1921	F	303226
1922	F	306244
1923	F	304350
1924	F	307232
1925	F	305310
1926	F	307799
1927	F	305877
1928	F	309173
1929	F	307301
1930	F	310158
1931	F	308306
1932	F	311020
1933	F	309118
1934	F	311031
1935	F	309126
1936	F	311552
1937	F	309658
1938	F	312510
1939	F	310614
1940	F	313134
1941	F	311255
1942	F	313674
1943	F	311717
1944	F	314490
1945	F	312633
1946	F	315306
1947	F	313355
1948	F	315932
1949	F	314033
1950	F	318434
1951	F	316516
1952	F	320876
1953	F	318949
1954	F	321403

3640	F	1157756
3641	F	1155862
3642	F	1160695
3643	F	1158788
3644	F	1162326
3645	F	1160468
3646	F	1163300
3647	F	1161413
3648	F	1163763
3649	F	1161842
3650	F	1164224
3651	F	1162283
3652	F	1164800
3653	F	1162908
3654	F	1165312
3655	F	1163427
3656	F	1165877
3657	F	1163960
3658	F	1166827
3659	F	1164936
3660	F	1168099
3661	F	1166212
3662	F	1168991
3663	F	1167093
3664	F	1169769
3665	F	1167907
3666	F	1170349
3667	F	1168446
3668	F	1170953
3669	F	1169031
3670	F	1171641
3671	F	1169703
3672	F	1172172
3673	F	1170256
3674	F	1173649

5360	B	762528
5361	B	764410
5362	B	763118
5363	B	765018
5364	B	763539
5365	B	765504
5366	B	764000
5367	B	765907
5368	B	765391
5369	B	767328
5370	B	767041
5371	B	768951
5372	B	768271
5373	B	770171
5374	B	768799
5375	B	770686
5376	B	769562
5377	B	771608
5378	B	770752
5379	B	772652
5380	B	771701
5381	B	773620
5382	B	773316
5383	B	775178
5384	B	773690
5385	B	775579
5386	B	774596
5387	B	776522
5388	B	776300
5389	B	778224
5390	B	775346
5391	B	777266
5392	B	775618
5393	B	777518
5394	B	777266

1955	F	319547
1956	F	322084
1957	F	320217
1958	F	322911
1959	F	321049
1960	F	323634
1961	F	321726
1962	F	325117
1963	F	323211
1964	F	326213
1965	F	324254
1966	F	327607
1967	F	325695
1968	F	328162
1969	F	326262
1970	F	328630
1971	F	326723
1972	F	329134
1973	F	327178
1974	F	330734
1975	F	328810
1976	F	332123
1977	F	330252
1978	F	334575
1979	F	332660
1980	F	335884
1981	F	333980
1982	F	337129
1983	F	335202
1984	F	337910
1985	F	335955
1986	F	338746
1987	F	336795
1988	F	339217
1989	F	337362

3675	F	1171759
3676	F	1174885
3677	F	1172999
3678	F	1175559
3679	F	1173649
3680	F	1176927
3681	F	1175025
3682	F	1178912
3683	F	1176985
3684	F	1179826
3685	F	1177910
3686	F	1180498
3687	F	1178666
3688	F	1181716
3689	F	1179839
3690	F	1182069
3691	F	1180140
3692	F	1183626
3693	F	1181716
3694	F	1184128
3695	F	1182244
3696	F	1185004
3697	F	1183084
3698	F	1185897
3699	F	1184029
3700	F	1187151
3701	F	1185251
3702	F	1186262
3703	F	1184361
3704	F	1189054
3705	F	1187160
3706	F	1190885
3707	F	1188990
3708	F	1191507
3709	F	1189579

5395	B	779200
5396	B	778224
5397	B	780087
5398	B	778396
5399	B	780301
5400	B	779557
5401	B	781481
5402	B	780503
5403	B	782380
5404	B	781419
5405	B	783311
5406	B	781747
5407	B	783680
5408	B	783004
5409	B	784912
5410	B	783820
5411	B	785752
5412	B	785255
5413	B	787155
5414	B	786655
5415	B	788572
5416	B	788671
5417	B	790554
5418	B	789164
5419	B	791064
5420	B	790001
5421	B	791900
5422	B	791734
5423	B	793679
5424	B	792944
5425	B	794875
5426	B	793809
5427	B	795692
5428	B	794580
5429	B	796450

1990	F	339999	3710	F	1191932	5430	B	795066
1991	F	338083	3711	F	1190008	5431	B	796966
1992	F	343144	3712	F	1192524	5432	B	795956
1993	F	341266	3713	F	1190640	5433	B	797855
1994	F	343699	3714	F	1192759	5434	B	797018
1995	F	341813	3715	F	1190869	5435	B	798918
1996	F	344108	3716	F	1193642	5436	B	798989
1997	F	342204	3717	F	1191742	5437	B	800875
1998	F	344851	3718	F	1193557	5438	B	800069
1999	F	342933	3719	F	1191657	5439	B	801944
2000	F	346148	3720	F	1194015	5440	B	799840
2001	F	344219	3721	F	1192120	5441	B	801701
2002	F	346493	3722	F	1195490	5442	B	801533
2003	F	344590	3723	F	1193560	5443	B	803445
2004	F	346815	3724	F	1196093	5444	B	802717
2005	F	344907	3725	F	1194215	5445	B	804581
2006	F	347836	3726	F	1196474	5446	B	803559
2007	F	345956	3727	F	1194592	5447	B	805419
2008	F	350379	3728	F	1197659	5448	B	804032
2009	F	348432	3729	F	1195724	5449	B	805931
2010	F	350856	3730	F	1198499	5450	B	805383
2011	F	348951	3731	F	1196578	5451	B	807291
2012	F	352008	3732	F	1199912	5452	B	806107
2013	F	350106	3733	F	1197986	5453	B	807988
2014	F	353209	3734	F	1200969	5454	B	806533
2015	F	351305	3735	F	1199133	5455	B	808430
2016	F	354224	3736	F	1202121	5456	B	806954
2017	F	352312	3737	F	1200227	5457	B	808724
2018	F	354781	3738	F	1202957	5458	B	807133
2019	F	352871	3739	F	1201058	5459	B	809033
2020	F	355223	3740	F	1202590	5460	B	808442
2021	F	353261	3741	F	1200694	5461	B	810357
2022	F	355393	3742	F	1203923	5462	B	808972
2023	F	353519	3743	F	1202049	5463	B	810896
2024	F	358901	3744	F	1204631	5464	B	809674



2025	F	357001	3745	F	1202753	5465	B	811557
2026	F	356594	3746	F	1205864	5466	B	810192
2027	F	354692	3747	F	1203964	5467	B	812105
2028	F	359240	3748	F	1206483	5468	B	811472
2029	F	357374	3749	F	1204592	5469	B	813357
2030	F	359721	3750	F	1207629	5470	B	813325
2031	F	357763	3751	F	1205727	5471	B	815179
2032	F	361071	3752	F	1208802	5472	B	813133
2033	F	359240	3753	F	1206909	5473	B	815134
2034	F	363605	3754	F	1209500	5474	B	813808
2035	F	361731	3755	F	1207557	5475	B	815737
2036	F	364142	3756	F	1210483	5476	B	815246
2037	F	362246	3757	F	1208584	5477	B	817168
2038	F	364567	3758	F	1211618	5478	B	815995
2039	F	362708	3759	F	1209745	5479	B	817892
2040	F	365039	3760	F	1212523	5480	B	817264
2041	F	363184	3761	F	1210554	5481	B	819164
2042	F	365445	3762	F	1213827	5482	B	817579
2043	F	363517	3763	F	1211927	5483	B	819491
2044	F	367040	3764	F	1214875	5484	B	818890
2045	F	365144	3765	F	1212992	5485	B	820733
2046	F	368825	3766	F	1215293	5486	B	819332
2047	F	366993	3767	F	1213430	5487	B	821217
2048	F	369698	3768	F	1216043	5488	B	820096
2049	F	367760	3769	F	1214183	5489	B	821951
2050	F	370141	3770	F	1216226	5490	B	820945
2051	F	368239	3771	F	1214374	5491	B	822870
2052	F	372329	3772	F	1216927	5492	B	821151
2053	F	370375	3773	F	1215064	5493	B	823079
2054	F	372779	3774	F	1219490	5494	B	822558
2055	F	370881	3775	F	1217534	5495	B	824449
2056	F	373223	3776	F	1219431	5496	B	823767
2057	F	371342	3777	F	1217534	5497	B	825634
2058	F	373939	3778	F	1220403	5498	B	825876
2059	F	372017	3779	F	1218475	5499	B	827737

2060	F	374849
2061	F	372953
2062	F	375351
2063	F	373487
2064	F	376316
2065	F	374416
2066	F	377737
2067	F	375828
2068	F	379537
2069	F	377660
2070	F	380033
2071	F	378160
2072	F	380789
2073	F	378889
2074	F	381238
2075	F	379279
2076	F	382969
2077	F	381124
2078	F	383293
2079	F	381425
2080	F	385178
2081	F	383278
2082	F	386271
2083	F	384392
2084	F	386780
2085	F	384891
2086	F	389383
2087	F	387504
2088	F	389901
2089	F	388001
2090	F	390700
2091	F	388732
2092	F	391612
2093	F	389763
2094	F	392346

3780	F	1221383
3781	F	1219499
3782	F	1223653
3783	F	1221767
3784	F	1224758
3785	F	1222881
3786	F	1226308
3787	F	1224409
3788	F	1225625
3789	F	1223654
3790	F	1227566
3791	F	1225677
3792	F	1227858
3793	F	1225937
3794	F	1228081
3795	F	1226189
3796	B	1019
3797	B	2954
3798	B	1843
3799	B	3739
3800	B	2694
3801	B	4545
3802	B	3694
3803	B	5513
3804	B	4290
3805	B	6238
3806	B	5924
3807	B	7846
3808	B	7687
3809	B	9583
3810	B	9189
3811	B	11095
3812	B	10261
3813	B	12119
3814	B	10982

5500	B	826583
5501	B	828435
5502	B	827511
5503	B	829428
5504	B	828829
5505	B	830729
5506	B	830262
5507	B	832158
5508	B	831286
5509	B	833182
5510	B	831946
5511	B	833848
5512	B	833372
5513	B	835267
5514	B	834125
5515	B	835992
5516	B	835267
5517	B	837193
5518	B	836111
5519	B	837952
5520	B	837844
5521	B	839751
5522	B	839381
5523	B	841221
5524	B	841127
5525	B	843073
5526	B	842409
5527	B	844323
5528	B	843691
5529	B	845602
5530	B	844244
5531	B	846153
5532	B	845319
5533	B	847139
5534	B	846411

2095	F	390463
2096	F	392540
2097	F	390639
2098	F	393487
2099	F	391609
2100	F	393904
2101	F	392025
2102	F	394703
2103	F	392782
2104	F	395024
2105	F	393098
2106	F	395705
2107	F	393791
2108	F	397607
2109	F	395705
2110	F	398807
2111	F	396957
2112	F	399848
2113	F	397886
2114	F	400914
2115	F	399008
2116	F	401183
2117	F	399301
2118	F	401964
2119	F	400060
2120	F	403450
2121	F	401527
2122	F	404124
2123	F	402206
2124	F	405765
2125	F	403865
2126	F	407131
2127	F	405243
2128	F	407456
2129	F	405563

3815	B	12839
3816	B	11463
3817	B	13355
3818	B	12950
3819	B	14850
3820	B	14425
3821	B	16332
3822	B	17477
3823	B	19400
3824	B	16296
3825	B	18161
3826	B	21128
3827	B	22976
3828	B	22265
3829	B	24185
3830	B	23701
3831	B	25599
3832	B	26350
3833	B	28258
3834	B	26350
3835	B	28258
3836	B	27241
3837	B	29113
3838	B	27977
3839	B	29896
3840	B	28804
3841	B	30700
3842	B	29727
3843	B	31642
3844	B	30253
3845	B	32158
3846	B	31775
3847	B	33657
3848	B	32511
3849	B	34422

5535	B	848300
5536	B	848760
5537	B	850653
5538	B	849242
5539	B	851174
5540	B	850753
5541	B	852649
5542	B	851795
5543	B	853690
5544	B	852696
5545	B	854596
5546	B	853938
5547	B	855846
5548	B	855338
5549	B	857240
5550	B	855982
5551	B	857873
5552	B	856786
5553	B	858722
5554	B	858783
5555	B	860735
5556	B	859824
5557	B	861787
5558	B	860442
5559	B	862329
5560	B	861415
5561	B	863252
5562	B	861677
5563	B	863558
5564	B	863171
5565	B	865099
5566	B	865021
5567	B	866922
5568	B	865497
5569	B	867408

2130	F	408841	3850	B	34214	5570	B	866808
2131	F	406901	3851	B	36114	5571	B	868732
2132	F	410478	3852	B	34765	5572	B	867342
2133	F	408573	3853	B	36664	5573	B	869242
2134	F	410725	3854	B	36289	5574	B	868064
2135	F	408832	3855	B	38186	5575	B	869974
2136	F	412263	3856	B	37759	5576	B	868732
2137	F	410363	3857	B	39682	5577	B	870664
2138	F	414168	3858	B	39585	5578	B	869974
2139	F	412268	3859	B	41496	5579	B	871880
2140	F	415013	3860	B	40942	5580	B	870857
2141	F	413111	3861	B	42840	5581	B	872753
2142	F	415636	3862	B	39640	5582	B	872149
2143	F	413743	3863	B	41543	5583	B	874087
2144	F	417033	3864	B	43329	5584	B	872758
2145	F	415114	3865	B	45196	5585	B	874658
2146	F	417163	3866	B	44025	5586	B	874131
2147	F	415332	3867	B	45979	5587	B	876122
2148	F	418166	3868	B	45048	5588	B	874903
2149	F	416265	3869	B	46970	5589	B	876793
2150	F	420186	3870	B	45582	5590	B	875548
2151	F	418259	3871	B	47472	5591	B	877437
2152	F	420697	3872	B	45979	5592	B	878078
2153	F	418861	3873	B	47901	5593	B	880011
2154	F	421313	3874	B	47216	5594	B	879478
2155	F	419437	3875	B	49128	5595	B	881385
2156	F	422172	3876	B	47791	5596	B	880874
2157	F	420342	3877	B	49689	5597	B	882771
2158	F	423342	3878	B	48196	5598	B	882771
2159	F	421412	3879	B	50126	5599	B	884644
2160	F	424008	3880	B	49180	5600	B	883542
2161	F	422073	3881	B	51105	5601	B	885447
2162	F	424585	3882	B	50231	5602	B	883777
2163	F	422711	3883	B	52149	5603	B	885689
2164	F	426021	3884	B	51697	5604	B	884430

2165	F	424107
2166	F	427407
2167	F	425513
2168	F	427936
2169	F	426053
2170	F	428592
2171	F	426717
2172	F	430475
2173	F	428558
2174	F	431378
2175	F	429417
2176	F	431927
2177	F	430046
2178	F	432609
2179	F	430710
2180	F	433005
2181	F	431082
2182	F	433712
2183	F	431812
2184	F	436521
2185	F	434640
2186	F	436897
2187	F	435057
2188	F	439741
2189	F	437882
2190	F	438296
2191	F	436377
2192	F	440475
2193	F	438538
2194	F	440281
2195	F	438394
2196	F	440989
2197	F	439080
2198	F	442121
2199	F	440252

3885	B	53619
3886	B	52917
3887	B	54735
3888	B	53619
3889	B	55476
3890	B	53910
3891	B	55816
3892	B	54416
3893	B	56326
3894	B	55107
3895	B	57009
3896	B	56693
3897	B	58586
3898	B	57489
3899	B	59394
3900	B	58749
3901	B	60649
3902	B	60086
3903	B	62002
3904	B	62375
3905	B	64275
3906	B	61715
3907	B	63633
3908	B	62699
3909	B	64601
3910	B	63981
3911	B	65858
3912	B	64268
3913	B	66227
3914	B	64423
3915	B	66309
3916	B	64834
3917	B	66756
3918	B	65705
3919	B	67611

5605	B	886335
5606	B	885834
5607	B	887782
5608	B	887528
5609	B	889442
5610	B	888432
5611	B	890292
5612	B	888879
5613	B	890775
5614	B	889595
5615	B	891481
5616	B	890119
5617	B	892034
5618	B	891428
5619	B	893320
5620	B	892050
5621	B	893950
5622	B	892259
5623	B	894158
5624	B	892701
5625	B	894611
5626	B	893194
5627	B	895056
5628	B	893347
5629	B	895263
5630	B	893787
5631	B	895711
5632	B	895642
5633	B	897542
5634	B	896759
5635	B	898650
5636	B	897802
5637	B	899694
5638	B	899665
5639	B	901565

2200	F	442121
2201	F	440221
2202	F	442780
2203	F	440879
2204	F	443285
2205	F	441384
2206	F	444276
2207	F	442406
2208	F	444472
2209	F	442568
2210	F	444960
2211	F	443040
2212	F	445556
2213	F	443681
2214	F	447565
2215	F	445676
2216	F	448396
2217	F	446496
2218	F	450057
2219	F	448133
2220	F	450444
2221	F	448555
2222	F	450988
2223	F	449054
2224	F	452212
2225	F	450329
2226	F	453450
2227	F	451581
2228	F	454643
2229	F	452718
2230	F	456004
2231	F	454124
2232	F	456785
2233	F	454897
2234	F	457749

3920	B	66228
3921	B	68163
3922	B	67538
3923	B	69404
3924	B	67961
3925	B	69841
3926	B	68796
3927	B	70662
3928	B	70984
3929	B	72885
3930	B	69392
3931	B	71314
3932	B	71365
3933	B	73287
3934	B	72253
3935	B	74167
3936	B	73916
3937	B	75760
3938	B	76398
3939	B	78328
3940	B	77734
3941	B	79610
3942	B	78592
3943	B	80517
3944	B	79577
3945	B	81476
3946	B	79968
3947	B	81861
3948	B	80203
3949	B	82108
3950	B	80665
3951	B	82565
3952	B	81257
3953	B	83184
3954	B	83370

5640	B	900460
5641	B	902360
5642	B	903450
5643	B	905354
5644	B	905307
5645	B	907291
5646	B	907290
5647	B	909083
5648	B	908055
5649	B	909955
5650	B	908358
5651	B	910273
5652	B	908900
5653	B	910831
5654	B	909607
5655	B	911450
5656	B	911760
5657	B	913589
5658	B	912584
5659	B	914529
5660	B	913054
5661	B	914956
5662	B	914208
5663	B	916113
5664	B	915388
5665	B	917272
5666	B	915880
5667	B	917747
5668	B	916886
5669	B	918778
5670	B	917940
5671	B	919827
5672	B	919070
5673	B	920972
5674	B	920107

2235	F	455856
2236	F	458132
2237	F	456205
2238	F	459216
2239	F	457348
2240	F	460692
2241	F	458792
2242	F	460133
2243	F	458230
2244	F	461228
2245	F	459327
2246	F	462183
2247	F	460269
2248	F	463120
2249	F	461220
2250	F	464355
2251	F	462444
2252	F	464842
2253	F	463010
2254	F	465346
2255	F	463451
2256	F	466061
2257	F	464143
2258	F	466780
2259	F	464842
2260	F	467462
2261	F	465578
2262	F	469419
2263	F	467538
2264	F	471324
2265	F	469419
2266	F	470463
2267	F	468587
2268	F	471822
2269	F	469897

3955	B	85203
3956	B	84202
3957	B	86080
3958	B	85032
3959	B	86902
3960	B	85520
3961	B	87367
3962	B	85648
3963	B	87548
3964	B	86155
3965	B	88052
3966	B	86806
3967	B	88768
3968	B	88389
3969	B	90207
3970	B	89174
3971	B	91107
3972	B	91319
3973	B	93151
3974	B	93306
3975	B	95184
3976	B	94311
3977	B	96210
3978	B	94761
3979	B	96578
3980	B	95640
3981	B	97452
3982	B	96835
3983	B	98743
3984	B	97685
3985	B	99639
3986	B	98655
3987	B	100585
3988	B	99680
3989	B	101592

5675	B	922088
5676	B	920666
5677	B	922554
5678	B	921412
5679	B	923307
5680	B	922216
5681	B	924104
5682	B	922661
5683	B	924538
5684	B	924024
5685	B	925893
5686	B	924192
5687	B	926063
5688	B	925245
5689	B	927137
5690	B	925672
5691	B	927558
5692	B	926744
5693	B	928659
5694	B	928169
5695	B	930064
5696	B	928543
5697	B	930439
5698	B	929238
5699	B	931109
5700	B	931227
5701	B	933127
5702	B	932291
5703	B	934184
5704	B	933738
5705	B	935651
5706	B	933127
5707	B	935001
5708	B	935969
5709	B	937869

2270	F	472471
2271	F	470610
2272	F	473208
2273	F	471319
2274	F	475143
2275	F	473243
2276	F	477091
2277	F	475181
2278	F	477375
2279	F	475475
2280	F	478473
2281	F	476586
2282	F	479058
2283	F	477158
2284	F	479829
2285	F	477916
2286	F	481237
2287	F	479312
2288	F	481769
2289	F	479903
2290	F	482435
2291	F	480535
2292	F	483976
2293	F	482075
2294	F	484899
2295	F	483029
2296	F	485593
2297	F	483674
2298	F	486401
2299	F	484498
2300	F	486762
2301	F	484859
2302	F	487287
2303	F	485366
2304	F	487487

3990	B	101592
3991	B	103448
3992	B	101950
3993	B	103878
3994	B	102534
3995	B	104467
3996	B	103031
3997	B	104947
3998	B	103754
3999	B	105653
4000	B	104281
4001	B	106192
4002	B	104786
4003	B	106618
4004	B	108635
4005	B	110512
4006	B	112299
4007	B	114196
4008	B	112839
4009	B	114713
4010	B	113960
4011	B	115829
4012	B	114352
4013	B	116272
4014	B	114932
4015	B	116831
4016	B	116002
4017	B	117886
4018	B	116781
4019	B	118702
4020	B	118284
4021	B	120181
4022	B	118749
4023	B	120691
4024	B	120124

5710	B	937305
5711	B	939223
5712	B	937448
5713	B	939423
5714	B	938633
5715	B	940533
5716	B	939032
5717	B	940928
5718	B	939478
5719	B	941392
5720	B	940021
5721	B	941918
5722	B	941017
5723	B	942925
5724	B	941392
5725	B	943238
5726	B	941586
5727	B	943496
5728	B	942787
5729	B	944657
5730	B	943043
5731	B	944971
5732	B	943404
5733	B	945286
5734	B	944025
5735	B	945981
5736	B	944302
5737	B	946175
5738	B	944654
5739	B	946533
5740	B	945633
5741	B	947515
5742	B	946073
5743	B	947974
5744	B	946645



2305	F	485642
2306	F	488811
2307	F	486942
2308	F	488918
2309	F	487001
2310	F	489740
2311	F	487772
2312	F	490300
2313	F	488400
2314	F	490880
2315	F	488969
2316	F	491167
2317	F	489268
2318	F	492066
2319	F	490096
2320	F	494600
2321	F	492697
2322	F	495778
2323	F	493845
2324	F	496350
2325	F	494396
2326	F	497139
2327	F	495210
2328	F	497504
2329	F	495651
2330	F	498216
2331	F	496381
2332	F	498990
2333	F	497076
2334	F	499284
2335	F	497401
2336	F	499563
2337	F	497644
2338	F	500555
2339	F	498645

4025	B	122009
4026	B	120691
4027	B	122601
4028	B	122655
4029	B	124563
4030	B	123173
4031	B	125141
4032	B	123579
4033	B	125526
4034	B	126570
4035	B	128539
4036	B	129398
4037	B	131325
4038	B	134942
4039	B	136814
4040	B	136628
4041	B	138531
4042	B	138117
4043	B	139995
4044	B	138531
4045	B	140363
4046	B	138525
4047	B	140361
4048	B	139778
4049	B	141692
4050	B	140577
4051	B	142487
4052	B	142067
4053	B	143981
4054	B	142919
4055	B	144787
4056	B	144478
4057	B	146417
4058	B	145520
4059	B	147378

5745	B	948517
5746	B	947646
5747	B	949545
5748	B	948344
5749	B	950219
5750	B	950104
5751	B	952004
5752	B	951301
5753	B	953207
5754	B	951505
5755	B	953387
5756	B	952382
5757	B	954257
5758	B	952927
5759	B	954794
5760	B	953711
5761	B	955611
5762	B	955556
5763	B	957444
5764	B	956049
5765	B	957977
5766	B	957358
5767	B	959202
5768	B	958136
5769	B	960022
5770	B	959490
5771	B	961374
5772	B	960507
5773	B	962439
5774	B	961892
5775	B	963792
5776	B	965000
5777	B	966954
5778	B	967076
5779	B	968975

2340	F	503868
2341	F	502008
2342	F	504574
2343	F	502741
2344	F	506571
2345	F	504671
2346	F	507498
2347	F	505565
2348	F	507615
2349	F	505777
2350	F	510441
2351	F	508522
2352	F	513523
2353	F	511660
2354	F	516834
2355	F	514938
2356	F	515101
2357	F	513277
2358	F	517031
2359	F	515093
2360	F	517620
2361	F	515698
2362	F	518070
2363	F	516181
2364	F	521162
2365	F	519241
2366	F	523023
2367	F	521123
2368	F	523865
2369	F	522003
2370	F	524373
2371	F	522530
2372	F	526029
2373	F	524115
2374	F	526479

4060	B	146972
4061	B	148872
4062	B	147545
4063	B	149452
4064	B	147756
4065	B	149677
4066	B	148484
4067	B	150382
4068	B	152436
4069	B	154325
4070	B	154353
4071	B	156228
4072	B	155395
4073	B	157286
4074	B	155740
4075	B	157613
4076	B	157002
4077	B	158902
4078	B	157861
4079	B	159764
4080	B	159219
4081	B	161121
4082	B	159569
4083	B	161484
4084	B	160221
4085	B	162109
4086	B	160670
4087	B	162572
4088	B	161075
4089	B	162983
4090	B	161789
4091	B	163728
4092	B	162380
4093	B	164291
4094	B	162671

5780	B	968474
5781	B	970326
5782	B	969039
5783	B	970930
5784	B	969718
5785	B	971619
5786	B	970080
5787	B	971991
5788	B	970371
5789	B	972257
5790	B	970832
5791	B	972738
5792	B	971481
5793	B	973403
5794	B	971909
5795	B	973810
5796	B	975372
5797	B	977234
5798	B	975634
5799	B	977548
5800	B	976739
5801	B	978639
5802	B	978543
5803	B	980448
5804	B	977907
5805	B	979832
5806	B	980997
5807	B	982862
5808	B	982167
5809	B	984051
5810	B	983206
5811	B	985082
5812	B	984344
5813	B	986279
5814	B	985741

2375	F	524580
2376	F	526756
2377	F	524823
2378	F	528167
2379	F	526263
2380	F	529315
2381	F	527408
2382	F	530372
2383	F	528484
2384	F	531842
2385	F	529945
2386	F	534077
2387	F	532190
2388	F	536335
2389	F	534585
2390	F	536858
2391	F	534931
2392	F	537710
2393	F	535810
2394	F	538105
2395	F	536211
2396	F	538901
2397	F	536979
2398	F	539360
2399	F	537421
2400	F	541059
2401	F	539160
2402	F	542198
2403	F	540335
2404	F	542650
2405	F	540840
2406	F	543589
2407	F	541677
2408	F	546376
2409	F	544486

4095	B	164573
4096	B	164340
4097	B	166222
4098	B	165693
4099	B	167632
4100	B	166627
4101	B	168472
4102	B	168668
4103	B	170565
4104	B	169244
4105	B	171102
4106	B	169734
4107	B	171575
4108	B	171259
4109	B	173158
4110	B	171701
4111	B	173585
4112	B	172018
4113	B	173925
4114	B	172759
4115	B	174706
4116	B	173718
4117	B	175602
4118	B	174902
4119	B	176765
4120	B	175869
4121	B	177781
4122	B	176181
4123	B	178083
4124	B	177158
4125	B	179120
4126	B	177599
4127	B	179539
4128	B	177928
4129	B	179888

5815	B	987653
5816	B	986106
5817	B	988045
5818	B	987667
5819	B	989585
5820	B	987418
5821	B	989315
5822	B	987936
5823	B	989842
5824	B	988447
5825	B	990355
5826	B	988979
5827	B	990875
5828	B	990066
5829	B	991966
5830	B	991268
5831	B	993171
5832	B	991858
5833	B	993763
5834	B	992722
5835	B	994621
5836	B	993082
5837	B	994988
5838	B	993290
5839	B	995230
5840	B	995015
5841	B	996927
5842	B	993839
5843	B	995750
5844	B	996203
5845	B	998090
5846	B	997094
5847	B	998977
5848	B	997835
5849	B	999728

2410	F	546731	4130	B	179693	5850	B	999224
2411	F	544872	4131	B	181621	5851	B	1001101
2412	F	549480	4132	B	180070	5852	B	1000267
2413	F	547547	4133	B	181968	5853	B	1002146
2414	F	550245	4134	B	182017	5854	B	1001594
2415	F	548328	4135	B	183925	5855	B	1003567
2416	F	551224	4136	B	182865	5856	B	1002100
2417	F	549328	4137	B	184809	5857	B	1003941
2418	F	552433	4138	B	184640	5858	B	1003571
2419	F	550520	4139	B	186551	5859	B	1005412
2420	F	554767	4140	B	185253	5860	B	1004381
2421	F	552882	4141	B	187108	5861	B	1006269
2422	F	555444	4142	B	185703	5862	B	1004753
2423	F	553541	4143	B	187661	5863	B	1006691
2424	F	557979	4144	B	186129	5864	B	1005890
2425	F	556089	4145	B	188059	5865	B	1007762
2426	F	557923	4146	B	186395	5866	B	1006199
2427	F	555988	4147	B	188339	5867	B	1008109
2428	F	561193	4148	B	188056	5868	B	1007050
2429	F	559292	4149	B	189840	5869	B	1008929
2430	F	559671	4150	B	191218	5870	B	1007819
2431	F	557777	4151	B	193089	5871	B	1009683
2432	F	561555	4152	B	191880	5872	B	1009446
2433	F	559655	4153	B	193768	5873	B	1011365
2434	F	563727	4154	B	193026	5874	B	1010314
2435	F	561828	4155	B	194899	5875	B	1012109
2436	F	564714	4156	B	193709	5876	B	1015234
2437	F	562803	4157	B	195592	5877	B	1017133
2438	F	566079	4158	B	194284	5878	B	1016571
2439	F	564180	4159	B	196187	5879	B	1018486
2440	F	567470	4160	B	194284	5880	B	1017755
2441	F	565569	4161	B	196187	5881	B	1019661
2442	F	568454	4162	B	196032	5882	B	1016781
2443	F	566609	4163	B	197932	5883	B	1018708
2444	F	569194	4164	B	196298	5884	B	1017022

2445	F	567291
2446	F	570873
2447	F	568996
2448	F	571678
2449	F	569809
2450	F	571983
2451	F	570083
2452	F	571837
2453	F	569998
2454	F	572927
2455	F	571022
2456	F	574804
2457	F	572868
2458	F	576267
2459	F	574354
2460	F	577925
2461	F	576082
2462	F	578598
2463	F	576721
2464	F	579758
2465	F	577878
2466	F	579620
2467	F	577731
2468	F	579950
2469	F	578022
2470	F	581080
2471	F	579248
2472	F	581459
2473	F	579555
2474	F	582128
2475	F	580221
2476	F	583209
2477	F	581305
2478	F	584650
2479	F	582828

4165	B	198245
4166	B	198296
4167	B	200200
4168	B	199677
4169	B	201577
4170	B	203050
4171	B	204943
4172	B	204776
4173	B	206682
4174	B	205877
4175	B	207768
4176	B	207568
4177	B	209477
4178	B	208009
4179	B	209935
4180	B	208490
4181	B	210396
4182	B	209832
4183	B	211779
4184	B	210948
4185	B	212834
4186	B	211360
4187	B	213221
4188	B	212036
4189	B	213948
4190	B	212409
4191	B	214308
4192	B	214299
4193	B	216199
4194	B	215173
4195	B	217077
4196	B	215689
4197	B	217544
4198	B	216374
4199	B	218284

5885	B	1018924
5886	B	1019233
5887	B	1021143
5888	B	1019674
5889	B	1021630
5890	B	1021020
5891	B	1022923
5892	B	1021630
5893	B	1023525
5894	B	1024510
5895	B	1026410
5896	B	1024936
5897	B	1026858
5898	B	1025836
5899	B	1027677
5900	B	1027197
5901	B	1029089
5902	B	1028022
5903	B	1029936
5904	B	1031445
5905	B	1033319
5906	B	1031943
5907	B	1033839
5908	B	1033277
5909	B	1035186
5910	B	1033697
5911	B	1035554
5912	B	1034009
5913	B	1035943
5914	B	1036282
5915	B	1038161
5916	B	1037178
5917	B	1039088
5918	B	1037902
5919	B	1039802

2480	F	585407
2481	F	583467
2482	F	586579
2483	F	584650
2484	F	587655
2485	F	585772
2486	F	587899
2487	F	586058
2488	F	589079
2489	F	587173
2490	F	590446
2491	F	588616
2492	F	592279
2493	F	590407
2494	F	592585
2495	F	590716
2496	F	593527
2497	F	591593
2498	F	594047
2499	F	592210
2500	F	595658
2501	F	593758
2502	F	596225
2503	F	594387
2504	F	596964
2505	F	595006
2506	F	597536
2507	F	595635
2508	F	598383
2509	F	596448
2510	F	599154
2511	F	597254
2512	F	600368
2513	F	598433
2514	F	600665

4200	B	216932
4201	B	218839
4202	B	217507
4203	B	219410
4204	B	218089
4205	B	220031
4206	B	218491
4207	B	220380
4208	B	218839
4209	B	220716
4210	B	219152
4211	B	221152
4212	B	220125
4213	B	221963
4214	B	221602
4215	B	223507
4216	B	222939
4217	B	224878
4218	B	223791
4219	B	225688
4220	B	224019
4221	B	225909
4222	B	224491
4223	B	226407
4224	B	225279
4225	B	227131
4226	B	225798
4227	B	227692
4228	B	227030
4229	B	228925
4230	B	228032
4231	B	229939
4232	B	228555
4233	B	230455
4234	B	228925

5920	B	1038167
5921	B	1040079
5922	B	1039198
5923	B	1041036
5924	B	1040803
5925	B	1042721
5926	B	1042560
5927	B	1044460
5928	B	1043630
5929	B	1045526
5930	B	1044850
5931	B	1046748
5932	B	1045609
5933	B	1047551
5934	B	1046761
5935	B	1048677
5936	B	1047741
5937	B	1049700
5938	B	1050218
5939	B	1052151
5940	B	1050831
5941	B	1052744
5942	B	1051223
5943	B	1053071
5944	B	1051974
5945	B	1053854
5946	B	1052287
5947	B	1054238
5948	B	1053379
5949	B	1055253
5950	B	1054458
5951	B	1056325
5952	B	1055816
5953	B	1057680
5954	B	1056172

2515	F	598769
2516	F	602011
2517	F	600087
2518	F	602418
2519	F	600513
2520	F	602921
2521	F	601009
2522	F	604391
2523	F	602468
2524	F	605571
2525	F	603671
2526	F	606334
2527	F	604452
2528	F	607133
2529	F	605167
2530	F	608673
2531	F	606773
2532	F	609710
2533	F	607794
2534	F	610711
2535	F	608882
2536	F	611524
2537	F	609623
2538	F	612119
2539	F	610213
2540	F	613820
2541	F	611861
2542	F	614604
2543	F	612704
2544	F	614960
2545	F	613056
2546	F	616387
2547	F	614471
2548	F	617574
2549	F	615586

4235	B	230828
4236	B	229587
4237	B	231371
4238	B	231239
4239	B	233111
4240	B	231737
4241	B	233660
4242	B	232306
4243	B	234186
4244	B	233044
4245	B	234873
4246	B	234599
4247	B	236504
4248	B	233738
4249	B	235682
4250	B	235454
4251	B	237347
4252	B	235569
4253	B	237469
4254	B	236954
4255	B	238812
4256	B	237891
4257	B	239761
4258	B	238568
4259	B	240472
4260	B	239227
4261	B	241122
4262	B	240341
4263	B	242266
4264	B	241805
4265	B	243697
4266	B	242570
4267	B	244401
4268	B	243155
4269	B	245067

5955	B	1058031
5956	B	1056825
5957	B	1058710
5958	B	1057197
5959	B	1059089
5960	B	1058522
5961	B	1060355
5962	B	1058919
5963	B	1060810
5964	B	1059646
5965	B	1061521
5966	B	1060801
5967	B	1062701
5968	B	1061774
5969	B	1063687
5970	B	1062682
5971	B	1064555
5972	B	1064300
5973	B	1066236
5974	B	1065489
5975	B	1067386
5976	B	1067725
5977	B	1069601
5978	B	1068285
5979	B	1070188
5980	B	1068930
5981	B	1070898
5982	B	1070188
5983	B	1072078
5984	B	1071383
5985	B	1073283
5986	B	1072658
5987	B	1074584
5988	B	1073699
5989	B	1075652

2550	F	619430	4270	B	243636	5990	B	1076111
2551	F	617510	4271	B	245538	5991	B	1077988
2552	F	618561	4272	B	244754	5992	B	1077010
2553	F	616679	4273	B	246679	5993	B	1078959
2554	F	619799	4274	B	246248	5994	B	1077598
2555	F	617886	4275	B	248169	5995	B	1079390
2556	F	621043	4276	B	248035	5996	B	1078260
2557	F	619133	4277	B	249968	5997	B	1080217
2558	F	622333	4278	B	249397	5998	B	1078959
2559	F	620411	4279	B	251305	5999	B	1080869
2560	F	623110	4280	B	251305	6000	B	1079354
2561	F	621211	4281	B	253161	6001	B	1081215
2562	F	623952	4282	B	252487	6002	B	1080217
2563	F	622052	4283	B	254380	6003	B	1082067
2564	F	624774	4284	B	253274	6004	B	1080742
2565	F	622872	4285	B	255156	6005	B	1082621
2566	F	625263	4286	B	254230	6006	B	1081580
2567	F	623369	4287	B	256130	6007	B	1083489
2568	F	625664	4288	B	255120	6008	B	1083400
2569	F	623773	4289	B	256980	6009	B	1085290
2570	F	626220	4290	B	256331	6010	B	1084927
2571	F	624297	4291	B	258223	6011	B	1086797
2572	F	627684	4292	B	257706	6012	B	1085868
2573	F	625785	4293	B	259578	6013	B	1087768
2574	F	628536	4294	B	258488	6014	B	1086965
2575	F	626655	4295	B	260396	6015	B	1088872
2576	F	629438	4296	B	258089	6016	B	1088185
2577	F	627541	4297	B	260005	6017	B	1090076
2578	F	631496	4298	B	259202	6018	B	1088704
2579	F	629606	4299	B	261035	6019	B	1090504
2580	F	633301	4300	B	261140	6020	B	1089236
2581	F	631397	4301	B	263031	6021	B	1091181
2582	F	637012	4302	B	261834	6022	B	1090076
2583	F	635112	4303	B	263716	6023	B	1091944
2584	F	638002	4304	B	263031	6024	B	1093259



2585	F	636114
2586	F	638598
2587	F	636682
2588	F	638836
2589	F	636938
2590	F	639333
2591	F	637471
2592	F	640506
2593	F	638598
2594	F	640730
2595	F	638885
2596	F	641468
2597	F	639550
2598	F	642029
2599	F	640162
2600	F	642785
2601	F	640954
2602	F	643129
2603	F	641229
2604	F	643440
2605	F	641522
2606	F	645316
2607	F	643376
2608	F	645552
2609	F	643613
2610	F	646025
2611	F	644186
2612	F	646773
2613	F	644904
2614	F	647678
2615	F	645712
2616	F	648128
2617	F	646249
2618	F	650179
2619	F	648244

4305	B	264890
4306	B	263293
4307	B	265179
4308	B	264599
4309	B	266560
4310	B	266208
4311	B	268109
4312	B	266867
4313	B	268783
4314	B	267558
4315	B	269472
4316	B	268249
4317	B	270042
4318	B	269121
4319	B	271051
4320	B	269709
4321	B	271643
4322	B	271051
4323	B	272920
4324	B	271761
4325	B	273662
4326	B	272570
4327	B	274469
4328	B	273370
4329	B	275313
4330	B	273884
4331	B	275821
4332	B	274219
4333	B	276115
4334	B	274796
4335	B	276716
4336	B	275980
4337	B	277886
4338	B	276241
4339	B	278138

6025	B	1095056
6026	B	1093403
6027	B	1095301
6028	B	1094437
6029	B	1096375
6030	B	1095839
6031	B	1097798
6032	B	1096858
6033	B	1098751
6034	B	1097305
6035	B	1099205
6036	B	1097835
6037	B	1099724
6038	B	1098097
6039	B	1100046
6040	B	1098615
6041	B	1100561
6042	B	1099098
6043	B	1100975
6044	B	1099614
6045	B	1101442
6046	B	1099747
6047	B	1101651
6048	B	1101298
6049	B	1103227
6050	B	1102435
6051	B	1104381
6052	B	1105179
6053	B	1107090
6054	B	1106770
6055	B	1108631
6056	B	1107502
6057	B	1109392
6058	B	1108337
6059	B	1110240

2620	F	651010
2621	F	649149
2622	F	652904
2623	F	651003
2624	F	653946
2625	F	652070
2626	F	655735
2627	F	653827
2628	F	656759
2629	F	654894
2630	F	658287
2631	F	656399
2632	F	659973
2633	F	658109
2634	F	662935
2635	F	661035
2636	F	664393
2637	F	662513
2638	F	665972
2639	F	664090
2640	F	666765
2641	F	664879
2642	F	667690
2643	F	665707
2644	F	668261
2645	F	666370
2646	F	668934
2647	F	667029
2648	F	670871
2649	F	668964
2650	F	670629
2651	F	668715
2652	F	672231
2653	F	670334
2654	F	672846

4340	B	276716
4341	B	278625
4342	B	277185
4343	B	279054
4344	B	277489
4345	B	279380
4346	B	277886
4347	B	279722
4348	B	278125
4349	B	280012
4350	B	278841
4351	B	280733
4352	B	279577
4353	B	281466
4354	B	280672
4355	B	282564
4356	B	281767
4357	B	283676
4358	B	282564
4359	B	284462
4360	B	284311
4361	B	286210
4362	B	284740
4363	B	286647
4364	B	285998
4365	B	287975
4366	B	286210
4367	B	288110
4368	B	287201
4369	B	289106
4370	B	287803
4371	B	289737
4372	B	288217
4373	B	290112
4374	B	288417

6060	B	1108653
6061	B	1110570
6062	B	1113632
6063	B	1115499
6064	B	1115225
6065	B	1117081
6066	B	1117154
6067	B	1119051
6068	B	1118403
6069	B	1120310
6070	B	1120257
6071	B	1122178
6072	B	1120776
6073	B	1122682
6074	B	1121660
6075	B	1123554
6076	B	1122120
6077	B	1123999
6078	B	1123243
6079	B	1125024
6080	B	1123752
6081	B	1125688
6082	B	1124484
6083	B	1126360
6084	B	1125020
6085	B	1126928
6086	B	1125790
6087	B	1127735
6088	B	1126747
6089	B	1128662
6090	B	1127899
6091	B	1129808
6092	B	1128819
6093	B	1130695
6094	B	1129798

2655	F	670946	4375	B	290319	6095	B	1131693
2656	F	674040	4376	B	289106	6096	B	1131563
2657	F	672139	4377	B	290961	6097	B	1133490
2658	F	674573	4378	B	289459	6098	B	1132846
2659	F	672674	4379	B	291358	6099	B	1134684
2660	F	675234	4380	B	289914	6100	B	1134070
2661	F	673377	4381	B	291796	6101	B	1136016
2662	F	675834	4382	B	290477	6102	B	1135089
2663	F	673906	4383	B	292423	6103	B	1137037
2664	F	676378	4384	B	290381	6104	B	1135815
2665	F	674477	4385	B	292309	6105	B	1137715
2666	F	676746	4386	B	291463	6106	B	1136186
2667	F	674888	4387	B	293372	6107	B	1138084
2668	F	677769	4388	B	292104	6108	B	1137365
2669	F	675834	4389	B	293999	6109	B	1139255
2670	F	678270	4390	B	293027	6110	B	1140364
2671	F	676378	4391	B	294951	6111	B	1142228
2672	F	679221	4392	B	293507	6112	B	1141611
2673	F	677325	4393	B	295409	6113	B	1143485
2674	F	679874	4394	B	293999	6114	B	1142478
2675	F	677978	4395	B	295838	6115	B	1144291
2676	F	681173	4396	B	294889	6116	B	1145907
2677	F	679288	4397	B	296750	6117	B	1147783
2678	F	680607	4398	B	295312	6118	B	1146953
2679	F	678674	4399	B	297219	6119	B	1148846
2680	F	682210	4400	B	296373	6120	B	1147769
2681	F	680303	4401	B	298305	6121	B	1149703
2682	F	682542	4402	B	298114	6122	B	1148415
2683	F	680607	4403	B	299985	6123	B	1150357
2684	F	683716	4404	B	298656	6124	B	1148758
2685	F	681842	4405	B	300623	6125	B	1150658
2686	F	684312	4406	B	299027	6126	B	1149462
2687	F	682410	4407	B	300899	6127	B	1151258
2688	F	684880	4408	B	299805	6128	B	1149932
2689	F	682916	4409	B	301692	6129	B	1151845

2690	F	685958
2691	F	684143
2692	F	687264
2693	F	685363
2694	F	687959
2695	F	685958
2696	F	688514
2697	F	686605
2698	F	689372
2699	F	687431
2700	F	690201
2701	F	688318
2702	F	691271
2703	F	689372
2704	F	692436
2705	F	690546
2706	F	694813
2707	F	692930
2708	F	695787
2709	F	693920
2710	F	696363
2711	F	694463
2712	F	698029
2713	F	696133
2714	F	699556
2715	F	697631
2716	F	702303
2717	F	700432
2718	F	702964
2719	F	701079
2720	F	704018
2721	F	702120
2722	F	705018
2723	F	703172
2724	F	705992

4410	B	300722
4411	B	302621
4412	B	301846
4413	B	303706
4414	B	302660
4415	B	304642
4416	B	303066
4417	B	304962
4418	B	303626
4419	B	305479
4420	B	304643
4421	B	306514
4422	B	305479
4423	B	307390
4424	B	306459
4425	B	308393
4426	B	307662
4427	B	309601
4428	B	308298
4429	B	310153
4430	B	309145
4431	B	311044
4432	B	310468
4433	B	312338
4434	B	311437
4435	B	313337
4436	B	311857
4437	B	313860
4438	B	311857
4439	B	313860
4440	B	313015
4441	B	314911
4442	B	313687
4443	B	315549
4444	B	313866

6130	B	1150814
6131	B	1152747
6132	B	1151409
6133	B	1153285
6134	B	1152540
6135	B	1154341
6136	B	1154863
6137	B	1156751
6138	B	1155886
6139	B	1157813
6140	B	1156963
6141	B	1158871
6142	B	1158093
6143	B	1159947
6144	B	1160998
6145	B	1162864
6146	B	1162864
6147	B	1164740
6148	B	1163244
6149	B	1165090
6150	B	1164244
6151	B	1166175
6152	B	1164517
6153	B	1166482
6154	B	1165167
6155	B	1167100
6156	B	1165789
6157	B	1167710
6158	B	1166376
6159	B	1168228
6160	B	1166872
6161	B	1168764
6162	B	1168598
6163	B	1170498
6164	B	1169447

2725	F	704105	4445	B	315784	6165	B	1171347
2726	F	706535	4446	B	314911	6166	B	1170043
2727	F	704685	4447	B	316804	6167	B	1171947
2728	F	707455	4448	B	315809	6168	B	1170689
2729	F	705553	4449	B	317701	6169	B	1172616
2730	F	708360	4450	B	316382	6170	B	1171556
2731	F	706385	4451	B	318284	6171	B	1173507
2732	F	708897	4452	B	318881	6172	B	1172305
2733	F	706997	4453	B	320778	6173	B	1174210
2734	F	709589	4454	B	321262	6174	B	1172562
2735	F	707689	4455	B	323214	6175	B	1174508
2736	F	709907	4456	B	321665	6176	B	1174018
2737	F	707963	4457	B	323565	6177	B	1175899
2738	F	711269	4458	B	322571	6178	B	1175429
2739	F	709396	4459	B	324461	6179	B	1177348
2740	F	711864	4460	B	323425	6180	B	1175793
2741	F	709985	4461	B	325316	6181	B	1177675
2742	F	714531	4462	B	324095	6182	B	1177347
2743	F	712594	4463	B	325977	6183	B	1179199
2744	F	715653	4464	B	325135	6184	B	1179316
2745	F	713725	4465	B	327001	6185	B	1181171
2746	F	717511	4466	B	326634	6186	B	1180309
2747	F	715615	4467	B	328557	6187	B	1182212
2748	F	718865	4468	B	328081	6188	B	1181048
2749	F	716993	4469	B	329959	6189	B	1182918
2750	F	720365	4470	B	328719	6190	B	1182162
2751	F	718471	4471	B	330596	6191	B	1184078
2752	F	722155	4472	B	328893	6192	B	1182528
2753	F	720253	4473	B	330825	6193	B	1184437
2754	F	722897	4474	B	329590	6194	B	1184078
2755	F	720989	4475	B	331485	6195	B	1186015
2756	F	723385	4476	B	331127	6196	B	1184698
2757	F	721493	4477	B	333069	6197	B	1186540
2758	F	724029	4478	B	332679	6198	B	1185631
2759	F	722081	4479	B	334592	6199	B	1187530

2760	F	724678
2761	F	722749
2762	F	726048
2763	F	724143
2764	F	726897
2765	F	724997
2766	F	727969
2767	F	726086
2768	F	728380
2769	F	726446
2770	F	729281
2771	F	727410
2772	F	729510
2773	F	727579
2774	F	729949
2775	F	728036
2776	F	730367
2777	F	728455
2778	F	731760
2779	F	729866
2780	F	732172
2781	F	730275
2782	F	733018
2783	F	731197
2784	F	733252
2785	F	731354
2786	F	733674
2787	F	731760
2788	F	734054
2789	F	732172
2790	F	734632
2791	F	732736
2792	F	735071
2793	F	733219
2794	F	735381

4480	B	334790
4481	B	336673
4482	B	336311
4483	B	338267
4484	B	337572
4485	B	339431
4486	B	338545
4487	B	340463
4488	B	339058
4489	B	341011
4490	B	339740
4491	B	341628
4492	B	340366
4493	B	342354
4494	B	343265
4495	B	345125
4496	B	344126
4497	B	345957
4498	B	344391
4499	B	346291
4500	B	345324
4501	B	347236
4502	B	346289
4503	B	348198
4504	B	347090
4505	B	348914
4506	B	347292
4507	B	349158
4508	B	347946
4509	B	349851
4510	B	350799
4511	B	352598
4512	B	351313
4513	B	353223
4514	B	352400

6200	B	1186079
6201	B	1188004
6202	B	1186704
6203	B	1188610
6204	B	1189251
6205	B	1191165
6206	B	1187609
6207	B	1189506
6208	B	1191165
6209	B	1193050
6210	B	1192378
6211	B	1194291
6212	B	1192265
6213	B	1194114
6214	B	1193058
6215	B	1194987
6216	B	1193224
6217	B	1195115
6218	B	1194035
6219	B	1195955
6220	B	1194384
6221	B	1196265
6222	B	1194291
6223	B	1196205
6224	B	1195955
6225	B	1197863
6226	B	1196570
6227	B	1198423
6228	B	1197051
6229	B	1198951
6230	B	1198058
6231	B	1199931
6232	B	1198960
6233	B	1200867
6234	B	1200490

2795	F	733445
2796	F	735852
2797	F	733957
2798	F	736244
2799	F	734401
2800	F	736982
2801	F	735071
2802	F	737321
2803	F	735397
2804	F	737566
2805	F	735696
2806	F	738491
2807	F	736564
2808	F	738797
2809	F	736935
2810	F	739513
2811	F	737626
2812	F	740420
2813	F	738526
2814	F	740457
2815	F	738599
2816	F	741553
2817	F	739676
2818	F	742518
2819	F	740565
2820	F	743344
2821	F	741509
2822	F	743875
2823	F	741984
2824	F	744240
2825	F	742365
2826	F	744725
2827	F	742858
2828	F	746380
2829	F	744493

4515	B	354357
4516	B	353522
4517	B	355411
4518	B	354690
4519	B	356610
4520	B	355158
4521	B	357057
4522	B	355676
4523	B	357681
4524	B	356995
4525	B	358866
4526	B	356173
4527	B	358074
4528	B	359607
4529	B	361536
4530	B	359550
4531	B	361442
4532	B	360135
4533	B	362033
4534	B	361536
4535	B	363461
4536	B	364013
4537	B	365905
4538	B	364716
4539	B	366707
4540	B	365000
4541	B	366941
4542	B	365513
4543	B	367447
4544	B	365892
4545	B	367873
4546	B	366877
4547	B	368725
4548	B	369265
4549	B	371167

6235	B	1202395
6236	B	1201512
6237	B	1203426
6238	B	1202606
6239	B	1204532
6240	B	1203139
6241	B	1205063
6242	B	1203691
6243	B	1205597
6244	B	1204382
6245	B	1206284
6246	B	1205249
6247	B	1207170
6248	B	1206651
6249	B	1208536
6250	B	1206976
6251	B	1208862
6252	B	1208092
6253	B	1210002
6254	B	1209115
6255	B	1210973
6256	B	1209979
6257	B	1211892
6258	B	1210739
6259	B	1212639
6260	B	1211761
6261	B	1213680
6262	B	1212985
6263	B	1214894
6264	B	1214299
6265	B	1216189
6266	B	1215132
6267	B	1217036
6268	B	1215714
6269	B	1217542

2830	F	746957
2831	F	745071
2832	F	747868
2833	F	746023
2834	F	748351
2835	F	746451
2836	F	749395
2837	F	747505
2838	F	749745
2839	F	747857
2840	F	750165
2841	F	748278
2842	F	751013
2843	F	749169
2844	F	752798
2845	F	750889
2846	F	754878
2847	F	752967
2848	F	755856
2849	F	754001
2850	F	756262
2851	F	754372
2852	F	760075
2853	F	758175
2854	F	761069
2855	F	759172
2856	F	761549
2857	F	759660
2858	F	761988
2859	F	760141
2860	F	762611
2861	F	760747
2862	F	763097
2863	F	761136
2864	F	763622

4550	B	370088
4551	B	371988
4552	B	370669
4553	B	372611
4554	B	372871
4555	B	374773
4556	B	373315
4557	B	375227
4558	B	373665
4559	B	375592
4560	B	374428
4561	B	376335
4562	B	375355
4563	B	377248
4564	B	375913
4565	B	377796
4566	B	376483
4567	B	378318
4568	B	377873
4569	B	379798
4570	B	380040
4571	B	381898
4572	B	380699
4573	B	382561
4574	B	381249
4575	B	383174
4576	B	381689
4577	B	383629
4578	B	383282
4579	B	385161
4580	B	383789
4581	B	385647
4582	B	385560
4583	B	387427
4584	B	386760

6270	B	1216541
6271	B	1218462
6272	B	1216828
6273	B	1218677
6274	B	1217166
6275	B	1218973
6276	B	1219876
6277	B	1221743
6278	B	1220892
6279	B	1222895
6280	B	1220288
6281	B	1222189
6282	B	1221657
6283	B	1223517
6284	B	1223930
6285	B	1225828
6286	B	1225211
6287	B	1227132
6288	B	1226090
6289	B	1227979
6290	B	1227132
6291	B	1229039
6292	B	1228061
6293	B	1229948
6294	B	1228293
6295	B	267
6296	B	1228524
6297	B	444
6298	B	267
6299	B	2068
6300	F	25997
6301	F	24032
6302	F	27128
6303	F	25189
6304	F	66744



2865	F	761742	4585	B	388588	6305	F	64845
2866	F	765438	4586	B	387508	6306	F	70130
2867	F	763525	4587	B	389369	6307	F	68200
2868	F	766664	4588	B	388984	6308	F	132477
2869	F	764747	4589	B	390900	6309	F	130559
2870	F	768045	4590	B	390387	6310	F	177854
2871	F	766196	4591	B	392260	6311	F	175906
2872	F	768329	4592	B	391202	6312	F	208127
2873	F	766429	4593	B	393055	6313	F	206180
2874	F	769107	4594	B	392044	6314	F	208688
2875	F	767244	4595	B	393959	6315	F	206807
2876	F	770507	4596	B	392615	6316	F	208732
2877	F	768633	4597	B	394499	6317	F	206877
2878	F	771618	4598	B	393218	6318	F	210051
2879	F	769725	4599	B	395123	6319	F	208141
2880	F	772865	4600	B	393909	6320	F	298801
2881	F	770975	4601	B	395807	6321	F	296907
2882	F	772865	4602	B	394566	6322	F	351495
2883	F	770970	4603	B	396498	6323	F	349572
2884	F	774810	4604	B	395027	6324	F	419727
2885	F	772927	4605	B	396931	6325	F	417822
2886	F	774131	4606	B	395531	6326	F	553133
2887	F	772232	4607	B	397467	6327	F	551247
2888	F	774604	4608	B	396227	6328	F	556301
2889	F	772782	4609	B	398132	6329	F	554410
2890	F	775851	4610	B	398070	6330	F	593567
2891	F	773934	4611	B	399935	6331	F	591675
2892	F	777314	4612	B	399189	6332	F	594641
2893	F	775412	4613	B	400970	6333	F	592748
2894	F	777677	4614	B	400351	6334	F	661934
2895	F	775781	4615	B	402208	6335	F	660041
2896	F	778400	4616	B	401465	6336	F	706309
2897	F	776472	4617	B	403507	6337	F	704409
2898	F	779281	4618	B	401705	6338	F	803092
2899	F	777333	4619	B	403666	6339	F	801192

2900	F	780063
2901	F	778150
2902	F	780885
2903	F	778994
2904	F	781333
2905	F	779431
2906	F	782524
2907	F	780674
2908	F	783349
2909	F	781433
2910	F	785138
2911	F	783238
2912	F	786197
2913	F	784328
2914	F	788274
2915	F	786387
2916	F	788679
2917	F	786778
2918	F	790090
2919	F	788213
2920	F	791608
2921	F	789711
2922	F	792499
2923	F	790605
2924	F	793324
2925	F	791440
2926	F	794068
2927	F	792185
2928	F	794998
2929	F	793098
2930	F	795457
2931	F	793582
2932	F	796831
2933	F	794931
2934	F	798455

4620	B	402461
4621	B	404410
4622	B	403507
4623	B	405356
4624	B	404421
4625	B	406295
4626	B	406160
4627	B	408052
4628	B	407645
4629	B	409450
4630	B	407922
4631	B	409744
4632	B	409039
4633	B	410960
4634	B	410673
4635	B	412559
4636	B	411193
4637	B	413064
4638	B	412049
4639	B	413946
4640	B	414525
4641	B	416425
4642	B	415622
4643	B	417559
4644	B	416072
4645	B	417968
4646	B	417351
4647	B	419259
4648	B	417789
4649	B	419748
4650	B	418569
4651	B	420453
4652	B	420345
4653	B	422177
4654	B	421003

6340	F	849060
6341	F	847142
6342	F	913050
6343	F	911152
6344	F	926614
6345	F	924714
6346	F	930121
6347	F	928238
6348	F	986297
6349	F	984362
6350	F	996001
6351	F	994109
6352	F	999731
6353	F	997877
6354	F	1009782
6355	F	1007891
6356	F	1010540
6357	F	1008671
6358	F	1012465
6359	F	1010540
6360	F	1028431
6361	F	1026524
6362	F	1086215
6363	F	1084362
6364	F	1118417
6365	F	1116527
6366	F	1169595
6367	F	1167713
6368	F	1180592
6369	F	1178709
6370	F	1182406
6371	F	1180498
6372	F	1194573
6373	F	1192667
6374	F	1195654

2935	F	796551
2936	F	799056
2937	F	797147
2938	F	799558
2939	F	797649
2940	F	801106
2941	F	799204
2942	F	802227
2943	F	800325
2944	F	803050
2945	F	801153
2946	F	803599
2947	F	801682
2948	F	804925
2949	F	803016
2950	F	805633
2951	F	803672
2952	F	806109
2953	F	804192
2954	F	806386
2955	F	804453
2956	F	806668
2957	F	804746
2958	F	807924
2959	F	806022
2960	F	808445
2961	F	806525
2962	F	809212
2963	F	807283
2964	F	809982
2965	F	808079
2966	F	811554
2967	F	809659
2968	F	812268
2969	F	810340

4655	B	422873
4656	B	421819
4657	B	423675
4658	B	422291
4659	B	424158
4660	B	423186
4661	B	425075
4662	B	424544
4663	B	426443
4664	B	424859
4665	B	426714
4666	B	426302
4667	B	428193
4668	B	427640
4669	B	429523
4670	B	428212
4671	B	430111
4672	B	428709
4673	B	430627
4674	B	430926
4675	B	432851
4676	B	431681
4677	B	433569
4678	B	432324
4679	B	434223
4680	B	433015
4681	B	434902
4682	B	433504
4683	B	435426
4684	B	434196
4685	B	436042
4686	B	436913
4687	B	438807
4688	B	437475
4689	B	439423

6375	F	1193753
6376	B	26870
6377	B	28721
6378	B	27835
6379	B	29730
6380	B	67456
6381	B	69351
6382	B	70820
6383	B	72708
6384	B	133173
6385	B	135068
6386	B	178637
6387	B	180518
6388	B	208864
6389	B	210727
6390	B	209376
6391	B	211305
6392	B	209483
6393	B	211383
6394	B	210875
6395	B	212766
6396	B	299694
6397	B	301582
6398	B	352312
6399	B	354200
6400	B	420390
6401	B	422291
6402	B	553822
6403	B	555736
6404	B	557050
6405	B	558930
6406	B	594583
6407	B	596527
6408	B	595405
6409	B	597289

2970	F	812712
2971	F	810799
2972	F	813355
2973	F	811466
2974	F	815198
2975	F	813243
2976	F	815798
2977	F	813917
2978	F	816879
2979	F	814940
2980	F	817571
2981	F	815676
2982	F	818388
2983	F	816489
2984	F	818884
2985	F	816921
2986	F	819597
2987	F	817680
2988	F	820485
2989	F	818555
2990	F	820764
2991	F	818878
2992	F	821982
2993	F	820080
2994	F	823403
2995	F	821559
2996	F	825235
2997	F	823320
2998	F	826405
2999	F	824501
3000	F	826945
3001	F	825046
3002	F	828489
3003	F	826588
3004	F	829813

4690	B	438591
4691	B	440490
4692	B	440583
4693	B	442491
4694	B	440583
4695	B	442441
4696	B	441274
4697	B	443135
4698	B	441459
4699	B	443353
4700	B	442412
4701	B	444339
4702	B	443184
4703	B	445100
4704	B	443131
4705	B	445100
4706	B	443800
4707	B	445789
4708	B	444771
4709	B	446620
4710	B	445100
4711	B	446962
4712	B	445229
4713	B	447187
4714	B	445974
4715	B	447872
4716	B	448028
4717	B	449927
4718	B	448958
4719	B	450858
4720	B	449850
4721	B	451753
4722	B	451103
4723	B	453045
4724	B	451482

6410	B	662614
6411	B	664530
6412	B	707138
6413	B	709063
6414	B	803951
6415	B	805790
6416	B	849771
6417	B	851730
6418	B	913917
6419	B	915796
6420	B	927331
6421	B	929238
6422	B	930857
6423	B	932735
6424	B	986987
6425	B	988912
6426	B	996771
6427	B	998623
6428	B	1000593
6429	B	1002496
6430	B	1010541
6431	B	1012452
6432	B	1011365
6433	B	1013249
6434	B	1013146
6435	B	1015044
6436	B	1029168
6437	B	1031036
6438	B	1087041
6439	B	1088885
6440	B	1119102
6441	B	1121033
6442	B	1170355
6443	B	1172218
6444	B	1181427

3005	F	827917
3006	F	830824
3007	F	828906
3008	F	831936
3009	F	830099
3010	F	833126
3011	F	831274

4725	B	453330
4726	B	452676
4727	B	454575
4728	B	453884
4729	B	455783
4730	B	455068
4731	B	456963

6445	B	1183338
6446	B	1183263
6447	B	1185158
6448	B	1195296
6449	B	1197175
6450	B	1196406
6451	B	1198306

**TABLE 6**

<i>clone Name</i>	<i>SEQ ID NO (B)</i>	<i>SEQ ID NO (F)</i>	<i>Chromosomal region</i>
790313H3#	6452	6648	A
790331B1#	6453	6649	A
790233A9#	6454	6650	A
790031G7#	6455	6651	A
890021E4#	6456	6652	A
790021E11#	6457	6653	A
790332G10#	6458	6654	A
790271B6#	6459	6655	A
790253H6#	6460	6656	A
790214E8#	6461	6657	A
790352D2#	6462	6658	A
790373F2#	6463	6659	A
790424A7#	6464	6660	A
790282F3#	6465	6661	A
790272F5#	6466	6662	A
790424F6#	6467	6663	A
890033H11#	6468	6664	A
790264H10#	6469	6665	A
790293A5#	6470	6666	A
790391E8#	6471	6667	A
890022B8#	6472	6668	A
790332B9#	6473	6669	A
790251B9#	6474	6670	A
790344E8#	6475	6671	B
790323F3#	6476	6672	B
790231G2#	6477	6673	B
790341C5#	6478	6674	B
790332H9#	6479	6675	B
890013A8#	6480	6676	B
790394F2#	6481	6677	B
790222G5#	6482	6678	B
790402A10#	6483	6679	B
790283F6#	6484	6680	B

790041H11#	6485	6681	B
790381C7#	6486	6682	B
790213E1#	6487	6683	B
790211C4#	6488	6684	B
790251B5#	6489	6685	B
790043H9#	6490	6686	B
790303F7#	6491	6687	B
790251G5#	6492	6688	B
790044H7#	6493	6689	B
790022E4#	6494	6690	B
790252A8#	6495	6691	B
790313E9#	6496	6692	B
790264G2#	6497	6693	B
790372A4#	6498	6694	B
790411C2#	6499	6695	B
790322B7#	6500	6696	B
790254F7#	6501	6697	B
790323B12#	6502	6698	B
790263E5#	6503	6699	B
790223C8#	6504	6700	B
790231H2#	6505	6701	B
790324E12#	6506	6702	B
790271D7#	6507	6703	B
790222E8#	6508	6704	B
790083G7#	6509	6705	B
790241D3#	6510	6706	B
790303C8#	6511	6707	B
790283F10#	6512	6708	B
790241B7#	6513	6709	B
790373F10#	6514	6710	B
790362F9#	6515	6711	B
790263H8#	6516	6712	B
790393D10#	6517	6713	B
790313D12#	6518	6714	B
890024C6#	6519	6715	B

890024B10#	6520	6716	B
790212E2#	6521	6717	B
790362E10#	6522	6718	B
790344G11#	6523	6719	B
890011D2#	6524	6720	B
790341B11#	6525	6721	B
790064E10#	6526	6722	B
790212E1#	6527	6723	B
790213G5#	6528	6724	B
790331F2#	6529	6725	B
890024B9#	6530	6726	B
790421F5#	6531	6727	B
890014D11#	6532	6728	B
790373F3#	6533	6729	B
790293D4#	6534	6730	B
790211A3#	6535	6731	B
790211H8#	6536	6732	B
790264E7#	6537	6733	B
790292B11#	6538	6734	B
790312A2#	6539	6735	B
890012D5#	6540	6736	B
790012D12#	6541	6737	B
790291E10#	6542	6738	B
790241C9#	6543	6739	B
790343F1#	6544	6740	B
790241D7#	6545	6741	B
790031H7#	6546	6742	B
790081C4#	6547	6743	B
790013B7#	6548	6744	B
790213F3#	6549	6745	B
790292F9#	6550	6746	B
790423F4#	6551	6747	B
790331F3#	6552	6748	B
790222B10#	6553	6749	B
790261G12#	6554	6750	B



790423G10#	6555	6751	B
790392A9#	6556	6752	B
790331B5#	6557	6753	B
790323H3#	6558	6754	B
890014H8#	6559	6755	B
790231B6#	6560	6756	B
790252F7#	6561	6757	B
790392C10#	6562	6758	B
790021D4#	6563	6759	B
790052D10#	6564	6760	B
790261E3#	6565	6761	B
890023E10#	6566	6762	B
790244B7#	6567	6763	B
790383E1#	6568	6764	B
790401B11#	6569	6765	B
790411B5#	6570	6766	B
790423A11#	6571	6767	B
790031A4#	6572	6768	B
790241G3#	6573	6769	B
790044F7#	6574	6770	B
790252B10#	6575	6771	B
790293F9#	6576	6772	B
790282H3#	6577	6773	B
790381C10#	6578	6774	B
790024H5#	6579	6775	B
790354H7#	6580	6776	B
790411F9#	6581	6777	B
790324G10#	6582	6778	B
790014A5#	6583	6779	B
790381F3#	6584	6780	B
790424D3#	6585	6781	B
790394A10#	6586	6782	B
790423C10#	6587	6783	B
790214D6#	6588	6784	B
790214C4#	6589	6785	B

790014F11#	6590	6786	B
790352F10#	6591	6787	B
790381H6#	6592	6788	B
790282G5#	6593	6789	B
790263C8#	6594	6790	B
890022B4#	6595	6791	B
790283C6#	6596	6792	B
790293B2#	6597	6793	B
790073A3#	6598	6794	B
790313E10#	6599	6795	B
790361D3#	6600	6796	B
790014A11#	6601	6797	B
790254G2#	6602	6798	B
790381C6#	6603	6799	B
790424E3#	6604	6800	B
790421G8#	6605	6801	B
790013C3#	6606	6802	B
790263E8#	6607	6803	B
790373C1#	6608	6804	B
790041C1#	6609	6805	B
790344A7#	6610	6806	B
790271D6#	6611	6807	B
790342H2#	6612	6808	B
890021A6#	6613	6809	B
790381E7#	6614	6810	C
790013G10#	6615	6811	C
790254A4#	6616	6812	C
790213D8#	6617	6813	C
790052A4#	6618	6814	C
790213D3#	6619	6815	C
790394D2#	6620	6816	C
790214D2#	6621	6817	C
790014A4#	6622	6818	C
790324H4#	6623	6819	C
790082B4#	6624	6820	C

790324A6#	6625	6821	C
790424A12#	6626	6822	C
790044G8#	6627	6823	C
790323C6#	6628	6824	C
790312G4#	6629	6825	C
790053C11#	6630	6826	C
890022B7#	6631	6827	C
790392A2#	6632	6828	C
890023D8#	6633	6829	C
790301F1#	6634	6830	C
790343A11#	6635	6831	C
790421A2#	6636	6832	C
790271G2#	6637	6833	C
790302G12#	6638	6834	C
790341E5#	6639	6835	C
790283B6#	6640	6836	C
790222A4#	6641	6837	C
790241B8#	6642	6838	C
790014C2#	6643	6839	C
790402C1#	6644	6840	C
790264E9#	6645	6841	C
790242G4#	6646	6842	C
790422F3#	6647	6843	C

TABLE 7

<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>	<i>SEQ ID</i>	<i>or.</i>	<i>5'position</i>
6452	B	29372	6583	B	547718	6714	F	519646
6453	B	30198	6584	B	547184	6715	F	520201
6454	B	31007	6585	B	547684	6716	F	520563
6455	B	31126	6586	B	547342	6717	F	521015
6456	B	32735	6587	B	548946	6718	F	521162
6457	B	32264	6588	B	549071	6719	F	521543
6458	B	32898	6589	B	550054	6720	F	521739
6459	B	33582	6590	B	549989	6721	F	522328
6460	B	33519	6591	B	550426	6722	F	522567
6461	B	34836	6592	B	550055	6723	F	522915
6462	B	35795	6593	B	550132	6724	F	523300
6463	B	35548	6594	B	550132	6725	F	523791
6464	B	35825	6595	B	551400	6726	F	523959
6465	B	37239	6596	B	551572	6727	F	524369
6466	B	36761	6597	B	551468	6728	F	524801
6467	B	37045	6598	B	550849	6729	F	525085
6468	B	36761	6599	B	552137	6730	F	525241
6469	B	37958	6600	B	552325	6731	F	525738
6470	B	38636	6601	B	552583	6732	F	526263
6471	B	39813	6602	B	553033	6733	F	526628
6472	B	41140	6603	B	553629	6734	F	526779
6473	B	40575	6604	B	553960	6735	F	527004
6474	B	40526	6605	B	553914	6736	F	527230
6475	B	501495	6606	B	554354	6737	F	527381
6476	B	502410	6607	B	555783	6738	F	527545
6477	B	502586	6608	B	555687	6739	F	527691
6478	B	503233	6609	B	556441	6740	F	527932
6479	B	503749	6610	B	557054	6741	F	527995
6480	B	504488	6611	B	556627	6742	F	528167
6481	B	504206	6612	B	557292	6743	F	528610
6482	B	504310	6613	B	557050	6744	F	529063
6483	B	505455	6614	B	815995	6745	F	529710
6484	B	505877	6615	B	817104	6746	F	531140

6485	B	506655
6486	B	506513
6487	B	507532
6488	B	507742
6489	B	508050
6490	B	507771
6491	B	509120
6492	B	509646
6493	B	510137
6494	B	510953
6495	B	511165
6496	B	511526
6497	B	511993
6498	B	513012
6499	B	512983
6500	B	512781
6501	B	514155
6502	B	515036
6503	B	515287
6504	B	516292
6505	B	516234
6506	B	516337
6507	B	517347
6508	B	517005
6509	B	516888
6510	B	516234
6511	B	517560
6512	B	517337
6513	B	518756
6514	B	518943
6515	B	519833
6516	B	520123
6517	B	520574
6518	B	520888
6519	B	522154

6616	B	817104
6617	B	816920
6618	B	820464
6619	B	821017
6620	B	821379
6621	B	821504
6622	B	822723
6623	B	823298
6624	B	823380
6625	B	824414
6626	B	824204
6627	B	825288
6628	B	825346
6629	B	825403
6630	B	826237
6631	B	824995
6632	B	826838
6633	B	828146
6634	B	827878
6635	B	827571
6636	B	828472
6637	B	828484
6638	B	828691
6639	B	829507
6640	B	829169
6641	B	828763
6642	B	829769
6643	B	831582
6644	B	830481
6645	B	831468
6646	B	831670
6647	B	832293
6648	F	28484
6649	F	29043
6650	F	29656

6747	F	531488
6748	F	531842
6749	F	532064
6750	F	532350
6751	F	532794
6752	F	533117
6753	F	533536
6754	F	533868
6755	F	534200
6756	F	534844
6757	F	535213
6758	F	535678
6759	F	535970
6760	F	536504
6761	F	537013
6762	F	537710
6763	F	538047
6764	F	538353
6765	F	538718
6766	F	539188
6767	F	539471
6768	F	539910
6769	F	540774
6770	F	540962
6771	F	541721
6772	F	542198
6773	F	542644
6774	F	543180
6775	F	543877
6776	F	544601
6777	F	544866
6778	F	545442
6779	F	545948
6780	F	546209
6781	F	546585

6520	B	523041
6521	B	522052
6522	B	522217
6523	B	523035
6524	B	524995
6525	B	523567
6526	B	523477
6527	B	523967
6528	B	525211
6529	B	525215
6530	B	526133
6531	B	525674
6532	B	526561
6533	B	526697
6534	B	526715
6535	B	526844
6536	B	527261
6537	B	527503
6538	B	528775
6539	B	528249
6540	B	530307
6541	B	527772
6542	B	529406
6543	B	527752
6544	B	529829
6545	B	529907
6546	B	529574
6547	B	529635
6548	B	530391
6549	B	531516
6550	B	532154
6551	B	532606
6552	B	533407
6553	B	533664
6554	B	533916

6651	F	30157
6652	F	30712
6653	F	31175
6654	F	31658
6655	F	31902
6656	F	32638
6657	F	33203
6658	F	33804
6659	F	34164
6660	F	34426
6661	F	35131
6662	F	35675
6663	F	36097
6664	F	36641
6665	F	36835
6666	F	37236
6667	F	38287
6668	F	38711
6669	F	39117
6670	F	39798
6671	F	500539
6672	F	501016
6673	F	501319
6674	F	501632
6675	F	502155
6676	F	502623
6677	F	503025
6678	F	503681
6679	F	504389
6680	F	504744
6681	F	505468
6682	F	505652
6683	F	505822
6684	F	505833
6685	F	506933

6782	F	546960
6783	F	547114
6784	F	547726
6785	F	548045
6786	F	548480
6787	F	548561
6788	F	548775
6789	F	549037
6790	F	549153
6791	F	549597
6792	F	550049
6793	F	550520
6794	F	550890
6795	F	550997
6796	F	551040
6797	F	551247
6798	F	551854
6799	F	552333
6800	F	552603
6801	F	552823
6802	F	553207
6803	F	553898
6804	F	554298
6805	F	554767
6806	F	555323
6807	F	555595
6808	F	555965
6809	F	556248
6810	F	815116
6811	F	815376
6812	F	815849
6813	F	816098
6814	F	818726
6815	F	819337
6816	F	820080

6555	B	534707
6556	B	533482
6557	B	534614
6558	B	534935
6559	B	536823
6560	B	535986
6561	B	536143
6562	B	537505
6563	B	537618
6564	B	538165
6565	B	538702
6566	B	540278
6567	B	539156
6568	B	539619
6569	B	540115
6570	B	540724
6571	B	541484
6572	B	540968
6573	B	542062
6574	B	541898
6575	B	543100
6576	B	543846
6577	B	543820
6578	B	544382
6579	B	545158
6580	B	545678
6581	B	545905
6582	B	546683

6686	F	507220
6687	F	507559
6688	F	508216
6689	F	508619
6690	F	509329
6691	F	509783
6692	F	510383
6693	F	510729
6694	F	511188
6695	F	511773
6696	F	511869
6697	F	512946
6698	F	513202
6699	F	513821
6700	F	514322
6701	F	514811
6702	F	515101
6703	F	515611
6704	F	515911
6705	F	516123
6706	F	516169
6707	F	516215
6708	F	516305
6709	F	517240
6710	F	517993
6711	F	518174
6712	F	518756
6713	F	519133

6817	F	820750
6818	F	821170
6819	F	821815
6820	F	822490
6821	F	822789
6822	F	823244
6823	F	823762
6824	F	823964
6825	F	824245
6826	F	824609
6827	F	824948
6828	F	825490
6829	F	826064
6830	F	826405
6831	F	826480
6832	F	827089
6833	F	827418
6834	F	827496
6835	F	827730
6836	F	828180
6837	F	828348
6838	F	828729
6839	F	830099
6840	F	830281
6841	F	830491
6842	F	830550
6843	F	830576

Publications Cited in the Specification

- Adames et al., 1985, Nature, 318 : 533-538.
- Aldous, M.B. et al., 1992, J. Infect. Dis., 166 : 646-649.
- 5 Alexander et al., 1987, Mol. Cell. Biol., 7 : 1436-1444.
- Allan, G. M. et al., 1995, Vet. Microbiol., 44 : 49-64.
- Altschul, S.F. et al., 1990, J. Mol. Biol., 215 : 403-410.
- Altschul et al., 1993, Nature Genetics, 3 : 266-272.
- Altschul et al., 1997, Nucl. Acids Res., 25 : 3389-3402.
- 10 Ansubel et al., 1989, Current Protocols in Molecular Biology,
- Arlinghaus, H.F. et al., 1997, Anal. Biochem., 69, 18, 3747-53.
- Bai, M. Et al., 1993, J. Virol., 67 : 5198-5205.
- Barany, F., 1911, PNAS. USA, 88 : 189-193.
- Beattie, K. et al., 1993, Clin. Chem., 39(4) : 719-721.
- 15 Bernoist and Chambon, 1981, Nature, 290 : 304-310.
- Borman, S., 1996, Chem. Eng. News, 74(50) : 42-43.
- Braun, J. et al., 1994 Ann., Rheum Dis 53 : 100-105.
- Brinster et al., 1982, Nature, 296 : 39-42.
- Buckholz, R.G., 1993, Yeast systems for the expression of heterologous gene products. Curr. Op.
- 20 Biotechnology 4 : 538-542.
- Burg, J.L. et al., 1996, Mol. and Cell. Probes, 10 :257-271.
- Campbell, L.A. et al., 1992 J. Clin. Microbiol. 30 : 434-439.
- Casas-Ciria J. et al., 1996
- Chatelier, R.C. et al., 1995, Anal. Biochem., 229, 1, 112-118.
- 25 Chee, M. et al., 1996, Science, 274 : 610-613.
- Chu, B.C.F. et al., 1986, NAR, 14 : 5591-5603.
- Chu, P.W.G. et al., 1993, Virus Research, 27 : 161-171.
- Clark, E.G., 1997, American Association of Swine Practitioners, 499-501.
- Cole et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc.,
- 30 pp. 77-96.
- Cote et al., 1983, PNAS USA, 80 : 2026-2030.
- Cserzo, M., Wallin, E., Simon, I. von Heijne G and Elofsson, A., 1997, Prot.
- Eng., 10 : 673-676.
- DeBoer et al., 1980, Scientific American, 242 : 74-94.
- 35 DeBoer et al., 1983, PNAS USA, 80 : 21-25.
- Derisi, J. et al., 1996, Nature Genet, 14 : 457-460.
- Distance Relationships: Atlas of Protein Sequence and Structure, Washington :



National Biomedical Research Foundation.

- Duck, P. et al., 1990, *Biotechniques*, 9 : 142-147.
- Dulac, G.C. et al., 1989, *Can. J. Vet. Res.*, 53 : 431-433.
- Edwards, C.P., and Aruffo, A., 1993, Current applications of COS cell based transient  
5 expression systems. *Curr. Op. Biotechnology* 4 : 558-563.
- Edwards, S. et al., 1994, *Vet. Rec.*, 134 : 680-681.
- Erlich, H.A., 1989, In *PCR Technology. Principles and Applications for DNA  
Amplification*. New York : Stockton Press.
- Falsey, et al., *J. Infect. Dis.* 168 :493-496.
- 10 Fanger and Drakeman, 1995, *Drug News and Perspectives*, 8 : 133-137.
- Felgner, et al., 1987, *Proc. Natl. Acad. Sci.*, 84 : 7413.
- Fodor, S.P.A. et al., 1991, *Science*, 251 : 767-771.
- Fontes, E.P.B. et al., 1994, *J. Biol. Chem.*, Vol. 269, N° 11 : 8459-8465.
- Fox, G. Et al., 1989, *J. Gen. Virol.*, 70 : 625-637.
- 15 Fraley et al., 1980, *J. Biol. Chem.*, 255 : 10431.
- Gardner et al., 1981, *Nucl. Acids Res.* 9 : 2871
- Gaydos, C.A. et al., 1994 *J. Clin. Microbiol.* 32 : 903-905.
- Grayston, J.T. et al., 1986 *N. Engl. J. Med.*, 315 : 161-168.
- Grayston, J.T. et al., 1996 *Rev., Med Interne* 17, 45S-47S.
- 20 Gonnet et al., *Science*, 256 : 1443-1445.
- Green Publishing Associates and Wiley Interscience, N.Y.
- Pearson and Lipman, 1988, *PNAS USA*, 85(8) : 2444-2448.
- Grosschedl et al., 1984, *Cell*, 38 : 647-658.
- Guateli, J.C. et al., 1990, *PNAS. USA*, 87 : 1874-1878.
- 25 Hackland, A.F. et al., 1994, *Arch. Virol.*, 139 : 1-22.
- Hahn, D.L. Et al., 1991 *JAMA*. 266
- Haidl, et al., 1992 *N. Engl. J. Med.* 326 :576-577.
- Haidl, et al., *Chlamydial infections* 1994
- Hammer et al., 1987, *Science*, 235 : 53-58.
- 30 Hanahan, 1985, *Nature*, 315 : 115-122.
- Hanson, S.F. et al., 1995, *Virology*, 211 : 1-9.
- Harding, J.C., 1997, *American Association of Swine Practitioners*, 503.
- Harding, R.M. et al., 1993, *Journal of General Virology*, 74 : 323-328.
- Hashiguchi, K. et al., 1992 *J. Laryngol. Otol.* 106 : 208-210.
- 35 Hayashi, S. and Wu, H.C., 1992, in N.M. Hooper and A.J. Turner (ed.) *Lipid  
Modification of Proteins: A Practical Approach*. Oxford University Press,  
New York, pp. 261-285.

- Heinkoff and Heinkoff, 1993, *Proteins*, 17 : 49-61.
- Herrera-Estrella et al., 1983, *Nature*, 303 : 209-213.
- Herrera-Estrella, 1984, *Nature*, 310 : 115-120.
- Heyraud-Nitschke, F. et al., 1995, *Nucleic Acids Research*, Vol. 23, N° 6.
- 5 Higgins et al., 1996, *Meth. Enzymol.*, 266 : 383-402.
- Horner, G.W., 1991, *Surveillance* 18(5) : 23.
- Houbenweyl, 1974, in *Meuthode der Organischen Chemie*, E. Wunsch Ed.,  
Volume 15-I et 15-II, Thieme, Stuttgart.
- Hueck, C.J., 1998, *Molec. Biology Rev.*, 62 : 379-433.
- 10 Huovinen, P. et al., 1989 *Ann., Intern Med* 110 : 612-616.
- Huse et al., 1989, *Science*, 246 : 1275-1281.
- Huygen, K. et al., 1996, *Nature Medicine*, 2(8) : 893-898.
- Innis, M.A. et al. 1990. in *PCR Protocols. A guide to Methods and Applications*.  
San Diego : Academic Press.
- 15 Inoue et al., 1987, *Nucl. Acids Res.*, 15 : 6131-6148.
- Inoue et al., 1987, *FEBS Lett.* 215 : 327-330.
- Jackson, L.A. et al., 1997 *Am., J. Pathol.* 150. : 1785-1790.
- Jantos et al., 1997, *J. Clin. Microbiol.*, 35(3) : 620-623.
- Kabat E. Et al., 1983, *Sequences of Proteins of Immunological Interest*,  
20 U.S. Dept. Of Health and Human Services.
- Kaneda, et al., 1989, *Science*, 243 : 375.
- Kelsey et al., 1987, *Genes and Devel.*, 1 : 161-171.
- Kievitis, T. et al., 1991, *J. Virol. Methods*, 35 : 273-286.
- Kleemola, M. et al., 1988, *J. Infect. Dis.* 157 : 230-236.
- 25 Kohler, G. et al., 1975, *Nature*, 256(5517) : 495-497.
- Kollias et al., 1986, *Cell*, 46 : 89-94.
- Kozbor et al., 1983, *Immunol. Today*, 4 : 72.
- Krone, J.R. et al., 1997, *Anal. Biochem.*, 244, 1, 124-132.
- Krumlauf et al., 1985, *Mol. Cell. Biol.*, 5 : 1639-1648.
- 30 Kuo, CC. et al., 1988, *J. Clin. Microbiol.* 26 : 812-815.
- Kuo, CC. et al., 1993, *J. Infect. Dis.* 167 : 841-849.
- Kwoh, D.Y. et al., 1989, *PNAS. USA*, 86 : 1173-1177.
- Ladany, S. et. al., 1989, *J. Clin. Microbiol.* 27 : 2778-2783.
- Laitinen, K. et al., 1997. *Chlamydia pneumoniae Infection Induces Inflammatory*  
35 *Changes in the Aortas of Rabbits.* *Infect. Immun.* 65:4832-4835.
- Lazarowitz, S. G. et al., 1989, *The EMBO Journal*, Vol. 8 N° 4 : 1023-1032.
- Leder et al., 1986, *Cell*, 45 : 485-495.

- Lee, C.A., 1997, Trends Microbiol., 5 : 148-156.
- Leininger, E. et al., 1991, PNAS USA, 88 : 345-349.
- Lipshutz, R.J. et al., 1995, Biotechniques, 19(3) : 442-447.
- Liu, H. et al., 1997, J. Gen. Virol. 78(Pt6) : 1265-1270.
- 5 Livache, T. et al., 1994, NAR, 22(15) : 2915-2921.
- Lockhart, D.J. et al., 1996, Nature Biotechnol., 14 : 1675-1680.
- Longbottom et al., 1998, Infect Immunol., 66 : 1317-1324.
- Luckow, V.A., 1993, Baculovirus systems for the expression of human gene products.  
Curr. Op. Biotechnology 4 : 564-572.
- 10 Lukacova, M. Et al., 1994, Infect. Immunol. June, 62(6) : 2270-2276.
- MacDonald, 1987, Hepatology, 7 : 425-515.
- Mankertz, A. et al., 1997, J. Virol., 71 : 2562-2566.
- Mason et al., 1986, Science, 234 : 1372-1378.
- Matson, R.S. et al., 1994, Analytical Biochemistry, 217 : 306-310.
- 15 Matthews, J.A. et al., 1988, Anal. Biochem., 169 : 1-25.
- McNeilly, F. et al., 1996, Vet. Immunol. Immunopathol., 49 : 295-306.
- Meehan, B.M. et al., 1997, J. Gen. Virol., 78 : 221-227.
- Mérel, P., 1994, De la PCR aux puces à ADN, Biofutur, 139 : 58.
- Merrifield, R.D., 1966, J. Am. Chem. Soc., 88(21) : 5051-5052.
- 20 Midoux, 1993, Nucleic Acids Research, 21 : 871-878.
- Miele, E.A. et al., 1983, J. Mol. Biol., 171 : 281-295.
- Moazed, T.C. et al., 1997. Murine Model of Chlamydia pneumoniae Infection  
and Atherosclerosis. J. Infect. Dis. 175:883-890.
- Mogram et al., 1985, Nature, 315 : 338-340.
- 25 Mordhorst, C.H. et al., 1992 Eur., J. Clin. Microbiol. Infect Dis 11 : 617-620.
- Morrison et al., 1984, PNAS USA, 81 : 6851-6855.
- Morrison, R.P. et al., 1995. Gene Knockout Mice Establish a Primary Protective Role  
for Major Histocompatibility Complex Class II-Restricted Responses in Chlamydia  
trachomatis. Infect. Immun. 63:4661-4668.
- 30 Murphy, F.A. et al., 1995, Sixth Report of the International Committee on Taxonomy  
of Viruses. Springer-Verlag Wien New York.
- Nakai, K. and Kanehisa, M., 1991, Proteins, 11 : 95-110.
- Nielsen, H. et al., 1997, Protein Engin., 10 : 1-6.
- Neuberger et al., 1984, Nature, 312 : 604-608.
- 35 O'Donell-Maloney, M.J., 1996, Trends Biotechnol., 14 : 401-407.
- Ogawa, H. et al., 1992 J. Laryngol. Oto 106 : 490-492.
- Olins, P.O., and Lee, S.C., 1993, Recent advances in heterologous gene expression

- in *E. coli*. *Curr. Op. Biotechnology* 4 : 520-525.
- Ornitz et al., 1986, *Cold Spring Harbor Symp. Quant. Biol.*, 50 : 399-409.
- Pagano et al., 1967, *J. Virol.*, 1 : 891.
- Peterson, E.M. et al., 1998, *Infect. Immunol.* Aug., 66(8) : 3848-3855.
- 5 Peterson, E. et al., 1988. Protective Role of Magnesium in the Neutralization by Antibodies of *Chlamydia trachomatis* Infectivity.
- Pierschbacher and Ruoslahti, 1987, *J. Biol. Chem.*, 262 : 17294-17298.
- Pinkert et al., 1987, *Genes and Devel.*, 1 : 268-276.
- Pugsley, A.P., 1993, *Microbiol. Rev.*, 57 : 50-108.
- 10 Puolakkainen, M. et al., 1993 *J. Clin. Microbiol.* 31 : 2212-2214.
- Rank, R.G. et al., 1988. Susceptibility to reinfection after a primary chlamydial genital infection. *Infect. Immun.* 56:2243-2249.
- Readhead et al., 1987, *Cell*, 48 : 703-712.
- Reeves, P.R. et al., 1996, in *Bacterial Polysaccharide Synthesis and Gene*
- 15 *Nomenclature*, Elsevier Science Ltd., pp. 10071-10078.
- Roivainen, M. Et al., 1994, *Virology*, 203 : 357-365.
- Rolfs, A. et al., 1991, In *PCR Topics. Usage of Polymerase Chain reaction in Genetic and Infectious Disease*. Berlin : Springer-Verlag.
- Salzberg et al., 1998, *Nucl. Acids Res.*, 26 : 544-548.
- 20 Sambrook, J. et al., 1989, In *Molecular cloning : A Laboratory Manual*. Cold Spring Harbor, NY : Cold Spring Harbor Laboratory Press.
- Sanchez-Pescador, R., 1988, *J. Clin. Microbiol.*, 26(10) : 1934-1938.
- Sani, 1985, *Nature*, 314 : 283-286.
- Sarver et al., 1990, *Science*, 247 : 1222-1225.
- 25 Schachter, J. 1980. *Chlamydiae*, p.357-365. In E.H. Lennette (ed.), *Manual of clinical microbiology*, 3<sup>rd</sup> ed. American Society for Microbiology, Washington, D.C.
- Schneewind, O. Et al., 1995, *Science*, 268 : 103-106.
- Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Karlin and Altschul*, 1990, *PNAS USA*, 87 : 2267-2268.
- 30 Segev D., 1992, in « Non-radioactive Labeling and Detection of Biomolecules ». Kessler C. Springer Verlag, Berlin, New-York : 197-205.
- Sheldon, E.L., 1993, *Clin. Chem.*, 39(4) : 718-719.
- Shiver, J.W., 1995, in *Vaccines 1995*, eds Chanock, R.M. Brown, F. Ginsberg, H.S. & Norrby, E.), pp.95-98, Cold Spring Harbor Laboratory Press, Cold
- 35 Spring Harbor, New York.
- Shoemaker, D.D. et al., 1996, *Nature Genet*, 14 : 450-456.
- Shor, A. et. al., 1992 *S. Afr. Med. J.* 82 : 158-161.

- Sosnowsky et al., 1997, PNAS., 94, 1119-1123.
- Struyve, M. et al., 1991, J. Mol. Biol., 218 : 141-148.
- Sundelof, et al., 1993 Scand. J. Infec. Dis. 25 :259-261.
- Sutcliffe, I.C. and Russell, R.R.B., 1995, J. Bacteriol. 177 : 1123-1128.
- 5 Swift et al., 1984, Cell, 38 : 639-646.
- Takeda et al., 1985, Nature, 314 : 452-454.
- Tascon, R.E et al., 1996, Nature Medicine, 2(8) : 888-892.
- Thom, D.H. et al., 1990 Am. J. Epidemiol 132 : 248-256.
- Thomas, GN. et al., 1997 Scand., J. Infect. Dis. Suppl 104, 30-33.
- 10 Tischer, I. et al., 1982, Nature, 295 : 64-66.
- Tischer, I. et al., 1986, Arch. Virol., 91 : 271-276.
- Tischer, I. et al., 1988, Zentralbl Bakteriell Mikrobiol Hyg [A] 270 : 280-287.
- Tischer, I. et al., 1995, Arch. Virol., 140 : 737-743.
- Tompson et al., 1994, Nucl. Acids Res., 22(2) : 4673-4680.
- 15 Urdea, M.S., 1988, Nucleic Acids Research, 11 : 4937-4957.
- Villa-Kamaroff et al., 1978, PNAS USA, 75 : 3727-3731.
- Wagner et al., 1981, PNAS USA, 78 : 1441-1445.
- Walker, G.T. et al., 1992, NAR 20 : 1691-1696.
- Walker, G.T. et al., 1992, PNAS. USA, 89 : 392-396.
- 20 White, B.A. et al., 1997, Methods in Molecular Biology, 67, Humana Press, Towota.
- Yamamoto et al., 1980, Cell, 22 : 787-797.
- Yershov, G. et al., 1996, PNAS., USA, 93 : 4913-4918.

WHAT IS CLAIMED IS:

- 1- An isolated polynucleotide having a nucleotide sequence of a *Chlamydia pneumoniae* genome, comprising
- 5 (a) the a nucleotide sequence of SEQ ID No. 1;  
(b) the nucleotide sequence contained within the *Chlamydia pneumoniae* genomic DNA in ATCC Deposit No. \_\_\_\_\_;  
(c) the nucleotide sequence contained in a clone insert in ATCC Deposit No. \_\_\_\_\_;  
10 (d) a nucleotide sequence exhibiting at least 99.9% identity with the sequence of SEQ ID No. 1; or  
(e) a nucleotide sequence exhibiting at least 80% homology to SEQ ID No. 1.
- 15 2- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. \_\_\_\_\_ or to a clone insert in ATCC Deposit No. \_\_\_\_\_ under conditions of high stringency.
- 20 3- An isolated polynucleotide which hybridizes to SEQ ID No. 1 or to the *Chlamydia pneumoniae* genomic DNA contained in ATCC deposit No. \_\_\_\_\_ under conditions of intermediate stringency.
- 4- An isolated polynucleotide having a nucleotide sequence of an open reading frame (ORF) of a *Chlamydia pneumoniae* genome, comprising:
- 25 (a) a nucleotide sequence chosen from one of ORF2 to ORF 1297;  
(b) a nucleotide sequence exhibiting at least 99.9% identity with one of ORF2 to ORF 1297; or  
(c) a nucleotide sequence exhibiting at least 80% homology to one of ORF2 to ORF 1297.
- 30 5- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under conditions of high stringency.
- 6- An isolated polynucleotide which hybridizes to one of ORF2 to ORF 1297 under  
35 conditions of intermediate stringency.
- 7- The polynucleotide of Claims 2, 3, 4, 5, or 6 which encodes the following polypeptides or fragments thereof:
- 40 (a) a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;

- 5 (b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;
- (c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;
- (d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;
- (e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;
- 10 (f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;
- (g) a *Chlamydia pneumoniae* polypeptide having involved in metabolism of fatty acids;
- (h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;
- 15 (i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;
- (j) a *Chlamydia pneumoniae* transport polypeptide;
- (k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;
- 20 (l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;
- (m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.
- (n) a *Chlamydia pneumoniae* surface exposed polypeptide;
- 25 (o) a *Chlamydia pneumoniae* lipoprotein;
- (p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;
- (q) a *Chlamydia pneumoniae* KDO-related polypeptide;
- (r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;
- 30 (s) a *Chlamydia pneumoniae* lipid A component-related polypeptide;
- (t) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;
- 35 (u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;
- (v) a *Chlamydia pneumoniae* Type III secreted polypeptide;
- (w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or

- (x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

8- A polynucleotide encoding a fusion protein, comprising one of ORF2 to ORF1297 of Claim 4, 5, or 6 ligated in frame to a polynucleotide encoding a heterologous polypeptide.

9- A recombinant vector that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

10- A recombinant vector that contains the polynucleotide of Claim 8.

10

11- A recombinant vector that contains the polynucleotide of Claim 4, 5 or 6, operatively associated with a regulatory sequence that controls gene expression.

12- A recombinant vector that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression.

13- A genetically engineered host cell that contains the polynucleotide of Claim 1, 2, 3, 4, 5 or 6.

14- A genetically engineered host cell that contains the polynucleotide of Claim 8.

15- A genetically engineered host cell that contains the polynucleotide of Claim 4, 5 or 6 operatively associated with a regulatory sequence that controls gene expression in the host cell.

25

16- A genetically engineered host cell that contains the polynucleotide of Claim 8 operatively associated with a regulatory sequence that controls gene expression in the host cell.

17- A method for producing a polypeptide, comprising:

30

- (a) culturing the genetically engineered host cell of Claim 15 under conditions suitable to produce the polypeptide encoded by the polynucleotide; and
- (b) recovering the polypeptide from the culture.

18- A method for producing a fusion protein, comprising:

35

- (a) culturing the genetically engineered host cell of Claim 16 under conditions suitable to produce the fusion protein encoded by the polynucleotide; and
- (b) recovering the fusion protein from the culture.



19- A polypeptide encoded by the polynucleotide of Claim 4, 5 or 6.

20- The polypeptide of Claim 19 which immunoreacts with seropositive serum of an  
5 individual infected with *Chlamydia pneumoniae*.

21- The polypeptide of Claim 19 which comprises the following polypeptides or fragments thereof:

- 10 (a) a *Chlamydia pneumoniae* transmembrane polypeptide having between 1 and 3 transmembrane domains;
- (b) a *Chlamydia pneumoniae* transmembrane polypeptide having between 4 and 6 transmembrane domains;
- (c) a *Chlamydia pneumoniae* transmembrane polypeptide having at least 7 transmembrane domains;
- 15 (d) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of sugars and/or cofactors;
- (e) a *Chlamydia pneumoniae* polypeptide involved in intermediate metabolism of nucleotides or nucleic acids;
- (f) a *Chlamydia pneumoniae* polypeptide involved in metabolism of amino acids or polypeptides;
- 20 (g) a *Chlamydia pneumoniae* polypeptide involved in metabolism of fatty acids;
- (h) a *Chlamydia pneumoniae* polypeptide involved in the synthesis of the cell wall;
- 25 (i) a *Chlamydia pneumoniae* polypeptide involved in transcription, translation, and/or maturation process;
- (j) a *Chlamydia pneumoniae* transport polypeptide;
- (k) a *Chlamydia pneumoniae* polypeptide involved in the virulence process;
- 30 (l) a *Chlamydia pneumoniae* polypeptide involved in the secretory system and/or which is secreted;
- (m) a *Chlamydia pneumoniae* polypeptide of the cellular envelope or outer cellular envelope of *Chlamydia pneumoniae*.
- (n) a *Chlamydia pneumoniae* surface exposed polypeptide;
- 35 (o) a *Chlamydia pneumoniae* lipoprotein;
- (p) a *Chlamydia pneumoniae* polypeptide involved in lipopolysaccharide biosynthesis;
- (q) a *Chlamydia pneumoniae* KDO-related polypeptide;

- (r) a *Chlamydia pneumoniae* phosphomannomutase-related polypeptide;
- (s) a *Chlamydia pneumoniae* phosphoglucomutase-related polypeptide;
- 5 (t) a *Chlamydia pneumoniae* lipid A component-related polypeptide;
- (u) a *Chlamydia pneumoniae* polypeptide that contains an RGD sequence;
- (v) a *Chlamydia pneumoniae* Type III secreted polypeptide;
- 10 (w) a *Chlamydia pneumoniae* cell wall anchored surface polypeptide; or
- (x) a *Chlamydia pneumoniae* polypeptide that is not found in *Chlamydia trachomatis*.

15 22- A fusion protein encoded by the polynucleotide of Claim 8.

23- The fusion protein of Claim 22 which immunoreacts with seropositive serum of an individual infected with *Chlamydia pneumoniae*.

20 24- An antibody that immunospecifically binds to the polypeptide of Claim 19.

25- An antibody that immunospecifically binds to the fusion protein of Claim 22.

26- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

- (a) contacting the sample with a polynucleotide primer of Claim 1, 2, 3, 4, 5, or 6 in the presence of a polymerase enzyme and nucleotides under conditions which permit primer extension; and
- 30 (b) detecting the presence of primer extension products in the sample in which the detection of primer extension products indicates the presence of *Chlamydia pneumoniae* in the sample.

27- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

- (a) contacting the sample with a polynucleotide probe of Claim 1, 2, 3, 4, 5, or 6 under conditions which permit hybridization of complementary base pairs; and

- (b) detecting the presence of hybridization complexes in the sample in which the detection of hybridization complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

5 28- A method for the detection and/or identification of *Chlamydia pneumoniae* in a biological sample, comprising:

- (a) contacting the sample with the antibody of Claim 24 under conditions suitable for the formation of immune complexes; and
- (b) detecting the presence of immune complexes in the sample, in  
10 which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

29- A method for the detection and/or identification of antibodies to *Chlamydia pneumoniae* in a biological sample, comprising:

- 15 (a) contacting the sample with a polypeptide of Claim 19 under conditions suitable for the formation of immune complexes; and
- (b) detecting the presence of immune complexes in the sample, in which the detection of immune complexes indicates the presence of *Chlamydia pneumoniae* in the sample.

20

30- A DNA chip containing an array of polynucleotides comprising at least one of the polynucleotides of Claim 1, 2, 3, 4, 5, or 6.

31- A protein chip containing an array of polypeptides comprising at least one of the  
25 polypeptides of Claim 19.

32- An immunogenic composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.

30 33- An immunogenic composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.

34- An immunogenic composition comprising the fusion protein of Claim 22 and a pharmaceutically acceptable carrier.

35

35- An immunogenic composition comprising the fusion protein of Claim 23 and a pharmaceutically acceptable carrier.

- 36- A pharmaceutical composition comprising the polypeptide of Claim 19 and a pharmaceutically acceptable carrier.
- 37- A pharmaceutical composition comprising the polypeptide of Claim 20 and a pharmaceutically acceptable carrier.
- 38- A pharmaceutical composition comprising the polypeptide of Claim 22 and a pharmaceutically acceptable carrier.
- 39- A pharmaceutical composition comprising the polypeptide of Claim 23 and a pharmaceutically acceptable carrier.
- 40- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 32.
- 41- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 33.
- 42- A method of immunizing against *Chlamydia pneumoniae*, comprising administering to a host an immunizing amount of the immunogenic composition of Claim 34.
- 43- A method of immunizing against *Chlamydia pneumoniae*, comprising: administering to a host an immunizing amount of the immunogenic composition of Claim 35.
- 44- A DNA immunogenic composition comprising the expression vector of Claim 11.
- 45- The DNA composition of Claim 44, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.
- 46- A DNA immunogenic composition comprising the expression vector of Claim 12.
- 47- The DNA composition of Claim 46, wherein the DNA composition directs the expression of a neutralizing epitope of *Chlamydia pneumoniae*.
- 48- A screening assay, comprising:
- (a) contacting a test compound with an isolated polynucleotide of Claim 1, 2, 3, 4, 5 or 6; and
  - (b) detecting whether binding occurs.

- 49- A screening assay, comprising:
- (a) contacting a test compound with the polypeptide of Claim 19;  
and
  - (b) detecting whether binding occurs.
- 5
- 50- A screening assay, comprising:
- (a) contacting a test compound with the polypeptide of Claim 22;  
and
  - (b) detecting whether binding occurs.
- 10 51- A kit comprising a container containing an isolated polynucleotide of Claim 1, 2, 3, 4, 5  
or 6.
- 52- The kit of Claim 51 wherein the polynucleotide is a primer or a probe.
- 15 53- The kit of Claim 51 wherein the polynucleotide is a primer and the kit further comprises a  
container containing a polymerase.
- 54- The kit of Claim 51 which further comprises a container containing deoxynucleotide  
triphosphates.
- 20
- 55- A kit comprising a container containing an antibody that immunospecifically binds to the  
polypeptide of Claim 19.
- 56- A kit comprising a container containing an antibody that immunospecifically binds to the  
25 fusion protein of Claim 22.

Figure 1.

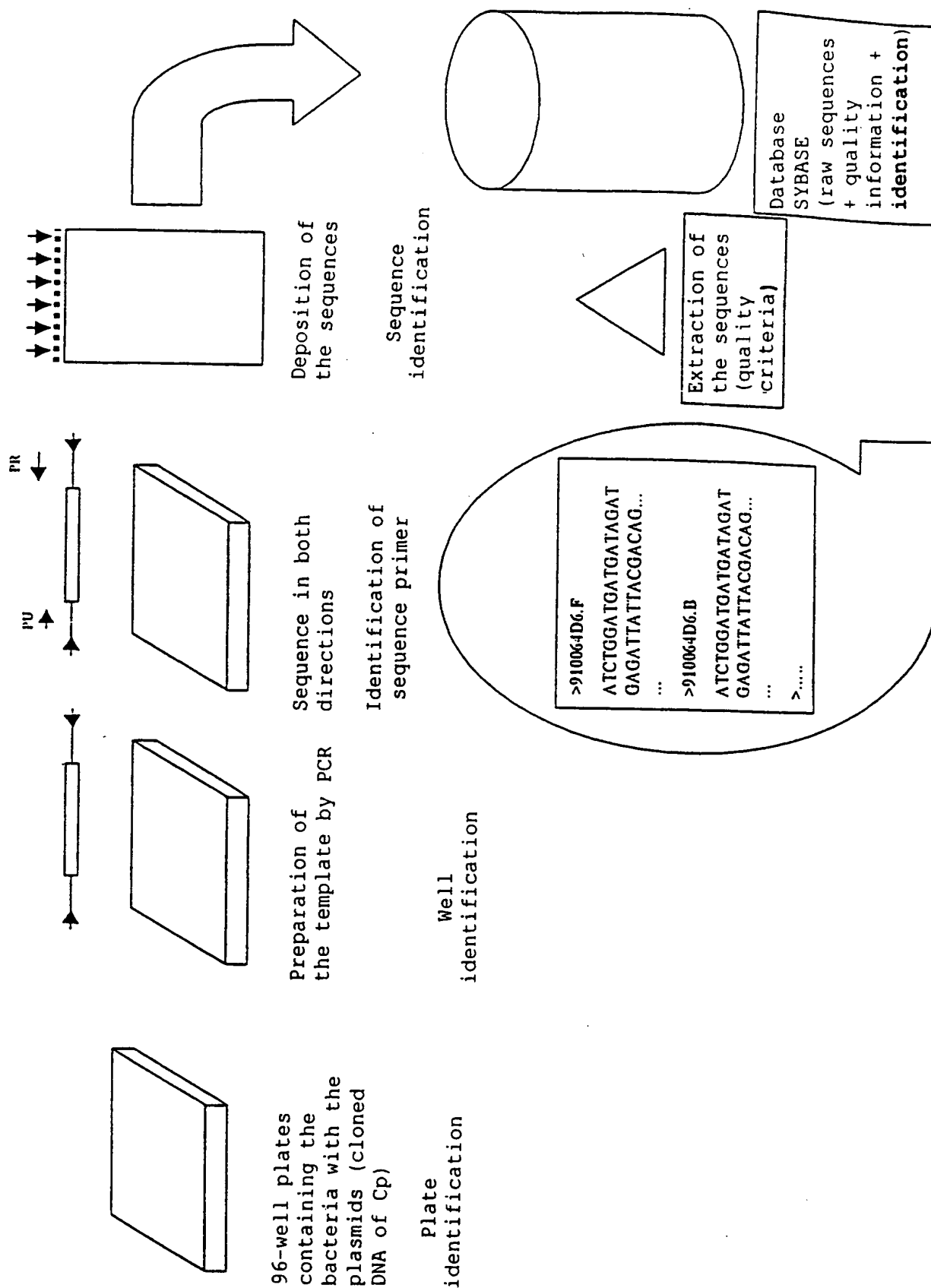


Figure 2.

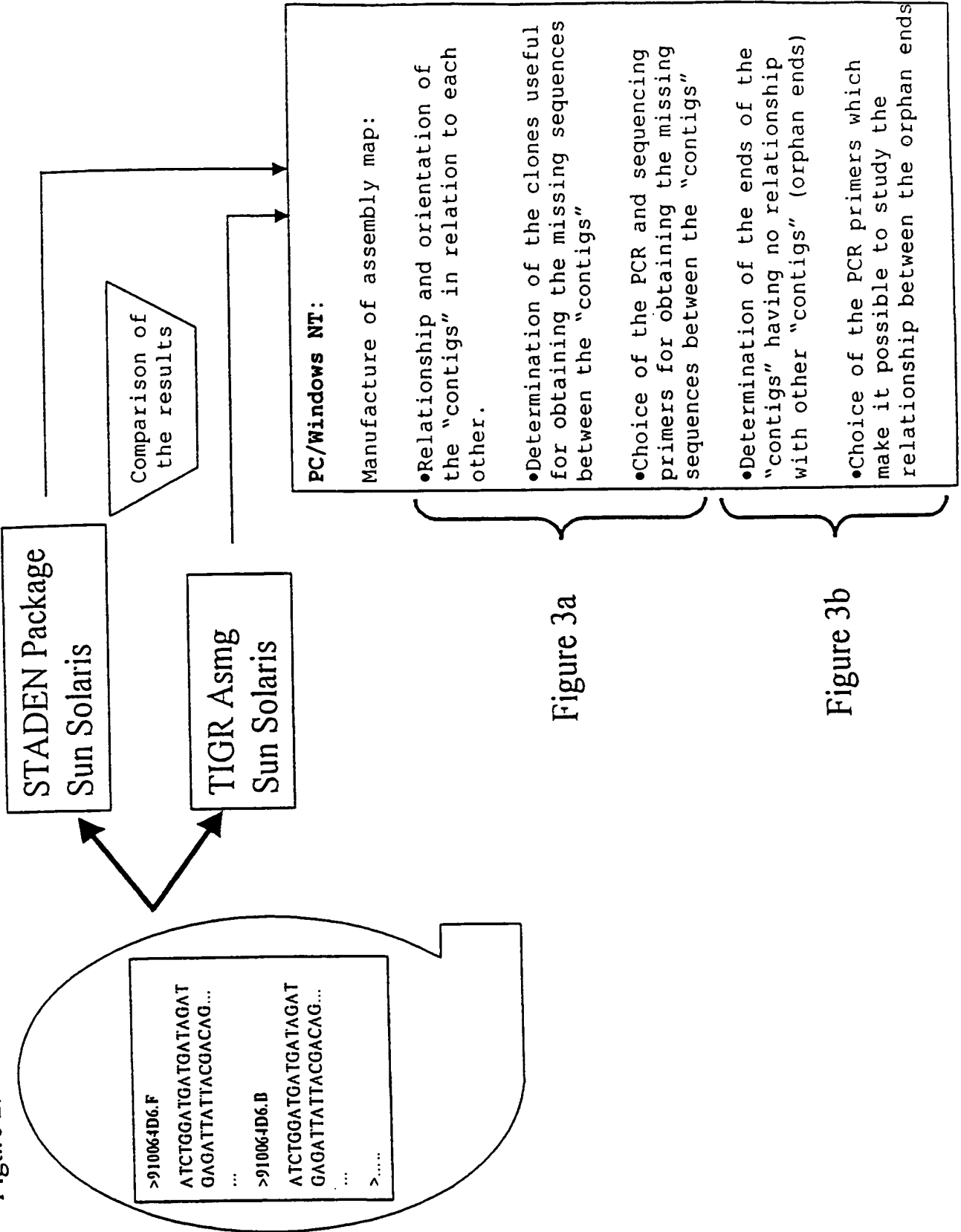
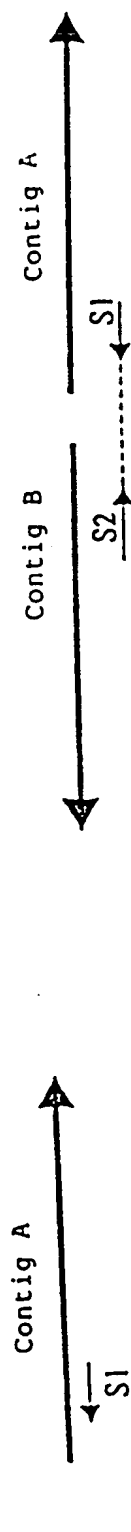


Figure 3a

Figure 3b

FIGURE 3A



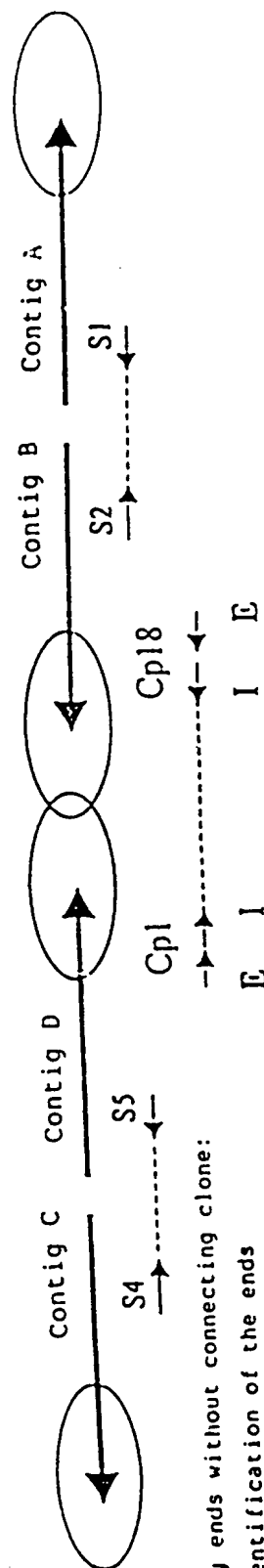
Distribution and position of the sequences on the contigs:

- 1- Define the arrangement of the contigs in relation to each other
- 2- Define the PCR primers which make it possible to fill the sequence

Statistical determination of the sequences:

- 1- Belonging to the same clone
- 2- Situated on two different contigs

FIGURE 3B



Contig ends without connecting clone:

- 1- Identification of the ends
- 2- Determination of outer and inner PCR primers for studying the relationships between the contigs

E: outer primers

I: inner primers



## SEQUENCE LISTING

&lt;110&gt;Genset SA

&lt;120&gt;Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

&lt;151&gt;1997-11-21

&lt;160&gt;6849

&lt;210&gt;1

&lt;211&gt;1230025

&lt;212&gt;DNA

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1

atagaaaact	attaaaaaat	cattgattct	gtcgggaaag	tatgcggata	aaattcagag	60
agaataagga	gaggaagatg	acaaggcaga	gttatgtttt	gggcaattgg	aaaatgcaca	120
aaacaatcca	agaagctaaa	gagtatgttc	aaacattagc	ttctntacta	caaggagAAC	180
ctcttttcctg	cactataggc	atagcttctc	catttacctc	tttgagagcg	attcatgaga	240
tgataaacac	tacgggagct	tttctctggg	tgggagcaca	aaatgtccat	cccgagcttt	300
cgggtgcttt	tactggagaa	atttccttac	ctatgcttaa	ggaggtagga	gtggaatttg	360
ttttagtagg	tcactccgag	cgtcgtcata	tttttgagga	gagtgatgcc	tttattgctt	420
caaaggtaaa	gtctgtagct	caggcgggac	tcgtgcctgt	tctttgtgtt	ggagagagct	480
tagaagttcg	tgaagaggga	aaggcgcatc	aggtaatcaa	aaaacagttg	cttttgggat	540
tggaacagat	ggataatggt	tccgaatttt	tgatcgcccta	tgaaccagta	tgggctatcg	600
gcacagggaa	ggtggcagaa	gcttcggatg	tgcaagatat	tcatatgttt	tgctgtgagg	660
tagtggcaga	gaggttctca	gaagctacag	ctgaagagat	ttcgattttg	tacggaggat	720
ctgtgaaggt	cgataatgct	cagcgatttg	ggcaatgtag	cgacgtcgat	ggtcttttag	780
ttggcggant	tcttttagang	ggcaaagttt	ttttgaagtc	gctaaaaatt	ttaatgtata	840
atttgtgaga	gttatgagat	ttttttgtct	attttttctt	gggttcctag	gatcttttca	900
ttgtgttgct	gaagacaagg	gcgtggattt	atttggagtc	tgggacgata	accaaattac	960
agagtgtgac	gatagttaca	tgacagaggg	tcgtgaagag	gttgaaaagg	tagtggacgc	1020
ttagtccatc	ggcttttatt	tatattctcc	ctaagggaag	cctgtattga	agatcgcttt	1080
ctcatagata	gaagtaattt	tcagatagtc	aataattggt	ttttttaaga	gaatgctagg	1140
cagggtgctcg	tgtttgggca	tttgattaag	tctacatgaa	tctggaggga	gagattcttc	1200
tggtattgag	aagtagaaca	aaaaacaagg	atcagacgtt	ctccgatgtc	ttcctaattcg	1260
atgtctttta	ataaggagat	tggcatgaca	gtgttggttt	acgcattttt	attcattttc	1320
ctttttctat	gtgtaattct	ttgtggctta	atcctggttc	aagagagtaa	gagcatgggg	1380
ttaggttctt	cgttcggcgt	ggattctgga	gattctgtct	ttggtgtctc	tactccagat	1440
attttgaaaa	aagtgacttc	atngtgtgct	gttgctttct	gcatagggtg	tttactactt	1500
tcattttcca	cgaatctctt	ggggaaaaag	ttagatgcta	aagaatttct	attgcctgct	1560
gctgaggaga	gcgacactca	agcttcttct	gagagcgttg	aagcagatga	atcctagcct	1620
atttgcggaa	ttaggtgttg	tctagattga	agtgcataaa	agctagcaag	tttttatctt	1680
catacgagat	atgagtgtac	ggtcggataa	gagtagaaat	ctttcttttg	ttcctatggg	1740
taagaagtcc	tttggcttcc	ttaaagagta	tgactcttat	caacccaaga	aatgttttag	1800
atccaagtgc	ttgtcgtacg	agatttcttc	acagagctct	gccaagccca	tgttcagact	1860
atgattagac	gtttagaata	ttacggcagt	cctattttta	ggaaaaagtc	ttccccaatt	1920
gcagagatca	cagatgagat	tcgtaatctc	gtgagtatac	tgtgtgatac	tttggaagca	1980
catcgtgggtg	tcgggttagc	cgctcctcag	gtagggaaaa	acgtcagttt	atttgtcatg	2040
tgtgtagata	gagagactga	ggatggagag	ttgattttct	ctgagtctcc	gaggggtattt	2100
atcaatcctg	ttctatcaga	tccttctgaa	accccgatca	taggtaaaga	aggatgtctt	2160
tctattcctg	gattgcgagg	agaagtattc	cgccctcaga	aaatcacagt	gaccgctatg	2220
gatctcaatg	gtaaaatatt	tactgagcac	ttggaaggat	tactgcacg	tatcattatg	2280
cacgagactg	accatctgaa	tggagtcttc	tatattgatc	ttatggaaga	acccaaagat	2340
cctaaaaaat	ttaaagcctc	tttagagaag	atcaaagctc	gctacaatac	acacttgagt	2400
aaagaagaac	tagtttctta	attgctcttc	agttctgatg	aggtgatatt	ttcttgtctc	2460
ttgcgtcaca	tttgttgta	gctttgtcta	tttccccgaa	caaatttcgt	caaagggtttt	2520
aaaatgtgtc	ttgctgattt	ttgctaagag	ctctttccct	cgttgcttag	cgatctctct	2580
tcctgtgctg	ttgacattga	atccagcacc	tttaggaagc	tgtacttgat	attgttcttc	2640
caacttctgt	atcgactgta	caaatgcate	tctagccaat	atagaagctg	ctgctacgac	2700
tacatcttgt	tctgcacgtg	gcttttgtat	taaagtaata	tcggtttctt	ttttttgaag	2760
tgcttttgagt	aggggtgtatt	ctgaagctgc	aaactgatct	gaaatagcaa	agacatctcc	2820
tgcagggtttg	ggtgctaagt	tgttgataac	agtagcgttg	gcccagcaag	gaagtgtatt	2880
taaattctgg	aatttcccat	atagctcggt	atatttttct	gggtatagaa	tgatgacatc	2940
gcagacacat	agtgagcgta	tgatactgtc	taaagaagcg	attttctgtg	ctttgagatt	3000
tttagagttc	tggactttat	tctcatagag	tttttttaag	atctctgcat	tcgatgcata	3060
gactgccgca	atacataaag	ggccaaaaaa	atcacctttc	cctgattcat	cgactcccaa	3120

ccttggaacga	aggctcttgct	ctacccttgc	atgggtgaag	gtatgaagga	tttctgggtc	3180
taagaaaaat	tctatgaatt	cctcacttcc	tttacccttg	attacgagtt	tcccggaggg	3240
gtatagagt	caggtaacag	tgtagagcg	agcttgaaat	acgggtattct	gtggctgaga	3300
aaagataaaa	tttttttctt	ttagctgatc	tcttaaattg	ttttgagcag	aagttgttaa	3360
agtaacaaca	aatgggtggcg	gcatgcagga	catctaccta	taaattatag	aaaaaattta	3420
gaacgattga	attcctagtc	ctaggaatcc	aggatgcaaa	gtgctcatac	tttttatttt	3480
tgcctactat	atcgtatagt	tatgacaact	tccaagtaca	aattaaacaa	caattttgta	3540
tatttctgca	aataactgcg	gggagccaaa	gatacaagag	tgtaagatgt	ctagtatttt	3600
acattcttaa	ggttttgaga	aacactatat	aggtaatcat	gcaagaacac	atacataaag	3660
aattgctaca	tctaggtgaa	atctttcgct	catcacgaga	gtctcaatcc	ctatcgtaa	3720
aggatgtaga	ggctgcaacc	tcgatacgat	atagttgttt	agaagctatt	gaacaggggt	3780
gtttaggaaa	attgatttct	ccagtttatg	ctcagggatt	tattaagaaa	tacgctacgt	3840
atcttgggtt	ggatggagat	agtatcttac	aagaacatcc	ttatgtcatg	aaaattttta	3900
aagagttttc	agatcataat	atggagatgc	ttttagacct	tgaatcgatg	ggaggaagga	3960
attctccgga	aagagcaatt	cattcttggg	cgaatctttg	gtgggcaggg	ctgatcatta	4020
taggtggcat	catggtgtgg	tggctcggat	cgttgttttc	tattttttta	cttaaggtct	4080
gttgggtctct	atttagacca	acagatagga	tggagtactt	cttaccctaa	tttgaatagt	4140
tgtgagactt	tctgagcccc	ttgcaaaagt	tgtctttgat	tttcaggaga	ccagggatct	4200
tcacccctac	cctcatcatc	ctcaggacct	aagggtctct	ctaaaccatc	acttctgtt	4260
gtactatcac	agccatcggt	tcggtctctt	ctctgttggg	agcttctctc	aacaccgaag	4320
gcactggcat	ggaatgccaa	atcctccgcc	tgtcacaata	ccatctcttt	ctatttctgc	4380
gtcatcccac	gggtcaggag	gtgggtggagc	ttgtctagga	gcttcgcctt	gggtttgtct	4440
ccaaatgttc	tctccagctg	tgggtggtgac	taataccttt	ctaagaattc	tttgccaagg	4500
accttggact	ctagggtcaa	gaacagtttg	ctctggatgt	agaggatcta	aaggaagata	4560
tccttttgaa	agaaggcata	gaaggacaag	gacttcaa	acctgagatt	ctaaactcaa	4620
accaatacca	ggacctaaga	aagtcgcaag	atcactggca	acaagtcttt	ttagtgattt	4680
ttttattaa	tccacaattt	gttttagcagc	ttgtcttaaa	ggacccttgt	aaccggattc	4740
taagctcaaa	acctctaacc	tggataat	ttgtaataaa	gtcctaaaat	tgagtttgca	4800
tgtaacacgg	cattcttgag	cggggtgctt	cttttgttga	ggagctggcg	cgcctcctac	4860
agcaccttgt	agctgttctt	cgtctgttgg	agggtggggga	cagggttgct	gttctggttg	4920
tagaatccaa	caagtaggag	gattgtcaga	tgaagttaga	aaggaaagag	cccccttga	4980
aacagcttga	agtatgagac	tccatgggtg	tgtctgttgc	atgtcttcgc	ctaagccgtt	5040
gttttgtaaa	agcttgacta	gagattcacc	catgcatctt	ggttgagctg	cttttagtag	5100
ttcccgatgt	agcttgcaac	cattttcaac	ctctgtttta	tcccgcgtac	ccaacggttc	5160
accttgctca	atcttctgtg	tacagtgcgg	tagctgttgg	aaagacatac	caacacaaat	5220
aggctccgtat	tgctgtataa	gttgttgtag	aaattgtgct	gagggattat	caggatcatc	5280
cacggctctct	aagcagcatg	cgcaacatcc	tccccatata	cattgtaaga	aaccaggaca	5340
atgtctctctg	caccagggag	tcccggttct	ataacaataa	tgtcctagac	gttgcatctc	5400
agcactatct	aagagattat	taagtaacga	gacctgttgt	tctaccatac	ctagcacatt	5460
gtctgatccg	agcgagatac	ccattttcacg	acctccagtc	ccaggctgtt	gtgtaattac	5520
acgtccacct	tgagagccag	attggcctcc	ttcttgcagt	ggaatatctt	ctcctccggg	5580
atttgggtggg	ggcgtttcgc	gataataaca	attacaattt	ccacatggaa	atgtcatgag	5640
gcttctcctt	tagtgaggtt	gagttgtatg	gatttttata	attacgagtt	cttctagaaa	5700
ggaattatag	aatgttcaga	tagagtattt	taaagcgggt	tatttcttat	tggatgatta	5760
agaaaaatag	gaaatcttga	ttatgttttt	ttgtcgagat	tactttttaga	gaaagagttt	5820
aaagtgatcg	cgggttatta	gtcaatttat	tttttaattt	aacatagatc	ctctcttaag	5880
tttccttgtt	tgtatgggag	aaatatttgg	ggaagaaaatg	ccgcaaaatt	ttttctaagt	5940
tctcaaaact	ttcaagaaaa	catagattct	gggatagaac	aaaagcttcg	cggcaaaaaa	6000
taggaatctt	attctttgtt	tattttttatc	cctaaaaata	gagtttgtaa	atgacccgag	6060
cattcaagga	tacgtgtttg	atacgccaaa	ttcccatcct	catcatcatc	ttcattttca	6120
tcttcttctt	cgagacttga	catgagaggg	acagattctg	caggggtagg	acaatcaaga	6180
ctttcctgtc	ttactaatga	gggtttcttt	tttaaaaacg	atgctgaagt	tttccctgtt	6240
ctatagctgt	attgtagtgc	atagaagatg	gtcataatcg	gatcatctat	catgtgtata	6300
tctacgacag	atgtctcatc	ggtatttgca	gggcaatagc	caatcgctaa	catcaataaa	6360
acgacgatag	cacgaaaatt	tgggcacgta	taacatattt	ctccacctgt	gtgctttaga	6420
atagaagatg	tgctttgtga	tgcagataag	agaaagctat	tcagcatttt	cacaatcagg	6480
agacaaaaag	gacctaaagc	tgaaaaatct	cctgttttta	gattgggtgac	ttggattttt	6540
cctaattgtc	tggccatgcc	attgtcattg	tatttttttg	ctacgtactg	gggctctgca	6600
ccgactgaag	atgggcgctg	cgcattctct	gatccacagg	ataggcgtga	cgctcgtaag	6660
gggctcgtat	ttaagatata	gcacgcagga	atgcgtgtag	aattagaagc	agaagatgtt	6720
cctgaggctt	cctctgatcc	tatagttttt	tcccaagacc	ttgtagcaat	aaagcttagc	6780
acggcttgga	ctagtgaatc	gtctagacct	cgttctctaa	tgctgttgac	tcttcaagg	6840
aaaaagtttt	gagaaaggct	ctgcatcggt	ccatagagct	gggttttagc	ttccgagcaa	6900
tgtctgtctaa	attcattttt	ctgttcttca	gacaaaatag	tgtttttttc	tacaagttcc	6960

attaagttga	ggcccatagt	tttagcagct	aaagcaacgg	caataggacc	atgggtctgt	7020
tcgcattcat	ggacaagtcc	agcaacctga	ttatcctctc	tgtctaagca	acacgcttta	7080
tacgttccac	aatgagctct	tccaaaagat	ccgcaacgct	gaccacatcc	agttgcgtaa	7140
ctgtcataac	aatactctgt	acatccttgc	gttcgtctat	gtgatagaat	ggagtctacc	7200
aattctcctg	cttcttggat	catgtgtatt	gtactttcat	caccttgagc	agtattaaat	7260
tggacacggt	tctctacttt	tgtaatTTta	gtaggttgcg	tagttatagg	agcagctcct	7320
ccactcgaac	cagcttcttc	gcttatactc	gaagccgatt	gccgcgttgt	ttcttctgtt	7380
gttggtactt	caacccattc	gcagttgaaa	tttccacaca	ttctgaacca	agaattatTT	7440
gggcaaacca	tagtcgtacc	TTTTtaatat	ttagattttat	ttaggtttta	gagagttgaa	7500
aagaactctc	taagaacagg	aaaagagtcg	gtatgctctg	cttgcgactg	tgctgtttgg	7560
aatgggaaac	gaagggatcc	cagtgtctat	agcacagtag	agtgaggcta	aacgtcaaaa	7620
ttgatttgaa	gaaatttgaa	ttgctgacaa	gagggggaga	ggaattaaaa	acgtcggacg	7680
gaagaagatg	tttagagcat	gtataaagaa	aattttaaat	tagatgcatt	atttcattggg	7740
tcttacctta	tttagactta	agatggtaag	gaagtctata	aaatcatttt	TTTTaaaatc	7800
tacggaattt	aaaaaattac	ttgataatga	tgtggagtgc	tagaagtgca	aactcactag	7860
aaatttcctg	aatttgagaa	ggagtttaaa	ataggtattc	ttgaaaagat	caatgcacgt	7920
gtagtggaaa	gaaaggcgta	acctacactg	gaaggagttt	cttttagaag	aaggtttctt	7980
ttttcgttgt	taatgacaaa	aactctctaa	gaacatcggt	tcaaccgttt	ttattgttgt	8040
gtttatttaa	aaaaaagatt	atatccttca	tgcaaattgg	tgctgttgga	aacaaatgtt	8100
gaaaatccag	aaaaaaagaa	tgtgtgtcag	cgtagtcatc	acggtagggc	ccatagtggg	8160
gtttttcaat	tctgcagacg	cagcaccaaa	gaaaaagaag	atccctatac	agattctcta	8220
ctcctttact	aaagtctctt	cctattttaa	aaacgaagac	gcaagtacta	tattttgcgt	8280
cgatgtggat	cgtggacttc	tccagcatcg	gtatttaggt	agtcaggat	ggcaggaaac	8340
cagacgtcgg	cagttattta	aatccttaga	aaatcaatca	tacggcaacg	aacgtttagg	8400
agaagaaact	cttgctattg	atattttcag	gaacaaagag	tgcttgagaa	gcgagatccc	8460
agagcagatg	gaagctatcc	ttgcaaattc	ctcggccttg	gtcttaggca	tctcttcttt	8520
tgggatcaca	ggaattcctg	cgactttgca	tagtttgctt	cgacagaatc	tatctttcca	8580
aaaacgctct	atagcatcgg	agagcttcc	tttaaagatc	gatagtggcc	cctcagatgc	8640
ctctgttttt	tataaaggcg	tgcttttccg	cggagagact	gcgatcgtgg	atgcgttaag	8700
ccaattattt	gccagctcg	atctttctcc	taaaaaaatt	atctttctag	gagaagacc	8760
tgaggtcgtt	caagctgttg	ggtctgcttg	tataggttgg	ggcatgaact	ttttaggcct	8820
ggtatactat	ctgctcaag	aaagcctttt	ttcttatgtt	catecttact	ctacagcaac	8880
ggagctccaa	gaagcacagg	gtttacaagt	aatttcagat	gaagtcgcac	agcttacttt	8940
aaacgctctt	ccgaaaatga	attaacatga	tgttagaaca	acaagcccta	cgtattctct	9000
ttccccctga	gggtgcttag	ggcccttttt	atctagcatg	agcggagatt	taggttttag	9060
tgagattttt	ggtaaatatg	aaaatatttt	cttaaaaaaga	tcatgaaaca	gtcatacttt	9120
tgcattgaag	gatctttatg	agacgttatc	ttttcatggt	tctagcttta	tgccctataa	9180
gagcagcccc	tctcgaagca	gtggtcatta	aaattactga	tgcgaggcca	gttcttaagt	9240
ttgctagaga	gaaaacttta	gtatgtttca	atattgaaga	tactgtggta	tttcttaaac	9300
agatggctcg	ccagtctgca	tggctctaca	atagagagct	cgatcttaag	actacactct	9360
ccgaagaaca	agccagagag	caggcggttt	tggagtggat	ggggatttct	tttcttgctg	9420
attatgaatt	ggtgagcgcg	aacttaagga	atgtactcac	aggcttatct	ttgaaacgat	9480
cttggtgact	cggtgattct	caaagacctg	tgcatTTgat	aaaaaatact	cttcgcattc	9540
tgcgttcttt	caacatagac	ttcacctcgt	gtccagctat	ttgtgaagat	ggttggtctt	9600
ctcatcctac	aaaggacaca	acattcgatc	aggccattgc	tatagaaaaa	aacattttgt	9660
ttgttggtct	tctcaaaaac	ggtcagccca	tggacgcagc	ccttgaaagt	cttctctctg	9720
ggatctcttc	tctccttagc	caaatcatct	atgtggatca	ggatgcagaa	cgtttgcgtt	9780
ctatcgggtg	tttttgtaaa	aaagcaaaac	tttattttat	agggatgctc	tacaccccag	9840
ccaagcagcg	tgtagaaagt	tacaatccta	aacttactgc	gatccaatgg	tcgcagattc	9900
gtaagaatct	ttccgatgaa	tattatgaat	ccctcttgag	ctatgtaaag	agcaaagggt	9960
agtgtcagca	aatcgatgtg	ggaatgggtat	cctgtggatg	gcatagacac	gcaaggcgtt	10020
ttttatgccg	tttttagatc	cttgtagggtg	cagaaaaaact	aaaaagatcg	gaagagaagg	10080
gattcgaacc	cctggttcct	gtaagagaac	ttctgatttc	gaatcagacg	cattcgacca	10140
ctctgccact	cttcgcta	gttcaatag	tttagaagat	ctacactcag	attgtctaca	10200
tgtatgtcac	aattgttttc	ataaattttat	gaaatcataa	tgaagattag	agaagatggc	10260
cgagtagtga	agacgaattc	ttagagaaaa	attagagtgt	tttcttgctg	atctaggcag	10320
aaaactaccc	tcaagaagag	gcttgagggt	gaaacatcta	atTTTTgtca	gaatgatgag	10380
agtggcagcc	tctgaagag	cagctgtctc	cgtgtgaatg	acgggacttc	ttgctgcaga	10440
aaggacaaaa	gcttagcaag	caaattgacac	cagcaattcc	aatgataata	taggtaattt	10500
gggtggcagg	agtagaaacg	cctccacaca	acttagcaat	aatattta	ttattgtgag	10560
tgattcctat	aagtcacacg	ttcaatgcac	aaagaataac	aataagagag	gataatcctc	10620
gaataatttt	gcctagcatc	gcttttctcc	taagttagtg	atacttaatt	tcatctttta	10680
atctttttta	taattttaata	aacagtTTTT	ttcaaaagac	ttctttgcta	aagtctctca	10740
gtctcgttga	cttttttgaat	acaaagggtt	aagttgttca	agaagttttt	gaactgtaaa	10800

caacttccag	tttttatgat	tagagagaca	gttcagaata	aaaacttcaa	ttttttaagt	10860
ttagataatc	tttctttact	tgcattgaga	aaagagcata	tttttataag	ccgcaattta	10920
ggataacata	tggagcaatt	tcatttggat	agggagaaa	ttttactttt	ggcaaaggcc	10980
tcagcactac	aactttctga	agagcttata	caggagtata	aaacttcttt	aagcgctgtg	11040
attacttcta	tgaagaagc	tcttgccata	gagattgatg	atgcggattc	atgcgaatct	11100
ctttttatgc	atgtagtaaa	tggtgaagat	ttgagagaag	attcgggtgac	ctctgatttc	11160
aatcgagagg	aattttttgcg	taatgttcca	gagtccttag	ggggattagt	gaaagtccct	11220
gcggaataca	agtaaggag	tctgaaaaat	tatgtatcga	tatagtgtct	tagaattagc	11280
aaaagctgtg	acttttagggg	aactgacagc	cacagggtg	actcaacatt	tttttcatag	11340
aatagaagaa	gctgaggggc	aggtaggtgc	ctttatttcc	ttgtgtgaag	aacaagcttt	11400
agaacaggca	gagctcatag	ataaaaagcg	ttcgcggtga	gaaccttttag	gaaaactcgc	11460
aggtgttcct	gtaggaatta	aagataatat	tcacgttaca	ggcctgaaga	caacatgcgc	11520
ctctcgtgtg	ctcgagaatt	atcaaccacc	gtttgatgct	actgtttag	aaagaatcaa	11580
aaaagaagat	gggattatct	taggcaaact	caatatggat	gagtttgcta	tgggatcaac	11640
aacgctatat	tctgcttttc	atcctaccca	caaccctgg	gatttatctc	gtgttcctgg	11700
aggttcttca	gggggatctg	cggccgcagt	ttctgctaga	ttttgtcccg	tagccctagg	11760
atcagatacc	ggaggatcca	tccgtcagcc	cgcagcattt	tgtggtgttg	taggttttaa	11820
gccttcttac	ggagccgttt	cgcgttacgg	gcttgtagcc	tttgccctct	cgctagatca	11880
aatcggtcct	ttagccaata	ctgtagaaga	cgtcgcccta	atgatggatg	tgttttctgg	11940
tagagatcct	aaagatgcaa	cctcaagaga	gtttttccgt	gattctttta	tgagcaagtt	12000
gtctacggag	gttcctaaag	tgattggggg	gcctagaaca	tttttagagg	gactccgtga	12060
tgatattagg	gagaatttct	tctcttcatt	agccattttt	gaaggagaag	gaacctatct	12120
tgtggatgtg	gagttggata	ttctcagcca	cgtgtatctc	atatattaca	ttttatcatc	12180
tgtctgaagct	gccacgaatt	tagcaagggt	cgatgggtg	cgttatggat	atcgttctcc	12240
tcaagcgcat	accatcagcc	aactctacga	tctctcacgt	ggagaaggat	ttggcaaaga	12300
ggtcatgcgc	agaatcctct	tagggaacta	tgcttctgtc	gcggagagac	agaatgttta	12360
ttataagaaa	gctacggcag	tgctgtgtaa	gattgtaaaa	gcatttagaa	ctgcatttga	12420
aaagtgtgaa	atcttagcca	tgcccgtctg	ttctagcccc	gcgtttgaaa	taggagaaat	12480
tctagatcct	gtgactttat	atctacagga	tatctatact	gtagctatga	atttagcgta	12540
tcttctctgcc	attgccgtac	cctctggatt	ttctaaggag	ggcctgccct	taggcctaca	12600
gattatcgga	cagcaaggac	aagaccaaca	agtgtgccaa	gtgggttaca	gtttccaaga	12660
gcattcgcaa	attaagcaat	tgttttctaa	gagatagcc	aaaagtgttg	ttctaggagg	12720
tcaatcatga	gtgctgttta	tgcagattgg	gaatcagtca	taggacttga	agttcacgta	12780
gaattgaaca	cagcatccaa	gttattttagc	tctgctttaa	atcgctttgg	agatgaacca	12840
aacactaata	tttctacagt	atgtacagga	ttgccaggat	cattgcctgt	attgaatcag	12900
agtgcctgg	agaaagctgt	gctttttggc	tgcgctgtcg	aagggtgaaat	ctctctattg	12960
agtcgtttcg	ataggaagtc	ttacttctat	cccgatagtc	ccaggaattt	tcaaattaca	13020
caattcgaac	atcctattat	ccgaggagga	cgcattaagg	cgattgtcca	aggggaagag	13080
cggtattttg	aattagccca	aaccatata	gaagatgatg	ccggaatgct	gaagcacttc	13140
ggagagtgtg	ccggtgtaga	ctacaatcgt	gccggagtcc	ccctaatega	aattgtttca	13200
aaaccctgta	tgttttgtcc	tgaagatggc	tgttgttacg	caacttcttt	ggtttccctg	13260
ttagactata	ttggaatttc	cgattgcaat	atggaagaag	gctccatccg	ttttgatgtc	13320
aatgtctccg	tacgccctaa	gggatcccca	gaacttcgca	ataaggtaga	aatcaagaat	13380
atgaactcct	tcgcttttat	ggcacaagct	ttagaagctg	aaaaacaacg	tcagatcgat	13440
gagtatctta	atcagccaaa	taaagatccc	aagctgggtga	ttccagccgc	tacctaccgc	13500
tgggatcccg	aaaagaaaaa	aactgtgtcg	atgcgtctca	aagagagtgc	cgaagattat	13560
aaatattttc	ccgagcctga	tctgccgaca	ctacaattga	cagagtccta	tatagaaagg	13620
attcgcaaga	ccttgccaga	acttccctat	gacaagtagc	atcgctatat	tcaggagtac	13680
ggtctatccg	aagatatcgc	aagtattctg	atcagcgata	agaatatcgc	aacgtttttt	13740
gaagtcgctt	gtaaagattg	taaaaacttt	aggtctttat	ctaactgggt	aaccgttgaa	13800
tttgagggcc	gctgcaaaac	cctaggagtg	aagttgccat	cttcaggaat	tttccccgag	13860
ggagtgcgtc	agctgggtcaa	cgcaatcgac	caagggtgtga	tcacagggaa	aattgctaag	13920
gaaatcgcag	atcttatgat	ggaatcccca	ggaaagaatc	ctgaggagat	tttaaaagag	13980
aagccagagc	tgcttcccat	gtcagatgaa	ggggaattgc	agaaaattat	cgcagaggtg	14040
gttcttgcaa	atcctgaatc	tatcgtagac	tataaaaaatg	gaaagactaa	ggctctagga	14100
ttcctagtgc	ggcagattat	gaagcgtaga	gcaggaaaaag	ctcctcccaa	gcgagtgaac	14160
gaactttttac	ttttagaatt	agataagggc	tagaattttc	tgtcacagtc	tgtcttaaaa	14220
aatcataaaa	gcatgttaga	gatctttcta	acatgctttt	tttatctaaa	tacacatttc	14280
taagttgcaa	aaacgaaagc	agaaaatttc	gatttgcctt	tctacctaca	ctttatggat	14340
ccatcagaat	taaattttgc	aaagccatgt	ctacgcggga	gataattctt	tttaagtgc	14400
aagaaattct	tgtgctcggc	ttgctttctt	attcttattg	acgtattgct	tgatcagata	14460
ttcattttga	tttaggtact	aaaatgcgat	tttcgctctg	cggatttcct	ctagtttttt	14520
cttttacatt	gctctcagtc	ttcgacactt	ctttgagtgc	tactacgatt	tctttaacct	14580
cagaagatag	ttttcatgga	gatagtcaga	atgcagaacg	ttcttataat	gttcaagctg	14640

gggatgtcta	tagccttact	ggtgatgtct	caatatctaa	cgtcgataac	tctgcattaa	14700
ataaagcctg	cttcnatgtg	acctcaggaa	gtgtgacgtt	cgcaggaaat	catcatgggt	14760
natattttta	taatatttcc	tcaggaacta	caaaggaagg	ngctgtactt	tggttgccaa	14820
atcctcaagc	aacggcacgt	ttttctgggt	tctccacgct	ctcttttaat	cagagccccg	14880
gagatattaa	agaacaggga	tgtctctatt	caaaaaatgc	acttatgctc	ttaaacaatt	14940
atgtagtgcg	ttttgaacaa	aaccaaagta	agactaaagg	cggagctatt	agtggggcga	15000
atgttactat	agtaggcaac	tacgattccg	tctctttcta	tcagaatgca	gccacttttg	15060
gaggtgctat	ccattcttca	ggccccctac	agattgcagt	aaatcaggca	gagataagat	15120
ttgcacaaaa	tactgccaa	aatggttctg	gaggggcttt	gtactccgat	ggtgatattg	15180
atattgatca	gaatgcttat	gttctatttc	gagaaaatga	ggcattgact	actgctatag	15240
gtaagggagg	ggctgtctgt	tgtcttccca	cttcagggaag	tagtactcca	gttcctattg	15300
tgactttctc	tgacaataaa	cagtttagtct	ttgaaagaaa	ccattccata	atgggtggcg	15360
gagccattta	tgctaggaaa	cttagcatct	cttcaggagg	tcctactcta	tttatcaata	15420
atatatcata	tgcaaattcg	caaaatttag	gtggagctat	tgccattgat	actggagggg	15480
agatcagttt	atcagcagag	aaaggaacaa	ttacattcca	aggaaaaccg	acgagcttac	15540
cgtttttgaa	tggcatccat	ctttttacaaa	atgctaaatt	cctgaaatta	caggcgagaa	15600
atggatactc	tatagaattt	tatgatccta	ttacttctga	agcagatggg	tctacccaat	15660
tgaatatcaa	cggagatcct	aaaaataaag	agtacacagg	gaccatactc	ttttctggag	15720
aaaagagtct	agcaaacgat	cctaggggatt	ttaaatctac	aatccctcag	aacgtcaacc	15780
tgtctgcagg	atacttagtt	attaaagagg	gggccgaagt	cacagtttca	aaattcacgc	15840
agtctccagg	atcgcattta	gttttagatt	taggaaccaa	actgatagcc	tctaagggaag	15900
acattggcat	cacaggcctc	gcgatagata	tagatagctt	aagctcatcc	tcaacagcag	15960
ctgtttttaa	agcaaacacc	gcaaataaac	agatatccgt	gacggactct	atagaactta	16020
tctcgcttac	tggcaatgcc	tatgaagatc	tcagaatgag	aaattcacag	acgttccctc	16080
tgctctcttt	agagcctgga	gccgggggta	gtgtgactgt	aactgctgga	gatttcctac	16140
cggtaagtc	ccattatggg	tttcaaggca	attggaaatt	agcttgga	ggaactggaa	16200
acaaagtgg	agaattcttc	tgggataaaa	taaattataa	gcctagacct	gaaaaagaag	16260
gaaatttagt	tcctaataat	ttgtggggga	atgctgtaga	tgtagatcc	ttaatgcagg	16320
ttcaagagac	ccatgcacg	agcttacaga	cagatcgagg	gctgtggatc	gatggaattg	16380
ggaatctctt	ccatgtatct	gcctccgaag	acaataaag	gtaccgtcat	aacagcgggt	16440
gatgtgtctt	atctgtaaat	aatgagatca	cacctaaagca	ctatacttcg	atggcatttt	16500
cccaactctt	tagtagagac	aaggactatg	cggtttccaa	caacgaatac	agaatgtatt	16560
taggatcgta	tctctatcaa	tatacaacct	ccctaggga	tattttccgt	tatgcttcgc	16620
gtaaccctaa	tgtaaacgct	gggattctct	caagaagggt	tcttcaaaat	cctcttatga	16680
tttttcattt	tttgtgtgct	tatggctcatg	ccaccaatga	tatgaaaaca	gactacgcaa	16740
atttccctat	ggtgaaaaac	agctggagaa	acaattgttg	ggctatagag	tgccggaggga	16800
gcatgcctct	attgggtattt	gagaacggaa	gacttttcca	aggtgccatc	ccatttatga	16860
aactacaatt	agtttatgct	tatcagggag	atttcaaaga	gacgactgca	gatggccgta	16920
gatttagtaa	tgggagttta	acatcgattt	ctgtacctct	aggcatagc	tttgagaagc	16980
tggcactttc	tcaggatgta	ctctatgact	ttagtttctc	ctatattcct	gatattttcc	17040
gtaaggatcc	ctcatgtgaa	gctgctctgg	tgattagcgg	agactcttgg	cttggtcccg	17100
cagcacacgt	atcaagacat	gctttttag	ggagtggaa	gggtcgggat	cactttaacg	17160
actatactga	gctcttatgt	cgaggaagta	tagaatgccg	ccccatgct	aggaattata	17220
atataaactg	tggaagcaaa	tttcgttttt	agaaggtttc	cattgctgtg	gtggttccgg	17280
atcttaacta	taaatcctgg	actatggatc	ataggcattg	ggtctctcga	acttggtgg	17340
agaataacga	cattttatat	gcataacgga	atactcgat	cacctcagcc	ccatagaca	17400
ttctttaggg	gttctttatt	tgtctaaact	tcgtatttta	tcgagaatcc	tttacgttct	17460
tggtttgctt	gtctccgagg	agttctctaa	cgaatcatag	ggattccagg	gttctgttcc	17520
ttgagtcctt	tggcagctga	tttgctctct	tctcaggagt	agagcgtgtg	gtttcagggc	17580
ttgggactcc	tagtaagacg	agccattctg	atagcctctc	taggagagcg	cttcgaagag	17640
gttcctgcaa	ctgcttctaa	gtaaaaattt	aaagagaagt	ctagtttttt	cgatacattg	17700
acttcttttt	tgaaccaga	cactcattgc	tagccgaatt	ttaagagtcc	atgagcatga	17760
tttctgtaaa	atcctcgcga	tgagcttttt	gtcttctcac	cttatgatgt	gctttctata	17820
agtattttaa	tgaactttta	ttaaaagagt	tttcgtcata	acctttcgct	cattttttcc	17880
tttcttgctg	tgataccgct	aactgatagc	actacaagct	ctctttcaac	gtctctctta	17940
gatgaaggaa	acccacaatc	catgaggaaa	cttcgtattc	ttgcgatcgt	tctcatagct	18000
ttgagcatta	ttttgattgc	aggtgggtgtg	gtattgctta	ctgtagcgat	ccctggatta	18060
agttcagtca	tttcttcccc	ggcagggatg	ggtgcctgtg	ctttgggatg	tgtgatgctt	18120
gctttaggga	tcgatgttct	tctgaagaaa	cgagaagtc	ctatagttct	cgcactctga	18180
actacgacac	caggaactgg	cagccctaga	agtggatttt	ctatttcagg	agctgatagc	18240
accatacgtt	ctcttctctac	gtatctcttg	gacgaggac	atccacaatc	catgaggaaa	18300
cttctgtatt	ttgcgatcgt	tctcatagtt	tttagcatta	ttttgattgc	aagtgggtgtg	18360
gtattgctta	ctgtagcgat	ccctggatta	agttcagtc	tttcttcccc	ggcagggatg	18420
ggtgcctgtg	ctttgggatg	tgtgatgctt	gctttaggga	tcgatgttct	tctgaagaaa	18480

cgagaagtcc	ctatagttct	cgcatctgta	actacgacac	caggaactgg	cagccctaga	18540
agtggatatt	ctatttcagg	agctgatagc	accatacgtt	ctcttcctac	gtatcccttg	18600
gacgagggac	atccacaatc	catgaggaaa	cttcgtattc	ttgcgatcgt	tctcatagtt	18660
tttagcatta	ttttgattgc	aagtgggtgtg	gtattgctta	ctgtagcgat	ccctggatta	18720
agctcgatca	tttcttcccc	agcggagatg	gggtgcttgtg	ctttgggatg	tgtgatgctt	18780
gctttgggga	tcgacgttct	tctgaagaaa	cgagaagtcc	ctatagtagt	tcccgcacct	18840
attcctgaag	aagtcgtcat	agatgatata	gatgaagaga	gtatacggct	gcagcaggaa	18900
gctgaagccg	cttttagcaag	acttcctgag	gagatgagtg	catttggaagg	ttacataaaa	18960
gttgctcgaga	gtcatttgga	gaacatgaaa	agcctgcctt	atgatgggtca	tgggctagaa	19020
gagaaaaacga	aacatcagat	aagagtcgtc	agatcttctt	tgaaggctat	ggttccagaa	19080
tttttagata	tcagaagaat	ttttgaagaa	gaagagttct	ttttctcttc	agctcgcaaa	19140
cgacttatag	atttagctac	tacttttagta	gagagaaaaa	ttttaacaga	gcaacttgag	19200
cgcaataaatt	taaggaaagc	gttttcttat	ttatatcagg	actcaatttt	taaaaaaatt	19260
attgataaact	tcgagaagtt	agcatggaaa	tttatgattt	tgagtaaate	aatttgtcga	19320
tttacaatta	tttttgaaaa	tcatgaacat	gggtgtacaa	agagcctgtt	acacaagaat	19380
gcagtgttac	tggagaaggt	aatctatagg	agtttgcaaa	aaagctatag	agatataggc	19440
atgtcatctg	caaagatgaa	aatcttgcac	ggcaaccctt	ttttctcttt	ggaagataat	19500
aaaaagacga	taatgaaaga	acacgcagag	atgcttgaaa	gtctcagtag	ctataggaag	19560
gtattttttag	ctctatctga	tgagaacgtt	gtagatacac	ctagcgatcc	aaagaaatgg	19620
gatttgtcag	gaatcccctg	tagggacgcg	ttgtctgaga	tttctcgtga	tgaacagtgg	19680
cagaagaaag	cacatctaaa	gcataagag	tccctctata	cgcaagctag	ggatcgttta	19740
acagaccaga	gctctaaaga	aaatcagaaa	gagttagaga	aagctgaaca	agagtacata	19800
tcttctttggg	aacgggttaa	aaaatttgag	attgagagag	tacaggagag	gatacaggca	19860
attcaaaagc	tttatcctaa	tatcctcgag	agagaagaag	aaaccacagg	tcaggagact	19920
gtgactccaa	ctgttcaagg	gacgacggct	tcacccgatt	taacagatat	tttaggaaga	19980
atagaggtct	ccagtaggga	ggataatcag	aatcaagagt	cttgtgtaaa	agtcttaaga	20040
agtcatgagg	tagaaatgag	ctgggaagtc	aaacaagagt	atggccctaa	gaaaaaagaa	20100
tttcaggatc	aaatgggttc	tttagagagg	ttttttacag	agcatattga	agagttagaa	20160
gtattacaga	aggactactc	taaaacacttg	tcttatttta	aaaaagtaaa	caataagaaa	20220
gaggttcaat	atgcgaagtt	taggttgaag	gttttagagt	cagatttaga	agggattcta	20280
gctcagactg	agagtgtctg	gagttctgta	actcaagaag	aacttccgat	tcttgcaact	20340
cggggagcct	tagagaaagc	tgttttcaaa	gggagtctat	gttgcgcgct	agcaagcaaa	20400
gcaaaaccct	attttgaaga	ggatcccaga	ttccaagatt	ctgatacgca	attgcgagct	20460
ctgactctaa	ggttacagga	ggctaaggca	agcctggaag	aagagataaa	gagattttca	20520
aatcttgaga	acgatattgc	agaggaaaga	cgccttctta	aagagagcaa	gcagacgttc	20580
gaaagagcag	gtttaggggt	tctccgagaa	attgcagtcg	agtctactta	tgatttgcgt	20640
tccttaacaa	atacatggga	agggacccca	gagagtgaga	aggtctattt	tagcatgtat	20700
cttaattatt	acaacgaaga	gaaacgtagg	gnnaaaacaa	gattggttga	aatgcacag	20760
aggtatagag	attttataat	ggccttgga	gctatgcagt	ttaatgaaga	agcccttttg	20820
caagaggaac	tctctattca	agctcccagt	gaataacaag	aatccgaggc	aagagctcgg	20880
catgtcgtc	gctataggct	acgagttgcc	caatctcggt	tggctgattt	agaagctgga	20940
gtcatccaga	aacgtaaaac	aatcaaagat	ttgttcaaga	aacgacagtc	tcaaccttct	21000
tctaagaaat	agaaaatttc	gtccatgctt	ccagggtttt	gaaatgagaa	aaagaccttg	21060
gaataaaaata	attgatatga	gtagcttagt	tgctttaact	tatgtttttg	agcatgatga	21120
catcacagat	tcataatgca	agtattctta	tctcctcaac	tacccccccc	ccccccgacg	21180
ctctctaggg	gtttcttgtt	ctaaactctg	tagtttatcg	atcactcttt	tagtttctgg	21240
tgtgcttttg	ttgaccttgg	ggattccggg	actcactgca	gggatctctt	ttggagccgg	21300
tttgggattt	tctgctttag	gaggagtgtc	cgtgatttctg	ggacttctat	tccttctagt	21360
aagacgagag	gttccgacag	tacgttcaga	ggaaattccc	agaggggttt	ctgtgacccc	21420
ttctgaagag	cctgctctag	agaaggctca	aaaagaaccg	gagacaaaga	aaatttttaga	21480
tcgggtgccg	aaggaattgg	atcagttaga	tacgtatatt	caggaagtgt	ttgcatgttt	21540
agagaggctg	aaggatcccta	agtacgaaga	tcgaggtctt	ttaacagagg	cgaaggagaa	21600
acttcgagtt	tttgacgttg	ttgagaaaga	tatgatgtca	gagtttttag	acatacaacg	21660
agtgttgaat	gaggaagcat	attatgtaga	acattgtcaa	gatcccctag	agaatatagc	21720
ctacgagatt	tctcttccc	aagagcttctg	tgactactac	tgtgcagggg	tgtgtgggta	21780
tttgcccttct	ggggatgctc	gagcggatcg	attaaagaga	tcagttaagg	aggtaaatgga	21840
tcgctttatg	agggtgacct	ggaaatcttg	ggaggcatca	gtcatgttgg	atcatagcta	21900
tggggtagcg	cgagagttat	tcaagaaggc	agtaggagta	ctagaggaga	gtgtctataa	21960
aattctgttt	aagagctata	gagatgcgtt	ttatgaatgt	gagaaggcaa	agatccagag	22020
ggatgggctg	ttcaaatggt	tataggatac	gagtgtcat	gcggaacaaa	ggtttaggga	22080
tatcaatggt	tgttgggagg	acttaaagca	aacgatcttt	tgggtaggag	aacatgattg	22140
tacggacata	gagaccgtac	gtaaaagctg	tatgtggctg	gatcgttatg	cagataaatt	22200
tattttgagg	gaaaaagagg	aaaagatgga	gcgtcatgag	ctctttcatg	cgactatggt	22260
ccgaaaaagca	tctgggcacg	cgtatgctaa	agctaaagca	gcctttgaaa	aggagagatc	22320

táatgagaat	cagaggaaag	tcaaggatgt	tgaaaaatgg	ttatctaaag	gtttagcgga	22380
gtttcgtaat	caagagtctc	gcagagctcg	ggagaggctg	agagagctgc	aaactttgta	22440
tcctgaggtt	tctgtagaag	agagagtgtt	agagagacaa	aggactaaaa	aagttaatct	22500
ggagaacttg	tatgcagata	tagaaaagaa	gtatcaccac	tgtgttcgag	agcaagagca	22560
ttactggaaa	gaggtagaga	acaaggaagc	agagtatagg	gagaacggag	aaaagggttct	22620
ctctgccgag	gaggtgtcag	agtgtcttca	gaggttgga	gattgtttag	agacgtggtc	22680
taagaaatta	acaaaagcgg	aagagagtgt	ctttgagatg	aagtttgatg	cgacagaaaa	22740
actagggaa	aaagtacttt	ctgatgtaac	gaaccgtctt	gagattttat	gtgaagatgc	22800
tgaggagatg	atttttcgaa	tcgaagagat	agagatgact	ctgcgtatgg	tagagcttcc	22860
actacttttt	atgaaaaata	cttttgagaa	agcctctcta	caatacaaca	gctgcaaaga	22920
gatgttagcc	aaagtagagc	cccaatgtaa	ggaaagccca	acctatagaa	gtagccaaga	22980
gcgcttagaa	aggttgaatc	aggatttaca	aacagcatat	acaaattgcc	aggagagact	23040
ccagggtttt	tcagatttgg	aatcaaaagt	acgtacatgt	agagatcatc	ttagagagca	23100
gatgaaacat	ttcgaagttc	aaggactgaa	ttttataaac	gaagagcttt	tatgggtcgg	23160
ggcagagctc	tttcacaaag	ccagattgga	cttagtagca	acagttccgt	atatggagtt	23220
ctatttgcag	taccataata	ttaaaagaga	aaaagttcga	tcccaatgga	tggcgaagac	23280
cgagaggtat	agagagattc	ggcaggcatt	tcaaggggtg	atgaaggaag	atttgttagc	23340
agaagatacg	atcttgaaag	aagaagatta	ttggctgctt	cgcgatgatt	ggttgctgcg	23400
tgatgagagg	aagaatagac	aaagacgttt	aatctgtaat	aagatagcag	cagcgcaaca	23460
gcgagtcaaa	ggcttctaac	ctgaagagat	ttaaaagatc	ctgaaagaga	aaacacctct	23520
tgtggctaga	gtgcgttctt	tatttactcg	cgaggaccat	acctagcata	aaactccagg	23580
agctgtgttt	ctttaaaaat	ctttgaataa	aatactatat	attagtagct	tagtgggttt	23640
aatttatgtg	tttgatcgcg	atggcaccac	agattcataa	tgcaagtact	tctatctccg	23700
cagctacccc	ccccccaac	actctgtagg	gtcgatttct	tctccatcta	aacttcgcgt	23760
tttagcgatt	acttttttag	tttttggtat	gctcttactg	atttcaggag	ctctctttct	23820
gacgttaggg	attccaggat	tgagtgcagc	aatttctttt	ggattaggca	tcggtctctc	23880
cgcattagga	ggagtgtgta	tgatttcggg	actactatgt	cttttagtaa	aacgagagat	23940
tccgacagta	cgaccagaag	aaattcctga	aggggtttcg	ctggctcctt	ctgaggagcc	24000
agctctacag	gcagctcaga	agacttttagc	tcagctgcct	aaggaattgg	atcagttaga	24060
tcagatatatt	caggaagtgt	tcgcatgttt	aagaaagtct	aaagattcta	agtatgaaag	24120
tcgaagtttt	ttaaacgatg	ctaagaagga	gcttcggcat	tttgactttg	tggttgagga	24180
tacctctcgc	gagattttcg	agttgcggca	gattgtggct	caagagggat	gggatttaaa	24240
ctttttgate	aatggggggac	gaagcctcat	gatgactgca	gaatctgaat	cgcttgattt	24300
gtttcatgta	tcgaagcggc	tagggatatt	accttctggg	gatgttcgag	gggaggggtt	24360
aaagaaatct	gcgaaggaga	tagtcgctcg	tttgatgagc	ttgcattgcg	agattcacaa	24420
ggtggcggta	gcgtttgata	ggaattccta	tgcatgggca	gaaaaggcgt	ttgcgaaagc	24480
ggtgggagct	ttagaagaga	gtgtgtatcg	gagctcgacg	cagagttata	gagataaaat	24540
tttggagagt	gagagggcga	agatcccact	gaatgggcat	ataacctggt	taagagatga	24600
tgcgaagagt	gggtgtgctg	aaaagaagct	tcgggatgcc	gaggaacggt	ggaagaaatt	24660
taggaaagca	gtcttttggg	tagaagaaga	cgggggcttt	gacatcaata	atctccttgg	24720
agactggggg	acagtgcctg	atccttatag	acaagagaga	atggacgaga	taacgttcca	24780
tgagttgtat	gaaaaaacta	cgtttttgaa	aagactgcac	agaaagtgtg	cgtagcgaa	24840
aacaaccttt	gaaaagaaga	gatctaaaaa	gaatttgcag	gcagtcgagg	aggcgaatgc	24900
acgtaggttg	aaatatgtaa	gggattggta	tgatcaggag	tttcagaaag	caggggagag	24960
attagagaaa	ctgcatgctt	tgtatcctga	ggtttcagtc	tctataagag	agaacaaaat	25020
acaagagacg	cgctctaatt	tagagaaaag	cttagaggct	atcgaagaga	actatcggtg	25080
ctgtgtccga	gagcaagagg	actactggaa	agaagaagag	aaaaggggaag	cggagttagg	25140
ggagagggga	aacaagattc	tttctcctga	ggagctggaa	agttcttttg	agcaattcga	25200
ccatggtttg	aaaaattttt	ctgagaaatt	aatggaattg	gaagggcata	tcttaaaact	25260
tcagaaagaa	gccacagcag	aggtggagaa	taaaatactt	tcagatgcag	agagccgcct	25320
tgagattgta	tttgaagatg	tcaaggagat	gcctgtcgca	attgaggaga	tagagaagac	25380
gctgcgtatg	gcggagctgc	ccctacttcc	tacgaagaag	gcgtttgaga	aggcctgctc	25440
acaatataat	agctgcgcag	agatgttgga	gaaggtgaag	ccttactgca	aggagagcct	25500
cgcctatgtg	actagcaaag	agcgtttagt	gagctgggat	gaagatttac	gacgagccta	25560
cacagagtgt	cagaagagat	tccaggggga	ttcgggtttg	gagtcggaag	taagagcctg	25620
tcgagagcaa	ctgcgagagc	ggatccaaga	gtttgaaact	caagggctgg	acttggtgga	25680
aaaagagttg	ctttgtgtga	gtagtagatt	aagaaataca	gagtgcgatt	gtgtatctgg	25740
tgtaagaaa	gaagcacctc	ctggtaagaa	gttttatgcc	cagtattatg	atgagattta	25800
tcgagttaga	gttcaatccc	gatggatgac	gatgtctgag	agattgagag	agggagttca	25860
agcatgcaac	aagatgttga	aggcaggcct	aagcgaagaa	gataagggtt	ttaaagaaga	25920
agagtatttg	ttgtatcgag	aggagagaaa	gaataaagag	aaacgtttgg	ttggtactaa	25980
gatagtagga	acgcagcagc	gagttgcagc	atttgatacc	atagaagttc	ctgagattcc	26040
tgaggcccca	gaggagaaac	cgagtgtgct	ggataaagcg	cgttctttat	ttactcgcga	26100
ggaccattcc	tagaactatt	ctaggagtct	atgtgcacta	ttttttaaga	ggtttattat	26160



tccgtgggta	tgtctgagag	acttttgatta	aatgggatat	tattatatcc	tagttgctct	26220
aatcaatatt	cctcttatga	tttttggtatt	cgatcatgac	tgcagcacca	gctattctac	26280
acgtatcccc	gacgccccct	gaagaaacaa	aattcggtat	tcctaaagat	agtaaactctc	26340
gcgctcttgg	gattacttta	ttagtcgtag	gcacccctct	ggtagtttgt	ggtgcgattg	26400
tactcagtg	agtgatttct	ggattgagtg	cactcattgt	ttgtggattg	ggtattagta	26460
cgatttctct	aggagtgtgc	ctatttgttt	taggattgat	attattactt	agaaagcggg	26520
aacttacctt	agaacagatc	gaggctaagc	aaattgcgga	gacctttgct	gatgaactga	26580
aagaactaga	aatgtacatt	cagtcgacag	agaaaaagctt	agagaagata	gaagggtccc	26640
gttatagtga	ccaagggttt	ctgaatcgtg	ccacccaaaa	aatccttagat	ttagaactctt	26700
cattgagctc	tattacttct	gagtttcgtg	atccttaggca	actccttgat	gaagaaaaaa	26760
tagagttact	ttctggagaa	aggcttttag	aatttattgc	agcgaattta	tttaaacaaag	26820
gaagagatgt	ctattttaa	ttagggaatt	tagcagacat	tcgtgcgtac	atggggccca	26880
acaattataa	agttgcgatg	gtcatagaaa	aagctaaagc	agttgtgcat	gagtttatag	26940
ttctgactac	aatggctagg	gaattagagt	tttttttcta	aaaaataaat	atggtttatt	27000
aaaggggatg	taccaggaga	atctaagatt	gttggaaggg	cttctttata	atagtgttca	27060
aaagagctat	gcggatcggc	tgttttccta	tgaaaagaca	aagatggtgc	acgatactcc	27120
gctgattcct	tgggaagagg	ataaggaaaa	atgtgctgaa	gctgagaaag	ctttcttaga	27180
gcaacagaag	attctcctag	attatggaaa	atctatcttt	tggctgaatg	agaacgatga	27240
gatcaattta	aacgatcctt	ggagttgggg	tcttaatacg	gtgaggacta	ggaaagtatt	27300
ccaagagggt	gacgacagtg	aacgttggaa	tcataaggta	ctcattcaaa	aactcgagga	27360
cgattatgag	aaacttctag	aggaaaagttc	aaaagagtct	actgaagcaa	ataagaagct	27420
tttatctgac	ttagtagatc	gtcctgaaga	tgctaagaca	aaatttttcc	tgaagaacaa	27480
ggaggagggt	gagactcgcg	ttaaggatct	tagagctcga	tatggaggca	cagtagtacc	27540
taagcaggat	acggaagcta	agaagaaagt	cgaattggag	gctagcttag	aaaccttttt	27600
agattccatc	gaatcagagc	tagtacagtg	tttagaagat	caagatatat	attggaaaga	27660
acaggatgtc	aaagatctag	cacgtacgca	agagctcgag	gaacaagata	ttgaagcgaa	27720
gagggaaagaa	gctgccgaag	acctaagaaa	gtccttaatga	gcgtttaaag	aagtcaaaaa	27780
ctatgttaga	taggggctaaa	tggcatattg	aaaatgctga	ggacagtatt	acctgggtgga	27840
ctagtcagat	agaaatgaag	gatatgaaag	caagactgaa	gatcttaaaa	gaagatataa	27900
caagtgttct	acctgaaata	gatgagattg	aaacgtgttt	aagcttagag	gagcttctct	27960
tgctttacgac	cagggaactc	ttaactaagt	cctacctaaa	gtttaagatt	tgttcggaaa	28020
cactattaaa	aatgacttct	gtgtttgaga	acaatatcta	tgttcaggag	tacgaggttc	28080
agctgcaaaa	tctaggggtt	aagttacaag	gtatatctca	gagattcgga	aagaaacaag	28140
acgattttgc	gaatctagag	gaacaggttg	ctttgcaaaa	gaaacgactc	agagagctca	28200
ctcagaattt	tgaataacaa	ggattcaatt	tcatagaaaga	agattttaag	gcagccgcta	28260
aagatcttta	tataagaagt	acagctgaac	aaaagatgaa	ctttgatgtg	ccttgcatgg	28320
agctcttccg	taggtatcat	gaggaggtca	acaagccgct	tcttgagttg	atgtacaatt	28380
gtgcagacag	ttatagagat	gctaagaaaa	agctttgctc	tctacgtctt	gatgaaaaag	28440
agttattaca	aaaagaaatc	aagaaagagg	aattttatca	aaagaaacaa	caaaggcatg	28500
cagatagatc	acgtcatact	aggtatcaaa	agctacgaat	tgtctgaagag	cttgctcttg	28560
agctgaagaa	gaaaatctaa	tcactaaagc	ctagttaagg	gttcttttga	attgggccct	28620
gtgtttccat	ttctctaggg	atcctcttag	ctgaggatct	tctttgtacc	tcttttgatt	28680
cgaaaagagg	tgctattgtg	agttgccaat	agcaacgatc	caccttcggt	tttgaaaaga	28740
tacatcagtt	gctaagggaa	cttttcagaa	aatatcataa	aaaactccca	agattttggc	28800
ttggaaagcg	agcctttctt	gctacttttg	ttacaacaaa	agtgttctat	tttaacgtgc	28860
gtatccattt	tgactaagag	atagacttgc	tttctttatc	taactctctg	tattgaaaag	28920
aaagccccct	gagggaaaaa	aaggttggtt	tgaagattcc	actccgcttt	ttattgatat	28980
cattagtagc	tacgctttct	atgtcgaatt	tattaggagc	tgtactacc	gaagagttat	29040
cggctagcaa	tagcttcgat	ggaactacat	caacaacaag	cttttctagt	aaaacatcat	29100
cggctacaga	tggcaccaat	tatgttttta	aagattctgt	agttatagaa	aatgtaccca	29160
aaacagggga	aactcagtct	actagttggt	ttaaaaatga	cgctgcagct	ggagatctaa	29220
atttcttagg	agggggattt	tctttcacat	ttagcaatat	cgatgcaacc	acggcttctg	29280
gagctgctat	tggaaagtga	gcagctaata	agacagtcac	gttatcagga	ttttcggcac	29340
tttcttttct	taaattccca	gcaagtagac	tgactaatgg	attgggagct	atcaatgtta	29400
aagggaaatt	aagcctattg	gataatgata	aggtattgat	tcaggacaat	ttctcaacag	29460
gagatggcgg	acaattaatt	gtgcaggctc	cttgaagatc	gcaaacataa	agtccttttc	29520
ttttatttga	aatagttctt	caacacgtgg	cggagcgatt	cataccaaaa	acctcacact	29580
atcttctggt	ggggaaactc	tatttcaggg	gaatacagcg	cctacggctg	ctggtaaagg	29640
aggtgctatc	gcgattgcag	actctggcac	cctatccatt	tctggagaca	gtggcgacat	29700
tatctttgaa	ggcaatacga	taggagctac	aggaaccgtc	tctcatagtg	ctattgattt	29760
aggaactagc	gctaagataa	ctgcgttacg	tgctgcgcaa	ggacatacga	tatactttta	29820
tgatccgatt	actgtaacag	gatcgacatc	tgttgtgtat	gctctcaata	ttaatagccc	29880
tgatactgga	gataacaaag	agtatacggg	aaccatagtc	ttttctggag	agaagctcac	29940
ggaggcagaa	gctaaagatg	agaagaaccg	cactttctaaa	ttacttcaaa	atgttgcttt	30000



taaaaatggg	actgtagttt	tgaaaagggtg	atgtcgtttt	aagtgcgaac	ggtttctctc	30060
aggatgcaaa	ctctaagttg	attatggatt	tagggacgtc	gttggttgca	aacaccgaaa	30120
gtatcgagtt	aacgaatttg	gaaatttaata	tagactctct	caggaacggg	aaaaagataa	30180
aactcagtg	tgccacagct	cagaaagata	ttcgtataga	tcgtcctgtt	gtactggcaa	30240
ttagcgatga	gagtttttat	caaaaagggt	ttttgaatga	ggaccattcc	tatgatggga	30300
ttcttgagtt	agatgctggg	aaagacatcg	tgatttctgc	agattctcgc	agtatagatg	30360
ctgtacaatc	tccgtatggc	tatcagggaa	agtggacgat	caattgggtc	actgatgata	30420
agaaagctac	ggtttcttgg	gcgaagcaga	gttttaatcc	cactgctgag	caggaggctc	30480
cgtaggttcc	taatcttctt	tggggttctt	ttatagatgt	tcgttccttc	cagaatttta	30540
tagagctagg	tactgaaggt	gctccttacg	aaaagagatt	ttgggttgca	ggcattttcca	30600
atgttttgca	taggagcgg	cgtgaaaatc	aaaggaaatt	cgcgcagtg	agtggagggtg	30660
ctgtagtagg	tgctagcacg	aggatgccgg	gtggtgatac	cttgtctctg	ggttttgctc	30720
agctctttgc	gcgtgacaaa	gactacttta	tgaataccaa	tttcgcaaag	acctacgcag	30780
gatcttttac	tttgtagcac	gatgcttccc	tatactctgt	ggtagtatc	cttttaggag	30840
agggaggact	ccgcgagatc	ctgttgccct	atgtttccaa	gactctgccg	tgtcttttct	30900
atgggcagct	tagctacggc	catacggatc	atcgcatgaa	gaccgagtc	ctaccccccc	30960
cccccccgac	gctctcgacg	gatcatactt	cttggggagg	atatgtctgg	gctggagagc	31020
tgggaactcg	agttgctgtt	gaaaatacca	gcggcagagg	atttttccaa	gagtacactc	31080
catttgtaaa	agtccaagct	gtttacgctc	gccaaagatg	ctttgtagaa	ctaggagcta	31140
tcagtcgtga	tttttagtgat	tcgcatcttt	ataaccttgc	gattcctctt	ggaatcaagt	31200
tagagaaacg	gtttgcagag	caatattatc	atgttgtagc	gatgtattct	ccagatgttt	31260
gtcgtagtaa	ccccaaatgt	acgactaccc	tactttccaa	ccaagggagt	tgggaagacca	31320
aagggttcgaa	cttagcaaga	caggctggta	ttgttcaggc	ctcagggttt	cgatctttgg	31380
gagctgcagc	agagcttttc	gggaactttg	gctttgaatg	gcggggatct	tctcgtagct	31440
ataatgtaga	tgcggttagc	aaaatcaaat	tttagcgatt	tctctttcga	tgctattttt	31500
ccatggctat	ttttaaaatg	atagccatgg	ttatagatac	gtagtcctta	tttcaaagaa	31560
gacactggtg	cattagatac	gctctctgat	ccctcaaaat	cacattttgg	tatctgattg	31620
ctaagattgc	aggataccac	gcactcttaag	agaaaggcgc	tcttacctag	tagagggtga	31680
gtgaatttct	tgacttggtt	ctcctattgg	tgtatctctt	aaaatattaa	attcaaaatc	31740
aaagtatata	ttttacaatg	aagtcttctt	tccccaagtt	tgtattttct	acatttgcta	31800
ttttcccttt	gtctatgatt	gctaccgaga	cagttttgga	ttcaagtgcg	agtttcgatg	31860
ggaataaaaa	tggtaatttt	tcagttcgtg	agagtcagga	agatgctgga	actacctacc	31920
tatttaaggg	aaatgtcact	ctagaaaata	ttcctggaac	aggcacagca	atcacaaaaa	31980
gctgttttaa	caacactaag	ggcgatttga	ctttcacagg	taacgggaac	tctctattgt	32040
tccaaacggg	ggatgcaggg	actgtagcag	gggctgctgt	taacagcagc	gtggtagata	32100
aatctaccac	gtttataggg	ttttcttcgc	tatcttttat	tgctgtctct	ggaagtctga	32160
taactaccgg	caaaggagcc	gttagctgct	ctacgggtag	cttgagtttg	acaaaaatgt	32220
cagtttgctc	ttcagcaaaa	acttttcaac	ggataatggc	gggtgctatca	ccgcaaaaac	32280
tctttcatta	acagggacta	caatgtcagc	tctgttttct	gaaaatacct	cctcaaagaa	32340
aggcggagcc	attcagactt	ccgatgccct	taccattact	ggaaaccaag	gggaagtctc	32400
tttttctgac	aatacttctt	cggattctgg	agctgcaatt	tttacagaag	cctcggtgac	32460
tattttcta	aatgctaaag	tttcctttat	tgacaataag	gtcacaggag	cgagctcctc	32520
aacaacgggg	gatatgtcag	gaggtgctat	ctgtgcttat	aaaactagta	cagatactaa	32580
ggtcaccctc	actggaaatc	agatgttact	cttcagcaac	aatacatcga	caacagcggg	32640
aggagctatc	tatgtgaaaa	agctcgaaact	ggcttcggga	ggacttacct	tattcagtag	32700
aaatagtgtc	aatggaggta	cagctcctaa	agggtggagcc	atagctatcg	aagatagtgg	32760
ggaattgagt	ttatccgccc	atagtgggtga	cattgtcttt	ttagggaata	cagtcacttc	32820
tactactcct	gggacgaata	gaagtagtat	cgacttagga	acgagtgcaa	agatgacagc	32880
tttgcgttct	gctgctggta	gagccatcta	cttctatgat	cccataacta	caggatcatc	32940
cacaacagtt	acagatgtct	taaaagttaa	tgagactccg	gcagattctg	cactacaata	33000
tacaggggaa	atcatcttca	caggagaaaa	gttatcagag	acagaggccg	cagattctaa	33060
aaatcttact	tcgaagctac	tacagcctgt	aactctttca	ggaggtactc	tatctttaaa	33120
acatggagtg	actctgcaga	ctcaggcatt	cactcaacag	gcagattctc	gtctcgaaat	33180
ggacgttaga	actactctag	aacctgctga	tactagcacc	ataaacaatt	tggtcattaa	33240
catcagttct	atagacgggtg	caaagaaggc	aaaaatagaa	accaaagcta	cgtcaaaaaa	33300
tctgacttta	tctggaacca	tcactttatt	ggacccgacg	ggcacgtttt	atgaaaatca	33360
tagtttaaga	aatcctcagt	cctacgacat	cttagagctc	aaagcttctg	gaactgtaac	33420
aagcaccgca	gtgactccag	atcctataat	gggtgagaaa	ttccattacg	gctatcaggg	33480
aacttggggc	ccaattgttt	gggggacagg	ggcttctacg	actgcaacct	tcaactggac	33540
taaaactggc	tatattccta	atcccagagc	tatcggctct	ttagtcctta	atagcttatg	33600
gaatgcattt	atagatatta	gctctctcca	ttatcttatg	gagactgcaa	acgaagggtt	33660
gcagggagac	cgtgcttttt	ggtgtgctgg	attatctaac	ttcttccata	aggatagtac	33720
aaaaaacacga	cgcggttttc	gccatttgag	tggcggttat	gtcataggag	gaaacctaca	33780
tacttgttca	gataagattc	ttagtgtctg	attttgtcag	ctctttggaa	gagatagaga	33840

ctacttttcta	gctaagaatc	aaaggtacag	tctacggagg	aactctctat	taccagcaca	33900
acgaaaccta	tatctctctt	ccttgcaaac	tacggccttg	ttcgttgtct	tatgttccta	33960
cagagattcc	tggtctcttt	tcaggaaacc	ttagctacac	ccatacggat	aacgatctga	34020
aaaccaagta	tacaacatat	cctactgtta	aaggaagctg	ggggaatgat	agtttcgctt	34080
tagaattcgg	tggaagagct	ccgatttgct	tagatgaaag	tgctctattt	gagcagtaca	34140
tgcccttcat	gaaattgcag	tttgtctatg	cacatcagga	agggttttaa	gaacagggaa	34200
cagaagctcg	tgaatttgga	agtagccgtc	ttgtgaatct	tgccctacct	atcgggatcc	34260
gatttgataa	ggaatcagac	tgccaagatg	caacgtacaa	tctaactctt	ggttatactg	34320
tggtatctgt	tcgtagtaac	ccgactgta	cgacaacact	gcgaattagc	ggtgattcct	34380
ggaaaacttt	cggtagcaat	ttggcaagac	aagctttagt	ccttcgtgca	gggaaccatt	34440
tttgctttta	ctcaaatttt	gaagccttta	gccaattttc	ttttgaattg	cgtgggtcat	34500
ctcgcaatta	caatgtagac	ttaggagcaa	aataccaatt	ctaattgcgtt	agcttttgga	34560
aagagctcca	tacatcgaag	ggaaaagagc	ttttaagatt	tcttgaaggc	tcttttcgat	34620
ttcgatttcc	attttagtgt	tttgctaaaa	cactttctaa	ttttttctt	ttgttttcta	34680
cattgaaaaa	aagagagtta	cggcagctgt	aaagttttta	atattgctcc	ccttggtcca	34740
tttatgttagc	gttcagactt	tgcaataaaa	cgagggtgtc	atatgagatc	gtctttttcc	34800
ttgttattaa	tatcttcata	tctagccttt	cctctcttaa	tgagtgtttc	tgcatagtct	34860
gccgatctca	cattagggag	tcgtgacagt	tataatggtg	atacaagcac	cacagaattt	34920
actcctaaag	cggcaacttc	tgatgctagt	ggcacgacct	atattctcga	tggggatgtc	34980
tcgataagcc	aagcagggaa	acaaacgagc	ttaaccacaa	gttggtttttc	taacaccgca	35040
ggaaatctta	ccttcttagg	gaacggattt	tctcttcatt	ttgacaatat	tatttcgtct	35100
actgttgacg	gtgttggtgt	tagcaataca	gcagctctcg	ggattacgaa	attctcagga	35160
ttttcaactc	ttcggatgct	tgcaactcct	aggaccacag	gtaaaggagc	cattaaaaatt	35220
accgatggtc	tggtgtttga	gagtataggg	aatcttgatc	ttaatgaaaa	tgctcttagt	35280
gaaaatgggg	gagccatcaa	tacgaagact	ttgtctttga	ctgggagtac	gcggtttgta	35340
gcgttccttg	gcaatagctc	gtcgcaacaa	gggggagcga	tctatgcttc	tggtgactct	35400
gtgatttctg	agaatgcagg	aatcttgagc	ttcggaaaca	acagtgcgac	aacatcagga	35460
ggcgcgatct	ctgctgaagg	gaaccttggt	atctccaata	acaaaaatat	ccttttcgat	35520
ggctgcaaa	caactacaaa	tgccggagct	attgattgta	acaaagcagg	ggcgaaccga	35580
gaccctatct	tgactctttc	aggaaatgag	agcctgcatt	ttctgaataa	cacagcagga	35640
aatagtggag	gtgcgattta	tacaaaaaaa	ttggtgttat	cctcaggacg	aggaggagt	35700
ttattttcta	atacaaaagc	tgcaaatgct	actcctaaag	gaggggcaat	tgcatattcta	35760
gattctggag	agattagcat	ttctgcagat	ctcggcaata	tcattttcga	gggcaatact	35820
acgagcacta	caggaagctc	tgcgagtgtg	accagaaatg	ctatagatct	tgcatcgaat	35880
gcaaaatttt	taaatctccg	agcgactcgg	ggaaataaag	ttattttcta	tgatcctatc	35940
acgagctcag	gagctactga	taagctctct	ttgaataaag	ctgacgcagg	atctggaaat	36000
acctatgaag	gctacatcgt	tttctctgga	gagaaactct	cagaagtaag	aaacctgaca	36060
atctgaagtc	tacattttaca	caggctgtag	agcttgctgc	aggtgcctta	gtattgaaag	36120
atggagtgc	tgtagttgca	aataactataa	cgcaggtcga	gggatcgaaa	gtcgttatgg	36180
atggagggac	tacttttgag	gcaagcgctg	agggggtcac	tctcaatggc	ctagccatta	36240
atatagattc	ccttagatggg	acaaataaag	ctatcattaa	ggcgacggca	gcaagtaagg	36300
atgttgccct	atcagggcct	atcatgcttg	tagatgctca	ggggaactat	tatgagcatc	36360
ataatctcag	tcaacagcag	gtctttgcct	taatagagct	ttctgcacaa	ggaacgatga	36420
ctactacaga	tatccccgat	accccaattc	taaatactac	gaatcactat	ggtatcaagg	36480
gaactggaat	aattgtttg	gtcgacgatg	caactgcaaa	aacaaaaaat	gctaccttaa	36540
cttgacttaa	aacaggatac	aagccgaatc	cagaacgtca	gggacctttg	gttcttaata	36600
gcctgtgggg	ttcttttgct	gatgtccgct	ccattcagag	cctcatggac	cggagcacia	36660
gttcgtttatc	ttcgtcaaca	aattttgtgg	tatcaggaat	cgcggaactt	ttgcatgaag	36720
atcagaaaag	aaaccaacgt	agttatcgtc	attctagcgc	gggttatgca	ttaggaggag	36780
gattcttcac	ggcttctgaa	aattttcttta	attttgcttt	ttgtcagctt	tttggttacg	36840
acaaggacca	tcttgtggct	aagaaccata	cccatgtata	tgcaaggcca	atgagttacc	36900
gacacctcgg	agagtctaag	accctcgcct	agattttgtc	aggaaattct	gactccctac	36960
cttttgctct	caatgctcgg	tttgcttatg	gccataccga	caataacatg	accacaaagt	37020
acactggcta	ttctcctggt	aagggaagct	ggggaaatga	tgccctcggg	atagaattgt	37080
gaggagctat	cccgtaggtt	gcttcaggac	gtcggcttgg	gggtgatacc	cacacgccat	37140
ttctaaacct	agagatgata	tatgcacatc	agaatgactt	taaggaaaaac	ggcacagaag	37200
gccgttcttt	ccaaagtga	gacctcttca	atctagcggg	tcctgtaggg	ataaaaattg	37260
agaaattctc	cgataagtct	acgtatgata	tctccatagc	ttacgttccc	gatgtgattc	37320
gtaatgatcc	aggctgcacg	acaactctta	tggtttctgg	ggattcttgg	tcgacatgtg	37380
gtacaagctt	gtctagacaa	gctcttcttg	tacgtgctgg	aaatcatcat	gcctttgctt	37440
caaactttga	agttttcagt	cagtttgaag	tcgagttgag	agggtcttct	cgtagctatg	37500
ctatcgatct	gggaggaaga	ttcggatttt	aatcctaagt	ttccaacga	gatagcatca	37560
gggtaagcca	gggtctctat	taagagattt	catagagccc	tctctttgtc	ttgctttttg	37620
tattttattt	ttatatttct	tgaatccggt	gttccaatgt	tcgaaaggta	tcctagatga	37680

gatttgctgtt	gtcttgtcct	atgctttttaa	tagctgcatg	tgcctcattt	tttggctttc	37740
aggaagaaat	gcaaggcaga	aatatacaat	ctcttgatgc	aaatgcttct	agtctagggg	37800
aacttttttc	tatttctacg	aagggagtgt	cttgcttaga	actccatagg	gagatcgcac	37860
gctaaatatg	agaatataat	atgaagactt	cagtttctat	gttggtggcc	ctgctttgct	37920
cgggggctag	ctctattgta	ctccatgccg	caaccactcc	actaaatcct	gaagatgggt	37980
ttattgggga	gggcaataca	aatacttttt	ctccgaaatc	tacaacggat	gctgcaggaa	38040
ctacctactc	tctcacagga	gaggttctgt	atatagatcc	ggggaaaagg	ggttcaatta	38100
caggaacttg	ctttgtagaa	actgctggcg	atcttacatt	tttaggtaat	ggaaataccc	38160
taaagtccct	gtcggtagat	gcaggtgcta	atatcgcggt	tgctcatgta	caaggaagta	38220
agaatttaag	cttcacagat	ttcctttctc	tggtgatcac	agaatctcca	aaatccgctg	38280
ttactacagg	aaaaggtagc	ctagtacgtt	taggtgacgt	ccaactgcaa	gatataaaca	38340
ctctagttct	tacaagcaat	gcctctgtcg	aagatgggtg	cgtgattaaa	ggaaactcct	38400
gcttgattca	gggaatcaaa	aatagtgcga	tttttgga	aaatacatct	tcgaaaaaag	38460
gaggggcat	ctccacgact	caaggactta	ccatagagaa	taacttaggg	acgctaaagt	38520
tcaatgaaaa	caaagcagtg	acctcaggag	cgcccttaga	tttaggagcc	gcgtctacat	38580
tcactgcgaa	ccatgagttg	atattttcac	aaaataagac	ttctgggaat	gctgcaaattg	38640
gcggagccat	aaattgctca	ggggacctta	catttactga	taacacttct	ttgttacttc	38700
aagaaaatag	cacaatgcag	gatggtggag	ctttgtgtag	cacaggaacc	ataagcatta	38760
ccggtagtg	ttctatcaat	gtgataggaa	atacttcagg	acaaaaagga	ggagcgattt	38820
ctgcagcttc	tctcaagatt	ttgggagggc	agggagggcg	tctcttttct	aataacgtag	38880
tgactcatgc	cacccctcta	ggaggtgcca	tttttatcaa	cacaggagga	tccttgacgc	38940
tcttactcca	aggaggggat	atcgatttcg	aggggaatca	ggtcactaca	acagctccaa	39000
atgtaccac	taagagaaat	gtaattcacc	tcgagagcac	cgcaagtgg	acgggacttg	39060
ctgcaagtca	aggtaacgct	atctatttct	atgatcccat	taccaccaac	gatacgggag	39120
caagcgataa	cttacgtatc	aatgaggtca	gtgcaaatca	aaagctctcg	ggatctatag	39180
tattttctgg	agagagattg	tcgacagcag	aagctatagc	tgaaaatctt	acttcgagga	39240
tcaaccagcc	gttcacttta	gtagagggga	gcttagtact	taaacagggg	gtgaccttga	39300
tcacacaggg	attctcgcag	gagccagaat	ccacgcttct	tttggatctg	gggacctcat	39360
tataagcttc	tacagaagat	attgtcatca	caaatttatc	tataaatgcc	gataccattt	39420
acggaaaaga	tcctatcaat	attgtagctt	cagcagcgaa	taagaacatt	accctaacag	39480
gaaccttagc	acttgtaaat	gcagatggag	ctttctatga	gaaccatacc	ttgcaagact	39540
ctcaagacta	tagctttgta	aagttatctc	caggagcggg	agggactata	attactcaag	39600
atgcttctca	gaagcctctt	gaagtagctc	cttctagacc	acattatggc	tatcaaggac	39660
attggaatgt	gcaagtcac	ccaggaacgg	gaactcaacc	gagccaggca	aatttagaat	39720
gggtgcgga	aggatacctt	ccgaatcccg	aacggcaagg	atcttttagt	cccaatagcc	39780
tgtgggggtc	ttttgttgat	cagcgtgcta	tccaagaaat	catggtaaat	agtagccaaa	39840
tcttatgtca	ggaacgggga	gtctggggag	ctggaattgc	taatttccta	catagagata	39900
aaattaatga	gcaccgctat	cgccatagcg	gtgtcgggta	tcttgtggga	gttggcactc	39960
atgcttttcc	tgatgctacg	ataaatgcgg	ctttttgcca	gctcttcagt	agagataaag	40020
actacgtagt	atccaaaaat	catggaacta	gctactcagg	ggctgtattt	cttgaggata	40080
ccctagagtt	tagaagtcca	cagggattct	atactgatag	ctcctcagaa	gcttgctgta	40140
accaagtcgt	cactatagat	atgcagttgt	cttacagcca	tagaaataat	gatatgaaaa	40200
ccaaatacac	gacatatcca	gaagctcagg	gatcttgggc	aaatgatgtt	tttggctctg	40260
agtttggagc	gactacatac	tactacccta	accagtactt	tttatttgat	tactactctc	40320
cgtttctcag	gctgcagtcg	acctatgctc	accaggaaga	cttcaaagag	acaggaggtg	40380
aggttcgtca	ctttactagc	ggagatcttt	tcaatttagc	agttcctatt	ggcgtgaaat	40440
ttgagagatt	ttcagactgt	aaaaggggat	cttatgaact	tacctttgct	tatgttcctg	40500
atgtgattcg	caaagatccc	aagagcacgg	caacattggc	tagtggagct	acgtggagca	40560
cccacggaaa	caatctctcc	agacaaggat	tacaactgcg	tttaggggaa	cactgtctca	40620
taaatcctgg	aattgaggtg	ttcagtcacg	gagctattga	attgcgggga	tcctctcgta	40680
attataacat	caatctcggg	ggtaaatacc	gattttaata	gggaactgag	agttccttat	40740
tgtagagagt	atttacaagg	attttgagac	gaaagagatt	tcttgttgta	ggtatctctc	40800
cacaggggtc	agttcaattt	ctatagttca	tggggtttct	ttttttataa	agaagaaacc	40860
ccatgtctga	cgagacctca	cctggatcta	ttgcattctc	tatggtaagg	gatccatgac	40920
ttgacacagg	aggttcattc	tcattgtctaa	gtcagagggt	agaagggagg	ttttttaagg	40980
tttgtcgagc	tttaagaaga	agaaaaatcg	actatctgct	tctcggcggt	catacacccc	41040
atagagctgc	caatgttcga	agatcttcgt	ccctagaatc	atctgggtatt	ctaggtagtt	41100
cggagtgtcc	tgcgatgcca	gccatagcgt	aaggataaag	ggtaattcca	acagggatga	41160
ggctgtacaa	ataatttccc	taaaatgaga	ttcctatgat	cagagagagg	ggagtctaaa	41220
agctgggtcaa	tgggacggct	gacatctaaa	atgaagttct	ccctgtcaca	cttaatcagg	41280
ctgtatttgc	ttctatgcag	ggattctaga	gtcatagcca	cattgtcatt	tcgatccac	41340
tcccaactga	tgttcatgtg	atcccaacag	tgctttttcc	aaatccattc	agcatctaag	41400
gagactgtat	ttttctttcc	aaaaggtaga	gatagctcgc	atgcagtttt	gggaaacgtg	41460
ggtttgcttt	ctgtattgct	caagatgtgg	gtagtccaca	gcttcgcatg	gattctcggg	41520

aatcgagggt	tagtcttact	cagtaccgag	gtatctatac	ccgctttcag	aagggtttaag	41580
gagtgaagg	catcttgaat	ggaaaagata	taatgatctt	cattcttagc	tagaggacga	41640
gtctctgtaa	tgaaggtaac	gaacggctct	ataatatggc	gtctttgaat	gtaggactta	41700
tgtaatagaa	agcgataatc	aagttgtagc	ttcgcggaaa	gctgactatg	gcgcgaggag	41760
atctcaggaa	catcgctata	gtaaatacaga	gaactcccta	gggtggagga	gagcggttct	41820
ataggttagag	gcacagtttt	atggagctta	gggcgcgcag	caagacgtag	tgaagagaaa	41880
ttctcgccaa	cgatatgata	gctaaaagca	aagtttaaat	acccacattc	tacgatgttt	41940
tcaaggtaca	ctcccgtatt	ataaatagaa	atcgggtact	gccttaatgt	taaataaggg	42000
agctcttggt	tggcattttg	gaaagagttt	accttaacag	aagaggtgag	atacccttca	42060
aaatagttgt	cattccaagt	gcaatcgaca	cgtgtggggc	ctgtattttt	caacatgaag	42120
ttgttgggga	aaatgtcagc	aacagtttcc	caactatcgc	tgagatggta	ttctccagaa	42180
aaatttacat	gcttatgctg	gaagcagaaa	tctccgtgta	ggcgatagcg	atcatgagct	42240
tctgccatat	cgatagcaag	gcggtgggca	taatagcttt	tcatattgaa	gacattctca	42300
ggaacctgct	tctgagaaca	atggaggttg	aatcccatgc	cgacgccatg	cttgaaaaag	42360
ctatccaaga	aaaatgtcga	ggagaaatgc	ttcttagaaa	tcggcgagta	gctcatcccc	42420
aaataggatc	ccagaaatcc	tcctgttcc	cctcgaaagt	ttatcggagg	cttagggatc	42480
tccataggca	tgatagaaaa	tgagggttaag	aaaagtatcg	gaatgcgaca	cacccttaat	42540
gttgtcttcc	ctatagaaag	aagactatct	gaagaatatt	ccaggtaatc	tccggagagg	42600
cacaggtctt	ttttgggacc	ctcggaggtg	gagatatatc	ccttccgaat	gactatgggt	42660
tctgggggta	gagtgatcat	agacccccct	agaaaccaag	gatacatcgc	gaatcttcca	42720
ttagtaagaa	gacaagagtc	tgtatcttcg	taatactcta	ggtaatcaca	aactaggggt	42780
tttgccctat	agttcaccat	aacattgcc	tgtgcgacaa	gcttcagggt	ttgaccaca	42840
gtatttttcta	catacacttt	attggcttgt	atccgcagg	tggtatggat	attcaatacc	42900
ccatcttcga	tggtcacaat	cccagaaaca	ctcttaaagt	gactaagata	ggagtttttc	42960
tttttcacag	cctcttgatg	agtcaaagca	tcagctgagg	aacccataag	aacaaaggaa	43020
gctagaaata	agaagcaacg	tttcataaga	cgtagggttg	ggttactcca	caatttttat	43080
gagtaagcct	gcaaggactg	ggaaattttt	tgcattctct	tccgtcatca	gttgtatcaa	43140
taaacggata	tcttcggaag	acttcgagg	ggctagtgtc	tctagaatat	ccaacatgag	43200
cttcgtacgg	ctttctgggg	tgacctgata	acgtagatag	ggcatgctgg	gatgggggtc	43260
ttggtttttc	gtgtccacaa	ataacaaggt	ttcctgaatt	agcttttttg	cataatcatg	43320
gagagaacgt	tttttttcag	gatcttttgt	gagattataa	atagcaagat	ctgcataggc	43380
gcggatgata	ggttctccag	gaagcttcgc	agcttgaaa	agtagatcta	aggcttctcg	43440
atgtgagggt	tgacttaaaa	aagaaatcgc	agtagtgga	agctgagttt	tctgactcgc	43500
caaaagctta	taaatacagg	ggaggtaagc	ttcttttaggt	aggcggaaga	gaaacgtaag	43560
gatctgctct	tcaagacctc	gggttgtgga	gagcaacctt	tccctctcct	ggggatcttg	43620
agggactatg	atgttcaccc	gcttccaatt	ttgtaaagta	cgcccccttag	agaaactcaa	43680
ggctagagtc	tcattataat	gtgggtggac	aagcctttcg	gtaatgtatt	ccagtagttt	43740
aggggtgtca	caccctaact	ctaagagagc	ttaaagctaca	ttcaacttgc	ttcgtgttcc	43800
ttagttttta	ggaatatcgg	cagggcaatc	ggaatcccta	tctcagagg	tagatggcgt	43860
aaggcataca	gggctcgagg	ccgctcctca	agtgcttgct	tttttatcac	gggaagagcg	43920
tcctcttctt	tcctcaaaag	aattaaagct	tgagctgctg	ctaaagtgc	atccacatca	43980
ggcttctgca	attgcttttt	tattattgtg	tagctctgac	catccttaag	cttccctaaa	44040
gcataaagaa	tagcttcttg	atcttgagga	gacgcactcg	ttagcaaatt	cctaagtgtc	44100
ggaagaaagc	gtttttgttg	gtattctccg	atctgcaaag	ctgtggcact	ccgaatcgcg	44160
cttttcttgg	cagctaagag	atcccgaata	taagcatcag	attcttcagt	ctccaagcgt	44220
aggaatatgt	ccgcagatag	gcattggatt	tcttcgggaa	gcttatgaat	gaaagaatgt	44280
agatgatcaa	tgactttagt	gttcttcaaa	ttagcaagtc	tataggcgcg	ttctaaagcg	44340
atgacaggat	aggagatgc	taaagcttta	aacagttaag	cgtcagaagt	tttcccaaga	44400
tgctctgaga	ctgccgataa	aaccagtagc	tgctgcagg	ggtctgcagt	ttccatagct	44460
tgaggagagca	cgtccaaggc	ttctgaagat	cccgccaggc	ctgctccaat	gatgggtgct	44520
tttctagttt	gcggatctga	ggagtggatg	ctttgcttga	gatagtcttc	tccgattttt	44580
cttaaaacga	agaagtcattg	atcaccgtag	gcattctagag	cttccagata	tggttgctaag	44640
gcctgctgtg	tagattgctg	acttatataa	aggatcttat	gacctacaga	ctcagggaat	44700
ttagcaacaa	gagaaatggg	aagactacac	aataaaagtc	caaagagagt	tagatggaat	44760
agtcctcatg	atcgatgttc	aactcctcta	gcaagtattt	caatgttttg	ataggagagc	44820
cttgaacatt	ataaacacat	ccatggacct	ttttcaaaat	caagccacca	tggaacacgt	44880
cataagcgcc	acaattattt	aatgttcccta	cagtgtcgat	ataagactct	atgcggtgat	44940
caggaatcat	agtaagtga	atctgagaag	tctctgacct	tgtgaggagt	tttcccttat	45000
gtaatacggc	aatactcgtg	accacatcat	gcgtctgatt	cctcaagggtc	tttaacatct	45060
ggatagcggn	tgctttgnct	tgaggttttg	tgaaaatac	gccatcgtaa	gaaacaatat	45120
tatcgccagt	gaggataata	cagtcacaag	gcgaatgtag	ctcagaaact	gcataggcct	45180
tttgtgcggc	aagttcttgt	gtataggcta	taggatcccc	agagttagctg	actttactct	45240
catcaaaatt	tgaaggatg	acagtaaagg	gaacacgaaa	tttttctaaa	ataaaattttc	45300
ttcttggcga	agaagaccct	aaaactaaag	gaagggacat	agaataaaaag	ctcctcgtgt	45360

tagatacatt	acaacaattg	cttatgacct	gcagtatagt	ctaccatagt	tccatcgaag	45420
aatgtaatct	tatctttatc	aaagatcaat	aacttcgtag	cacaatcttg	aatcagtcct	45480
ctgtcgtgag	agacaaaaat	cgctgtgccc	ttatagtcac	tgatagccca	agaaagagca	45540
gacacagact	ctaagtctaa	gtggttggtc	gcttcatcaa	ggataaggac	attatgggtt	45600
tctagcatca	tccccgccat	gagaagacga	gctgtttctc	ctccagataa	tgcttggatt	45660
tgcttgaaa	catcatcgcc	tccaaaaagc	attttcccta	acacactgcg	gatttcttga	45720
tcgttaattc	cgggttttgcg	attgcggtanc	actcaaatag	cgtttcttga	ccacaatcag	45780
ctagaacatc	gctgtgggtt	tgaggaaaaat	atgaacagat	agcttgatgg	cctaacttga	45840
tacttctcga	agaaggagcc	tcaacacctg	caagtaactt	cattaatgta	gttttaccce	45900
atccattggt	cccagataata	ccaagcttgt	ctccttgata	aatctctaaa	gaaaaaggat	45960
ggattacctg	atgatcccca	taatcctttg	taatcgcttc	taaagacaaa	acgactttcc	46020
ctgaggattt	gtcagatagg	gggaaacgaa	tgtaaggacg	ttggatattg	gattttttta	46080
attccttggtg	ctgaagcttc	ttaatctctc	ttaatcgaga	ctgcacttga	ctcgcctcgtg	46140
atccccgacc	aaatttagca	acaaattcct	taagctgaga	aattttcttt	tccttagatt	46200
tgatgtcggc	cttttcttgc	tcgcgagacg	cggttttcat	ctctaccata	tcgtcatagt	46260
ttccagggta	gataatgatc	gtgtcgtaat	caatgtcagc	aatgtgagtc	gtaattgtat	46320
tttaagaaatg	acggtcgtga	ctgactacaa	tgacagtgcc	ttcataatct	tttaaaaagt	46380
ttcccagcca	attaatggaa	tagaggtcca	agtgggttgt	tggtcatca	agaagaagtg	46440
cttcgggggtg	accaaagaga	gcctggcaaa	gaagaactcg	aaattgtagg	tctatgggaa	46500
tcatagccat	tttcttatca	aacatctcat	tggggatgcc	aatgcctgtg	aggagtctct	46560
cggcttctga	atctgctcgg	tacccatttt	cctcgccgat	gatctcttca	atttcaccaa	46620
gtccatttcc	aatggcgctca	gtaaaattctt	gtagatagag	attatcacgg	cgttgtaaaag	46680
cttcccaaag	acgagtattt	cccataatga	cacaatctaa	gactgttgtg	tcgtgaaagc	46740
tatcgatatt	ttgacgcagg	atccccactt	ttttaggtaa	ggaaatcgaa	cctcttgtag	46800
gttctatcat	tcccataatg	atttttaaaa	gggtggactt	tcctgcgcgg	ttaggaccag	46860
taagaccgta	gcagttcccg	gggttgaaaa	cgacggaaac	atcatcgaat	aaaattcgag	46920
tgccataaaga	tttgccaatt	ttatctaata	ctatgtcat	agcagacagc	ataacaaagt	46980
gctgcttaga	gtacaagagc	tttgccctgt	tctcttaggc	atggggatgg	gcttcttgggt	47040
gggtctgttt	ttttaacttt	acagagactt	gcgtatagac	cgttgttgtc	tctaaagaac	47100
tatgaccaag	aagtgcctgg	attgttttta	aatccatacc	actctctagc	caatgggtgg	47160
ctatagtgtg	acggattgta	tggggggtga	tgtgccctga	aagtccagaa	cgctgaagat	47220
attcttgaaa	acttctgtca	atagatcgtg	ttgaaatgcg	cctcccaaag	cgattgagaa	47280
agatggcttg	aggatccttt	tccaaacgct	ttctatccgg	atgggttcagg	tagatttgga	47340
tccattgtat	ggcattcgat	gtcacgggaa	taatcctttc	ttttttccct	ttcccacgga	47400
tgcgaaatcag	atgagtactc	aaatcaaagt	cctgtttatt	aacagcgaca	atctcactaa	47460
tcctcaaacc	cgaactatag	aacagctcca	tgagacagcg	atcacgaagt	ccgtgatatt	47520
tagaaatgtc	aggagtgcgc	atcagcactt	caacttgcgc	ataggtcac	ggggaaggca	47580
gctccttagg	aagacgaggt	ccgtggatag	tttccgcaga	ttttccaaaa	gaatcttttg	47640
aataacacag	taatgggcaa	agcttttaat	ggaagagagg	caacgcttaa	ttgttctctt	47700
agctttgcca	ttttctatca	gttttcgcgat	gtacatgcgt	acatgctctt	tggtgaataa	47760
ggaaaaagga	agttcagaga	ctttgcgctt	ctctgtggct	aactgtaaag	gagaagaagg	47820
agcgagggtta	ccacgttccn	ctaaaaaaat	tttcaatcca	ttaagatcta	gacaataatt	47880
tcttaatgta	tgcgagagag	cactttttac	cattttcaaa	tagtctaaga	acgaatatag	47940
agaggcaatc	ataacttctc	tttaccttac	aataaagatc	gtaaaaagac	ttcctcttag	48000
cttttaggaag	gctagcttct	tactattctt	tccgagctat	ttatttagaa	gaggattttt	48060
cggaaagggg	tagctgcgat	attcttgtgc	tacggacaca	ttaggaaata	ctgccgaggc	48120
ttctttataa	aaatcatcca	gatttaagta	acgtgccgag	aagtgtgtga	gaataagctt	48180
ttgtgttgcg	gcacgtttcg	caagagtcgc	cgcttgtttt	gcagtcatat	gaaaatggct	48240
ctcagcaaga	tggtgggtgct	gttcgaggta	ggtgctttca	cacaacatca	tgcagctatt	48300
ttttgcgaga	tctatagcag	cttggaagg	caaagtatcc	gcaataatcg	caatgctatc	48360
ccccttgcg	acgtagctaa	catcactaag	atataccgta	gaaccgccta	tcgaaatttc	48420
ttgggtcacga	ataagatctt	ggataatcag	accacgaatg	cctcgagatt	ccagctcttt	48480
aggaagaaat	tttatagtgt	ctggttccgt	gattctccat	cctaaagtgt	ctacttgggtg	48540
ttggagtcgc	tgtgcttcaa	tacgaaaaact	accaaaatct	tcgacaattc	cttcttcaga	48600
gattggatgc	tccaccacct	ggatggtttc	gtgataaatt	gttccataac	gtaagcggtc	48660
aaagtatttt	ttccctgaag	caggatagta	gcaatggata	gggtgcgaaa	ccttgtccaa	48720
gttaagacgc	atcaacatgg	agcctagacc	caaacaatga	tctccatgga	aatgactcac	48780
aaaaattcta	ttgactgttg	taggagcaat	atttgcaaaag	atgaattgcc	tttgagtgcc	48840
ttcaccagga	tcaaaaagta	gaccctcacc	attccagcga	aataggtagg	ctccttgatt	48900
gcgtgttcgt	gtaggctgtt	ggctcgagca	ccctaaaata	attaactctc	tagaactcat	48960
aaggattttac	tttaagaaaa	agtcacagaa	taaactaagt	gaaattatat	acgccactac	49020
aacttttgaa	tgacaacttt	tttatcattt	aaaattttgt	tttcttataa	ctcctgcatt	49080
gttgtcttca	tatttatagg	aatcgcaaga	tagttatggg	tctgtcgggt	gcttgcagaa	49140
ccaagggagt	atcgctttcc	gttgtacggg	tggaggagat	gaagaatcag	aactctcatt	49200

gcctgatgat	tgatgttcta	gatcttctat	agggaggggg	acggtttttt	tcaatagcac	49260
aggtttttctt	tttttcgacg	gaaccatggg	ttttggtgct	gatctcttat	gtatgctact	49320
tgctgttcta	tgtaaggagt	gttttagttt	cttcttcttc	tttgagcttt	ctgttggtga	49380
agtttttagac	ccttttgtag	ttgccgtatg	aggtgctttt	cccttggtctt	tgcatgaggag	49440
ttcaggggaa	gattcatcag	aggattcaat	ttcagaagaa	cgcttgcttt	gcctaggtga	49500
atggtgttca	tcagagatgt	gaggactctc	ttcaccactt	ttgaatttgt	ttgttacata	49560
ggtgacgcct	ttttcttaatt	gcgttcttat	gaagtttttt	ggttcgtggt	catgatgtgg	49620
ggagagttgc	gggctccctt	ttctagacgc	agattttgta	ggttgtgatt	cagaggcatc	49680
ttttggggca	atttcttttg	ttttttttgt	ggatatccaa	ttaatgagac	acggattgaa	49740
aatactcaag	agcactagaa	gtgccaatga	gcttaaacaa	agaggaattc	ctacagaggg	49800
aataaacatg	cacagcatag	ctccaacaag	aactacgacg	acgagaacgc	atataatgat	49860
taggtaagca	atgttgcaaa	tgtctcgaat	cgatttgga	ggagccgctt	gtttgatcgg	49920
ttgaggttta	tggaaatacg	aagtcactga	gttgcgcagg	ctaggaataa	gatgggacat	49980
agcaaagtta	gattaaagct	ctctgaaaag	aacagcttat	gtattcaagg	tctgtttgta	50040
aataacaga	cttttttata	cgcattaaat	ctaccttaat	gcgtataaaa	atagtatttc	50100
tcaagagaac	aagggttcaa	cttggtcttc	tatttttagct	tgggaaaagc	aactttgaga	50160
acatcatcat	agtgtgaaac	aaaatgtatt	ttcaaccctg	ttttcagata	tgcatggaagc	50220
tcttcatagt	ctctacggtt	gtcttcaggg	aaaatcaaga	tgttcaatcg	tgatcttcga	50280
gctgcaatca	gtttctctcg	aatgcctcct	acacctaaaa	cacgacctgt	aagagtaatt	50340
tctccagtca	ttcccaaatt	attcactacc	ggagtttcca	acagcaacga	aaggagagag	50400
gtcaccatag	taattcctgc	agaaggaccg	tcttttagggg	tggctccctc	aggaatgtgg	50460
atatgtactt	gagactttgg	aaagaacgta	tagcctgggg	cataccgatg	gagagcactg	50520
tgaaggtagg	tccaaagcaat	ctgagaagac	tcttctatta	cttcccagc	ctgacctgta	50580
aggtgcattg	ctgttttgag	tgaggacacc	tgtacacttt	ctatatataa	cgttgctcca	50640
cctaaagagg	tccaggcaag	tcctgtggcc	actcctacag	gagtggattc	atagaagcga	50700
tcgctagaaa	atatacggtt	ccctaagtag	gtctgcagat	ttttcgaaga	gattttaaaa	50760
gtaatcttct	tagatttggt	tttttcttga	ttttgaacaa	tctttaaagc	aactttcctc	50820
aatacttttt	tgatattccc	attaagagta	cgtaacccag	cttctcgtgc	atagttattg	50880
atcatgtact	ttaaagcttc	aggttgga	ttcacttcgc	ttgctgttaa	accgatttct	50940
ttgcgagctt	tgggaactag	atacttttta	gcaatttgaa	gtttctcttc	taaaatgtag	51000
ccagaagctc	ggagaatctc	catgcgatct	aaaagaggat	ccggaatggt	atctagaaca	51060
ttggcagtta	aaatgaatag	tacattggat	agatcaacac	gtacgtctaa	ataatgatca	51120
agaaaatctt	tgttttgctc	aggatctaaa	acctctaata	aggcagaggc	aggatctcca	51180
tgataactcg	caccaatttt	atctacctca	tcaatcataa	tcacaggatt	catagcttgg	51240
ctttgcttga	gcgcctggac	catttttctc	ggcattgccc	caatataggt	gcggcgatgc	51300
cccttgatct	cggcctcatc	acgcatgcct	cctactgaga	aacggaagaa	ctttctatgc	51360
aggactttag	caatgtgcgc	cctatgcttg	ttttcccaac	tcctggaggg	cctacaagac	51420
agatgatact	tccttttaat	cctttggaaa	gcttacctac	actgattaac	tcgagaatgc	51480
ggtgtttaat	ctcatcaagg	ccatagtgat	cctgtttcag	gacgatttct	gctttcttta	51540
agtcatggta	tcttttactt	tgtatgcccc	aaggaatgat	tgtcagccaa	tccaggtaat	51600
tgccgcatac	ggtatattcc	gccgaagaag	tttctaaagt	ctgaagtttt	tcaatttcat	51660
cttgaatcac	ttccatagca	taatcaggaa	catggcgttt	tcttagcctt	tccgaaaact	51720
tctctatata	aatagcgcg	tcttctttct	ctaaccctag	ttctttttta	ntcgttttta	51780
actgctcttt	taagaagaat	tccttttggt	ttttngtaat	cgtagcttca	attttttgat	51840
taatgctgct	ctggaggcgg	cctaagtcta	attccttttt	tagtaagatc	agtgccctat	51900
caatgcgatc	atgcatgttg	gtggctctta	agacctcttg	gagctcttcc	cgagctctcg	51960
ttgttaaagc	aacagagaaa	tccgcaagct	tgcttggttc	agtaaaatcc	gaatgaccac	52020
gaaaaatttg	tagttcttct	ttaaagagag	gatttagttt	taaaagggtc	ttgatgacag	52080
agacaatact	aatagagtac	gcttttagct	cttctgtaag	ctctttattg	tccgcatgat	52140
aggaaactcg	agctttaaga	tatttgtctt	taatgggttc	tataatccga	atacgctctt	52200
caatgcttaa	aagaacttga	gcactgccac	cctcgattgg	catgatacgg	aggattcttg	52260
cggcaactcc	agttttatgc	agctggttga	agctcacttt	taaaatatcg	gcgttctctt	52320
ttttggttaa	gacaagacca	atatattttt	gagacgactt	cgctaaaacc	tttaataact	52380
cataataagg	accgactca	ataagaatgg	gagccggcat	tccggggaaa	aaaggctcgt	52440
tatttaattg	caggataaat	aactcagaag	gcagcaaacg	ctccgtagac	tgatcttcgg	52500
attcctcttc	agattcatct	aaaagctttt	caacatcttc	tggatttgga	tctaagatgg	52560
gggagtcgct	attgggttga	gagtcacaaa	ttgtccttat	gctcggctat	atttgtctgt	52620
cgctccagta	aatacggctc	tttttctcta	gggtaaaaag	agggagcgat	tttaaaagat	52680
tgcatatttc	gctatactac	aaaatagatg	caattaggcg	catatataca	acttctaaaa	52740
aatatctaga	agggattaaa	gattaggaaa	gactcgtggt	taaggcaaat	cgtctttttt	52800
tattttttca	aaaaaaatag	tttgtatcta	ctgttttaaa	ttgctcagag	ataagggatt	52860
aagaaaaact	ccattgtttt	tgagtttttt	acttttatag	ggggtagatt	ttccaaagga	52920
aaaacgtcag	tagtccaaat	ccagcctttt	tgtccttcgt	ttgcattgaa	ggtaaatgca	52980
gggatcgga	gacaaaagaa	cacgcttgca	ttgttttttaa	tttaacagcc	atttctctct	53040

gttggttcttt	atgataatta	agagcccggt	cctcgctga	aatatttggga	acagatacca	53100
aggaatgaaa	atagaagtta	gggagaaggg	aattataaga	gaagccaata	tcttgctttg	53160
gtgaaggagc	ttgaccaaga	tctgtgat	tagtgaaaga	aaacccttct	tgtataagct	53220
cgttataggt	ttttccagaa	cgcactaaaa	tgtgtagcgc	atgaattttc	tttaagtgtg	53280
taggagatgg	taaaggaaga	ctgaggtttt	cttgggtcagg	tgtaatgtgt	tttttccaaa	53340
tcttccttct	taacatctng	gattagacca	cgatacttga	ngaataagat	aatncgtaaa	53400
acgatcttaa	taaagagagc	tagaatcaga	ggaagaatta	aaatatagga	gagaattttt	53460
attatttttt	cagatttcga	gattgggagg	gcatgatcaa	cagatagaaa	ggtagctcca	53520
gaaactcctg	tgatgataac	agaagtgtct	cctcccaaat	gtaaatagtg	ttcaacgata	53580
ttggaacatt	tttcaataat	gccagagctt	tttcctaagt	aaggaagaaa	agataaggac	53640
tgatccgaga	agactatagg	atgaaaaaac	tgaagaaaca	tacgttagaa	tttttatttt	53700
ttttatatta	taacgtacta	gccttcaaaa	agtaactatt	ctttatggct	tagtcttggt	53760
tctctcagaa	tttagataaa	cataaaattt	gatcttccagt	tccataacag	aacgactcca	53820
aataatctct	tgtaattgtg	cggccatagt	tggggggagt	cttggatctt	caatctcaaa	53880
tgaattcaga	tattgaaaac	gggacgtccc	atagagaata	tccgattggg	tagcttctcg	53940
ttgcctagt	tggtggcgta	agcttattaa	actactctta	atagaagtag	ttctcaattt	54000
gatttgaat	tttttcaaga	gttcctgacc	ccctttccta	agcaagggaag	aatcgagtag	54060
cattggggcgt	aaaagtatat	aggagtaaca	aaatcgcaac	ccatcgttcg	tcttatattt	54120
tagagcggcg	agaatcttaa	tgtatctgaa	taaattaaaa	caataaatgt	tttcatttct	54180
ttcattttta	tttgattaaa	aggggtttgt	tggtatagtt	tattttttta	tatcaaaaaa	54240
cgacgcatgt	acttctataa	gtatgttatc	atagatactt	ctggatacta	tccattctta	54300
gcttgtgtgg	ataatcaaca	agtgtctggg	cattggctct	tgccagtcgg	tccagatctt	54360
ggaattgttt	tagagtttct	ttttaaaagt	aaaaatctct	cttttccagg	agttgcgggtg	54420
gctctaggtc	caggaacttt	tctgcaacac	ggatagggat	ttctttcgtc	caaggattgg	54480
caatggcaaa	gaatgtgect	ttgctaggat	atagctcttt	ggaaggatac	ttattatcta	54540
aagatgaaaa	aaaagcttta	atgcttcctt	tggggaaacg	tggaggcgctc	ctgactttaa	54600
gctctgagat	tcttgaagag	ggcttgaatg	aaaaaaggag	aggggtgggg	ccgggagctt	54660
tgctctctta	tgaagaggcc	tctgattact	gcgttgctca	tggatattat	catgtgattt	54720
ctcctaatec	gcagctcttt	gcgagcagtt	tttctgataa	gatcacgcta	gaagaagttg	54780
ctccttcggt	agaacagatc	cgcaggcacg	tgatttctca	attcatgttt	gtagaatatg	54840
acaagcgaat	ctctcctgat	taccgtagct	attcatgtat	tttttgattt	gtattttcta	54900
aatatttttt	acattgttgc	ttccgaatcg	attcaactat	cccttgaagc	ctaataagaag	54960
tagtgggtaca	atcgaggctc	ttctaaaaga	catagtaaaa	agattattat	tgtgtttata	55020
gaaggccaga	gatttgttat	ttattgctga	ataataaggt	aatgcatgcc	cagtgttaaa	55080
gttcgagttg	gagagcctgt	agatcgtgct	ctgcgcacat	taaaaaagaa	aatagataaaa	55140
gaagggattt	taaaagctgc	taaatcccat	cgctttttatg	acaagccttc	tgtcaagaaa	55200
cgagctaaat	ctaaggctgc	ggctaagtat	cgtagtcggt	aattggcaat	gtcgtattcg	55260
ttggtagtgt	ttcagggtatg	gattattatt	caatttttagg	catttctaaa	actgcttcg	55320
cagaagaaat	taaaaaaagcc	tatcgcaaat	tagctgttaa	atatcatccg	gataaaaaatc	55380
ctggggatgc	tgcagcggaa	aaacgcttca	aagaagtttc	cgaagcttat	gaagttctca	55440
gtgatcctca	gaagcgcgac	tcttacgatc	gtttcggtaa	ggacggtcct	tttgctggag	55500
ccggtggctt	tggtggcgct	ggaggcatgg	ggaacatgga	agatgccttg	cgcactttca	55560
tgggagcctt	tggcggagag	ttcggagggtg	gaagcttctt	tgatggctct	tttggtgggc	55620
ttggtgaagc	ttttggaatg	cgctcagatc	ctgcagcgcc	tcgtcaagga	gccagtaaga	55680
aagttcatat	taatttgact	tttgaagaag	cagctcatgg	tggtgagaag	gaactgttag	55740
tttctggata	taaatcttgt	gaaacctgtt	ctgggtcaagg	agctgtaaac	cctcaaggga	55800
ttaaatcctg	cgaacgttgc	aaagggttcgg	gacaagtggg	acagagtcgt	ggatttttct	55860
ccatggcctc	tacatgtcca	gaatgcgggtg	gcgaaggccg	tattatcaca	gacccttggt	55920
cttcatgtcg	cggccaagga	agagttaaag	ataaacgtag	tgtccatgtg	catatccccg	55980
caggtgtgga	ttctggaatg	cgcttgaaga	tggaaaggcta	tggagatgca	ggccaaaatg	56040
gagctccctc	cggagatctc	tatgtcttta	ttgatgtaga	gtctcatccc	gtatttgagc	56100
gtcgtggaga	tgacttgatc	ctagagcttc	ccattggttt	tgtagatgct	gctctcggtg	56160
tgaagaaaaga	aattcctacg	ttattgaaga	cagaaggatc	gtgtcgtctt	acgggtcctg	56220
aaggaattca	aagtggaaac	attttaaaag	taagaaatca	gggctttcct	aatgttcatg	56280
ggaaagggtcg	tggagatctt	ttagttcgca	tttctgtaga	aactcctcaa	aatttatcag	56340
aagagcaaaa	agaactttta	cgtacttttg	cttctacaga	aaaagcagag	aactttccta	56400
agaagcgtag	cttttttagat	aaaatcaaag	gttttttttc	tgacttcaca	gtataagaag	56460
gagaaaagac	cgacttttagc	tgagagagat	ccatgggagt	agtacaaaat	caagttattt	56520
cttctataag	agatgtttta	aagctagtct	gggaattgctg	gttcgcagag	cataagatgc	56580
ttctcctctc	taggcagagc	ggctcgggctg	gcacatttca	gttgtcttgt	gcaggtcatg	56640
agcttgccgg	ggttcttgct	ggtaaaagtc	tcattctctg	ttaaagactgg	tccttccctt	56700
attatagaga	cgaagggttc	cctataggct	tgggttggtga	tctctctgag	atctttgctt	56760
cgtttctagc	tcgtacaact	ccaaatcatt	cctctgcgag	gatgatgcct	tatcactatt	56820
ctcataaaaa	attgctgatt	tgctgtcagt	ccagtgttgt	aggaacacag	tttttacaag	56880



ccgcaggtcg	tgcttgggct	gtcaagcact	cgtcagctga	tgaagttgtc	tatgtttctg	56940
gaggcgatgg	agctacatct	caggggtgaat	tccatgaaat	gttgaacttt	gtagcactac	57000
accaactgcc	tttaatcact	gtaatccaaa	ataatcattg	ggcaatttct	gttccttttg	57060
aagaccaatg	tggagccgac	cttgccagct	tgggtcgttg	ccatcaagga	ttagctgtct	57120
atgaggtaga	tggaggcaac	tatacttctc	ttacagaaac	tttttctcat	gccgtagatc	57180
aagcgcgtca	acattcgggtg	cctgcattga	ttttaatcga	tgtggttcgc	ttgagctctc	57240
atagcaattc	cgataatcag	gaaaaataac	cctccgcttt	agacctgaaa	ctatccatgg	57300
ataaggatcc	cttaatcctt	ctagagaaaag	aggctatcaa	tgtttttggt	ctgtctccct	57360
ttgaaatcga	ggagatcaag	gctgaagctc	aagaagaagt	tcgaaaatct	tgtgagattg	57420
ctgaagctct	tccttttccc	tctaagggat	ctacaagcca	tgaagtcttc	tctccttata	57480
ccgagactct	cattgattat	gagaattctg	aaagcgctca	gaatttgctg	aactctgaac	57540
ctaaagtgat	gcgtgatgct	atctccgaag	cccttgtaga	agagatgact	cgagattctg	57600
gagtcattgt	ctttgggtgag	gatgtcgtcg	gagataaagg	aggagtcttc	ggtgtcacca	57660
ggaatttgac	agaaaaattc	ggaccacaac	ggtgtttcaa	ttctccctta	gctgaagcaa	57720
ccattatagg	aaccgccata	ggcatggcct	tagacgggat	tcataagcct	gtcgttgaga	57780
ttcagttcgc	agattatatt	tggccgggga	tcaatcagct	attttctgag	gcctctagca	57840
tctactatcg	ttcagctggc	gaatgggaag	ttcctctggt	aatacgagcc	ccttcaggag	57900
gctatatcca	gggaggaccg	taccattcgc	aaagtataga	agggttccta	gcacactgtc	57960
ctggaattaa	agttgcctat	ccttctaattg	ctgctgatgc	taaagctttg	ctaaaggcag	58020
cgattcgaga	cccgaatcca	gtagtgTTTT	tggagcataa	ggccctctat	caaaggcgta	58080
tttttagtgc	ctgcccagtt	ttttctcatg	actatgttct	gcctttccgc	aaggccgcta	58140
ttgttcatcc	cgggaaagat	ctcacgatag	ttctctgggg	aatgcctctg	gtattgagtt	58200
tagaggttgc	tcagggaatta	gcctctcggg	ggatttccat	agaagttata	gatttgcgta	58260
ctatggtgcc	ttgtgacttc	gctacggttc	taaaatcctt	agagaaaacc	ggaaggttgt	58320
tgggtgattca	cgaggcttca	gagttttgtg	gctttggcag	tgagcttgct	gctactatgt	58380
cggaacaagg	atacgcttat	ttagatgctc	ctatccgtcg	tcttgggtggg	cttcatgtct	58440
ccgttcccta	ctctaagggtt	cttgaaaacg	aagtgcctcc	tcataaggag	tctattttac	58500
aagccgcgaa	aagtctcgca	gaattctagg	cgattctcca	gcttctttct	aggccgggat	58560
tttaattcaa	aaagagagcc	cgacacgctg	tttgtagagg	tacttgggag	atgctattta	58620
ctgaaacatt	agagagtgcg	tactcttctt	tggatgctaa	taaaatgcgc	acggattcta	58680
aaagagcaag	atggcaacaa	ctctcccatg	tagtaaatct	ctcttgatct	gcgctgaggt	58740
tatttaattcc	aaaaacttct	aactgtacac	tttcaagatt	gtgctcaata	cagatatcaa	58800
agcattgcaa	ataagccagt	actaaattag	taaatgcctc	tttcatacta	aaatctttca	58860
atgtaattgc	gcggcgcat	ttttccttaa	tgagagtttc	taatgtaggg	ggattgataa	58920
caatcagatg	agaggtgtac	agttgcgcgc	cctcttctac	atcccaaggg	ccagaaacgc	58980
atgaacctat	aggcaagtgt	ttttctggag	tgggaatgtt	gtttttgatc	ttttcccagc	59040
agctcctttg	taaacatggt	gtaacagcaa	acgctcttcc	taatgttgtg	gagaaatcca	59100
tgctagaatg	tgaagagata	acaacagccc	ctgatttttt	atttagaatt	ttatcatgag	59160
aaaaatgtcc	tttaaagcag	tgaaaacgga	atccagattt	ttcttttagat	ctcaggagaa	59220
tacttgctag	cttgttgga	tacttacgat	cttcgggtct	ggtttctgga	tctagagaga	59280
atagctgctt	gagtaacgaa	aaacaagcct	taggatcata	cgtagaggga	taatgtatat	59340
caggattgca	ggtcagtttt	gttctatcga	ctttaggtag	agttggaggt	aagggtattc	59400
ctggagctgg	cgcggttatt	tctggagtta	gtgtgggtgc	tcttagagtt	ggtgagggtg	59460
gaggagtggg	gagtggctca	ggaatcttag	gtttttctag	gtagtgata	aaatacaaca	59520
acgtaaaagc	aataaagact	gcggtaaagta	tgaatagagg	catggtgatc	tctagggaac	59580
accctaggca	aatggcaaaa	actcccccta	ggcaagatag	gaatgctaaa	atggcaaaag	59640
caattgcgtt	gactattgaa	gatggagtct	ctttcttgcg	ttgaggttta	aaaggtgcct	59700
gcgtggggat	tgtagggata	tggtcaggag	aagaatctgg	atccggaaca	ggcgggtgtct	59760
tctgggatac	aatagaggag	tcgggtaaag	atggagtcca	tatttccgcc	ataagaattc	59820
ccctacaagt	tgttggtcaat	aaaaaattta	cttaatttta	atataaaaaac	aatcagaaa	59880
aacaaagatt	attttgattt	gtcattagaa	tattgttggt	ttataggggt	tcgatgaagc	59940
gataagaagt	cgcagaagtt	gatgcatagg	gggagacgtt	tgtgcgtaaa	attccaatga	60000
agaataaaat	aagagaagct	aaggtaagca	tccaaggagg	gacaggagca	aaggaaagag	60060
tcttttaggat	attgggggtg	tgtagccaag	gatgtgagag	gaatccctgg	ataagcgctt	60120
cggtgatagg	ggagcaacat	ggcaagatga	ttgttgcaat	gaggaaaaca	atgatgggga	60180
gaatggtaaa	aggaacaatg	agattataga	ggagaccctc	aaggggtaag	ctcccaaagt	60240
actgcatgat	tggcagaaca	ataaagagtt	gtgccgatag	tgaaattgcc	aaagtcattg	60300
caagatagcg	gataggatag	aaccaaagt	gagagagaaa	ctgagtccaa	ggggtgtaga	60360
gaaaggaaaa	gatcttcggg	aaaaagagta	gaatccccaa	cgtcgctaag	aagcttaaaa	60420
caaaggtagg	agagaagcgc	gaaaaaaaaga	tagaacataa	aataaagcct	gcgcctagac	60480
gatttagccc	cgaacaggac	ccagaaaaaac	accatgaaaa	acaaagtagg	gttacggaga	60540
tccaagagcg	ccataccgag	agagacatag	ggaaaatata	ggatagagaa	gtcagaacaa	60600
tgaagcttaa	gatttttttg	attttttaag	gaagaagagc	acagagcatc	cagagagtag	60660
tagcacacag	agagaaatgc	cagccccgaga	tagcaaagag	atgagataac	cctttttgtc	60720



tgaagaggtc	tctgagattt	tgaggaaggg	gagttcctag	cagaagactc	gaagcaaagg	60780
ggcctacctc	agaagaggga	aacctatggt	tcaggaaatg	gcagctagat	tctcggcatt	60840
tctctttcat	gatatagaac	ctagacctag	gaattttctt	gtagcaagca	ttagacttaa	60900
aaacaatttg	agatgtatga	tgtagtgtcc	cttcgagctc	gtaaaccttt	ttaagctcta	60960
aacgggattc	tgatagaatt	tgacacnaga	gggtggtggg	tcttttnccc	acagggcgctc	61020
tgaatacaaa	gagcttctcc	gtagtagntc	cttgcccccc	tgcgtggtga	atcacaaaag	61080
tccctgatat	agggccgtca	tggaggaatg	gcgcaggagt	taacatcaaa	gaaatgatcc	61140
aagcacttgc	taaagggagc	cattgttttag	ggttgctgag	aaggaacatt	cctaagaaaa	61200
taagaatcag	agcactacat	tctgggtagc	cacgggatgt	gatgccagca	agccaataga	61260
gcccacataa	gaaaatagga	tgtcttttgt	ggaagcactc	acaagaggcg	cgtaatcgaa	61320
tgagccaaga	gcttatggga	tagcgaaaga	aaaaagatga	aaaaacctga	caacgattcc	61380
acatttgatg	ttcgcctctt	ctttcccttc	gatgtgttat	gtatagagca	gttgcgcaag	61440
gaaatgtctt	gggaagtggg	ttcagcgaa	atccccgcgtc	ttcctcgagg	gtggtacgag	61500
ctcatgggac	tatcaaaaaga	agatcgtata	gatttttgcg	tagacttctg	gtgttccgta	61560
ctagggatgt	agcataaaga	atctccaagt	atttgtcggt	ttttttcttt	actagagacc	61620
attgaagtgt	acatctatcg	cttggaaaaa	gaaccttatc	aactaaagat	gttttatgta	61680
ttcgtgatg	gtcgttgtgg	gtttcaagga	gagcctcttc	ttctagattt	tttagggcat	61740
cataggctgc	ctccttttag	ggaccgccat	tacgagaaat	ttttctctat	tcataatgga	61800
ttcgggaaat	gggaggatga	ggggattttc	cccatgagg	ctttagcaaa	ggtacaacaa	61860
aaattacgtc	agcagctcgt	tgtaatgaat	aagatgcagg	cggaagataa	ttgttattct	61920
ttaggtatct	ttccttttta	tggctatgaa	gagccttttg	cttatcagag	tttctttttt	61980
gatcctgaaa	tacgcagaga	ccttccttct	cgaatgtgt	tgtaaatga	agagagcttg	62040
gagcatcgaa	gcttagaaac	tattgagttg	ttgcatctgt	ctaagagcta	ttatccttct	62100
ttcctctcgt	gggtggagaa	ctatctacat	agtgaggagg	tgtataatga	atgagcctac	62160
tcgcacttat	ctagaaagtg	agaaagatac	acaagatcag	atcgaagagc	tccaggcaac	62220
ttgtatagtt	aagaatgcag	caggaatcca	tgtgcgtcct	gcagggtgta	ttgttcgact	62280
ctttgatgga	gagccttggt	atgtgcattt	cacctacgca	ggtaaaacga	taaatgcaaa	62340
gagtatcatg	agtattctta	tgttgggagc	tccacaagga	ggagagattc	ttgtgactat	62400
tagaagcaaa	gaagctcatc	gtatcttaca	aaagatacaa	gatgcgttta	gttcgggttt	62460
tggagaacta	taaatggata	cacagtcttc	tataggtaac	gaagaatggc	gtattgcagg	62520
aaacctctgt	gtttctggga	tggccttagg	taaagtattt	tttttgggaa	catccccctt	62580
gcatgttcgt	gagctgactc	tacctcaaga	agaagtcgaa	catgaaatac	atcgttatta	62640
taaagctttg	aatcgctcga	agtctgatat	cgtagcttta	gaacaggaag	ttacgggaca	62700
gcaaggcctt	caagagggtt	cctctatcct	acaagcacac	ttggagatta	tgaagagccc	62760
tctccttacg	gaggagggtg	tcaatactat	ccgtaaggat	cgtaaaaatg	cagaatatgt	62820
cttttcttca	gtcatgggta	aaatagaaga	gtcgttaaca	gcagtcgcgc	ggatgccttc	62880
tggttgatag	cgtgttcaag	atatccatga	tatctccaat	agagttatcg	gccatctgtg	62940
ttgccaacat	aagagttcct	taggagaatc	tgatcagaat	ttgatcatat	tctctgagga	63000
attgaccccc	tcagaagtcg	ccagtgcata	ctctgcctat	atccgagggt	ttgtctcatt	63060
agtgaggagca	gccacatcac	atacagctat	cgtctcgcga	gcaaagagca	ttccctatct	63120
tgctaataatc	tccgaggagc	tttggaaacat	cgcaaagcga	tataatggca	agttagtctt	63180
aatcgacggt	tatcgtggag	agctaattctt	taatcctaaa	ccagcgactc	tacaaagctg	63240
ctataaaaaa	gagctttccg	tggttgccc	tacctctcag	agattagtaa	gaaagtcctt	63300
acacccgatt	gtttcttcgc	atgcaggcag	tgataaggac	gtagaagatc	tattagagaa	63360
cttccctcaa	acctccatag	gcctctttcg	ttctgagttt	ttagctgtaa	ttttaggacg	63420
cctacctaca	ctaagagagc	aagtagatct	ttacgagaag	ctcgcacgtt	ttcctggaga	63480
ttcgccctca	gtactgcgcc	tctttgattt	tgggtgaagac	aaaccttgct	ctggaataaa	63540
aaataagaaa	gaacgttcta	tacgatgggt	gctagactat	agtgtgattc	ttgaggatca	63600
gctccaagca	attgctaaag	cctctttgca	aggctccata	aaggttctca	ttccaggagt	63660
gtctgacgtt	tctgagatta	tagaagtcaa	aaagaaatgg	gagaccatcc	agacgagggt	63720
ccctaaaagg	ccataagggt	tcttggggga	ctatgataga	atttccttct	gcagtttgga	63780
tgattgaaga	gatccttcc	gaatgtgatt	ttctctctat	agggacgaat	gaccttgctc	63840
aatatacttt	gggaatttcc	agggaaatcg	ctcttcttaa	acatctaaat	gtaactttgc	63900
ccccagcagt	gatccgcatg	attcaccatg	tacttcaagc	tgcaacaaa	atcagggtcc	63960
tggttagcatt	tgtggagagg	ccgcagggca	gctcagctcg	actcctttat	ttataggcct	64020
gggagttcaa	gagctctcag	tagctatgcc	tgtaatcaat	agacttcgca	atcatatcgc	64080
cctgctagag	ttgaactcct	gccttgaaat	tacagaagcc	cttttacaag	ctaaaacatg	64140
ctctgaagtt	gaagaacttt	taaatagaaa	caacaaaatc	acatcataaa	aattccatta	64200
tacttttttt	atataaagat	cttttatgat	gtataaaagt	tgtaaaaact	gtgttttcta	64260
gtcgtgccaa	tgtgcaatag	gaaaaaatac	caactccacg	gcggatctct	agttctagaa	64320
aggcattgtg	gaacgcataa	gagacatttc	ttgatccatc	tgctcttttg	caagtttgaa	64380
tgcagcacgg	aaagaagtctt	caatgacttc	tggatcttca	gggtctaagc	acgtaggttg	64440
tacttttact	gaaattaagt	cacactttcc	gttgatgaca	acagagacaa	gaccgttgcc	64500
agcttgccct	tcgtaacgct	tttctaatag	tgaggcctcc	atttctagga	attgctgttc	64560

cataatttta	gcttcttttt	ttttcttagc	gtatccgctg	cccatgctta	tctatcctta	64620
ggtgaaatat	tgatctttcc	tctcatgaaa	ttttctaaga	ggttcttgct	tattgtctta	64680
aaatttcctga	aaattctaca	acagcaaact	gtaataatgt	gtctacagct	gcagatttta	64740
ttgaagctga	gcttttaact	tctacagata	taattttacc	ttccgcagca	ggttgatttt	64800
ttttctctaa	aaaactctgt	tctttgtagg	tgggctgagg	ttgaggagct	gatacttgct	64860
gcgtcaaggt	gggctcctta	atattgcgaa	gcccttcaaa	ctgccgactc	ttaatagaag	64920
agatcaactc	tgataaaaca	ggcctttgat	aaatgcgaat	gatatgaatg	atgacggttt	64980
ctaaaaatgt	ctgttcgaag	atgggtatttt	gtagggtgctt	agcagattct	ccaaggaaat	65040
ctattattttc	tagaagctgc	tccgtcttat	actgagagct	gaacttgctt	gttgtagaat	65100
tcgtaagaag	aagattacga	taaaataatg	taaggctcatg	gagaaatgtg	acagggtgcta	65160
ccccagaatt	taagaagtc	gttacgatcc	ctaaggctgt	cgcatagtc	ctttgaagaa	65220
tcgcattgtc	taaagtccgg	agagaatcct	gggaagcaaa	gcctaaagct	tgggcaaccg	65280
tgctcgggaga	gagagattta	ggaaataaag	atattacgta	ggtcataaag	agattctgca	65340
tcacgcaagc	ttccttgctg	tgcacgggag	atcggcgcca	atgcttcttg	cgacgcctca	65400
ataatggctat	cttgagccat	aagcgatagc	ttctccagga	tcgttttttc	aggaatcctt	65460
tgaagatgca	ttttttgaca	acgacttaaa	atagttccgg	gaattttatg	gattttctgta	65520
gttgcaaga	aaaattttac	atgttggtga	ggctcttcta	aagtcttcaa	taaagcattg	65580
aaggcttcct	tagtgagcat	atgaacttca	tctatgat	aaattttaaa	ctttgctttt	65640
acaggagtga	ataatacagt	ttcattaatt	tgacggatat	cttcgatacc	acggtgggag	65700
gctccgtcaa	tttctaaaac	gtctaaagag	gatcctgaag	caatctcttt	acaagaaaaa	65760
cactgggtgc	agggtctgcc	atcctcgcta	agatgcacgc	agttcagagc	ttttgctaaa	65820
atgcgagcta	gtgtgggttt	ccctgtacca	cgaattccag	aaaatagata	ggcgtgggag	65880
gctcgggtga	agaccaaggc	attttttaaa	acagcgacaa	cagagctctg	acctggaatt	65940
tctcgaaaga	tttctgggag	gtactttcta	gaggatgctt	ggtagggttg	tagagtcatt	66000
gtataacca	gagaatgtgt	atagaaagct	cattttctca	tttaagagat	ttttcttga	66060
agaccttttc	tgattttcat	aagaaaattc	ttttcgcaga	gatggaatga	ttttccttct	66120
aaaatagaat	ttgtgaattc	ttcttttagaa	ggaaaatgaa	tctctttgaa	taaaatacta	66180
tatattagta	gcttagtggtg	tttaacttat	gtgtttgatc	gcgatggcac	cacagattca	66240
taatgcaagt	acctctatca	ccacagctac	ccccctcccc	aacactctgt	agggctcgatt	66300
tcttctcgat	ataaacttcg	cgtttttagcg	attacttttt	tagttcttgg	tgtgtcttta	66360
ctgatttctag	gagctctctt	tttgacgttg	gggataccag	gactcactgc	aggggtctct	66420
tttggttag	gtataggtct	ctctgcgtta	ggaggagtgc	ttgttgcttc	aggactacta	66480
tgccttctag	taaaacgaga	ggtttcgaaa	gtatgtcccg	aggagattcc	ggcagtaaa	66540
ccagaagaga	ctcctgaagg	ggttcctgtg	actccatttg	agaagccagc	tctagatgaa	66600
gcccagaagg	agcagaagac	tcagaaaatt	ttagatcagc	tgctcaaga	attggatcag	66660
ttagataggt	atattcagga	agtgttcgca	tgtttaggac	cgctgaaaga	tcttaagtac	66720
gaagatcaag	gttttttaca	agacgtcaag	gaggagtctt	aagtttttga	ctttgttcaa	66780
aaagatatga	ttgcggagtt	tgtagagcta	cagcagattc	tatgtcaaga	agggagggtg	66840
ctagagtctg	taatcaatca	gacacgat	ataggaaag	atctttttta	aagagaggat	66900
agtttatata	aattatggga	atggcttggtg	tatttacctt	ctgggggatgt	tcgaggggag	66960
cgggttaaaga	aatctgctcg	tgagggtgtg	gatcgcttta	tgagaacgac	ttgtaacata	67020
cgggaagatag	ccatgacttt	tgataggcat	gtttatagt	tgccgaagac	ggcctttgaa	67080
aaggcatttg	gagccttgga	gacgtgtgtg	tatgagagta	tgagagagag	ttatagagag	67140
gcattttgtg	agtatgagaa	ggcgaagctg	cttggggatg	aggagaagag	tgacatgccc	67200
gagcaaaggt	ttcaggatat	aaagaaccgt	tgggaggatg	taaaggatgc	attcttttgg	67260
gtaaaagaag	atgggggaaga	ttgaaattga	tgatgcaatt	ggaaacagtt	gtaaaaggag	67320
tgagcgttat	gaagagcaca	ggattactcg	agcaagatgg	tataaggctcg	cggagcatca	67380
gttgtttaat	gcgactatga	gagtgaagaa	ttcgttacga	gagcataatg	aagcaagagt	67440
cgcttttgag	aaggagagat	ctaaggagaa	tcagaggcaa	gtccaaaaaa	agaaagaaaa	67500
gagggtgcga	gatttaaagg	aattgcatga	tcaggagctt	ccgagagcac	aggagaggtt	67560
gagagagctg	caagctttgt	atcctgaaat	tgcatctctt	gttgtagagg	ccaggagaga	67620
ggtagcctct	gatttagaga	aagctcatga	gagtattgac	aagcactatc	aaagctgtgt	67680
tcgagagcaa	gagctctact	gagaagaaga	agagaaacag	gaagcggagt	ttagggagaa	67740
cggcacaaaag	attcgctcta	tggaggaggt	gtctgagtat	cttcagcaag	tagaaaatca	67800
gttggaattcc	gtttccaagc	gattaacca	gatggaaact	tttgccttag	gtgtgaggtt	67860
ggaagctaaa	gaagagatag	agtctatcat	actttctgat	gtagtgaacc	gttttgaggt	67920
tttatgtaga	gatattgaag	atatgctatc	tcgagtcgag	gagatagagc	ggatgttacg	67980
tatggcggag	cttctgttac	ttcctataaa	agaagcgctt	accaaggctt	ttgtacaaca	68040
taacagctgt	aaagagaagt	taaccaaggt	agagccttac	tttaaagaga	gccctgcata	68100
tctaactagt	gaaaaccgat	tgcagagttt	gaatcagact	ttacaacgtg	cgtacaaaaga	68160
gtcccaaaag	gttttcagggt	tagaatcgga	agtgaagacc	tgctgagagc	agcttaaaga	68220
tcaagtaaga	cagtttgaaa	ctcaaggagt	gagcttgata	aaagaagaga	ttctctttgt	68280
gactagtacc	tttagaacta	aatttagcta	tcattcattt	cgattacatg	ttccttgcat	68340
gagggtgtat	gaggagtatt	atgatgacat	tgatctagag	agaactcgag	ctcgatggat	68400

ggc gatgtct	gag aggtata	gag atgcttt	tcagg cattc	cagg agatgt	tga aggaagg	68460
cct agttgaa	gaag ctcagg	ctct tagaga	aacc gagtac	tgg ttatatc	gag agggagag	68520
aaag agtaaa	aagaa acatt	gatt ttgcgt	aag ctaacag	cag cgcagca	gcg agttgca	68580
gcatt ttgaat	ccat agaagt	tcct gagatt	cct gagggccc	caga agagaa	acc gaggttg	68640
ctgg ataaaag	cggt ttcttt	attt acccga	gaag atcggt	ctt agaacca	ctc taggagt	68700
ctct agggccc	tgt tttttta	aatt ctcttga	ataaa atact	atat attagt	ggct gagttta	68760
gttta actta	tgtgt ttgat	tcc gatagca	ccac agacgt	ata atgcaag	tacct ctatc	68820
accac agcta	cccc cccccc	cccc cccccc	cag accaatc	tgt aggggct	tct ttttgtc	68880
tgt ctaaat	tcgt gtttta	gca atcactt	tttt agttct	tgg tgtgctc	ttact gattt	68940
cagg agctct	cttt ctaacg	ttagg gattt	cagg agtctc	tct tggagtt	ggt ttggggc	69000
tct ctgcatt	agga agtgta	ctc gttattt	cgg gatttct	att gctttta	gaa agacgag	69060
agg ttctcggg	agt ggggtta	gag ggggattc	cgac aggtat	tct tgggggt	cct tctgcag	69120
aac ttctctc	agag gaaata	caga agaagc	aaaa agcaaa	gcaa atttta	gat caattgc	69180
ctc aggaact	agat cagtta	gata cggata	tcc agacgt	gct ctcatgt	ttagg gaaac	69240
tga aagatct	taagt gcaaa	gat cgaggtc	tttt aaaaga	tgcc aaggag	aaact gcaag	69300
tttt ttgactt	tgt ttggaaa	gac atgatga	tgg agtttgt	agag ctacag	cagg tcatgg	69360
atca agagag	ccgt tatctta	gag ggcctga	tcc atgagg	acaa agtata	gcac acaaac	69420
tttt ttgtaga	tgat gtaaat	att agatccc	att tagggga	gtc gtgcggg	tatt ttacctt	69480
ccg aggatgt	tcg aggggaa	ctg tttaaaga	gatt cgcata	agag gtcgta	gct cgcctta	69540
tga aagtga	tcg cgacata	cgga agatag	caat ggcttt	taac aaaaaat	gcct atgggg	69600
cag caaaaaa	tgct tttgat	aagg ctcttg	gaag ctctga	aac gtgtctg	tata agagtc	69660
tgact aagag	ttata gagat	acct ttttgt	act ataagag	agca aagatc	ctt ccggtg	69720
aga ataatag	cgct cgtgcc	gag caaaggt	ttagg gaaag	caag gatcat	tgg gaggact	69780
taa acgaaac	ggt ctctttg	gtaa aagaag	acgg tctgtat	tgac atagaa	gtg ctactg	69840
cag tcgggtg	gtgg ccagat	cg ttatccag	agc atcttat	tct tgaaaaa	agaa aggata	69900
agg taatgag	ccat cagttg	tgg gaggcga	ctat gcgtgt	gaa aagaagc	gaag taacgt	69960
atag tgtagc	aag agtcgcc	ttt gaaaagg	atgg atctca	gcag aatcag	aagaa attcc	70020
aag aaaagac	aaa agagagg	ctgc gatgtt	taa aggattt	gcgt gatcag	gag tgtcatc	70080
gtgc acaaga	gag attagaa	aaact gacgg	cttt gtattcc	tgag gtttca	gtct ctgtag	70140
tag agacaga	gag agagagg	aaatt taatt	tag aaaaagc	ctat gggaat	ctc gaagagc	70200
gct atcagag	cg ttgtgcaa	gat caaagg	act actggac	aga acaaaaag	aac aggggaag	70260
caga atttag	ggc gaaagga	act aaggttc	gct ctatgga	ggag gtggca	gag catcttc	70320
agat cttaga	aaat ctattg	gaag actgtt	ata agagatt	atcaaaaagca	gaa acttttg	70380
cct taggggt	ggag aggggaa	gct acagaag	agat agagta	tacc atactc	tct gatgcag	70440
cga accgtct	taagg ttttta	tgt gaagata	ttg aggcacac	cct gcctcga	gtc gaagaaa	70500
tag agatgat	gct gcgtatg	gcag agcgtc	cact ccatcc	tataa agcaa	gcatt ttacca	70560
agg ctctttg	aca atataac	agg tgcaaa	agag gtttagc	aaag gtagag	ccct attata	70620
aag agagccc	gct atatgta	aat agcgaag	agc gattgca	gag ttgtgat	cagg ctctcac	70680
agt gcataca	aag agtccca	aaagg tttca	agt tttagaaa	cgga agcatg	tac atataga	70740
gag tatctta	gaga acaagt	aca acagttt	gaa actcaag	gag tgagctt	gataaaaagaa	70800
gag ctctctc	tttta agcag	tact ctcaaa	agt aaattga	gct atgatcc	atta atagca	70860
aac attccct	gtat gaagtt	ttatt acccag	tatt atgatg	acatt gataa	agc gagagct	70920
caat cccgat	ggct ggagaa	gtct gagagg	tat agaaatg	cta agaggag	att ccaagag	70980
atc gtgaaga	aagg ccctatt	caa agaagct	aag cccttga	aaa aagagga	gtat aggtta	71040
ctt caagagg	agaga agcaa	taagg gagaag	cg ttgtattt	aca ataagat	ggc agtagct	71100
cgg caacgag	ttca agaatt	tga atcgatg	gag attccag	aat agaaaagt	aagt ctctatg	71160
gataa agcgc	gtt ctcttatt	tact cgagaa	gat cgttcc	agc acaactc	tagaa acccta	71220
tgag ttgtgt	tgt ttttaaaa	att ttttttga	ataaa atgct	atgt attagt	agct tagttg	71280
gttaa actta	tgt attttggt	cac gatggca	tcac agattc	ata atgcaag	tac acgtatc	71340
acc caccaca	gct acccccc	gat cactcgg	tag ggggctac	ttct tggcaa	ccta agcttc	71400
gtatt ttaac	catt actttt	ttag ttcttg	gtgt gctttt	act gatttca	ggag ctctct	71460
ttcta acggt	ggg agttcca	ggact tgcgt	cag ggcctctc	tttt ggatta	ggc atcgggc	71520
tct ccgcat	agg aggcgta	ctgg ttgttt	cagg acttct	att ctcttctc	ata agacgag	71580
gggt ttcgaa	agtt cgtcca	gaag agattc	ctgt gactcc	ttccc atgaa	gcc cagaaga	71640
tttt atgtca	gct acctcag	gaact ggatc	agtt agatac	gtct attcag	gaag tagtct	71700
cat gtttagg	gaa actgaaa	gat cttaagt	acga agatca	agg gctttta	acag aggtac	71760
agg agaaaact	tcg agttttt	gact ttgtca	ggaa agacat	ggg tacagag	tttt tagagc	71820
tac agcaggt	tgt ggtcaca	gaagg acaat	ttct agatta	ccta atcaat	cagg tgcaaa	71880
gcata tcaca	caa acttttt	gtac ctgatg	taa atattgg	agct cattta	gcgg agttgt	71940
gtgg gtattt	acct tctggt	gat gtttcgag	tgg agcgttt	aaag agatct	gct cgtcagg	72000
ttgt agatcg	cttt catgag	ggg tacttgt	gcac gcggga	agg tggcaat	ggc ttttgac	72060
gaga atgctg	tgg agtggca	aaaa atgcct	ttg ataaggc	tttt ggggca	ttaga agagt	72120
gtgt gtataa	gagt ctgaca	gag agttata	gag aggcatt	ttat gaatat	gaga aggcga	72180
agat ccttag	gaat gaagat	gtaga atggc	tgc aggataa	gaata agagc	gcac gtgctg	72240

agcagagatt	tagggaagtc	aaggatcggt	gggaggactt	aaaggaaacg	gtcttttggg	72300
taaaagaaaa	cggttgatt	gacctagaag	tgctcactgc	agtgggtggg	tgcccgatc	72360
gtggtccaga	gcattcttatt	cctgaaaaaa	gaagggaataa	ggtaatgagc	cataaattat	72420
gggaggcgac	tatgcgaatg	aagggagcag	aaggaacgta	tagtgtagca	agagtcgcct	72480
ttgaaaagga	tggatctaga	agaatcaga	agaaattcca	agaaaagaca	aaagagtggg	72540
tgcatgttt	aaaggatttg	catgatcagg	agtgtcatcg	tgacgaggag	agattggcag	72600
aacttgaagc	tttgtatcct	gaggtttcag	tctctgtagt	agagacggag	agagagacaa	72660
aattttaaatt	agagactgct	tatgggaatc	tcgaagagcg	ctatcagagc	gttgtgagag	72720
atcaggagga	ctactggaaa	gaagaagaaa	acaaggaagc	agagttagg	gaaaaaggaa	72780
caaagggttcg	ctctccagag	gaggtggtag	agtatcttca	gatcttagaa	aatctgttgg	72840
aagactgttc	taagcaatta	actatagcgg	aagtgggtgt	cttaggtgta	gagctggaag	72900
ctacagcaga	gttcgagtat	accatactct	ctgatgcagc	gaatcgtctt	aaggttttat	72960
gtgaagatat	tgaggacatc	ctgcctcgag	tcgaagaaat	agaaatcatg	ctacgtatag	73020
cagagcttcc	attccttccct	ataaagcaag	catttactaa	ggccttttta	caatataaca	73080
gctgtaaaaga	taagttagca	aaggtggagc	cctactgtca	ggagagcgtg	gactatagaa	73140
gaaacaaaga	gcggtttcag	agtttgaatc	aggatttaca	aaatgtatac	caagagtgcc	73200
agaaggctac	aggttttagaa	tcggaagtga	gtgcatatag	agatcatctt	agagagcaga	73260
tcacagagtt	tgaaactcaa	gggctggacg	tgataaaaaga	agaacttctt	tttgtgagta	73320
gtactctcaa	aagtaaattg	agctatgatc	cattaatagc	agacattccc	tgtatgaagt	73380
tttatgagga	gtattatgat	ggcattgata	aagcgagagt	tcaatcccga	tggtctggaga	73440
agtctgagag	gtatagaaaag	gcgaagaagg	gattccaaga	gatgctgaag	gaaggcctat	73500
tcaaagaaga	tcaggctttg	aaaaaagcag	agtatagatt	acttcgagag	aagagaattga	73560
ataaggagaa	gcttttgatt	tgcaataaga	tagaagcagc	tcagcagcga	gtccaagaat	73620
ttggaccctc	gttttcataa	tgaaaaatga	catatcggct	cttctccctc	tgatatttca	73680
ggagtctcaa	gcaatgtttt	tcgcctagtg	ctctattttg	tctaaatttt	agagaggaag	73740
gtcgcagctg	aaggctttca	tttgtagaca	ttttatagaa	aaatcagaaa	aataccttta	73800
gaaaaataaa	gaacactttc	atcttaaagt	gactatagtg	ggatttttta	gatttgtttt	73860
agaaggcatt	ttaacgatgt	atcattttca	aaagattcgc	atgacactta	caactcaggg	73920
atttgttctt	aataaatctt	taaggaagga	ttatgaactg	tggtttgtct	atggatcatg	73980
tccagaatct	aaggtaaaac	tacagacttc	ctctcataaa	tggttgtgag	acgaagtttt	74040
ctaagtgtgt	ggtagatag	atgaaagaac	ttagacatga	atcctataac	cgtgcattac	74100
ataagctaag	ccatcaatgg	gttcgctact	ttctctatac	tttcgtatcg	tgttccttca	74160
tagtcgccat	atttactttt	gcatgggtta	aggctctcta	tgttcccgaa	tgnaaggctg	74220
gtgagatctc	acgtattttt	ctgacagctc	ctatggattt	tnctttaagt	tggaagcgtc	74280
ataaatttta	taaacgtact	gcccacattt	cagaagcctt	tggaagggtc	tatcatctta	74340
cactctctcc	cggtagtctc	ctcagcaaag	aggggaacgc	cgatgaaaac	actgactatt	74400
ggtttaaaaa	agcagctgat	tttttgttgt	ctaccaactt	tgctgatagt	tcaactcaaa	74460
aatgtcttaa	ggacttgtgt	atatatcctc	ctttattggg	gaaagaaaag	aaaaccttag	74520
aaatcaatat	caactcgaat	aaagggaatg	ttattgtctc	gtgcttctgc	cacttaaaaa	74580
tttttcttat	acaagaaaat	tgtccccagc	cctgttttga	tgcaatcatg	gatattttga	74640
agatcgccaa	cttcgaagtg	gccgtggata	aggaaatgtc	aggttgtgtg	aaaggagagc	74700
ttctcggaag	acgttgcatc	gagaaaatta	ccaagggcac	acctatatta	gaaaagtatc	74760
agagaatcga	tgatcgggat	gctaaaattc	taaagcagct	tcgagcgcaa	ctcctttcag	74820
tgcatacctt	attttcctgt	agatccttat	ggggggctat	ttttgtagtt	ttactcatac	74880
ttctatgggg	ctacgggtgct	ttgaaagccc	tgtgtcctga	gatgttgaaa	tctccccagc	74940
gctttatgct	ctatattgct	attctaactc	tttcgttgct	gtggtgcaga	gggacagaaa	75000
tcttttgctc	ctattgggtt	tcctatctat	ctatcccacc	gattttacca	tttacagctg	75060
tactcctagg	atatttttcta	ggtcttccca	tagcaggatt	ttcctgtacg	tttcttgccc	75120
ttctctacac	cttgggatcc	gatctttgga	ataatagtgt	gtttctatct	ataaacctac	75180
tttggttcttg	gagaacttta	gtgagcttac	atcgctcag	tcgcctttct	tcgggtgttt	75240
gggcgtgtat	gaaacttgga	ggcgtagcta	tggaagcct	gctcatgttt	cggtatattta	75300
caaatacaat	atcaagagaa	gccctatatg	ctgatgggat	cgaaagcttc	gttttatagtc	75360
tgatcaccgc	aatcagcgtt	gttgctttga	tccctgtctt	cgaggcttct	ttcggagctt	75420
ctacaaaact	ttcgctcttc	acctatttat	ctcccgaaaa	cgcattgctg	aagcgtcttt	75480
tcaaagaagc	tccaggtacc	taccagcatt	ccgtattagt	tggaagctta	gcagaagctg	75540
cagctcaagc	tataggtgca	gatagcctct	attgcttggg	tgacgtcat	taccatgata	75600
tcgggaaact	gattaatcca	ggatttttca	gtgaaaatca	aaaaatctta	caacaatctg	75660
gtcattegct	atccccatta	gagtgcgcta	agatgattat	gcgccatatt	cctgaagggg	75720
tgaatcttgc	taggcaggna	gggcttccctg	agtctgatat	ccagggtgata	gaagagcatc	75780
acggaacctc	tgtgatccgc	tcagcatact	acagccatat	ggtagagaac	ccttctacag	75840
ggagctttga	tgaggaaatta	ttccgatatt	ctggaaataa	accctcctct	aaagaaacta	75900
caatcattat	gatcgcggat	tcttttgtaag	cagcctcgcg	atctctaaaa	aatgccagtc	75960
ttccagatct	tcaaagactc	atcgatcaga	ttatccaagg	gaagttacaa	gacggtcagt	76020
tttcttgctc	tccaattacg	ttagatgaac	tcgctttgat	tagcaagagc	atggtgcaaa	76080

ccctctacgg	agctctacat	tctcggatga	aataccctga	aatatcgtat	caaatttcta	76140
tggattcctg	ccccaaaccc	tctataggag	gaacttagtt	ctctagatta	cgtggcggtt	76200
gatttccagc	aaatgtgctt	tgaaatataa	ttttttatgc	tctcatatgt	agaaagagaa	76260
aaaagcatta	gaatgccaa	aagcagtagc	gacaaaacga	ccaaaatgag	aataggggact	76320
aaaattccca	gtcctcctag	gatggaaatg	caaattaggc	cgtatccgtt	tacgaaggcc	76380
tgcacacact	ctttctgttc	gcaagaaagc	gaaggcgagt	acccgatctg	aactgtagtc	76440
cgatctaggg	atTTTTTTat	ttgataagca	cggaccaaac	ccgcaattgg	tactagactc	76500
acaaatatca	aaaacacgtt	cgaaaagcag	tctaaactaa	aggggttttc	atccacccaa	76560
atagcacggc	tttttttctg	gaatagtttg	tttgagtcct	tgtgagtgtg	acctgggata	76620
tatatcgtgt	ttcctgtcaa	tattttgtca	tagtaagggt	gatgtagcat	agtaagccaa	76680
aaaatttctt	gatagataac	tagcaggtaa	acgatattcc	ttctttttctc	tttcagtcaa	76740
tggatttttt	tataagtcac	taagaataaa	aactcataaa	gatgggtctag	cttcgctttg	76800
cttattttta	acttctacag	tgtctaaagg	gaaagaaatg	tagtaaaaaga	ctacaaatga	76860
gacatgcaat	tacgccaaag	tgttatttag	caacaataaa	tttgtaacag	tatcagagga	76920
cactgattga	cgcaaagcaa	agcaacaaag	gcgaaatggc	aacatgatta	actgaaaaag	76980
cacagaaata	agtaggatag	ctaggagcag	aagaaatata	gggagaagga	ttccacatcc	77040
accaagaatt	ccagcgggtct	ttatagagct	tgtcagtcct	gatgacatcc	tacatagcgc	77100
atTTTTgcag	ttagtatgag	gggagatagc	ctaagttagc	cttgacattc	tcgctattcc	77160
agtttggttg	atgctttgca	tatctcattg	catagaaata	ttccgagaat	gggaaacccat	77220
gagacctata	tacatccagg	agtgtctccg	agtagtcatg	ctcaggatgt	tagcagatct	77280
acagtttacc	ccagtcgaag	ttttatcatg	agacgtatgc	tcatgggctg	gaatttcaat	77340
cgtgttccct	cgaagagctc	cgagcagtta	atggatggct	atcgcatacc	tcttatattt	77400
tttgggaagc	atcctctac	tatatctatt	ttaaatgtca	atagattttc	ttggctctcc	77460
atTTTTtaca	atggagaaag	gggggttttg	gaagaaaacc	aaactcacca	tacagattaa	77520
agtacaacaa	aatctaagga	agaccagttt	gtatttttagc	agcatcatag	aaatacttga	77580
tggtttatga	gagctatata	ggaggaccct	ctatccacat	agtgtctcca	gattcaggta	77640
gtctctcctg	cgattctatg	aaaagcgagg	ggagagttat	gaggagtggc	agtgtatagg	77700
ggtaaataac	tgtttccatt	tacctgcgtg	atccttggct	gtaattgcta	aggatccttg	77760
tagggcatgg	tatggaggag	gaagttctat	actataagca	tgatgcaggt	gaagtcttaa	77820
actcgcagct	ttcgcaagaa	caatagcatc	ataatgacca	cgttgaggct	gatccagcct	77880
ctcttcaata	gtgcctcgaa	tatccaagat	ctgtccttga	ggaaacagtt	gttttagtac	77940
tgcacttcga	cgtagagaag	aactccctag	ccggggactc	aagggtaggg	gctcatgaac	78000
atagtgggtca	gcatacacta	acaggtctgc	aggatgtaga	catcgtgtta	tggaactac	78060
aggaagagag	ggagtctcag	gaagatcctt	agcagagtgt	atcgccagat	cgcagactcc	78120
tttatggact	aaggcatcga	cgccatcagt	gaaaaataaa	gagttttcta	caagatgtaa	78180
ggggattttc	ttctcacgat	ccccagtagt	ctctgtagtg	cttaactgga	accaagttt	78240
gggataccac	gagcgcanaa	aagaaatata	ctcatgtact	tgagctttcg	ctaaaatttg	78300
aattttctaga	aagcaataac	gaagggggcg	cttgccctga	caggaaatca	cttaaacagg	78360
ggtcagagta	acagacggat	agcatctttt	tattgttttc	actccttgta	aacgaaagtt	78420
ttctcgaatt	tccttgggaa	gagatgaaat	ttgacctca	ggaagaattg	caccttcaaa	78480
tcccatgagt	tttccctctt	taatgcgtct	ctctaaatga	gccacatgac	ggatttctcc	78540
tccaagacct	acctctccaa	ttacaatgga	attgttaggt	aacaggcggt	tgtatagcga	78600
ggaagcaacg	gcaagtagag	cccccaagtc	cgcagcaggc	tctataatct	ttaaaccccc	78660
cgtaatggat	aggaagacat	ccatggtaaa	tagtttgact	tgagcccttt	tttctaatac	78720
agctaaaagt	aaagaaaagc	gattcggatc	gaatcccgca	gtcttcttta	ctggattagc	78780
aaagggagag	gaagagacca	aagcctgcag	ctcgataaga	agagccccag	agccttctat	78840
aataggaatg	atcatagacc	ctgtcgttgg	ccccgtcttt	tcctgaagga	aaagtcttga	78900
agggttgcta	acctctttga	gaccatctgc	atgcatcgag	agaatcaata	gttcatttgt	78960
agggccaaaag	cgatttttca	cagagcgaat	catacggtaa	ttcgcatggg	aattccccctc	79020
aaagtaaagt	acagtatcta	caagatgttc	caatacccta	ggacctgcga	tctctccaga	79080
ttttgtcacg	tggccgataa	taaatgtcgt	gatctgcgca	cttttagcaa	tctgcattag	79140
ttcataagta	acttctcgga	cctgagctac	cgatctctgt	gcagagttta	gcgtgggggtt	79200
aaatataatc	tgaatggaat	caataattaa	aatatcaggt	tccaaagtcg	ctatttgcgtg	79260
cttgatattg	tccaagtttg	tttcaggaaa	taaataaaatc	aaaggtgatg	agatatttag	79320
cgcttcgctc	tcaaagacgt	ctgcgttaca	gattcttcac	cacaaacata	aagaacttta	79380
tacttttgcg	atgccaatct	ctccgcagtt	tgaagaagga	gtgtcgactt	tccaatgccg	79440
ggatccccac	caagaagagt	gaggcttcca	cgaacaaccc	ctcctccaag	gatgcgatcc	79500
caccccgcat	gatcaataaa	tatccgagat	tcattctcta	attcgataga	gcttaatgca	79560
atcgcaactg	tagaagatcg	cgacgaagtc	ccagatcgag	cctggggggac	atattcttca	79620
accaaagagt	tccagtttgt	gcagcctgga	cattgccccta	accatttagg	agcagtacct	79680
ccacattgat	tacacgtcca	ttgtgttttg	gtttttgttg	ccatacgtat	ctagtgcctg	79740
ttgtgctgca	atTTTTtctg	cttctttttt	ggatgcagca	tttccctctc	cccaaaccctc	79800
ttgattcaca	agaacctgga	tctggtaact	gacatttctt	tgagcatccg	taactgccgt	79860
ggattgatat	accggaagaa	cgcgaaactg	cttttgtgtg	aactgctgaa	gaaggttctt	79920

aggattgcca	gacattaaag	gaagaatttc	ttctctagga	ggaaggaggg	gaacgtaagt	79980
ttcctagctg	gagaaagacc	cccatccaaa	tacacagcac	ctaaaataga	ttcaaataga	80040
ttggcatagg	cagaaagacg	tcctcgctca	ctctggattt	tttccctttt	tcctataaga	80100
agataatccc	caatccctag	catgggttgta	taacgacagc	acgctttttg	attcactaaa	80160
gaagcccgtg	ccgtggatag	agttccctca	tccatcgaag	gaaagagaag	aaaaagatgc	80220
tcagtaacaa	tgagaccaag	gacagcatct	cctaaaaatt	ctaaacgctc	actatcttca	80280
atttgcaccg	ccgactcggt	tttatatgag	gggtgagtc	gcgctatttc	taagagctta	80340
ggttgtgtaa	atgtaaaatt	taacttagct	tcaatagccg	tgatgtctat	aggggggatgc	80400
atagataggga	gggcgccgtc	cttaaaactta	gagttgggaa	tttttatagg	cggaaaaaag	80460
cttaaggtct	atagtgtctt	tggatttgtt	atcttattcg	gatacgtatg	aggtctgctc	80520
tacacctcca	acacttgccg	catttccata	accacggctc	tattttattt	gaaaatcttc	80580
tgactataaa	agattgtttt	ttattagaaa	caaaattaca	aaattttatt	gccaaagcat	80640
caaaaactat	agacactgtg	cggtggagag	agaatatatt	tcgctcaatg	ccagagattt	80700
atacagtcgt	tcgtaaacgg	cgtttggatt	tctttgcagc	ggaattgggtg	caccgcccc	80760
agctttccct	cgttcgagat	ctctgggtct	ctccaggaga	agagatcctt	gaaggagaag	80820
aagattgcct	gcttttcctt	ttactttcag	gagatcgctc	aggaagcggt	atattcttta	80880
caggacccta	tccttcagat	ctttatgaat	tggagaaggg	aactacgggg	ttgcttttag	80940
ctttctcttc	tgtagggatt	ccagtaattt	aatctttctt	ctctcgctct	agaaacagaa	81000
ataagagaca	gggacttaca	gttcttattg	cctccatggt	ttgattcagc	atctttctga	81060
aggaaaaatc	accatattct	ttacaaagag	cttctcatgt	tttagttccc	cgcttgcttt	81120
caataacttaa	ttacaaaaac	cacaggccga	agtataacgg	ctttgagtga	tcaagtgtat	81180
tctataggat	ttattttgaa	gggtggattc	ttaattaaag	aaacctttct	caaacaattg	81240
attataccag	accaagcttg	aagaatccct	ggactttatg	caaaaagggt	gttaagagtt	81300
cctgaaacta	tccttacata	ggattttctt	aatgaaagaa	gtagaacaac	gtatccgggtc	81360
attatacgat	gcagtaacag	ctgaaaatat	ttgtagatgg	ttgtccaatg	attgtaccca	81420
acaagatgca	aagactatcc	taggatgggt	agatacagat	cctgcacagc	ttgaagatct	81480
attcggagcg	actcttacct	ttggtaccgg	aggactccgt	agtcttatgg	gtatcggaac	81540
aaataggatc	aacctgttta	ctatacgctc	aacgacgcaa	gggctgggtc	aggtgctccg	81600
cgctcatctt	ccccatcccc	gagatcctat	gcgtgtagtt	gtcggttgtg	ataccgcgca	81660
taactctata	gaatttgctc	aagaaactgc	aaaagtcctc	gcaggtaatg	gctgcgaagt	81720
tttcttggtt	cagtatcccg	aacctttggc	tttagtctcc	ttacgggtga	gatacgaaag	81780
ggccatcgcc	ggagtgatga	tcaccgcctc	tcataatcct	cccaattaca	atgggtataa	81840
agtttatatg	gcttcgggag	gccaaagttc	ccctccctta	gatcaagaga	ttgttgccgc	81900
ctgtagtgca	gtgaacgaaa	ttttatcagt	gccctcgata	gatcatccca	atattcacct	81960
cattggaaaa	gaatacgaag	ccctttacag	agacactttg	aagcaactgc	aactctatcc	82020
cgaagcaaac	cggatttcag	gaaggtcttt	atctatttcc	tattcgccat	tgcatggaac	82080
aggaatttct	ctcgttcctc	atgtttctca	agactgggga	tttttatccg	tacatcttgt	82140
ggaaaaacag	gccatagggt	acggcgattt	cccaaccgtg	cagctgccaa	cagtgaggga	82200
tcagaggct	ctgactctgg	gcactgagca	aatgctcgct	aatgacgatg	atctttttat	82260
agctaccgac	ccagatgccg	atcgcggtgg	cgtgggttgt	ctagaagacg	gccaaacctc	82320
ccgatttaac	ggaaatcaaa	tggcgagcct	tttagcagac	cacatcttag	gagcttggag	82380
caaaacaaga	cacttaggag	aacatgataa	attggtcaag	agcttgggtga	ctacagaaat	82440
gctctctgct	atcgcaaagc	actatcatgt	ggatcttatt	aatgtcggaa	caggatttta	82500
atacatcgga	gagaaaattg	aatcctggcg	caattccaca	aacaaattcg	tatttggagc	82560
cgaggaatct	tacggttgtc	tctacggcac	tcacgtagaa	gataaagacg	ctattattgc	82620
gtcagcattg	attgcagaag	ccgcactaca	acaaaaatta	caaggaaaaa	ctctatgcga	82680
cgcactcctt	tctctttacg	aaacatacgg	atactttgct	aacaaaacgg	agtcgtgggt	82740
tttttccgca	aaaactgacg	aacaagaaat	aagaaaaaaa	ctttcacacc	ttgaggaaat	82800
cagttctgcg	aattttttct	cagggaaata	ccaagtagag	aaatttgaaa	actataagca	82860
agggatagggt	ttcaatcttc	tatcgaagga	ttcctacgcc	ctcaccctgc	ctaaaacatc	82920
tatgctctgt	tattatttta	gtgggggagg	tcgggtaatc	atacgaccct	caggaacaga	82980
acctaaaatc	aagttctact	tcgaaatgtc	aactcattat	ccagagcgcg	ttaccgataa	83040
agaaatacaa	aaacacgtga	agcagagagt	tttcaacatt	tagacgattt	tatttttgat	83100
tttaaagaga	aattttccaa	tttgtgagtg	gaaaaatcat	cttgagaaat	atcctaaagc	83160
tatttacact	tggtgtaaat	ctccttcaga	ataaggcctt	ctttcaaggc	cattgttgta	83220
tccgaaacaa	gggttagtag	agtacttgct	ttcctagcaa	aactttctga	acttaaatca	83280
aggaggttaa	atactaaaaa	ggtatgttgt	tatgagtttt	gttccttatt	ctttaccaga	83340
gttaccctat	gattatgacg	ctttggagcc	tgtaatttct	tctgaaatta	tgattttaca	83400
ccacaaaaag	catcatcaga	tctacattaa	taatcttaac	gcggctttga	agagattaga	83460
tgctgcagaa	acacaacaaa	accttaatga	actcattgct	ttagaacccg	ctctccgctt	83520
taacggggga	ggacacatca	accactctct	attctgggaa	actcttgctc	ctatcgatca	83580
agggggagga	cagcctccaa	atcatgagct	cttttctctt	attgaaagat	tttggggtac	83640
ggtggacaac	tttttaaaaa	aattaatcga	agttgtcgca	ggagttcaag	gctccgggtg	83700
ggcctgggcta	ggattttgtc	ccgcaaaaac	agaacttgct	ttacaagcaa	cagcaaatca	83760

ggatcctcta	gagcctctca	cagggaaact	ccctctgctt	ggcgtggatg	tttgggagca	83820
cgcctattac	ctgcaatata	aaaatgttcg	tatggattat	ttaaaagcct	ttcctcaaat	83880
aattaattgg	ggacatatag	aaaatagatt	ttctgaaata	atatcatcta	aataatttga	83940
atttgggtgat	tttaattgca	gtgttaataa	cattaattta	aaattgcttc	ctaacagaac	84000
ctagattagg	tggcttgtgc	gtctattttc	ttacgacaaa	cccaagatta	aagtgcataa	84060
aatcaaggca	gatggtttta	gtggttggct	caagtgtaat	cattgtcacg	agatgattca	84120
cgcaaatgag	ctaggacaaa	attataattg	ttgtcctaag	tgtcctatc	attaccgtat	84180
tactgcgctc	gaaagagtca	agctgcttgc	agacaaagat	tcttggcgtc	ctctttatac	84240
ggatctgaaa	tccaagatc	ccttggaatt	tatagatacc	gatacctacg	caaatcgctt	84300
agaaaaagct	cgaaagaata	ctacagaaa	cgaaggcgtc	attgtaggta	tatgtactat	84360
aggcctccac	cccgtagccc	tgcgcgttat	ggattttcaat	tttatggcag	gatctatggg	84420
tgtctgttga	gggganaaac	tgaccagact	tatagaggaa	gccattgaaa	ccaggctccc	84480
tgtaatattt	gtcagcgtct	ctggaggcgc	acgtatgcag	gaatctgtat	ttcttttaat	84540
gcagatgggtg	aagacctcag	cagctctttg	taagcttcat	gaagcaggtc	taccttatat	84600
ttcagtcctc	accaacccaa	cttcagggtg	agtgcacagc	tctttcgtcg	ccctcggtga	84660
tattataata	gcagaaccta	aagcactgat	ttgtttcgca	ggacctcgag	tcgtcgctca	84720
ggtgatagga	gaagatctcc	ccgaaggctt	caaaaatctg	aattcctact	agaacatggc	84780
atgattgata	aaatcgttga	gcgtaaagaa	ttgaaaacca	cccttcagac	tttacttgat	84840
tacttttttag	cccaagaata	cactggcggg	aaaagtaaag	ctcctagaga	tctttcgaaa	84900
aggcttaaaag	agattttttt	gttgacagat	gacagtgaat	aaaacatcat	accgcatctt	84960
gcaatgataa	cattatctgt	aacgctatcc	ttatgactgt	attttgtgaa	ttggattcag	85020
gaggagaact	tcttgaatat	actacgccag	gagccgctgg	tgcggatctt	agggcacaaca	85080
tcgaagaacc	catcgctctg	ctgcctggac	aacgtgcttt	gatccctacc	ggaatcaaaag	85140
cagaaattcc	cgaagtacga	gctacaggtc	cgctctcgga	gcgggtttggc	tttaaagcac	85200
ggcattactg	ttttaaattc	cccagggact	atcgattcag	attatagggg	agagattcgt	85260
gtaatcttaa	tcaacttcgg	tgatagtaca	ttcattattg	aacctaaagat	gcggatagct	85320
caagttgttt	tatctcctgt	agtacaggca	acgtttgttg	ttaagcaaga	nagtttagcg	85380
gaaactgccc	gaggaagtgg	aggtttttgg	catactggag	caagctaaga	tgccatccta	85440
ttgtcaaaa	caacaagatt	ttctctttat	ctctcttttg	tctcctagac	ttgtaatgtt	85500
tttaggcaaa	cactcccgag	atgaaatcct	ccaagatctt	acagatcttg	tggatgctgc	85560
aggcctactt	gaagacaaac	aagccttttt	tgatgtctct	gtccgtcgtg	aaaacatcat	85620
gtccacagga	atcggaatgg	gcgtggctat	tcttcacgga	aaactcgaaa	gctgctctaa	85680
ttttttttatt	gctataggca	tccatacgca	aggcatttta	tgggacgcta	ttgacggagc	85740
cctcgtacgc	ctcgtcttct	tgatcggagg	tccagaaaat	gctcaagccg	aatatctcaa	85800
gttattatct	actttgactt	tatcttttgag	agaagagtct	cgctcgtcaac	agttgttaca	85860
ggtgaatacg	attgaagaag	tcatgaatgt	atttgtgggg	atgtaaaaat	ggatttaaaag	85920
ttagatgaag	tcgcctcttt	gttagatgtt	tccgaacata	cagttctgca	atggcttaaa	85980
gaaggagcca	ttccaagcta	tagtatgaat	aatgaatacc	gctttagtgc	tgaagaaatc	86040
gaagactggc	tattgcataa	ccaagcactc	atgatccaag	aacgcggcga	agataaagaa	86100
gcacttaaaag	atctttcttt	gaaatatagt	ctctacaaaag	caattcatcg	tggcggcgtg	86160
ctttgcatg	ttgtggttca	tagtaaagaa	gaagctctcc	aatacgcttc	taaatacatc	86220
gccccaaaagt	ttcaattaga	cgaaaagcgta	ctttttgaaa	tgctctccca	cagagaaaat	86280
cttatgtcca	caggtatagg	agaaggaatt	gccctgcccc	atgccaaaaga	cttttttaatt	86340
aatgcctact	atgacattgt	ggttcctatg	tttcttgacg	agcccataga	atacggggct	86400
ctagatggaa	aacctgtagg	cattcttttc	ttcctttttg	cttgccagga	taaaagtcac	86460
ttaaactttag	taaaataaat	agtccatctc	gggatgtctt	taaatgcccg	aagctttttt	86520
aaaaattatc	ctaacaaaga	tcaactttta	gcgtacgtta	aggaatggga	gtcccaaact	86580
cattaatagc	tagagtttta	aaagattttt	aagtcctaag	tgtgaaaaaa	atccttttgt	86640
tgctatgggtg	atcctcatag	gcttccagga	gattgtagtc	gcatgatgag	ctctaagcgt	86700
acctcgaaaa	tagcgggtgct	ttcaattttta	ttaacattta	ctcactctat	agggttcgca	86760
aatgcgaatt	cgctccgtagg	tcttggcacg	gtctacatta	catccgaggt	tgtaaagaag	86820
cctcagaaaag	gatcagaaaag	gaaacaagcc	aaaaaagaac	ctcgtgctcg	taaaggatac	86880
ttagtccctt	cttcaaggac	tctttcagct	cgagcccaaa	agatgaaaaa	ctcctctcgt	86940
aaagagtctt	caggtgggtg	taacgaaatt	tctgcaaatt	ctacaccag	atctgtaaaa	87000
ttacgaagaa	acaaacgtgc	agaacaaaag	gcagctaaac	aaggattttc	agctttttct	87060
aacctaactt	tgaaaagcct	acttcctaaa	cttccttcaa	aacaaaaaac	ttcaattcac	87120
gagagagaaa	aagcaacctc	aagatttgtt	aatgagtctc	agcttagttc	cgcacgaaaa	87180
cgctactgca	caccatcttc	agccgctcct	tccctatttt	tagaaacaga	aatcgttcga	87240
gtcctgttag	aaagaactaa	agaacttcaa	gataatgaaa	ttcatattcc	tgtagtgcga	87300
gtccaaacga	accccaaaga	acaatacata	aagacaacta	aacagttggc	atcccaagcc	87360
tcgattcaac	aactcgaagg	aaccgagcaa	tactgctgag	agctcgccca	aggtgctagc	87420
ctacctgtct	tagtgcgctc	taatcctgaa	gtgtctgtac	aaagacaaaa	agaagagtta	87480
ttaaaagaac	tcgtagctga	acgtagacaa	tgtaaaagaa	agtctgtaag	acaagctctt	87540
gaagctcggt	ctttaactaa	gaaagttgct	agaggcggtt	ctgtgacctc	gactttacga	87600



tacgatccag	aaaaagcggc	ggaaatcaaa	agtagacgca	attgcaaagt	aagtcctgaa	87660
gcacgtgaac	aaaaatattc	atcttgcaaa	agagatgctc	gcgctaattg	gaaacaagac	87720
aagacaactc	ctagtgaaga	tgcttctcaa	gaagaacaac	aaactggggc	aggactcgtg	87780
cgcaagactc	ctaaatctca	ggttgcaagt	aatgctcaga	acttctaccg	aaattctaaa	87840
aatacaaaac	tagatagcta	tcttacagct	aaccaataca	gctgtagttc	tgaagaaaca	87900
gattggccat	gttcttccctg	cgtctctaaa	cgcagaactc	acaacagtat	atctgtatgt	87960
accatggtag	ttactgtcat	tgcgatgac	gtaggggctt	tgattatagc	taatgctaca	88020
gaatctcaaa	caacatcaga	tccaactcct	ccaactccta	ctccatagtt	gtatagccct	88080
tgctggacgt	gtagctctac	ccaaaatctt	agatagcctt	cttatctatg	atcttagtgg	88140
gtagagcttt	ccctcccgac	tcgtcttctt	ttcaattttc	tctttgtaat	tacactttat	88200
ctctctttct	atctttttcg	ggagtacctt	cttatttttag	atagagaaag	cttagttttt	88260
cttttgttta	agaaataatt	ataagctcgt	taatataatc	aatttgcctt	taagtaaaat	88320
gataaaacta	tctaacttat	agtgatttgt	gttgtagagc	attattatat	tgcatcgtgt	88380
cagatttgcg	tgttcattct	aggggaacac	cgaccagac	tcatagttag	atctgtgtgt	88440
cccacccac	caacagattt	ttgaaaaaac	accctacact	tgacctatgt	atgcgaattg	88500
taagcacaat	tgtctctgtc	tttatgattt	tagcagacat	cgttctcttc	ctgggctccc	88560
tcttactttt	accctcctt	atagttttac	tttggaatc	ttcttaggaa	gatgcctttc	88620
tacgtcta	attgttttat	tataatttta	aaaatgatta	taatttctta	ttcaactcat	88680
gaatattttac	atttaataaaa	agtataatgt	ataattagtt	atgactaaaa	ttcaatgtag	88740
tgctcagtat	tatagatctc	gaccggccga	gagggcccaa	actcctccgc	aacctttcct	88800
tgctagggat	cgcgcggtat	tttgggagag	acatcctaga	ttcagtgcac	gttgtcgtgt	88860
cttattactc	gttgcttggg	tggttctcgc	tctactgttt	ctctttgtta	tgcttcttcc	88920
tctagccgct	gggtcgtatt	tacttgcctt	tttaaggatt	cttcacctaa	aaacttgtgt	88980
tttgggtgcc	tgtagctatt	tcaaaggcat	gtttttatcg	atcggagctt	ctctttgttt	89040
gggagagtc	gttcgtatct	ttgtaattct	tctacgattt	agttttatcc	ttatcttaga	89100
ccaacctctt	cataggtgga	tcctgtagag	gaactattcg	actcaggagt	cgtagacctt	89160
aggtattcgt	gtttaaagat	aaaagtttta	ttttctaaga	gtttttta	tattaagatt	89220
tttattttaa	aatatatctt	ttgattagat	ctctaatacg	attattataa	atataaatag	89280
tttttcaaaa	aaaattatat	gacagatttt	cctactcact	tcaaaggacc	caaacttaac	89340
cccattaaag	taaatccaaa	cttttttgag	aggaatcccta	aagtcgcaag	ggtagtgcaa	89400
attacagccg	tagtcttagg	aatcattgcc	ctcttatccg	gtatagtact	cattataggc	89460
accctctcgc	gagctcctat	aagtatgac	ctcggcggtat	gtcttttagc	ttctggaggc	89520
gccttatttg	ttggtggtac	gattgctacg	atattgcaag	ctagaaatag	ttataagaag	89580
gccgtgaacc	aaaagaaact	ctcagagcct	ttgatggaa	gccccgaatt	gaaagcctta	89640
gattattccc	tagatctgaa	agaggtatgg	gacctacatc	attcttggtg	tcaacatctt	89700
aaaaaaatag	acctgaatct	ttccgaaacc	caaagggaag	ttctaaatca	aatcaaaaat	89760
gatgatgagg	gaccctccct	aggggaatgc	gccgctatga	tttcagaaaa	ctacgacgca	89820
tgcttaaaga	tgctcgcgta	tcgtgaggag	ctcctgaaag	aacaaaccca	ataccaagag	89880
acacgattca	atcagaacct	cactcataga	aataaagttt	tgctctccat	cctctcaagg	89940
atcacggaca	atattttctaa	agcgggcggt	gtcttttctt	tgaaattttc	cacgctaagc	90000
tcgcggtatg	cacgaattca	taccaccacc	actgtgatcc	tggttttaag	tgccgttggt	90060
tctgtcatgg	tcgtagcagc	tctaattcca	ggtggcattt	tagcactacc	tatacttttg	90120
gctgttgcta	tttctgcagg	agtgtattgt	accggacttt	cctatctagt	tcgtcagatt	90180
ttaagtaaca	ccaagcgtaa	tcgtcaggat	ttttataaa	atctttgtaa	aatgttagat	90240
atagagcttc	ttaaccaaac	ggtaacttta	cagcgattcc	tctttgaaat	gctcaaaggt	90300
gttctgaaag	agaagaaga	agtctcctta	gaaggtcaag	attggtatac	acaatacata	90360
accaatgcac	ccatagaaaa	aagattgatc	gaagagatca	gagttacctt	caaagagatc	90420
gatgctcaga	ccaaaaaaat	gaagacagac	ttggagttct	tagaaaaatg	ggtgcgttcc	90480
gggagactgt	ctgtagcgtc	cccgtcggaa	gatccaagtg	aaactcctat	ttttactcaa	90540
ggtaaggagt	ttgcaaagtt	acgtcgccaa	acctctcaga	atatatccac	gatttatggg	90600
ccggacaatg	aaaatattga	tcccgaattt	tccttaccct	ggatgcctaa	aaaagaagaa	90660
gaaatagacc	atagcttaga	acctgttaca	aagtgggaac	ccggttcaag	agaagagttg	90720
ttgttggttag	aggggggtcaa	cccaacctta	agagaactca	atatgagaat	tgcaacttcta	90780
caacaacaac	tatcaagtgt	ccgaaaatgg	agacaccttc	gaggggaaca	ttacgggaat	90840
gttatctatt	cgatatacaga	actcgatcgt	attcagatgc	tagaaggcgc	atctttataat	90900
cacctcaggg	aagctcaaga	ggaaatcacc	cagtctctcg	gagaccttgt	tgacattcaa	90960
aaccgtattt	tagggatcat	agttgaagg	gactcagatt	caagaacaga	agaagagcct	91020
caggaatagg	attctcatat	aaataacaac	aaactaagag	ctgttttttt	ctcttacagc	91080
tctttctaga	caggatctct	aaggctcctaa	attcatgttt	tccattatca	tccttgcccta	91140
cgacctaggc	tgcatccgga	ttctataagt	acgtactctc	agttgctttt	tctacaagtt	91200
gggctagccc	acaggctgca	aacagaaatt	ttatttcttg	aaatctattt	tcttattttac	91260
aaatttattt	ccctaaaaatg	aataaaactaa	ggagtttata	tggaacaatcc	cacacaatcg	91320
cgaccaccga	gtccggagat	aagtatagaa	gaactagagc	ttcaagaact	tgccagatcc	91380
tcgaatactg	agactatttc	taatacacct	cccccgctcat	gcgctgctac	tgccgaagaa	91440



gtatctcttt	ttattgaggg	aggccgtaga	aactcagaag	atgaggagggg	acctctagga	91500
tcttgtgagg	tgtacgatgt	tgtctgtata	acaaaccaag	gagatcctga	ggttagagat	91560
cacgaagtca	gagttatgta	cattaacggc	agcggtcgaa	cacaacatga	gggtattctt	91620
gatgctatga	acatctgtga	tctcagagga	gaacccgtca	ggttcatata	caatagtggg	91680
tatggtttag	ggagctgctt	cttagggatt	cgaaatcgta	ttcctcctag	agataatgtt	91740
attagccaag	caatacaagc	acgatggaat	gagtttttta	ttttcgcaga	aaatgcaaat	91800
cgagattaca	tcgttctttt	ctctggtaat	ggagggtctct	atctttcaagt	cgcttttagat	91860
aactccatat	actcacatca	tattctttgt	gttggcattg	gaagcagtta	ttatatccaa	91920
ggaaattatc	gtgttcacaa	ctaccgtgtg	acaggggatt	ggacgaccct	cctggatcgt	91980
cggggggcaa	cagcagtaaa	tactacaacg	ttgccttatg	cagattctgc	tgaaggactc	92040
tttttaccct	cagtacgctg	tccctcatat	caatgggcat	tgcgttggtg	agaacagtgc	92100
ctgatcatgg	ataacaacca	acaagttggg	tttcgcccc	aagattcctc	ttcagaaatc	92160
gccttagtag	taaatttaaa	tcaggaccac	agcacctgga	ctcgtctgat	tgaatggata	92220
gatcgggggg	attctcaggc	tgttctagaa	ttgaatcctc	aaccgagtca	ttgtcgtgat	92280
attgcattga	ctgcactata	cgctacaaca	aggatttctt	ctttacttca	agagtgccta	92340
atgatttctg	tgacttatgc	tccagagggt	ttcgtcacct	atgctatcgt	tacaggatac	92400
tctataatga	ccttgcgcta	ttttattcta	ttattaacaa	atcgtccagg	ctgccggcgg	92460
cattttctgtg	ttttaagatt	agcggcttta	gggttgacgt	ccttaggatt	tttgactgta	92520
ttgcttgatc	atatcaatgt	aacacggaga	gtcaatcgcc	gccccccctt	aatatcagta	92580
atcttctgta	ctgctagtgt	tgccacagga	agtttcatct	atgtagactt	aacacgcagt	92640
tttttcacga	gcttacgttc	gcgcttgcaa	ttgtttgttc	aaagaagatt	aacaggaaga	92700
gggttaccac	tgagaagggt	ttttgtaaat	cacctagact	ctttgagatt	ttctcaaaat	92760
gctttgataa	cctttcatgg	gggacttttt	atgcctctca	taatagggtt	ttttaatcag	92820
ctggctattc	aggttcctcg	agttgtcatc	agaccaaata	ccactgccgt	ttatgatctc	92880
aaccagacct	cacaggaagc	gtgggactct	ggagacgtat	tagctatagg	acagaccata	92940
aacttcttgc	tttgcatgat	tctattgggtc	atcaatacct	ttttcttcgt	gagatccgta	93000
cgaaggaatt	tgcatcgtag	acctcatcga	tagcaactgt	gcagaaccct	actctttaga	93060
tttcaaaaaat	aactgatacc	gaaatgcccc	tgtactatag	gtgccattgt	tccttagaaaa	93120
tctaaagaga	tcggcctctt	tcctttatat	ctgaaatcat	gactagggaat	aaggagttaa	93180
ctgtctttta	acgcattctg	ttgacattaa	aaccaaataa	aaacatgttt	ttatttggtc	93240
tattctgtta	aaatagatag	gtttttttta	actctgatcc	taaagtgtca	ttgaaaagggt	93300
tcagggtatt	cttatagagg	tccccctatg	gcagtagaag	gaagagtaaa	tagttctcaa	93360
gccttaaatc	aagattgtca	agaagtctta	gcaaataaac	aatcgaaagg	cctcctaagg	93420
tgagaattc	tatctatagt	agtagctgtt	atcaccttta	tcgccgggggt	tgtgttgata	93480
gctttaacat	tagcctctat	tttaacttct	gttccttact	tagcgttagg	agtgttttta	93540
ctgattgtca	ctctgggatg	tataatat	gctctttgct	ctgagaaaaat	aaaaaaagggt	93600
cccccgactc	ctatttcaca	taaagaggag	atcattgcct	ggttcgaaga	gaagaaaaat	93660
attgatattg	aaaaggaaaa	agaagatccg	gagcattttg	gaagaaccgc	tacggatatc	93720
ccaatgagat	ctgcattaga	tcagtttaac	cactcttgtc	accatattca	cgagagcccc	93780
gcgttaacag	aaacttatag	aagccatcaa	gatgttctcc	tctttaagga	ctgggtgtcct	93840
gttacgttgc	ctgatgtaac	ctcagaagaa	gaagtcttaa	tacgcagtgt	ggttggtagc	93900
tattttattaa	tggaggcggtg	cgttccaaaa	gtatccatgc	ttatcgacga	actccataat	93960
aagcttatnt	ctccttcgga	aagagagtgc	ctcttttatag	ataaaaaaac	attgcagcga	94020
aaagctagtt	ttctttttcac	tcagaaagat	ctcgcaacat	tctttcttga	cttatacgcg	94080
ggtgaatgat	ggtcatttag	caccgtttcg	agcaggagca	aaatggatct	taatacatta	94140
cgttaggtta	agacgtcaac	acaatcagaa	cgactttttt	actccaggac	attcttggtta	94200
ctatgctcgt	ctagccttta	accaaaccga	acgactctat	catcaattat	tcaatgtaga	94260
aaagcttcgt	agtatctatg	cgaacatgga	taaagaccct	ctatgtcacc	catgggctnt	94320
cattcctatc	tatgatttat	tgaaaacaga	ggaccatgga	gatgggtttc	tagaacaaca	94380
agaagatcgg	gaatatccaa	gtagagctgc	tcaagatcaa	ttttggggct	aatgtttaaa	94440
ggatcagttt	tttaaaacac	ggattctaaa	ttgtaattca	ggattactat	ttttcttcag	94500
aaagcttaga	cctactgctt	gtgaggcagg	ggagtagtct	tacaccccaa	aggaaatata	94560
ccgaataaaa	atatctagaa	gaggctctag	atacatcttt	ggaaatagac	tctccgttct	94620
tagatactct	agattatcta	aatttcatga	ggagagatca	aaagaaaatg	ttccaagatg	94680
ttatggaaca	ttttctctct	agttttattt	tttaatagca	taagagtttg	tttaatatct	94740
tgttcacgtt	gaaatgctag	ctcgcggctt	actttttctt	tattccaatc	taaaatggac	94800
tttttaaaact	ctaaatcctt	ctctcggagc	tctaattcgc	gattttttcaa	ctccaattcg	94860
cggttccgaa	tgtcaaattc	acgattaaaa	caatcgataa	tttgggcaac	ttgtccagat	94920
tgacacatct	tagaaatgcc	ctctaattctt	tgaaccatgc	tatcgaaaaa	atctaagaca	94980
tattcattag	aagactcttt	atcagtcttt	tcagaaaagc	cttctgagtc	agaagtacca	95040
caactttctc	gaactctctc	cgaacttttt	tgcccgtcgg	aaattgcttg	tagttcatta	95100
cgatatctct	tgccctcttc	gattgggggtt	tcaatcagct	cattgagttg	tgttattaaa	95160
acttcaggat	cctcctcaat	tctggactga	gaagagacat	cctcattgca	aatgcctttt	95220
aggggagcgg	agaaactgca	ggagaaaaat	aaactataaa	taaaaaattt	cttaatcata	95280

aaactttaaa	gtaattaatt	taataaatcg	attttaatgg	tattatagaa	atataaaaaat	95340
caaaatacaa	aagaaatttg	tgaataaaaa	aaagaatagc	aaattatttt	ttgttcataga	95400
tttgtgaatt	ttaaaaaata	ttatttatta	aatacaaaacc	tgtaacaat	agggtgtgaa	95460
aggagattac	gatttttttg	agatatcctt	attaactaca	aatgggtctt	acctatatta	95520
ggttaattaa	aataatataa	attattttatg	tgttattgat	ttataattaa	attttcttta	95580
tgtttatcta	ctcatattta	atcttggtat	aatgacaann	ccccaccat	cccgatcctc	95640
ctctcctcct	ccctatgatt	ggatagaact	tcaagatctg	gggaatacga	ataacaatag	95700
cagtcgagct	accccccccc	gaagtaggcg	gtgagctgcc	cccgtatttt	tcagctagca	95760
actttgttgt	aatagagcgg	ggcgctccta	gtctgccttc	tccacagcaa	cttttatctc	95820
ttccagaata	ttctaggcag	ccgccaccag	gatattttga	tgaacacagca	agcataacta	95880
gcagaacgag	tgaagagatg	tttggtagct	tggtctctac	cttggtgtgt	cctgccaact	95940
cggaaagggg	ttgggaagat	cacgaggtaa	attgtattta	tattgctagt	accagtgaca	96000
ctcaacttga	agctgttcaa	ggtgggatgc	atatcactga	gttacgtggg	gaacccgtaa	96060
gagttcttta	tgagacgggt	cacttatatc	catttgctag	agaaaataca	tgctattccc	96120
gtttagaagt	tagccatata	gttagagcta	tgacgtactt	ttgggaccga	tttttttagtc	96180
gccactggaa	cgtggggcga	cgtttcctag	tattttacca	gggaaacgga	ggcgctatg	96240
ttcaggcagc	cctcgattca	tccatgcata	ctcaggatat	ctatgttcta	gggctctctc	96300
cgactgtcta	tattagaggg	aactatcacg	tacagcacta	ccgtgttcga	ggattttggc	96360
cctcttgctt	ggattctcta	gcggcctgtg	cggaaaatac	atcagtactt	cctacgggga	96420
atcgagtgc	ggaatctttt	acccctctct	attcagccac	acatttgata	acgcgatacg	96480
gtatggtgag	agatgcctgt	tggtttgttc	tgagggcatg	ggaatgcttc	cagaaacgca	96540
acaacaaaca	tctcctttta	cttcactaga	agggggacat	gaggtagctc	tagttctcaa	96600
tccccagcag	aaacccagag	ctctaagtat	tgctcttaga	ttgatgcag	aagaaagagg	96660
tgggagatta	gaactctaact	atatgcctgg	acgttctagt	aatcctttca	tgacaagtat	96720
gtatgttctc	gtacggctga	atacacttgc	tcagatctac	ctgatgtctc	cttattattc	96780
tttccaaagc	aacgacattg	tatgccttat	ctttataagc	agtgtctgtg	tagagacagt	96840
aagctacata	ttcctgactg	taactgactc	aacttgtggg	cgtcggtacc	tgcgtgtccc	96900
acggctagtt	tgtacagggt	tacgtaacct	ggcgttaccc	acaactctac	tagagctact	96960
tattttgtca	taccctcgat	cagtagaggg	ggtacctttc	aatgttagat	tcattcttgg	97020
atatatgtgc	actactagag	ttgtattttt	tgcatggaac	ttgatcctcc	actggccttt	97080
ccgatgtcta	cgccatggaa	tccaatttgt	ttgtcataga	agtataatag	gacatacgtt	97140
gggagcaaga	ttactgatt	taaccctagc	aagtatgcga	tacgcaatag	tgtttccatc	97200
tatagtaagt	tcattgctgt	taactgctct	tgctcatgca	aataactaaca	tacttgctct	97260
ggacccttat	agattgatcg	aatctggaga	tttaagacgt	cccgcattta	atgatgatga	97320
aatgcaacaa	gcagataatc	cttgggatgc	ttactctatc	ggcttagtta	taaacacgtg	97380
tatctacatg	ttaattttat	tcgcaaacct	aattttcatg	gtgtactctg	tacgaagata	97440
ccatagatcc	cgccgctaag	agtagcttgc	cttaagtttc	gtactatcta	ttcttcggca	97500
atgcaagata	agaaaacatt	gattaagagc	gaatagaacc	ctaaaaaact	gtgtttattt	97560
tttattacag	tttttttagat	ataaagatct	cttttttagt	ccgtatctct	aaatgaaatc	97620
aaagggttcc	ttgtgaagaa	aaccctacag	attgcaaccg	aagaatagac	tcgaaatgag	97680
gggacacctt	tggaatctc	tgctcgtagg	tgctgactg	attagaaaaa	aagttttgat	97740
ttttcaaagt	aaataagcct	actttgtatt	agaggctgat	tcataaaact	tcctaagaaa	97800
tatatgataa	gaaaaacttg	gggaggacag	gatttgaacc	tgtgacctac	gggttatgag	97860
tccgcagctc	taaccactga	gctaccgccc	cccaaggtaa	gagagcaatg	ctaacacata	97920
attttctaat	gatcaaggga	tatccacgcc	tgaacggaat	gtagttagtg	ttgaggcggc	97980
tttaagtatt	gtaccgctat	ttgcttcata	cgcatgtaca	gagattctct	accattcaac	98040
ctacaaaaag	aaagataggg	agtcaggcgc	tgaaaaaaaa	ttggcttgca	tgtaaaaatt	98100
gtagaaggag	tttctccaga	atataacctca	gtaataaaag	aggcgattcc	tgaagacact	98160
aaagctttcg	tataagtga	aaaaaataaa	attccatctt	gatataacct	gtaaagatat	98220
aaatcactct	gacaacctac	aaccaagttc	tccttcaaca	tgcgcttctt	gtcaaaaagca	98280
tcccttgaag	aactattttc	catcaactta	agatacagat	gatctttttg	aaaagggtct	98340
ggaaatagct	cctcaataat	tttatgctgt	tttttttaaac	acctagcgtg	ttgcagagga	98400
cagataaatt	ccaaaatact	tctcaatgat	ttgattcaat	gatacgatca	ggctcttttt	98460
tgatttgttg	caaagtctga	gataaggcca	taatacattg	gtcagctctt	gcaataatat	98520
ctcaggagct	gttgattttc	aagtcaagg	atgagctagt	tacaccacat	tctggcatcg	98580
aaaaacaata	gggcataggc	tgattttaagt	ttagtttcaa	agaagctaaa	agattcgcgtg	98640
tggcaggatc	cgtttggttg	ttgcgattta	tctctataag	cgcattcaac	tgcttttgat	98700
tgatcatttg	gtgcttgatg	atttgatgct	ggttgatcgc	ttgctcaatg	ttctctatct	98760
gttttttggtg	ggccttgcca	tcaatagcat	aagtagcctc	atctcctaag	cgcgccccat	98820
aaacagtatt	aataactta	tgattttccaa	tggaaaaaac	tataacaaga	ccaacagcct	98880
gaggaaccgc	ataaatcaac	gctgaaatag	aggctatcat	cgtggctaaa	agaatttgtc	98940
gtgttcctgt	cggatctaat	tgcaaaatc	catggtttat	caaattccat	agactgttta	99000
catgcctatg	cttgttctct	ttatctaaac	atgtcgctgt	aaaaatgcc	aaaacaacgc	99060
caatccctag	accacccctt	aaccaaattg	ttagagttaa	agcaaccgta	tgatgacata	99120

ctaaaattaa	tgcccaagct	aaaatataaa	gtaatatata	tttccaattc	ctttggagga	99180
ataaaccaat	tttttcaacc	gcgtttttta	aacgagttgt	ccaagaaaat	gaattttgat	99240
tataaggaac	taatttcaga	tcagttaatg	caactaacgc	tgaaatagga	gggctgacta	99300
taggagagtc	ccctgaagca	tttgaatcag	gagagttcga	tctagaagag	ctcagtcgtg	99360
cacaaaatag	ttcttgagga	acgtattggt	cagaaggcga	aattcctcca	gaagatagtg	99420
gagtagacat	tcgatagtga	aaaaaataaa	acaataagca	ctatattaaa	ataaggactt	99480
tttctttgta	aacagagggt	tttgtgcttc	tatagccctc	ctagtttact	caatatttta	99540
ttggtagtat	tcgcaagggt	ttgtgaaaag	gatttgactt	tttctaaata	acaaatataa	99600
tcctaagtgcg	tttatagaat	aggggaaatg	aagagcaccg	ttctattttt	agggtcgaat	99660
ctaccacta	ggccagccag	tcacaggctt	aggcttaaaa	gattttgtta	aggataattg	99720
atcaatggcg	aaaaaagaag	atactcttgt	actcgaaggt	aaggtagaag	agctccttcc	99780
aggaatgcat	tttcgtgtaa	tactagaaaa	cggtatgcc	gttacgcgcc	atttgtgcgg	99840
aaaaatgcgt	atgagtaata	ttcggattgc	ttgttgagga	ccgcgttact	gtcagatagt	99900
ccgcctatga	cttaacaaaa	gctagggttg	tctacagaca	tcgttaatta	tattttctat	99960
tgatgtttta	aaataagtga	catagactag	gcggtttttc	aagaccggga	agcaatgcat	100020
aagtaagccc	agatagctca	gtggtagagc	acttgcatgg	taagcaagcg	gtcgtagggt	100080
caattcctat	tctgggcaga	aagaatggtt	ggagtaatca	ataattttta	agaggatttt	100140
gagatgtcaa	aagaaacttt	tcaacgtaat	aagccccata	tcaatattgg	gacgatcggg	100200
cacgttgacc	atggtaaaac	tacgctaaca	gcggcaatta	cacgcgcgct	atcaggggat	100260
ggattggcgt	ctttccgtga	ctatagttca	attgacaata	ctccagaaga	aaaggctcgt	100320
ggaattacta	tcaacgcttc	tcacgttgaa	tacgaaaccc	caaatcgtca	ctacgctcac	100380
gtagactgcc	tcggtcacgc	tgactatggt	aaaaatatga	ttacaggcgc	cgctcaaattg	100440
gacggagcta	tcttagtcgt	ttcagctaca	gacggagcta	tgccacaaac	taaagaacat	100500
atcttgctag	ctcgccaggt	tggagttcct	tatatcggtg	ttttcttgaa	taaagtagat	100560
atgatctctc	aagaagatgc	tgaacttatt	gaccttggtg	agatggaact	tagtgagctt	100620
cttgaagaaa	aaggctacaa	aggatgccct	attatccgtg	gttctgcttt	gaaagctcct	100680
gaaggtgatg	caaattatat	cgaaaaagtt	cgagaactta	tgcaagctgt	ggatgacanc	100740
atccctacac	cagaaagaga	aattgataag	cctttcttaa	tgccatcga	agacgtattc	100800
tcaatctctg	gtcgtggtac	tgtggttaca	ggaagaatcg	agcgtggaat	cgtaaagggt	100860
tctgataaa	ttcagctcgt	gggattagga	gagactaaag	aaacaatcgt	tactggagtc	100920
gaaatgttca	ggaagaagct	tcctgaaggt	cgctgaggag	aaaacggttg	tttactcctc	100980
agaggtattg	gaaagaacga	tgttgaaaga	ggtatggtgg	tttgtcagcc	taacagcgtg	101040
aagcctcata	cgaaatttaa	gtcagctggt	tacgttcttc	agaaagaaga	aggcggacgt	101100
cataagcctt	tcttcagcgg	atacagacct	cagttcttct	tccgtactac	agacgtgaca	101160
ggagtcgtaa	ctcttcctga	aggaactgaa	atggtaatgc	ctggagataa	cgttgagctt	101220
gatgttgagc	tcattggaac	agttgctctt	gaagaaggaa	tgagatttgc	aattcgtgaa	101280
ggtggtcgta	ctatcggcgc	tggaaacgatt	tcaaagatca	atgcttaaaa	atgaattctg	101340
cgatgatttt	catcatcgcg	attttctggg	tgtgtagctt	agctggtaga	gcagtgccct	101400
ccaaagcgc	cggtcggggg	ttcgattccc	ttcgaccccg	tagatttaat	ttttaatcta	101460
gaagttggtt	tatgaaacaa	caacacaatc	gtaaggcttt	atctcgcaag	attggcacag	101520
tgaaaaaaca	agccaaattt	gcagggaagct	ttttagatga	gattaaaaaa	attgaatggg	101580
taagcaagca	cgatcttaag	aaatacataa	aagtagttct	tatcagtatt	tttggttttg	101640
gatttgctat	ttatttcgta	gatcttggtg	tgcgtaagtc	aatcacatgt	ttagatggta	101700
taacaacctt	tttggttcggt	taattgcatg	tataaatggt	atgtcgttca	agtttttaca	101760
gctcaagaaa	agaaagtaaa	aaaggcttta	gaagatttta	aagagtcttc	aggaatgact	101820
gattttatac	aggaatttat	cttgccattt	tggaaagtga	aaaaggagaa	101880	
cataaggtcg	ttgaaaaata	catctggcct	ggatacctct	tagttaaaat	gcacttgact	101940
gacgagtctt	ggctctatgt	taaaagtaca	gcaggtatag	tcgagtttct	tggaggcgga	102000
gtccctgtag	ctctttctga	agatgaagta	agaagtatct	taacagatat	agaagagaag	102060
aaatcgggag	tggtgcaaaa	acatcagttc	gaggttggtt	ctagagtga	aattaatgac	102120
ggagtctttg	tcaattttat	cggcacggtt	tccgaagttt	tccatgataa	aggacgcctg	102180
agtgttatgg	tttctatctt	tggaaagagaa	actagggtag	atgatttaga	attttggcaa	102240
gtggaagagg	tagccccagg	gcaagaaaag	gagttagatg	gttaaaatca	gtgtattctt	102300
attcctttat	ttcttataat	tttagttttt	cgtttcttac	cctctgtttg	ttagaggtgtc	102360
tcagtgcaaa	gtaagggttta	gtatgtcggt	aaaaaaggta	atcaaaaata	ttaagttgca	102420
aatccctggg	ggtaaagcaa	atcctgcgcc	acccatagga	ccagctttag	gtgctgctgg	102480
agtcaatatt	atgggcttct	gtaaggaggt	taatgctgca	actcaagata	agcctggaga	102540
cttacttcca	gtagtcatca	ctgtttatgc	tgataaaact	tttactttta	taaccaaaaa	102600
gcctccagtc	tcctctttta	taaagaaaac	tttgaatctg	gaatcaggat	ctaaaattcc	102660
taatcgtaat	aaagtaggaa	aacttactca	ggctcaagtt	gaagcaattg	ctgaacaaaa	102720
aatgaaagat	atggatattg	tccttctaga	atctgcgaaa	cgtaggttgg	aaggaaactgc	102780
ccgtagtatg	ggtatagacg	tagaataaat	tgttacttgt	agagctgtag	aattatgaca	102840
aaacatggaa	aacgtatacg	aggcatctta	aagaactatg	atttctcaaa	atcatattct	102900
ttgcgggagg	ctatagatat	tttaaaacaa	tgtcctccag	tacgcttcga	tcaaactgta	102960

gatgtatcta	tcaagtttagg	gatagatcct	aaaaagagcg	accaacaaat	tcgtggagcc	103020
gtttttttac	ctaattggtac	aggaaaaaact	ttaagaattt	tggtttttgc	ttcaggggaaac	103080
aaagtcaaag	aagctgttga	agcgggcgca	gactttatgg	gaagcgacga	tcttgttgaa	103140
aaaattaaat	ccgggtggct	ggaattcgat	gttgctgtcg	ctaccccaga	tatgatgcgt	103200
gaagtaggaa	aattaggaaa	agtcttagga	cctagaaatc	taatgcctac	acctaaaaca	103260
ggaacggtaa	ccacagacgt	tgctaaagca	atctccgaat	tgcgtaaagg	aaaaattgaa	103320
tttaaagcag	accgcgcagg	cgtatgtaat	gtaggcgtag	gtaagtgtgc	ttttgaaagc	103380
agtcaaata	aagaaaatat	tgaagctcta	agtctgtcct	taattaaggc	caaacctcct	103440
gcagctaaag	gtcaatatatt	agtctcattc	actatttctt	ccactatggg	gcctgggtatt	103500
tctatagata	ctagagaatt	aatggcatct	taatcttaaa	gagggaaaat	gaaacaagaa	103560
aaaacattac	ttcttcaaga	ggtagaagac	aaaatttccg	cagcacaggg	attcatttta	103620
ttaagatacc	ttagattttac	cgccgcgtat	tctagagaat	tcagaaactc	actttctgga	103680
gtttctgcag	aattttgaagt	tttaaagaag	agaatcttct	ttaaagctat	agaagctgca	103740
ggttttagagg	tagattgtag	tgatacacat	gggcatctcg	gtgtagtctt	ttcctgtgga	103800
gatacctgtt	ctgccgcgaa	gcaggtactg	gactttaata	aacaacataa	agactcttta	103860
gttttctctg	ctggaaggat	ggacaatgct	tctctgtctg	gtgcagaggt	agaagctgtc	103920
gccaaattgc	catctcttaa	agaacttaga	cagcaggttg	ttggtttatt	cgctgtctca	103980
atgtcccaag	ttgtaggaat	tatgaattct	gtcctttctg	gagtgatctc	ctgtgtggat	104040
caaaaggcag	gaaagaacta	aagaattaaa	attaaaactc	tcaaaataag	taagggtgac	104100
aaaagtgcag	acagaaaagt	tggaaaactt	agtagagaag	ttaagtaatt	taactgtact	104160
agaactctct	caattgaaaa	aattattaga	agagaagtgg	gatgttactg	cttctgtctc	104220
cgtagttgct	gttgctgctg	gtggtggcgg	agaagctcct	gttgctgccg	aacctacaga	104280
atgtgcagta	accctcgaag	atgttctctg	agataaaaaa	atcggcgtct	taaaagtcgt	104340
tagggaagta	actggattag	ctttaaaga	agctaaagaa	atgacagaag	gtttacctaa	104400
aactgttaaa	gaaaaaactt	ctaaaagtga	tgctgaagat	actgttaaga	agttacaaga	104460
tgctggcgca	aaagcctcat	ttaagggact	gtaatttgta	gaaaagaaaa	atcgaaagat	104520
ttttcttttc	ttttcttttt	catgtataaa	aaaccgaatg	ctcccttttag	aagcatatcg	104580
aggcttaatt	tagggaaatt	ttgtcgcctc	aaaatagcag	gagaactcgc	acgttgaagt	104640
gccctgaacg	ggtcagtggt	aaaaaaaaag	aagatatccc	agaccttcca	aatcttatcg	104700
aaatccaaat	taagtcttat	aagcagtttt	ttcaaattgg	aaaatttagca	gaagaaagag	104760
aaaatactcg	tttagaagag	gttttcaggg	aaatttttcc	cattaaatcc	tataacgaag	104820
ctaccgttct	tgagtacctt	tcatataatt	tgggtgtgcc	aaaatattct	ccagaagaat	104880
gtatccgtag	aggaattacc	tatagcgtca	ctttgaaagt	ccgttttctg	ttaaccgatg	104940
aaacgggaat	caaagaagaa	gaagtctata	tgggaacgat	ccctctaatt	actgataaag	105000
ggacatttat	cattaatgga	gctgaaagag	tcgttgtttc	ccaagtccat	cgttctccag	105060
gaattaactt	tgaacaagaa	aaacattcca	aaggtaatat	tttattctcc	ttcagaatca	105120
ttccttatcg	tggaaagtgg	ctcgaagcta	ttttcgatat	taatgactta	atttatatcc	105180
atattgatag	aaaaaaacgt	agaagaaaaa	ttctagcaat	cacctttatc	cgagctcttg	105240
gatactcttc	agatgcagat	atcatcgag	aattcttcac	aataggagaa	agttctctta	105300
gaagtgcagaa	agactttgct	cttcttgttg	gaaggatttt	agcagacaat	attattgatg	105360
aagcctcttc	tctagtttat	ggaaaagccg	gagaaaagtt	aagtacagca	atgttaaaac	105420
ggatgctcga	tgctggaatc	gcttctgtta	agattgctgt	agatgctgat	gaaaatcatc	105480
ctattatcaa	aatgctcgct	aaggatccta	cagattcata	cgaagccgct	ttaaaagatt	105540
tttatcgtag	actacgtcca	ggagaacctg	caactctagc	taatgcacgt	tctactatca	105600
tgaggctctt	ctttgacccc	aaacgttata	atctaggacg	tgtagggcgt	tataagctca	105660
atcgcaaact	aggcttctct	atagatgatg	aagctctgtc	tcaagttact	ttgagaaaag	105720
aagatgtgat	cggagcctta	aagtatctga	ttcgtttgaa	aatgggagat	gaaaaagctt	105780
gtgtagacga	tattgatcat	cttgctaata	gacgtgtccg	ctctgtcgga	gaactcattc	105840
aaaatcaatg	tcgttcagga	cttgctagaa	tggagaaaat	tgtagagag	agaatgaatt	105900
tattcgattt	ctcctcagat	acgttgactc	caggaaaagt	tgtctctgct	aaaggtctcg	105960
ctagcgtggt	aaaagatttc	tttggccgct	cccagctttc	gcagtttatg	gaccaaacca	106020
accctgtagc	tgagttaact	cacaaacgac	gtctttctgc	attaggtcca	ggaggactaa	106080
atagagaacg	cgcaggattt	gaagttcgtg	acgtgcacgc	aagtcattat	ggacgttatt	106140
gtcctattga	aactcctgaa	ggtccaaata	ttggtctgat	cacctctctt	tctctttttg	106200
ctaaaattaa	cgaatttgga	ttcattgaaa	ctccttatag	aattgtaaga	gatggaatcg	106260
taacagatga	aatcgaatac	atgacagccg	atgttgaaag	agaatgtgtg	attgcacagg	106320
cttcagcaag	cctagatgag	tacaatatgt	ttacggaacc	cgtctgttgg	gtacgttatg	106380
ctggagaagc	tttcgaagca	gatacaagca	ccgtaaccga	tatggatggt	tctccgaaac	106440
agctcgtttc	tattgttaca	ggattgattc	ctttcttaga	gcacgacgat	gcgaaccgcg	106500
ccttgatggg	ctccaatatg	caacgtcaag	cggttccctt	acttaaaacc	gaagctcctg	106560
ttggtggcac	tggattagaa	tgtcgtgctg	ctaaagattc	tggagctatt	gttggttcag	106620
aagaagatgg	tgttgttgat	tttgttgatg	tttacaaggt	agttgttgct	gcaaaaacata	106680
atcctacaat	taaacgtacc	tatcatctga	aaaagttcct	tagatctaata	tcaggaactt	106740
gcattaacca	acagcccttg	tgtgcagtcg	gtgatgtcat	aactaagggt	gatgtgattg	106800

ctgatggacc	cgcaactgat	cgtgggagaac	ttgcttttagg	taaaaatgta	ctcgttgcc	106860
ttatgccttg	gtatggatac	aacttttgagg	atgcgatcat	tatctctgaa	aaattgatca	106920
gagaagatgc	ctatacctct	atztatattg	aggaattcga	actaacagcc	cgagatacaa	106980
aattaggaaa	agaagagatc	actcgtgaca	ttcctaacgt	atctgatgaa	gtattggcca	107040
atctcgggtga	ggatgggac	attcgtatcg	gtgctgaggt	taaacctggg	gatattcttg	107100
ttggtaagat	cacacaaaa	tcagaaacag	aattagctcc	agaagagcgt	ctgctccgtg	107160
ctatttttgg	tgaaaaagct	gctgacgtta	aagatgcac	tttaacagtg	cctccaggaa	107220
ctgaaggcgt	cgttatggat	gttaaagctc	tcagtagaaa	ggatagattg	tcaagagtg	107280
atgacgaact	tgtagaagaa	gctgttcac	ttaaagattt	gcaaaaagga	tataaaaacc	107340
aagttgcaac	tttaaaaaaca	gaatatcgtg	agaaattagg	agctctctta	ttaaattgaga	107400
aagcacctgc	agccattatt	caccgtcgta	cagcagaaat	cgttgttcat	gaaggcctac	107460
tctttgatca	agagacaata	gaacggatag	aacaagaaga	tttagtggat	cttttaatgc	107520
ctaactgtga	aatgtatgaa	gtgttgaaag	gacttctatc	agattacgaa	acggcattac	107580
aacggctaga	aatcaattat	aagactgaag	ttgagcatat	tcgtgaggga	gatgcagatt	107640
tagatcatgg	tgtcattcgc	caagttaaag	tctacgttgc	ctctaagaga	aaacttcaag	107700
ttggagataa	aatggctgga	cgacacggaa	ataaagggtg	tgtttccaaa	atcgttccccg	107760
aagcggatat	gccatatctc	tctaacggag	aaactgtaca	aatgatcctg	aacccccctg	107820
gggtgccttc	aaggatgaac	cttggacagg	tattagaac	acacctaggt	tatgcagcaa	107880
aaactgcagg	cattttacgtg	aaaaccctcg	tttttgagg	attccctgaa	caacgtatct	107940
gggatatgat	gatagaacag	ggattaccag	aagatgggaa	gtccttctta	tatgatggga	108000
agacaggtga	acgctttgat	aacaaggtag	tgataggcta	tatctatatg	ctaaagctca	108060
gtcacttgat	cgctgataag	attcacgcaa	gatctatatg	gccatattct	ttagtcaacg	108120
aacaacctct	cggtggtaaa	gctcagatgg	gaggacaaa	attcggggaa	atggaagttt	108180
gggctctaga	agcatatggg	gttgctcata	tgctccaaga	aattctaacc	gtgaaatctg	108240
atgatgtctc	aggaagaaca	aggatttacg	aatctatcgt	taagggggaa	aacctcttgc	108300
gacaggaac	gcctgagtcg	ttcaatgtgc	taattaaaga	gatgcagggt	ctaggacttg	108360
atgttcgtcc	tatggtcgta	gacgcttaaa	aaatgacgtt	ttggagaaaa	taatgttcgg	108420
agaaaattct	cgagacattg	gagttctttc	taaagaagga	ctatttgata	aattagagat	108480
aggcatagct	tcagatatta	caattcgtga	taaatggtct	tgtagagaaa	tcaaaaagcc	108540
agaaactata	aattaccgta	cgtttaaac	tgaaaagggc	ggtctatttt	gtgaaaaaat	108600
ccttggtcct	actaaagatt	gggaatgttg	ctgcggaaaa	tataaaaaaa	taaaacataa	108660
aggaattgtc	tgcatcgat	gaggagttga	agttactctt	tcaaaagtcc	gtcgtgaacg	108720
tatggctcat	atcgagttag	cagttcctat	tgctcatatt	tggtttttca	aaacaactcc	108780
atcacgcatt	ggtaatgttc	ttggaatgac	agcttcggat	ctggaacgtg	tcatttatta	108840
tgaagaatat	gtagttattg	acccaggtaa	gacagaccta	actaaaaaac	aacttcttaa	108900
tgatgcgcaa	tatcgtgaag	ttgttgagaa	gtggggtaag	gacgctttcg	ttgctaaaaat	108960
gggtggcgaa	gctatctatg	atttgcttaa	atccgaagat	ctccaaagct	tgcttaaaaga	109020
tcttaaagag	cgtttacgca	aaacaaaatc	tcagcaagcg	agaatgaagt	tagccaaacg	109080
tcttaaaatc	attgagggat	ttgtttcttc	atccaaccac	ccggagtggg	tggtattaaa	109140
aaatatccca	gtagttccac	ctgatctccg	tcctcttggt	cctttagatg	gcggtcgttt	109200
tgcgacttct	gatttaaacg	atctctaccg	ccgtgtaatt	aatcgtaaca	atcgtcttaa	109260
agcgatctta	cgtttaaaaa	caccagaggt	tattgttcgt	aatgaaaagc	gtatgcttca	109320
agaagctgtt	gatgctcttt	ttgataacgg	tcgacatggg	catccgggtca	tgaggagctgg	109380
aaaccgacca	ttgaaatcct	tgtcagaaat	gttaaaggga	aaaaatggac	gcttccgtca	109440
aaatctttta	ggaaaacgtg	ttgactactc	tgagcgttct	gtaattattg	ttggtcctga	109500
attgaagttt	aatcaatgcg	gattgcctaa	ggaaatggct	ttagagctat	tcgaaccctt	109560
tattattaan	agactaaaag	atcaaggcag	cgtttatacc	attcgttctg	ctaagaaaaat	109620
gattcaacga	ggagccccag	aagtttgga	cgttctcgaa	gagatcatta	agggacatcc	109680
agtacttctt	aaccgagcac	ctacattgca	ccgtttagga	attcaagctt	tcgaacctgt	109740
attgatagaa	ggtaaagcga	ttcgtataca	ccccctagtt	tgcgagcgtg	ttaacgctga	109800
cttcgacgga	gaccaaattg	ccgtgcacgt	tcctctatct	gtagaggcac	aactggaagc	109860
taaagtttta	atgatggctc	cagacaacat	cttcttctct	tcctcaggaa	agcctgtggc	109920
tattccttcg	aaagatatga	cttttaggatt	atattatctg	atggcagatc	ctacctattt	109980
tcctgaagaa	catggaggaa	aaactaagat	atttaaagat	gaaatcgaag	tattgcgtgc	110040
tttaaaatac	gggtggattca	ttgatgatgt	tttcggagat	cgctgtgatg	aaacaggacg	110100
cggtatccat	attcatgaaa	agattaaagt	gcgtattgat	ggacaaatta	ttgagacaac	110160
cccaggaagg	gtattgttca	acagaattgt	tcctaaagaa	ctcggcttcc	aaaattacag	110220
catgccaaagt	aagcgtataa	gtgagcttat	tttacagtgc	tataagaaag	tcggtttaga	110280
agctactgta	cgtttcttag	atgaccttaa	agatcttgga	tttattcaag	ctacaaaagc	110340
cgcaatctct	atgggattga	aggatgttcc	tattcctgat	atcaagagtc	atatcctcaa	110400
agatgcctac	gataagggtg	ctatcgtcaa	aaaacaatat	gatgatggga	tcattactga	110460
aggggagcgt	cattccaaaa	ctattagtat	ttggactgaa	gtttccgaac	agctttcaga	110520
tgccctctat	gttgaaatta	gcaaacaaac	acgtagcaag	cataaccctt	tgctcctgat	110580
gattgattct	ggagccccgag	gtaataaatc	ccagttgaaa	cagttgggag	cgttacgagg	110640

attaatggcg	aagccaaacg	gagcaattat	tgaatctcca	attacttcga	acttttagaga	110700
aggattgaca	gttttagagt	actccatctc	ctcacacggt	gcgagaaaag	gttttagccga	110760
tacagctcta	aaaactgccc	actccggata	cttaacacgt	agacttgtag	acgtagccca	110820
agacgtgatc	attaccgaaa	aagattgccc	tacgttaaata	cacattgaga	tttctgcaat	110880
aggatcaagg	tctgaagaac	tcttgccctc	taaagatcgt	atctatggac	gtactgtagc	110940
tgaagatgtc	tatcaaccag	gtgataaaag	tgcactactt	gctcaatcgg	gtgatgtact	111000
caactccgta	caagcagaag	caattgatga	tgccgggtatt	gagacaatta	agattcgttc	111060
tacattaacg	tgcgaaagtc	ctcgcggagt	ttgtgcaaaag	tggttacggcc	tcaatttagc	111120
taatggtaga	ctcattggca	tgggtgaagc	tggttggtatt	attgctgctc	agtcgattgg	111180
ggaacctgga	actcagttaa	caatgagaac	gttccaccta	gggggtattg	ctgctacgtc	111240
ttcaactcct	gagattatta	cgaatagtga	tggtatctta	gtctacatgg	atctccgtgt	111300
tggtctgggg	caagaaggtc	acaatcttgt	cttgaataag	aagggagctt	tacatgttgt	111360
aggatgatgaa	ggctgctact	tcaatgagta	taaaaagctg	ctttcaacca	agtcctataga	111420
aagcctagag	gtatttctctg	tagaactagg	agtgaataat	cttggttgctg	acggaactcc	111480
tggttctcaa	ggacaaagaa	tgcgagaagt	tgaactacac	aatattccta	tcatttgcca	111540
taagcctggc	tttattaaat	atgaagattt	gggttgaggga	atctctacag	agaaagttgt	111600
gaacaagaac	acaggacttg	ttgaacttat	tgtgaaacag	caccgagggg	agttacatcc	111660
tcagattgct	atctatgatg	atgctgactt	gtcagaactt	gtcggaaact	atgctgattcc	111720
ttcaggagcg	attatctctg	tagaagaagg	acaacgggtt	gatccaggta	tggtgttagc	111780
tagacttctc	cgcggagcta	tcaaaacaaa	agatattact	ggcggtttgc	ctcgtgttgc	111840
tgaattagta	gaagctcgta	aacctgaaga	tgctgctgac	atcgccaaaa	ttgatgggtg	111900
tggtgacttc	aaaggaattc	aaaagaacaa	acgtattctt	gttgctctgtg	atgaaatgac	111960
aggatggaag	gaagaacatc	tgattccatt	aaccaaacat	tgattgtac	acgtggaga	112020
tagtgtgatt	aaggcgagca	gcttaccgat	gggttagttg	ttcctcatga	aatcctagaa	112080
atttgcgag	ttcgtgaact	tcagaagtac	ctggtaaatg	agggtgcagga	agtttaccgt	112140
ctgcagggcg	ttgacattaa	cgataagcat	attgaaatta	ttgttcgtca	gatgttataa	112200
aaagtacgaa	ttactgaccc	aggatgatac	actctgctct	ttggcgaaga	cgtgaataag	112260
aaagagtttt	atgaagaaaa	tcgtcgtacc	gaagaagacg	gtggtaagcc	agctcaagct	112320
gttcccgtct	tattgggaat	tacgaaagct	tctttgggta	cggaatcgtt	tatatcagca	112380
gcttcttttc	aagacacaac	tcgagtctta	acagatgcag	cttggtgtag	caaaaccgac	112440
taccttcttg	gatttaagga	aaatgtgatc	atgggtcata	tgattcctgg	tggtacaggc	112500
tttgaaacgc	ataagcgtat	taagcagtat	ctagaaaaag	aacaagaaga	tctcgttttt	112560
gattttgtta	gtgaaacnga	gtgtgttttn	taactaggtg	acacagtctt	ttatcaagga	112620
ggttatgttt	acaacctcct	tgataggaat	gttttttttt	gttaacgttg	cctagagatc	112680
aacagtgatg	ccaaggtgcc	tatgtctaac	caatttgatc	aattaaagaa	gttgagcact	112740
atcgtttgtg	atagcggaga	cccagagcta	gttaaagcct	cgggatctca	agacgctaca	112800
acaaaccctt	ctttgatctt	aaaagtggcc	caagaaccca	aatttcaaga	gctatttaa	112860
gaagctgtag	tttggggaat	ccgacagaac	ggatgatgat	ttcagactct	ttcttttatt	112920
ttagacaaaa	ttcaggttaa	ctttgctcta	gaaattatca	aaaatatccc	tggtagaatt	112980
tctcttgaaa	ttgacgctag	gctttctttc	aacgttgaag	ctatggtaca	gcgtgcccga	113040
ttcctttcgc	agcttttcga	agctatggga	ggagataaaa	agcgcctgtt	agtaaagatt	113100
cctggaactt	gggaaggat	tcgagctgtt	gaatttttag	aagcaaaggg	catagcatgt	113160
aatgtcactt	tgatttttaa	tttagttcaa	gcgattgcag	ctgctaaagc	taaagcaact	113220
tttaatttctc	cttttgttgg	ccgtatttat	gattgggtga	tcgcccgtta	tggtgatgaa	113280
ggttactcta	tagatgcaga	tccaggtgtc	gcttcagtat	caaataat	cgcgatttac	113340
aaaaaattcg	gtattcctac	gcaaattatg	gcagcatctt	ttcgtacaaa	agagcaggta	113400
ctagcattag	ctggttgca	tcttttaacg	atatctccaa	agctgctgga	tgagctaaag	113460
aaatctcaac	accagtaaaa	aaaagaatta	gatcctgcag	aagctaaaaa	gttagatgtg	113520
cagccaatag	aactcacaga	aagctttttt	cgctttttta	tgaatgagga	tgctatggct	113580
acaganaaac	ttgctgaagg	aattcggata	tttgcaggag	atactcaa	tcttgagact	113640
gcaattacag	agtttataaa	gcaaattgct	gcagaagggtg	cgtaattgct	tactaaatta	113700
agccgatattg	gggataccac	cttaaagcga	aatgaaaaat	aagatggact	ataaatcgca	113760
actagtattt	tcttgccctt	gttggtgcaa	aggcaattgt	tggttctcag	tttttaactt	113820
agacgttatt	ttacatgta	acgtttgtct	atctacttat	acattcgatt	ctgtcatac	113880
taatgagatt	cgtcagtttg	tagcactatg	taaaaggata	catgatgcta	attctatact	113940
tggaatgct	actgtgtcgg	tatcggtaga	agacaaccaa	atggatattc	cctttcaatt	114000
gctgttttct	cgtttccctg	tagtattaaa	tctctcttta	gatggaaaga	aaatagctat	114060
tcgtttcctc	tttgatgctt	taaatacaag	tatcttacac	caagaaagcg	atcttatttc	114120
ttaatcctaa	gtttatttgt	tttcgttttg	cagagcttcc	aaagcttttt	caaggattgc	114180
atctcctgaa	gtagcctctt	taccaccgag	aatttgga	gaagagacta	cttttaaaaa	114240
ggtaaatgaa	agttctgcat	agtcatacaa	agttgcagtg	cttgtaaaaa	tataagcagt	114300
atgggtcaatg	actggtgtcg	cttgtaaaaa	aaatacacgt	ccccatgaag	agtttttctc	114360
tggtttgata	atagtaaaact	ctccgctagg	agattgaatt	tggtgtaata	ttccagattc	114420
taaagtcac	tcattggctt	tatgataggc	taagatttcc	tcaatatact	cttttgaaga	114480

tttggaagtg	atttcctgag	caatgttgat	ggtaggagtg	agatttcctt	tccccttgcc	114540
tataaggaga	acatctaatt	tttctgggag	ctgtgtttta	tcgtcaatac	actgccaaag	114600
agagggtgtc	tgtatgctat	agtttttccc	tgaatagcga	acccattgga	cgggggagag	114660
cgagggtttt	ttctcaaatt	ttcctatttt	tttccgcgca	gtgctcttgt	tttatagcga	114720
gaaacactcg	cattcgttgc	tgccgaagat	cgtatcctag	aggctcttct	tgcttttgc	114780
tgctttgagt	gagatgcaga	gacttgagtt	cttggctgag	cagagaaaagc	agggaaattga	114840
gctacaatca	aaataaaaag	aataaaaaat	ttcatagaaa	attatgtagt	tagttgtaca	114900
ttaaagataga	ttcaaagcac	atagcatagc	tctctacctt	atacaagatt	gtatcgtttt	114960
cagaaaaata	ttcccaatag	ggaatctttg	gatctagaag	aaggcctact	ttcaaacaaa	115020
catagaaagg	caattcttct	tttttgaatt	ctatgtttat	aggaattttt	tcttagagag	115080
ttagaggaga	gcatgggatt	tatcttgaag	atatcaaagc	aattttcttc	tagaacatct	115140
ctgcaaccgc	tttcttatatt	gtggatcagt	tgaattaaat	gctagaatga	cataaactgt	115200
tagattagtg	gaatcataat	aacatctttt	ttaaagaaaa	ttcttttcta	aaagaattga	115260
cggtaaaata	ttatggcgaa	tcttaatgcc	gatggtaagc	ttaagcaaat	ctgcatgct	115320
ttgcgttttag	acactctaaa	gcctgcagaa	gacgaggctg	cggcggttatt	gcataatgct	115380
aaagaacaag	cgaaaagaat	tattcaagaa	gctcaagaag	aagccagaaa	aatcttagag	115440
acggcagaag	agagagctca	tcaaaaagata	aaacaaggcg	aagttgctct	aagccaagca	115500
gggaagcgcg	ctttggaagc	cttaaaacag	gctgtagaaa	acaaaatatt	tagagagtct	115560
ttagtagagt	ggctggagca	tgtaaccacc	gatcctgagg	tttctacaaa	gttaattcaa	115620
gcttttagtgc	aggcttttgg	agctcaaggg	gtttcaggaa	atctgaccgc	ctatatagga	115680
aaacatgtga	gtcctagagc	tgtaaatgag	ctcctaagga	aaggctgtaa	caacaaaaac	115740
tacgaaagaa	aagtgtagtt	gttggaagtt	ttgttggtgg	gttcaatta	aaagttgaag	115800
aaaagaactg	ggttctggat	cttagttcct	cagctcttct	tgagattttc	acacgttatt	115860
tgcaaaaga	ttttcgtgaa	atgatttttc	aaggatcttg	actttaataa	agtcatgaaa	115920
agatcttctc	aatattttaa	gttgctcgta	tgactcaata	ttatttttta	tcttcatttt	115980
tacctactca	gctaccagaa	tccgtacctc	tattttctat	ttcggactta	gacgatctac	116040
tttattttaa	cctatcagaa	aacgatcttt	gcaattacgg	acttcttaaa	cgtttttttg	116100
atttcgaaaa	tttcgctttc	ttttgggctg	gtaaaccgat	tcccttctct	tttggggagg	116160
tgactcagga	aaatgtagaa	agaatgcttt	cctctcagca	gtggctgat	gacaatgatt	116220
ttgaagattt	ctttaaggat	tttttaatga	atcataagtc	ttctcaagat	cgtttgaatc	116280
acttttcaga	tttattttaga	gagtttcttt	cctatcatca	aacgaattct	tcaaagtttc	116340
ttcaagatta	tttcagattt	caacaacaac	ttcgtgttgt	actcgcggga	ttcctgcaa	116400
gagtcttgaa	tatggatgtt	tcctatgttt	tgccgcgacga	agatagttcc	gatccagttg	116460
tgctcgaggt	gctcatgcag	aaagattctc	ctaattatga	gntcctgaa	gagtttncgg	116520
atttacaggg	cgttttggat	gactaanggc	cttctngcct	nanacactga	atngngcgc	116580
ntngccnnta	taccaatttc	ataaactcga	gggattttgt	tccngactcc	tactttgatg	116640
ggaatgtcat	tttagcaaga	tgtgtctacat	atatgtttgc	tattcgtaca	gcttagcaag	116700
tgttgaaaaa	ggaagagaaa	ttattaatca	tatagaaaag	gcaatcaaat	ggtaacagtt	116760
tcagaaccaa	acttgctcag	ggacatgtta	tagaagctta	tggaacttg	ttacgtgtac	116820
gctttgacgg	atatgttaga	caagggtgaag	ttgcataatg	caacgtagat	aatacctggt	116880
taaaagcaga	agtgattgaa	gttgctgatc	aagaagtcaa	ggttcaggta	tttgaagata	116940
cacaaggcgc	gtgtcgagga	gctcttggtta	cgttttcagg	acatctttta	gaagccgagt	117000
tagggcctgg	cttgcttcag	ggcattttcg	atggacttca	aaatcgtctt	gaggtgctag	117060
ctgaagatag	ttctttcttg	cagagaggca	agcatgttaa	tgctatttct	gatcataatt	117120
tatggaatta	tactcccgtta	gcttctgttg	gggatacttt	aagacgagga	gatcttctag	117180
gaacagtacc	tgaaggacga	tttactcata	agattatggg	tcctttttct	tgctttcaag	117240
aggttaccct	gacttgggta	atttctgaag	gaacctataa	tgctcatact	gtggctcgcaa	117300
aagctcgaga	tgctcagggt	aaagaatgtg	cctttactat	ggtgcaaaga	tggccgatca	117360
aacaagcttt	tattgaagga	gagaagatcc	ctgcgcataa	gattatggat	gtgggtttgc	117420
gaatctttaga	tacgcaaatt	ccagtatgtga	agggggggaac	tttctgtacc	ccaggacctt	117480
ttggtgcagg	gaaaacagtc	ttacaacacc	atcttttctaa	gtacgctgct	gtagatattg	117540
tgattttgtg	tgcgtgcgga	gagcgtgctg	gtgaagtgtg	tgaggtatta	caagagtcc	117600
ctcatcttat	cgacccccat	accggaaaag	ctttaatgca	cagaacatgt	attattttgta	117660
acacatcatc	catgcctgtg	gctgcccag	agtcttcgat	ctatttagga	gtgacgattg	117720
cagaataacta	tcgccagatg	ggactagata	ttctgctttt	agctgattct	acatcccgat	117780
gggcacaagc	ccttagagag	atttcgggac	gtcttgaaga	aatccctgga	gaggaagcat	117840
ttcctgcata	cctgtcttct	agaatagctg	ctttttatga	gcgaggagga	gctatcacca	117900
cgaaagatgg	ttctgaagga	tctttaacta	tatgtggtgc	ggtgtctcct	gcaggaggaa	117960
actttgaaga	accagtcact	caatctacat	tagctgtagt	cggagcgttc	tgtggtcttt	118020
caaaagcacg	actgacgcac	gtaggatatcc	ttcaatagac	cctttgattt	cttgggtctaaa	118080
atatttgaac	caggtaggac	aaatttttaga	agagaagggt	tcaggctggg	gtgggtgctgt	118140
gaaaaaagca	gcacagtttc	tagagaaagg	ttcagaaatc	ggcaagcgta	tggaagtgtg	118200
cgggtgaagaa	gggttttcta	tgggaagacat	ggaaatctac	ttaaaggcag	aactttatga	118260
tttttgttat	ctccagcaga	acgcattcga	tcctgtggac	tgttattgtc	cttttgagag	118320



acagatagag	ttattttcat	taatcagtcg	tatttttgat	gctaaatttg	tttttgatag	118380
tcctgatgat	gcaagaagct	ttttccttga	gctgcagagc	aagattaaga	cattaaatgg	118440
cctgaaattt	ctttcagagg	aatatcatga	gagtaaagag	gtcatagtta	gactgttgga	118500
aaaaacaatg	gtacaaatgg	cgtaaggata	tgcaacaat	ctacacaaaa	ataactgata	118560
ttaaaggcaa	tttaatcact	gtagaagcag	agggagctcg	tttaggggag	cttgctacaa	118620
tcacaagatc	cgacggaaga	tcttcgtatg	cttcgggtatt	gcgttttgac	cttaagaaag	118680
taactctcca	ggtttttggg	ggcacatcgg	gcttatccac	tggagatcat	gtcacgttct	118740
tagggagacc	catggaggtc	acatttgagg	gctcattatt	aggcagacga	ttgaatggta	118800
tagggaaacc	cattgataat	gagggggagt	gttttgagg	acctatagag	attgctactc	118860
caacatttaa	ccctgtctgt	cgtattgttc	ctaggagtat	ggtacggaca	aatattccta	118920
tgattgatgt	tttcaactgt	ttagtgaaat	ctcagaaaat	tcctattttt	tcttctctctg	118980
gagaacatca	taatgctttg	ttaatgcgga	ttgctgcaca	gacagacgcg	gatatagttg	119040
tgattgggtg	gatggggcct	acattcgtag	attacagctt	ttttgttgaa	gagtcctaaga	119100
agctaggatt	tgcagataag	tgtgtgatgt	ttattcataa	agctgtagat	gctcctgtag	119160
aatgtgtttt	ggttcctgat	atggccctag	cttgtgctga	aaaatttgct	gtagaagaga	119220
aaaagaacgt	cttgggtttg	cttacagaca	tgacagcggt	tgctgatgct	cttaaggaaa	119280
tttctatcac	tatggatcaa	attcctgcc	atcgtgggta	ccccggttcc	ctatatctctg	119340
atctagcttt	acgctatgaa	aaagctgtag	aaattgccga	tggggggtcg	atcaccttaa	119400
ttactgtaac	tacgatgcct	agtgcagaca	ttacacatcc	tgttcctgat	aacacaggat	119460
acattacaga	gggacaattc	tacttgagga	ataatcgtat	agatccgttt	ggttctcttt	119520
caagattgaa	gcagctgggtc	attggtaagg	tgactcgaga	ggatcatgga	gatcttgcca	119580
atgctttaat	tcgtctttat	gcggattccc	gtaaagctac	agaaagaatg	gctatgggag	119640
tcaagttatc	gaattgggat	aagaaattac	ttgcgttttc	cgagcttttt	gaactcgttt	119700
tgatgagttt	agaggtaaat	attcctttag	aagaagcttt	agatattggg	tggaaaattc	119760
tagctcaaa	tttccacttct	gaagaagtgg	gaattaaagc	ccagttaata	aataagtatt	119820
ggccaaaagc	atgtctgtcc	aagtaaagct	aacaaagaac	tccttttcgac	tagaaaaaca	119880
aaaactagca	cgattacaaa	cgtaccttcc	gacattaaaa	cttaagaaag	ctttattgca	119940
ggctgaggta	caaaacgctg	ttaaagatgc	tgcagagtgt	gacaaggact	atgtacaggc	120000
ttatgagcgg	atttatgctt	ttgcggaatt	gtttagtatt	cctctctgta	cagattgtgt	120060
agagaagagt	tttgagattc	agagtataga	taacgacttt	gaaaacatag	ctgggtgtga	120120
ggtccctata	gtccgtgagg	taacactatt	tccagcttcg	tattctcttt	taggggcccc	120180
gatatgggta	gatacgtatgc	tctcagcatc	aaaagaactt	gtgggtcaaaa	aagtcattggc	120240
cgaagtctcg	aaagaacgtc	taaagatctt	agaagaagaa	ttacgagccg	tttcaattcg	120300
agtcaattta	tttgagaaga	agctcattcc	tgaaactacg	aagatactca	agaagattgc	120360
ggttttctta	agtgatcgta	gcatacccca	tgtagggtcaa	gttaaaatgg	caaaaaagaa	120420
gatagaactc	cggaaagcaa	ggggggatga	gtgcgtttta	atatacataa	gtatctcttt	120480
ataggacgca	ataaggcgga	ttttttttct	gcaagtagag	agcttggtgt	tgtagagttt	120540
atttctaaaa	agtgtttcat	taccacagaa	caggggccatc	gttttgtaga	atgcttaaaa	120600
gtttttgatc	atttgaagc	cgaatactcc	ttagaagctt	tagagtgtgt	taaagatgag	120660
agtgtttcag	tcgaagatat	tgtctccgag	gtccttactt	taaataagga	aatcaaggga	120720
cttttagaaa	ctgtaaaggc	attaaggaaa	gagattgtta	gagtcaagcc	cctaggggca	120780
ttttcttctt	cagagattgc	agagctgtct	agaaagacag	gaatatctct	acgatttttc	120840
tataggacgc	ataaagataa	tgaggattta	gaggaggact	ctcctaacgt	tttttatctt	120900
tctacagcgt	ataattttga	ttattatcta	gttcttgagg	ttgtggatct	tcctagagat	120960
cgctacacag	agattgaagc	tccacgttct	gtaaatgagt	tgcaagtaga	ccttgcaaat	121020
cttcagcgcg	agattagaaa	cagatccgac	cgtctttgtg	atctctatgc	ctatcgtaga	121080
gaagtcctgc	gagggctttg	taattatgac	aatgaacaaa	ggcttcatca	agcaaaagag	121140
tggtgagagg	acttggttca	tgggaaagtc	tttgctgttg	cgggttgggt	catcgctcat	121200
agaatcaaa	aattacaaag	tctttgcaat	cgttatcaaa	tttatatgga	aagggttctt	121260
gttgatcctg	atgagacgat	ccctacctac	cttgagaata	aagggttagg	tgtgatggga	121320
gaggatcttg	tacagattta	tgatactcca	gcataattccg	ataaagatcc	ttccacttgg	121380
gtattttttg	cttttggtgct	cttcttctct	atgattgtca	atgatgctgg	ctacggcctg	121440
ctattttctaa	tgtcttcgct	tctattctct	tggaatttcc	gtcgttaagt	gaagtctctt	121500
aaacatctct	cacgcattgt	gaagatgacc	gctatttttag	gtcttggttg	tatatgttgg	121560
ggaacgacaa	caacttcatt	ttttggaatg	agtttttagta	aaacgagtgt	gttttagagaa	121620
tactctatga	cgcattgtct	ggctttgaaa	aaggccgaat	actacctgca	aatgcgtcct	121680
aaagcctata	aggaactcac	gaatgagtac	ccctcggttaa	aagcgattcg	tgatcccaag	121740
gccttcttgc	tagcaactga	aataggaagt	gcaggatag	aatctcggtta	tgtagtctac	121800
gataagttta	tcgataatat	ccttatggaa	ttagcgctgt	ttattggagt	cgtaacacct	121860
tccttaggta	tgttgcgcta	tcttcgttat	cgttattctg	gcattgggtg	gattctcttt	121920
atgggttagcg	cctatcttta	tgtgcctatt	tacttggtta	ctgtatcttt	gattcattat	121980
cttttccatg	ttccctatga	attaggagga	caaataagat	attatggcat	gtttgggtga	122040
attgggcttg	ctggtgtact	ggcaatgata	cagaggaggt	ggcggtggagt	tgaggaaatc	122100
atttctgtga	tccaagtgtt	ctctgatgtt	ctctcgtatc	tccgtatata	tgcttttagga	122160



cttgctgggtg	ctatgatggg	agccacgttt	aatcaaatgg	gagcaagatt	gcctatgctt	122220
cttggttcta	tagttattct	tcttgggtcac	tccgtgaata	tcattctttc	tattatggga	122280
ggagtgattc	atggacttag	gttaaatttt	atagagtggg	accactacag	ttttgatggg	122340
ggaggtcgtc	ccttacgtcc	tctgagaaa	attgtctgta	gcgaagatgc	tgaggcttcg	122400
gggattcact	tagataataa	ttcaatagtt	tgataaaactt	cccttgccct	taagagagga	122460
acatgaaaga	aatccttgta	agtttcgta	tattttaaagg	tatttgaagg	gagcacatga	122520
ggtaagtatg	attgatattg	ctgttggttg	gcctgctttg	gttttaggct	tagctatgat	122580
tggaagtgc	ataggatgtg	gcattggctg	agtcgcttca	catgcagtaa	tgtctcgat	122640
agatgaagga	catgggaagt	tgataggaat	gtcagcgatg	ccctcatctc	agtcctatct	122700
tgggtttatt	ttgatgttgc	tgatgcaagc	agcaataaaa	aatggaaccc	tatcgccagt	122760
aggagggatc	gctataggtt	tatctgtggg	agccgccctt	ttagtatctt	ccgtgatgca	122820
aggcaagtgt	tgtgtcagcg	gaattcaagc	ttatgtctga	tcttcgtcaa	tatatgggaa	122880
gtgttatgca	gcgattggga	ttgtcgaatc	tttttcattg	tttgcgtgtg	tttttgccgt	122940
actactactc	taaaacttgta	tttgggctta	cagttctgtt	agccgcaata	agtggtgatt	123000
gcttattggg	ttgttcagaa	ccttcattat	cctcttttac	agaatacgt	gggtccagagt	123060
atagtgcagc	agcccaactc	agtatcgagc	agagttgtca	tgatgaggtg	tatggacagc	123120
aggttgtagt	gacctggagt	cctccctcac	gtatgaggaa	atgccttccc	gtgactttgt	123180
atctctgggt	atattatggg	aatggcaagg	tagagaaatt	gacctatgag	gtcaatcaaa	123240
gtgcggggta	tcgagtgtat	tgcctcaagg	gactagaata	caaagaactc	cagggcatta	123300
tctcctatcc	gttgcggtat	gtagcgggaa	tcaagagatt	gtgagtaggc	gtcaccatct	123360
ttggatggag	gttatctctc	tggattctcc	ttaataaaaa	atatcaaatc	ataaacatgc	123420
cctattttta	gaaaaagcag	cataaagata	ataaaataga	actatgctac	ttgctctaag	123480
tttacagggt	atcttcttagt	agagatcaca	aatgtggatt	aagaattatg	acaacagaag	123540
atcttccaaa	agcatataac	tttcaggata	cagaacccga	gttgtatgtg	ttttgggaaa	123600
agaatgggat	gtttaaggct	gaagcttcga	gtgataagcc	tccatattct	gtaatcatgc	123660
cgcccccaaa	tgttactggg	gttttgcata	tgggccaatgc	tttgggtcaat	acccttcaag	123720
atgttcttgt	tcgttacaaa	cgcatgtcag	gatttgaagt	ttgttggatt	ccaggaactg	123780
accatgcagg	aattgctacc	caggctgtag	tggaaaggca	tctccaagct	tctgaaggca	123840
agcgtcgtac	ggactatagc	cgagaagact	ttttgaagca	tatttgggca	tggaaagaaa	123900
agagcgaaaa	agtcgttctc	tcccaactgc	gacagctggg	gtgttcctgt	gattgggata	123960
ggaaacgctt	tactatggag	ccgcttgcca	atcgtgcggg	caaaaaagct	ttcaaaaccc	124020
tatttgaaaa	tgggtatatt	tatcgtgggt	actaccttgt	aaactgggat	cctgttctcc	124080
aaaccgccct	ggcggtatgat	gaggtggaat	acgaagagaa	agatggatgg	ctctattata	124140
ttcgctatcg	tatggtagg	tctcaagagt	ctattgttgt	agcaacaaca	agacccgaaa	124200
cctcattagg	agacactggg	atcgagatgt	ctcctaacga	cgagcgctat	gcacatgga	124260
ttggtgcgag	cggtgaagtg	ccttttgtaa	atcgtcagat	tcctatcatt	ggagatgctt	124320
ctgtagatcc	tactttcgga	acaggagctg	taaaagtgc	tcctgctcat	gataaggacg	124380
attatcttat	ggggaccaac	catcatcttc	ctatgattaa	cattctcacc	ccctcaggag	124440
gaatcaatga	gaatgggtga	ccttttgctg	ggatggctaa	agagaaagca	cgcgaggaga	124500
tcctcattgc	actagaagaa	caggggttat	ttgtaaggaa	agagccttat	aagcttcgtg	124560
tcgggtgttc	ttatcgatct	ggagctgtaa	ttgagcctta	tctttctaaa	cagtggtttg	124620
tctctgtgtc	agagttccgt	ggagctttgc	gagagtttgt	agaaagtcaa	gatattaaga	124680
ttttccctaa	agactttgtc	aaaaattact	tgctcctggg	caaccacctt	agagattggg	124740
gtattagtag	gcagctgtgg	tggggaatc	gtattcctgt	ttggtatcat	aaaaatcatg	124800
acgaacgggt	cctttgttat	gatggagagg	gcattcctga	agaagtcgct	caagatcctg	124860
attctttgga	ccaggatccc	gatgttctag	atacctgggt	ctcttcaggc	ttatggccac	124920
tgacctgctt	gggtggccct	gatgaaaatt	ctccagattt	gaagaaattt	tacccaccg	124980
ctctattagt	tacagggcac	gacatcttgt	ttttctgggt	aaactcggatg	gtgttactat	125040
gttcttcaat	gtcaggggaa	aagccttttt	cagaagtttt	ccttcatgga	ttgatatttg	125100
ggaagtctta	taagcgttat	aacgactttg	gtgaatgggt	ctatattttc	gggaaagaga	125160
agctagctta	tgatattggg	gaagcgcttc	ccgatgggtg	tggtgcaaaa	tgggaaaagc	125220
tctctaaatc	caaaggggaa	gttatcgatc	cctttagagat	gatcgctact	tatggtaccg	125280
atgcggtacg	ccttgactttg	tggtcttgtg	caaatcgccg	agagcagata	gatcttgatt	125340
acaggctatt	tgaagaatac	aagcactttg	caataaaggt	ttggaacgga	gctagggtta	125400
tctttgggtc	tatctcagat	cctcagggca	aggattttgt	tgaggttatt	gatgaagact	125460
ccttagggct	tgaagatttt	tatattttag	atggttttaa	ccaactgatt	catcagcttg	125520
aggaggctta	tgctacctat	gcttttgata	aagtggcaac	tttagcttat	gaatttttcc	125580
gtaatgatct	ctgttccacg	tatatggaga	ttattaaacc	cacactcttt	ggtaagcagg	125640
gaaacgaggc	ttcgcaatct	acgaagcgga	ccttacttgc	tggtcttctt	attaatgtat	125700
taggagttct	tcactcctga	gctcctttca	ttacagaatc	tttattttta	agaattcagg	125760
ataccttagg	agcccttcc	gaaggagatg	gggagtcatt	tacaggtcat	gctttacgta	125820
tgctacgttc	tcgtgcttgt	atggaagctc	cctatccaaa	agcttttgat	gttaagatac	125880
cccaagatct	tagagaatct	tttactttag	ctcaaaggct	cggtttatact	attaggaata	125940
tccgtgggga	gatgcaactg	gatccgcgtt	tacatctgaa	agcttttggt	gtttgttctg	126000

atactaccga	gattcagagc	tgtatcccca	tacttcaggc	attaggaggg	ttagaatcta	126060
tacagctcct	agataaagag	cctgaaaagg	gcctctatag	ctttggtggt	gttgatacta	126120
tacgcctggg	gatttttgtc	cctgaagagc	atcttcttaa	agagaaaggg	cgtttagaaa	126180
aagaaagagt	taggttagaa	cgagctgtgg	agaacttaga	gcgcttatta	ggagatgaga	126240
gtttttgcc	aaaggcaaac	ccgaatcttg	tagttgcgaa	gcaagaagct	ttaaagaata	126300
atcgatatga	attacaaggc	attcttgata	agcttgcac	gtttgcttag	acagagagga	126360
ccaacgatct	ttggagcgct	atgatattgt	tagaattatt	ggaaagggag	gcatgggtga	126420
agtctatctt	gcctacgac	ctgtatgttc	tcgtaaagta	gctcttaaaa	aaattcgtga	126480
agatcttgca	gaaaatcctc	ttttgaaaag	gagggtttta	cgagaggcaa	gaattgccgc	126540
tgaccttatt	catcctgggtg	ttgttcctgt	ctatactatt	tacagcgaga	aagatcctgt	126600
atactacacg	atgccctaca	tagagggata	tacactaaaa	accttactga	agagtgtatg	126660
gcaaaaggaa	tccctgtcta	aggaattagc	agagaaaact	tctgtagggg	catttctttc	126720
tatctttcat	aagatctgct	gcactataga	atatgtccat	tctcggggca	ttcttcacgc	126780
cgaccttaaa	cccgataaca	tcttattagg	tctttttagt	gaggctgtaa	tcttagattg	126840
gggagcagca	gttgccctgtg	gagaagaaga	ggatcttctt	gatataagtg	tcagcaaaga	126900
ggaggtgctc	tcttcaagaa	tgacaattcc	aggaagaata	gtagggactc	cagattatat	126960
ggctcctgag	aggctcctgg	gccatccagc	ttctaaaagt	acagacattt	atgctttagg	127020
agtggttctt	tatcagatgc	tcactctctc	ttttccttat	agaagaaaaa	aaggaaagaa	127080
aatagttctt	gacggtcaga	gaattccaag	tcctcaagag	gtagctcctt	atcgagaaat	127140
ccctccgttt	ctttccgctg	tagtgatgag	aatgttggct	gtagatcctc	aagagcgcta	127200
ttcttcggta	acagagctta	aggaagatat	cgagagtcat	ctgaaaggga	gtcctaagt	127260
gactttaacc	acagccctgc	cacctaaaaa	atcttctagt	tggaagctaa	acgaacctat	127320
tttactttct	aagtattttc	caatgttggg	ggctcttcca	cgctcatggt	acagtttagc	127380
aatctctaatt	attgagagtt	tttctgagat	gcgcttggag	tatactcttt	ctaaaaaagg	127440
cttgaacgaa	ggctttggta	ttttacttcc	cacgtcagaa	aatgctttag	ggggagattt	127500
ttaccagggg	tatggctttt	ggctgcata	taaggagaga	accttatccg	tgtctctggt	127560
gaaaaatagc	ctagaaatcc	agaggtgctc	tcaagatttg	gaatctgata	aagagacctt	127620
cttgatagct	ttagagcagc	ataatcatag	tttatctttg	tttgtcgatg	gtacgacttg	127680
gcttatccat	atgaattatc	tgccaagtgc	tagtgggcga	gtcgctatca	tagttcgcg	127740
tatggaagat	atcctggaag	atataggcat	ttttgaaagt	agtggctctt	tgagggtcag	127800
ttgtcttgct	gttccgagc	cttttcttgc	tgagaagtta	tatgatcgcg	ctttagtgtc	127860
ttaccgaagg	atcgcagaat	ctttcccagg	acgtaaagaa	ggttatgaag	caagggttcag	127920
agcaggaatt	acagtttttag	agaaggcctc	tacagataat	aatgaacagg	aatttgctct	127980
agccattgaa	gaattctcaa	aattacatga	cgggggttgc	gctcccttag	aataccttgg	128040
taaggcttta	gtatatcaga	gactccaaga	gtataatgaa	gaaattaaga	gtttgctatt	128100
agcattgaaa	cgttattcgc	agcatcctga	aatcttttagg	cttaaagacc	atgtggttta	128160
ccgactccat	gagagctttt	ataaacggga	tcgccttgct	ctgggtgttca	tgattttagt	128220
attggaaata	gctccccagg	caatcactcc	agggcaggaa	gaaaaaatcc	tggtttggtt	128280
aaaggacaaa	tctcgggcta	ccttattttg	cctcctggat	cccacggctc	tagagctgcg	128340
ctcttctaaa	atgggaattat	ttttaagtta	ttgggtctggg	tttattcccc	atctcaatag	128400
tctatttcat	agagcttggg	atcaaagcga	tgtgcgagct	ttgatcgaga	ttttctatgt	128460
tgcttgtgat	cttcataaat	ggcagtttct	ctcttcttgt	atcgacatat	ttaaagagtc	128520
tcttgaggat	cagaaagcca	cagaagagat	tgttgagttc	tctttcgagg	atthaggggc	128580
atcttctttt	gctattcaga	gcatctttta	caaggaagat	gcagagaaga	tctttgtttc	128640
taatgatcaa	ttatcgccaa	tccttcttgt	ttatatattc	gatctttttg	caaactgtgc	128700
tcttctggaa	tctcaaggag	aggctatttt	tcaggctttg	gatctcatcc	gaagtaaaagt	128760
tcttgaataa	ttttatcatg	attacttgcg	gaatcatgaa	atccgagcgc	atctttggtg	128820
ccgcaatgag	aaggctctaa	gcacgatttt	tgaaaactat	acagagaaac	agctaaagga	128880
tgagcaacat	gaactgttcg	ttctctatgg	atgttacctt	gctcttatac	aagggtgctga	128940
ggcggcaaa	cagcattttg	atgtatgtcg	tgaagatcgc	atcttccctg	cttcattatt	129000
agctagaaat	tacaatcggt	taggtcttcc	caaagatgct	cttagctatc	aagagcggcg	129060
tttggttattg	cgacaaaagt	ttctctattt	ccattgtctt	ggtaaccacg	acgagcgtga	129120
cttatgccag	actatgtatc	acctcttaac	cgaagaattt	cagcttttaa	tgatttgtgt	129180
atgggtctcag	gatcttagat	tctaagttct	taagaatcga	gttcttcatt	gcagatatat	129240
tttttcagca	acgagtcctt	acttgcatag	atatctttgg	gagatcctga	aaaaagaagc	129300
tttctcctt	gtttcccgag	tcccgggcct	atctctatga	ggtagtccgc	agattttaac	129360
aacttcacat	cgtgatctat	gtagattacc	gagtggccgc	tatttatgag	ggagcgaagt	129420
ttttctggaa	gatgttgttt	tttgattgga	tctagagaag	aaaagagctc	atcaatgaga	129480
aatagggtgg	gagtctctgg	agtttgatag	agaaaaataag	cagtttttcag	tgctgttttt	129540
tcacttacag	ataaggaaga	gagtttttgg	ccgataggaa	gatagccgag	tcctatgtca	129600
agaagtgcct	ttagaggttt	ttgtatcttt	ttaataaagg	gaaatcggag	ggctacagtt	129660
tcaatcggag	tatgcaaaa	ttctccgaaa	tgcttgcctt	cataaaggac	ttctcgagca	129720
agaggttggg	tacgaaatcc	tgagcaggta	gggcaggggac	gcttttctaa	agcgtaaaaa	129780
gcccgatcta	tccattggta	cccaagtcct	tggcaatccg	agcattgtcc	ttgttttcta	129840

tttgtactga	acatcgtaga	tgaaatattc	agggcctttgg	cttgtgttag	cgaagcataa	129900
aaagctctca	aggaaggagc	aatatcgaaa	taggtgctga	tatcagagcg	ttgcgatgaa	129960
gctattggat	gagagtcgat	cactacaagg	tcggaaaatg	ttgtagttcc	ttttgctatc	130020
aggagctcag	cttgtttttt	aaatccttct	aaaagtagag	aggttttccc	agatcctgaa	130080
actcctccaa	tggcaaccaa	agcatggaga	ggagccgata	ctttcaaatt	ctgaatatgg	130140
tgtatcgata	gatttacctt	taatgtacga	tcggatcctc	gggtatgggt	tgccctactt	130200
atagaaagtg	gagccttggg	acaaacctca	gtttggggaa	cgtagcggtg	taggtctaca	130260
gatgggcaaa	cctcagtatc	agaatccatg	agaaatcctc	cttgagggtcc	agatcctgga	130320
cccaagaaga	tcgcgtgata	ggcatggggg	attaaagaac	aggaccgatc	ggtagcaatt	130380
actgtgttgt	tatttgctac	gagctcttta	agtagctgaa	ctatggtagg	aagatcctgg	130440
gggtgcagtc	cagaaagagg	ctcttcgaat	aagtagacga	tggtggtaag	atttatagag	130500
atcttttttg	caaggtgtaa	acggtagttc	tcaccatcac	tgagagtgtc	ttgcctttgc	130560
ccaagggtaa	tatagctcag	gcctacttta	ctaagtgaag	taaggcgatt	catcaaatct	130620
tggattatgc	ttcttgtatc	atcggttcct	atagtgttta	ggaaagattc	taagaatgtg	130680
gcactcttct	gataaatatc	caaaagcgag	gtattgttga	ttcgcacata	gttggcataa	130740
tcgttttagtc	ctgagccttt	gcaggcagga	caggaggtaa	gagcaagcag	aggttttatc	130800
aggggagagt	cagattcagt	atctagctgc	tccataagta	gtgcgttcat	tcctggaaac	130860
tctgaggaac	ctcggcaaaa	atttaggaac	tctttcgtag	ttagcaactt	tagtggttga	130920
gaggcattct	catctttaag	cagcttttgt	acaggcttca	tatagctctt	tggaaagaat	130980
aaactaaaaa	actctaaagg	agtgtagtga	gcaatttttt	ctttatgctc	ttctagggag	131040
attttttagga	tttcgccacg	acctccacat	gtaaggcaac	gacctcggg	atggtcagaa	131100
gnaagtatgt	gatgtgtaat	ctcgggatag	agtcctcctt	tcttatcttt	ccaccctaag	131160
gaatacgaga	gttttctgtg	ctttttctga	gagatataga	tccagatttc	tgaggataga	131220
gaaaaagcta	ccgagattgc	ggataataaa	gaggaactat	ttttcgggga	tacttttgta	131280
tgttgtatga	ctatagcagg	ttctatgaga	tttagaggca	gcctctcatc	taaatacatag	131340
aggttccccct	cagaatataa	ctttatgaat	ccctcttttt	gtttttcttg	aaggaagatt	131400
tccagatcag	aaccaagagg	aatcggagag	gttatagtga	cgtaatcgct	tttatagctt	131460
ttgagtaggc	tatcgatgat	ggtctgaggt	gtagttttag	agagtttttc	ttctgttaagg	131520
ggagaaaaag	gttctcctaa	gatggcaaag	agctttttcca	gaccattgct	taatccgaga	131580
gccgaggcta	ttgtatggta	cgagcgattg	gaggagctac	attttcttac	cgaaatgact	131640
ggagagagtc	cttttacctc	tcctacagag	ggtagaggag	tctccttaag	cagaccctgt	131700
ctaagttagg	gagggaagag	ctcggcataa	gcgatatttc	ctgatgcata	gagtatatca	131760
aagactaaag	aatgtttccc	tgaggctcca	ggaccgcgaa	ttgctattag	ggagtttctc	131820
ggaagagcaa	gatctatgtg	tttgagatta	ttttgatagg	catccttgat	aaggatatca	131880
caagatttag	gagaggatgg	cggttcagat	tttactaccg	gtatgtctag	agaaccttca	131940
atataggggg	ccaacgcttt	tgctgttgga	gtattttagt	ggataagatc	cttaggggtg	132000
caggatgccca	ggaggatatcc	tccgagatcc	ccctcttcag	gacctaatc	caaaacataa	132060
tcacaaaact	tgacaacgtg	catgttatgt	tcgataacaa	ggactgtgtg	ccctagatat	132120
gtgagggata	gaaggacctc	gatcagtgct	tggatatcat	gagtatgaag	gcctgtcgta	132180
ggttcatcta	ggacatagag	tgtttgctta	ggagaagcaa	agagaagctc	gtgagcgagt	132240
tttagccttt	gaatttcccc	tccggataat	gtggaaagag	gtcttcctaa	gggcaggtaa	132300
tctaggcgta	gggaacatag	agcatggatt	ttttcatgaa	ttttaggatg	tgaaatgaaa	132360
aatttttctg	cttcgtacgc	tgatcatatc	aaaatatcag	cgatgttctt	cccttcatag	132420
aggatttcca	atacttctga	gtgataacgc	ttcccttggc	attcagaaca	ggggatgggt	132480
gtatcatcat	cggagatggg	catcgttctc	aacctctgac	actgaataca	aggtccttga	132540
ggttgggtga	agctaaaaatg	agcttttgtc	agtccttgac	gtaggctgcg	aggttgagag	132600
gcgaagagtt	cccggatatc	atcaaaggct	ttaatatagg	tcaaagggtat	cgaacgctgt	132660
gagcgtcctg	gaagatctcg	ggtaatgtga	atcaagcggc	ctatgcatcc	ccactcaaaa	132720
tgagatttt	tagggttctc	ttgtttcaag	aagctttcta	tagcaggcac	taacgtatta	132780
ttaattaaag	aggatttccc	cgatccagag	actcctgtaa	ctccgattag	ccgagctaac	132840
ggcagacgaa	tagaaagatt	tttaagggtg	tggatcggtg	cttctgttag	caagagccaa	132900
gatgtgggag	cttcccggga	ttctggaatg	ggaatcgtaa	gctcttgacg	caagtatttt	132960
gctgtcagag	atgaggagtt	catgaggaag	tcctcaggct	ttccattaaa	gaggacctcg	133020
cctccgaaaa	ttcctgctcc	agggccgatg	tcaataatcc	tatccgcaag	agaaatcatc	133080
cgttcttcat	gctcaacaag	aatcacctga	ttgccttgat	ctcgtagctt	tttaatgaca	133140
ccgatgagct	tttcagtgtc	ttgtggatgc	aagcctatgg	agggctcatc	taggatatag	133200
gtaattccaa	aaagtctctc	tcctaggtgt	tttgctattg	ctgtacgttc	ttgttctcct	133260
ccagaaaggg	tagctaatac	gcgatttgga	gtgaggtagc	ctagccctaa	gtcaataaga	133320
aaagagagcc	tttgcttttag	tccttgacgg	atttcttgaa	tagagagaga	aggagatttt	133380
accttagaaa	aaaatacgtg	ccagtatttt	agagacattc	gttggaattc	agtgaaatgtt	133440
tttccttccc	aagtagctac	ggaagcgtag	tctcctaggc	ctgtaccttt	acatagggaa	133500
caggaatgtg	ctgacatgcc	tttggagaga	taacgtgagg	gcttcgtggg	ataacgaact	133560
ttatctccta	tatcgtttaag	tacacctctc	catactttat	aggtgagatt	cttttttccct	133620
aaagtttgat	cgaagagtcg	tacaggaaga	accaagttat	tttttccctt	aagaaaaata	133680

ttttggattt	ctggggaaa	atctttccat	ggagttttcta	gattgaaatt	taaggcatca	133740
gcaagagctt	ggtatatagt	atgatagaga	taggaagaac	aatttccagc	aaagctacag	133800
caattctctt	taatcgaaag	atcttcatcg	ataagaaggg	gattatctat	ggaaataaag	133860
atcccggatc	cttgacaaa	agagcaacgg	ctctccaggg	catgaggaga	aaataattgt	133920
tgagtttagag	gggtataggt	gacgtcatcg	atctgtttgct	ttgtggagaa	tgcatgagc	133980
tcttcgtcac	taagaactga	gcaatgaccc	tctccgaatt	ccaaagctgt	gaataggcta	134040
actttgagcc	ttgcaatatt	atcttcaact	ttgattagag	tatcaataac	aatatcaaca	134100
gagcagtcct	caggaatccc	tgaagttagg	aaggagtaaa	tgggggtggat	cgtgccgtta	134160
caacgtactt	ttgtaaattc	ctgtttgtgca	tactcatgga	ttgcagcaat	atctttacgt	134220
agcagaggag	ctaaaataga	gatctgtaca	ccttcagaga	gctccataat	ggtactaaga	134280
actttctcct	tgctgtagag	atctaagact	tcttttagtct	taggatctcg	agcctgtcct	134340
tctagcgtga	agagaagagc	aaggtgcgaa	aaaagttcag	tagtgctccc	gacagtcgca	134400
tgactatagt	gtgaaaagtg	gttctgtttt	attgctattg	ttggtgagag	accatgaatt	134460
tcttctactt	taggattggg	cagcgtcggt	atcgtagtga	cgaagaatgt	cggaagtgtt	134520
gaaatatagc	gttttcttcc	agcagcatat	agggtatcaa	aggctatcga	ggattttcct	134580
gatcccga	ctcctgtgag	tagaacgatt	tccctcggagt	taaaatggat	agaaacgttt	134640
tttagatttc	taactttgat	cccagaaaca	tatacaggaa	gtgatttcat	aaagaattct	134700
cgtaatatat	ttagaaaggt	ctcttaccta	accttgagaa	aagagtcata	tccgcactga	134760
tatcttggga	tttcaagtac	aaattaaacc	gcaatattgt	atattcctgc	aagtatcctc	134820
cctctcaaga	gtttgagtta	ataaagagaa	ttttttaata	ttttttcaaa	aaagaatata	134880
aaatatttca	ttataccatg	agtttttcat	tgaatagaca	ataggacagt	atgatcacac	134940
gcactaaaat	tattttgact	atagggccag	caacgaatag	tccagagatg	ttagcaaaac	135000
ttctagatgc	tgggtgaac	gtagcaagat	taaatattag	tcatgggagt	cacgaaactc	135060
atggacaggc	tattggattt	ctcaaggagt	taagggagca	gaagcgggtt	cctttagcaa	135120
ttatgctaga	tactaagggg	cctgaaattc	gttttagggaa	tattcctcag	ccaatttcgg	135180
tttctcaggg	acaaaagctt	cgtctggtaa	gtagtatat	cgatgggagt	gctgaagggg	135240
gagtgtctct	ctatcctaag	gggatatttc	cctttgttcc	tgaggggtgct	gatgttttaa	135300
tagatgatgg	ctacattcat	gctgttgttg	tctcttcaga	ggctgattct	ttagaattag	135360
agtttatgaa	cagtggcctt	ctcaagtctc	ataaatcttt	gagtatccga	ggtgttgatg	135420
ttgctcttcc	ctttatgaca	gagaaagata	ttgctggatct	taagtttggg	gtagagcaga	135480
atatggatgt	gggttctgca	tcttttgtgc	gtcacgggtga	agatattgaa	actatgcgca	135540
agtgttttagc	agactttaggc	aatcctaaga	tgcccatcat	tgcaaaaata	gaaaatcgtt	135600
taggggtaga	aaattttctct	aagattgcca	agcttgcgga	tgggaattatg	attgctagag	135660
gagatttagg	aatcgagctt	tctgtcgttg	aagtcccaaa	tttgcaaaag	atgatggcta	135720
aggtttctag	agaaacaggt	cacttctgtg	tgactgcaac	gcagatgcta	gaatctatga	135780
ttcgcaatgt	cttacctaca	cgagctgaag	tctctgatat	tgccaatgca	atztatgatg	135840
gttcttcagc	agtgatgttg	tcaggggaaa	ctgcatctgg	agcccatccc	gtggctgccg	135900
tgaaaatcat	gcgttctgtg	attttagaaa	cagaaaagaa	tctctcccat	gattcttctt	135960
taaaatttaga	cgaaagcaat	agcgctcttc	agggtgtccc	ctatctctca	gccattggat	136020
tggcaggcat	tcagattgca	gaaagggcag	acgccaaagc	tcttattgtt	tatacagaat	136080
caggaagtct	tccgatgttt	ctctctaaat	atcgctccgaa	attccctatc	attgccgtga	136140
ctccaagcac	ttctgtttac	tatcgcttag	ctttggaatg	gggggtctat	cctatgctta	136200
cccaggaaa	tgatcgcgct	gtatggagac	atcaggcctg	tatttatggc	atagaacagg	136260
gcattctctc	taattatgat	cggattcttg	tgcttagcag	aggagcctgt	atggaagaaa	136320
caaataatct	taccctgaca	atagtgaatg	atattttgac	tgggtcgga	tttcttgaaa	136380
cctagaattt	ttgcttttaa	atccaggact	tgcgaaattt	ttcgagaata	tacagatggt	136440
ttcgtaaaata	tgaattagg	cttttactcc	actgtaagtc	agggccctt	cgacttcacc	136500
ttgaagtttt	ttctctcttt	atctttaaga	tttttagaat	agaagatcct	caaagagttt	136560
tttagaggag	cttgggggtg	gtctagagat	ttttctagga	atctttttaga	gtacacagca	136620
caagaacctg	tttttctaaa	atgcttgat	aaatgctgta	gattgttagt	gagatcaaaa	136680
atagcaggat	agcaattcgg	tagagctaga	atgtcttgat	catttcggag	ttggatcaag	136740
gagtactctg	ggaattgttc	ttgaagttct	tcaagatgat	ccgcatttcc	tagtggttaga	136800
tgaagagtgg	ttcctgaaaa	gcattctgct	agagctttca	gaaaagaaaa	gtgtgaggag	136860
acttgatcta	caaaaactag	aatatggcta	tagcggtagt	tcttttttat	tacgttagag	136920
atctttctct	tccacttttt	atgaaatccac	atccattgtt	caggctgact	ggcgatccct	136980
ttttctaaaa	atcccatcat	ctgatccata	aggatagcca	cggattcttt	catagggagg	137040
cttttattag	catacagctt	ggcactcgga	atcacttcga	agccttttagc	ttggcgagaa	137100
acattaacag	caatcacagg	aaaacctgtt	ttataagcta	atagtgtctg	agatgtcgtt	137160
gtgaatgctg	gagagccaaa	gagaggatac	gtgtatgaag	acatcaacaa	ggcttgatct	137220
ccaacaatcc	ccacgagttt	cccttgattc	agagcttcta	tgccctgttg	gattccgttt	137280
tttgggggta	caatcttacc	tttgaaaact	tctctaaagag	caaagatttt	cttgctgagc	137340
ctttgatttt	ttatagcctt	agcdaaggcg	attccaggat	agtttttagt	gatataaaga	137400
aaaggaaagt	cccagtttgc	ctggtggcca	caaaaataaaa	taaggccctg	cttctcttgt	137460
agattcttaa	aagtcttctc	ttaaattctca	ttggaaatga	cctcttcaga	agaaaaacct	137520

ttgggggtttc	gtgaggatgt	cacgatttga	atgagtttgt	ctatatattcc	gacaagttgc	137580
tcgattgcga	gtaattctaa	gagtgttaatt	ataagatgct	gcaaagattg	acgagctatt	137640
ttataacgct	catcaaattgt	tttttctgga	aacgctaattg	ctaagtttgt	gagggctgtt	137700
tttcgataat	cgctgatgat	ataaaaggct	agaaatccaa	aaccttttcc	taatcctgtt	137760
aaaaaagatc	ttgggggatg	cctgcataaa	gcaataatac	cagagactag	gtaatacaga	137820
ggggcttcta	ggattgttct	cttgatctga	tggaaattttt	tgcccacaag	ctaatttgac	137880
tttcgcaaat	cacttttaaat	aatactattg	tgtctcttac	tatctcaaga	tttctcgttt	137940
tgacgcgaag	acgctccaga	aaggaacatg	cttaacagta	tcgtaactaa	gagaactagg	138000
acagcagcaa	cattactcat	tccgaaagtc	atcccagaag	ctccaagcac	tccagtacaa	138060
atcaaaatga	tcagtataaa	agaaacaata	gcagtaagag	ctaaaagtcc	tgacagact	138120
gtcgctacat	ttgctttgga	ttctgagcta	tcagaacaac	aacaaactgt	gttgattgca	138180
gcttcaaagc	cctggcccaa	gcaatctatt	aagcacataa	agtttccctt	aactaaattt	138240
tagtgagtct	gcactaccac	tcttttttat	ataatttagt	tgtttccttt	gtttttgtct	138300
ggatcacaa	tttattattt	ttgattttctg	caataagatt	taaaggttca	ccgtctgctg	138360
taaaaagtgc	aagctttctt	aaatattctc	ggaatctatg	acgaattcca	gcctcatcaa	138420
taagggtctat	atcgtgtaaa	attccatggt	cttgggctat	aatagtctga	agaaaagtat	138480
tttctaaagt	tttttcatct	aaaaattcta	tagcccgatt	gatcgaagaa	gggtcttgtg	138540
gtgagggcat	cacaattggt	aagaccatgt	tgttctttac	gacatctaaa	aactgtctac	138600
ttacatcctt	aacatataaa	ggaatattta	tttgatgaat	tccatgattc	agaataatgg	138660
gagggacagg	atctaagctg	tactctagag	gattcatcgt	ttgaatgaag	gttacaggaa	138720
agaatagaaa	gaccggtaaa	tttaaaattta	ggggaaatgca	ttcccttttt	aaaaataaaa	138780
ggcgaagaaa	atctgcttga	gggtcattga	gacccatgaa	ggatatttca	aagggatacca	138840
aaattttctt	ccattcttta	ggaatgggga	aaataatttc	gtcatgactt	ccctgagcaa	138900
tgcgatttct	ttctaactct	tcgaacgaaa	ttttattcaa	attaaagggt	agctcaagac	138960
cttgctcttt	caaagcattg	atatattctt	tggggccact	gactttttga	ttcaagtact	139020
tcggccagac	atccaaatac	tcatatcctt	tcgggggact	ccctataggt	ttcgttatag	139080
ttaataaaaat	gtcttcgggt	acatattgtg	taagtcggac	aaaaatatcg	ttagcgtcaa	139140
cgctatggat	gtctttgcgt	atggtgatct	catgatctac	agagacaagg	ttatgcttat	139200
ctatagtggc	aatccaactt	tccgtatggt	ttgctgcact	gatcaattacc	tctaaatttg	139260
aaggacggag	gtcttgaacg	gtatttttat	tcccagtgat	tgttaaagag	acttttttat	139320
tcaggaatcc	gcttttttgt	agtccaagaa	cggttttggtc	tggtatgtag	tctacgatgc	139380
gcacagggac	atttgtgagt	gttcgcgtga	tggtaacact	ttgtcctacg	aggatccaaa	139440
tgatgatggc	aaaacctaag	gaaacaactt	ttctaggcca	atgccgaata	aagagttgag	139500
ataaaaaattt	tatcatcggt	tccaaatcca	agagaataaaa	ggttttcttt	tgtgttcttt	139560
aggggaaaga	atactgcgga	gtaccgcttt	gaatctatct	attttttactc	cgcgtgttag	139620
aaggccgtct	ctagacaaag	agacacttcc	attttcttca	gatactgtga	taattagagc	139680
atcagatcgt	tggctagctc	ctagagctgc	gcgagtcctt	gtcccatgg	atcgggaaag	139740
ctgcgtcgta	tcattgagcta	gtggggagaa	gacgcgagca	taggctagaa	tgtctcctct	139800
tagaatgacg	gcaccatcgt	gcaatggaga	tgaagggttcg	aaaatcgtct	ctaaaagttc	139860
ttcagagaaa	gttgcattga	ttttcaccga	agaaaaactt	aggtattcat	cgaaagaatc	139920
tttgttttct	aaaacaacaa	gagccccgat	ttggcgttct	gatagctgat	aaatactggc	139980
agctaattgc	tctacgaact	gctcttgagt	atctatgaag	aattttttcc	catgaaatcg	140040
tatacgagag	agagccaaac	gaatttcttg	ttggaaaata	ataaagacca	cgatggcagc	140100
gatattgact	acgtggagca	tcaatctacg	gatgataggg	aggtggagtt	tatcggctag	140160
gacaaataga	aagagaaacg	caagcaagcc	aaagacaaca	tccatagctc	gggtgcccc	140220
gaaaaatttt	aataggtagt	ttaacattac	ccaaatttaa	atgatttcta	gcaaagggtg	140280
tgtataataa	gtaatatcaa	agggcatagt	tttactaggt	ccttgggtag	tatactgaga	140340
aaagttgcac	aaagtgtctg	gctattgtcc	taggaaaggt	aacctattat	cttagcatac	140400
gaacaaaaag	gttaacagca	aagtattttg	tagttgcaat	actttgtttc	atcgttcaca	140460
ttacagtttc	taattttata	tacaattctg	gaagtttatg	gatgcgctta	tcttatctag	140520
aatacaattt	ggattgttta	taacttttca	ttaccttttt	gtgcctctga	gtatgggttt	140580
gagcatgatg	cttgtgatca	tggaaaggct	ctacttggtt	acaaaaaagc	aaattttata	140640
gcaaatgaca	tgggttttgg	ttgggatttt	tgccctaaca	tttgttcttg	gagtcggtac	140700
tggaaatcatg	cagatatttt	ctttcggttc	taactgggca	aatttctcag	aatatacagg	140760
aaatattttc	ggcaccttat	taggtagtga	aggtgttttt	gcttttttct	tggaaatcagg	140820
atttttagga	attttgttat	ttggctcgca	caaggtctct	aagaaaatgc	atttcttttc	140880
tacgtgcatg	gtagcttttag	gagctcatat	gagtgccctt	tggattattt	gtgcgaattc	140940
ttggatgcag	actccttcag	gttacgagat	gggtgatgat	aaaggaaaac	tcacccctgc	141000
tttaacctcc	ttctggggag	tggctctctc	tccaacaact	atagatcgct	ctattactgc	141060
agtcttagga	acttggctgt	caggagtttt	ctttgttata	agtgtatcag	tatatatttt	141120
atggaaaaaa	cgtcatcatg	agtttgctaa	acaaggatg	aagataggga	cgatttgtgc	141180
agttatagtc	ttagtttttac	aatttggtgc	tgcagatgta	acggctaggg	gagttgctaa	141240
aaatcagcct	gcgaagtttag	cagcttttga	aggtatcttc	aaaaccgaag	aatatactcc	141300
tatatgggct	tttggttatg	tagacatgga	aaaagaacgg	gttatagggc	tgccattatcc	141360

aggagcactt	tcttttcttg	ttcatagaaa	tataaaaacc	ccagtcactg	gttttagatca	141420
aattcctaga	gatgaatggc	ctaagtgtaca	ggctgtcttt	cagctgtatc	acctgatgat	141480
catgttggtg	ggggttatgg	tcgctttaac	tttgatttcc	tggctctgcat	ataaggggatg	141540
gcgatgggcg	ttaaaaccct	ttttcttagt	cattttaact	ttttctgtct	tattaccaga	141600
aatttgtaac	gagtgtgggt	ggtgcgctgc	tgaaatggga	agacaacctt	gggtagttca	141660
aggattatta	aaaaccaaag	atgcggtgtc	tcctatagt	caggcgaata	aaattgtaca	141720
atctttggta	atatttagct	tagtattcat	tgctctctcg	actctcttta	ttactgtact	141780
ttgtaaaaaa	ataaagcatg	gtcctgaaga	ggaaaatgat	cttacagaat	ttgaagtga	141840
atagagggtat	ttttatggaa	ctttctctaa	caagcctttt	accacttgcg	tggatgtga	141900
ttcttgaggt	tgctgtcttt	gcgtattctt	ttggcgacgg	ttttgatctt	gggctcggag	141960
ctgtttatct	taaagctaag	gaggataaag	aacgtcggat	tcttcttaat	tccataggac	142020
ctgtatggga	cggcaatgag	gtctgggttag	tgatcattgt	cgggtgggtta	tttgcaggat	142080
ttcctgcatg	ctatgccaca	cttctctcga	ttttctatat	gcctatctgg	actttgggtac	142140
tcctttatata	ttttagggga	tgttcttttag	aattccgaag	taaatcggaa	tcagtgtctt	142200
ggaaaaatatt	ttgggatatt	atctttatatt	gttctgggac	tgccatcagc	tttttcttag	142260
gcacgattgt	tgggaatctg	atccttggat	tgctttgttc	tccagacacc	tcttatgtct	142320
ctttatcctg	gattttatatt	ttccgtcctt	atgcagcctt	atgtggcgct	gtagttgcca	142380
gtgcgtttgc	tactcacggg	tccttcttcg	cattaatgaa	gacttcggat	tctttaaattg	142440
ctaggattgc	tcagcaattt	ccttatattc	tttctctctt	ccttctcttc	tatgttctct	142500
tcttaggagc	aagtttaate	tctattccca	agcgttttga	tgctttccct	acgtatccac	142560
tcttgatttt	gctcattgct	ttaacgagct	gctgctgtgt	tgctgctaag	acgagcgtgt	142620
ctaagaaaca	ttatggtacg	catttatatta	ttctacactg	aacttggtgt	ctctcattct	142680
gtcggcagct	accctaacgt	tccctaatat	tcttctctct	actgtagatc	cacagtatag	142740
ttatactatc	tacaatagcg	ctgttgaaac	taaaacgtta	aaaagccttt	tgattatagt	142800
gcttataggc	cttcccttca	tcattactta	tacgtgttat	atttatcgtg	tgtttagagg	142860
aaaaactaat	tttccctcta	tatattgagt	ttcattttaa	gagtccgaag	ccttcattcc	142920
atgagggctg	gatttagatt	aaagagactg	tgattgcgta	tagatccaag	aatgaatcga	142980
agaacagagg	atctagaaaa	tgaagagctt	ccattggaat	cctttggaag	ctatcattat	143040
acttcgttat	gaagcttctt	taattccaac	tacataataa	gcaggaaaag	caaaatgggt	143100
gtaggacgt	gggagacatt	ccacagtgc	acgcttctct	aaccattgct	ctaagtgtat	143160
acttgtagcg	ttaaagaaaag	caatcgtggt	ttcctgagct	tttagtaggt	aatccccggg	143220
attgttcttt	actacatgag	gatacacttc	taatacaccc	gcaagcactt	gttttttctt	143280
ctgttcagcg	cgataaaacg	cttcttgtgt	tagtgcttca	gagtggatcat	tgcttctgtg	143340
catactggcc	cagattctga	agagagaata	ctctaggttt	tctcttcctt	gggtaagagg	143400
agctgttttt	aatgcagttt	gcttacgaat	atgacgtgaa	agtaaatgaag	ttgtaacttc	143460
agaagaagaa	accttaggag	tgggaacattg	tgagcttgca	atcgaagtat	tttgagattc	143520
tagagattta	gaaagatagg	catcttggat	ttcttcttaa	gctttttgta	taagcccttg	143580
aattcctgga	acatctttaa	actcttcgga	ttgtacaagg	ttgatctttt	tataaaattgc	143640
ttccagatca	atctcattga	ggcttttctc	aagctctata	tgagcaaagt	ttaaagcaga	143700
attgataagg	tccatggcaa	tctttttttg	tccctcgcgt	tgcgatatata	gctcgatggg	143760
tcctttgtta	gcaacaaagt	tttttgcaac	atagaatacg	cattgtgagg	gcaagaccac	143820
ctctaaccat	ttcccatgtg	gctcttgaga	agctggctgt	atttgtgtgc	ctcgggagag	143880
tctcacaagt	actggagctg	atgttgaggg	ttctaaacga	acattgactt	gttcaccttc	143940
aacgacatta	tctaaaacaa	atgagcggaa	cacataacct	gtaattcctg	gaggcgcaga	144000
aattacgtag	tagtctttgc	tttctccgat	aacagcaaca	agatctcctt	tagaaaatttc	144060
cctaattgat	gtcccatcag	tatgaggtgc	tagacgcatac	cgtacgtggt	ttcccttaatt	144120
ttctccagta	aatgaagagg	gaagttgttc	tggaaaaggat	acggattggg	aatcggcagc	144180
atagattgct	ggtgagttga	ttgcagttcc	taaagctaaa	agaagcatag	aaatctggag	144240
cattctcatg	cttttctcct	acaaatatat	ttcgtctaac	cgttggttga	aaacatcgct	144300
tacagcaaaa	aggagattaa	cccctagaaa	aagaattata	ttgacttcaa	ggaaaaagtc	144360
aatcggctta	ccaaaagctt	aattatgaat	gcagttctac	taagtatata	aaacagcttt	144420
tatatgttca	cagttgggtt	cgccacaagt	acagcctatg	gggggtccca	agtagacgct	144480
aaactgatca	ctaggattta	agggattcgt	tacaatatat	aactttatcc	ccactttgca	144540
taatgtccca	agtgcggaaa	gtcagatctt	tatcgaaaac	cgcagggtta	tcttcttcat	144600
tcatgacctt	tccaatttgg	cagtgcatat	aattgcaatg	gggttctggt	ctgggtaaaa	144660
gcgttgcat	attccctgaa	agtacccgaa	tgacatcagc	cattttctct	aagacgtcgg	144720
taggagcatc	aggatgatct	ttatgttctg	gagtatgttg	tagtattgct	tcgatgggat	144780
ttgttccaga	aaagagaggg	gaaattagat	ttttaggtaa	tacttgaatg	tcgtttccct	144840
tagttatctg	ctgcaataca	ttcataagga	cccctacacc	tagtttatca	tcatcacgag	144900
aatcctcttt	ccccgattga	gaagtttcta	ggtagagaag	gtgctcttga	aaagcaatgt	144960
caataatcga	ctgatctaaa	ttaggaatag	aaatgatttt	gccatcaata	aggtggagcc	145020
ttagtgttcc	ttgttctttg	ttttctcctt	cctgggattc	aataaatgca	ttttggctcc	145080
atcttgcaga	gatgaatggg	ggaatacaaa	tcagttgatc	attaattttg	actttcatag	145140
cgatcttggg	ggtgaatcta	atcttagcag	tttgaggcca	ttgtaaatgt	atctcttttt	145200

ttttacaata	aatttagcagc	ataggggtttt	gatttgctaaa	ttttctaaaa	ggcacgtatc	145260
atgtaaatgg	atTTTTtatt	atgaatatat	tttttgcaat	agttccctgat	agaaaaacga	145320
aagtatggta	gttggacctt	aacaacacaa	tacgtctttt	aatgaaaaga	aggggttttct	145380
ttggaagtta	tgtagagatt	gttttaggca	aaaatttgta	tctgataaag	aataaaaggt	145440
tcagtaagag	aaggtgagga	cgcaaatgaa	gaaaacaatg	gtcattgata	caagtggtgt	145500
catctatgat	ccagaagccc	ttttttcttt	tgaaaatact	cgaattatca	ttcctttccc	145560
agtcattgaa	gagctagaag	ccttcggaaa	atntagagat	gagtcctgcta	aaaacgcgtc	145620
tcgagcatta	agtaatatc	gtttgctttt	agagaatgca	aaaactaaag	ttacagatgg	145680
tgtgctctta	cctagtggta	gtgagttgcg	tatcgaggtg	gcgccccttt	ctaagatga	145740
taggcgaggg	aaacttctta	ccttgaggtt	gctcaagatt	attgctaaac	gagaacccat	145800
ggtttttgtg	actaagagct	tgggacgcag	ggtgcgtgct	gaagcactac	aaattgagtc	145860
tcgagactat	gaaagtaaac	gctttttctt	tcgttcctta	taccgtggat	ttagagaact	145920
gcaagtttct	caggaggata	ttgaaaactt	ctataagaat	ggctacttag	atcttctct	145980
agacgtggct	tcttcgcca	acgagtattt	tttcatgtcc	gcaggagaaa	accattttgc	146040
tttgggtaga	tactacgtaa	gcgaaggaaa	gattatcgca	ttaaaggcaa	tggataagag	146100
tgtttgggga	atcaagcctt	taaatacaga	acagcgatgt	gccttggatt	tggtgcttag	146160
ggatgatgtc	aagttagtca	ccctaatecg	gcaagcagga	tctggaaaga	ccattttggc	146220
tttagcagct	gctatgcata	aagtttttga	taaggaaacc	tataataaag	ttttggtaag	146280
ccgtcccata	gtccctatgg	gaagagatat	agggtttctt	ccaggattaa	aggaagataa	146340
actgatgcat	tggatgcaac	ctatatatga	taatatggaa	gtgttattta	gcattaacca	146400
gatggggaa	tcttcagagg	ctctccaagg	tcttatggat	gctaaaaaat	tggaaatgga	146460
agctcttacc	tatatccgag	ggcgctctct	acccaaagct	tttattatta	ttgatgaagc	146520
tcaaaacctc	actccccatg	aatcaagac	aattatctca	agagctggga	aaggaacgaa	146580
aattgttctt	acaggagatc	ctacacaaat	cgatagtttg	tattttgatg	aaaattctaa	146640
cggactcacc	tatctagttg	ggaagttcca	tcacttggcc	ttatatggac	acatgtttat	146700
gacacgtaca	gaacgttccg	aacttgcagc	tgcggccgca	actatcctat	agaaccttcg	146760
atgtttataag	tgacttttct	tcttcggatc	tgtaatatga	ggagttttca	agtctgtaag	146820
gacaatcaac	attcttctgt	ctgtatttcc	gggttctatt	ccaaattctt	gcatagcggc	146880
aacaagagcg	catttttacag	cgtgtatcca	tctcatcgcg	actttattct	cttcactatt	146940
aggctttttt	ctattttcag	gaggcgcgta	gatcccgaga	gaaattagag	ggattttgtag	147000
gaaggttaca	cctaaagtgt	gagctaagct	gaagcagttt	aggtaggcgt	ttttgcagcg	147060
atcaaaggct	gcttgagact	tgttatgatg	atccactgct	ttaggcccaa	gaagtgtgtc	147120
taggtagtgt	ggtttacctt	gttttctctg	gtggttggat	ccatcggcac	ttctccacat	147180
gcctgcccga	cattcaccct	cattaagagg	agtcctctgg	cgttcaggat	ttagaggctc	147240
ttgcgacagc	cccaagaatc	gacactgact	gctgcccata	gaacttgatt	tgtaccgcgc	147300
ccatctcgac	tcattgttct	attggctgcg	tttacaatca	tcatagacat	actatcagtg	147360
acaagacgag	gtttgtgcaat	atttctgac	gtcgagacaa	aaatcagctt	tgattgattt	147420
agtgccagag	caaagatttt	ctgggttttt	tctgctgggtg	gccatgggaa	cggctcctct	147480
acaggagtcc	aatttctcaa	gagcatctta	tgaacacagag	atagaggaga	aaccatagag	147540
tctggtgacg	gtttcttgcc	taggatgggg	gaagcttcta	tacttccagg	tacaatgtga	147600
tctgtaggtg	taggggagac	ctctgggtctc	tgagggtatgg	gtgggttagg	ttgtgtcggg	147660
atttcttttag	gtgttacagg	tgggggggctt	tttttttatc	ttcttgtaac	agatcatcca	147720
ggaacggatc	tttgaatcct	gttggagagg	taggagttaga	aaatatggcg	tctatttgc	147780
gccccatgtc	aaggggagta	ggtgtttaag	ggttttgagg	ttctcttggc	tctggaggac	147840
ggcagcaagg	acaaagatac	cgaacgatca	actttataat	cttaatgact	cctaagacca	147900
ggtaatacag	agctttaatg	ccgaaaattt	ctagccaagc	ttcttttcta	actttaggaa	147960
gttcctcata	gatctcagga	cagggtaatg	ttttacacac	tgaagagaag	ttccctgtca	148020
ttagaaccat	agaatattga	agagaactaa	ttccttttaa	ggttttgata	cctataaatg	148080
tactaaatat	cggaatatag	cttgcaatac	gttgtaaatt	tgtgcggtgt	aagggattca	148140
ctaaaggagt	atttcttagt	gcggttgagg	tttgaccag	aggcgtgtgc	cgatggctaa	148200
ttataaagac	ttcttcatta	aaaatgctca	taagaatcgc	cttataatga	aataaatttt	148260
ttcataaga	attataaaac	aacttatctt	tcttttctat	ttctatgaaa	tctagaaggg	148320
ttttttaatg	gatatttgat	ttcttttaaag	actttaggaa	gacattgtct	aaatttggtg	148380
aaaaagacag	attctcctcg	ttaagagggg	atgagtagca	ttttaaaata	atttttttaa	148440
ataatggagg	tggagagact	cgaactctcg	tccttgacaa	actccctgct	aacctctaca	148500
tgcttatctt	ctagaattgt	ttacattgga	ctcccttagc	tagaagcctc	tatagcagcc	148560
aatgactctc	aaaaatctcg	aacgaacttc	cttgagaatt	agagaaagta	agttccaacc	148620
agataaatga	cggtattttg	caagcctctg	gtggagctcg	cagataccgg	gttacctaga	148680
gattatctag	ctaacaactt	ttgctaatta	agcagctagt	ctttcctcta	ctgagtcaaa	148740
caagctaata	atttcgcatt	cagccttagg	ttcggcattt	attgttttgt	tgggttttta	148800
ggaggccagc	caacgccctc	cgcatgcaat	taacacttca	ttttcaagtc	gaaacctata	148860
cacccccaca	acaatttttag	aagctgggta	gctttttatc	aatcatcgta	ttttgggtcaa	148920
gttctaagaa	cttcttagag	atctctagag	aggtgggcta	tggacgaaaa	cctaaaaaac	148980
ctctattgta	aatatgtttt	catatcaaaa	tgttcctaaa	ggcaaaagat	gacagcagat	149040



gaggtagggga	aaaatagctt	tgcaaaaaaa	gaagaacagg	ttttgaagtt	ttggaaagac	149100
aatcaaattt	ttgaaaagtc	tttgcaaaat	cgtcagggaa	aaaccctata	ttctttctat	149160
gacggccctc	cttttgctac	aggtcttcca	cattacggtc	acttattagc	aagtaccatt	149220
aaggatgttg	ttggacgcta	tgctaccatg	gacgggtact	atgtgcccg	acgttttggc	149280
tgggattgcc	atgggggttc	tgtggaatat	gaggtggaaa	agtctctgag	tttaacagca	149340
cccggaccca	tcgaagattt	tggtatagca	tcctttaacg	aagagtgtcg	taaaaatcgta	149400
tttagatacg	ttcacgagtg	ggaatactat	atcaatcgta	taggacgttg	ggtagatttt	149460
tcttctactt	ggaaaactat	ggacgcttct	tttatggaaa	gtgtctggtg	ggttttccaa	149520
tctctatata	accaaggatt	agtgtacgaa	ggtacaaaag	ttgtcccttt	ttcaacagca	149580
ttaggaacac	ctctctctaa	ttttgaagca	agccaaaatt	ataaagaagt	cgatgaccgc	149640
tctcttggtg	taagaatgcc	tcttcagaat	gattccgcat	ccttgcttgt	atggacaacg	149700
actccatgga	cattgccttc	taatatggct	atagctgtag	gggaaactct	ggtttatgtc	149760
cgtattcaag	ataaaaaaag	tggagagcag	tggatcctaa	gtcagggatg	tgtttctcgt	149820
tggttttcaa	attccagaaga	atttgtaat	ttagagagtt	tttctgggaa	agatccttgt	149880
ggtaggactt	atgagccccc	ttttactttt	ttccaatcta	agcgagagga	aggagctttt	149940
cgtgtcattg	cagcttcggt	tggtgaggaa	agtgaaggaa	caggagtcgt	acatatggct	150000
ccagcgtttg	gtgaaggaga	ctttttagtt	tgtaaggaga	accatgttcc	tttagtctgt	150060
cctgtagatg	ctcacggaag	ttttacagaa	gaaatacctc	aatatcaagg	gcaatacatt	150120
aaacatgctg	acaaggaaat	catcaagttc	ttgaagaaaag	aaggaaaggat	tttttaccac	150180
ggaacagtaa	aacaccggta	tcctttctgt	tggagaacgg	atactccttt	gattttataaa	150240
gccgtgaatt	cttggttcgt	cgctgtagaa	aagattaaag	ataagatgct	tcgtgctaac	150300
agctcgatcc	attgggttcc	tgaacatac	caagaaggcg	gttttggaag	atggttggaa	150360
ggcgtctcgtg	attgggctat	cagtagaaaat	cgttattggg	gaacgcgaat	tccgatttgg	150420
aaaagtgctg	atggcgagat	tcttggtgta	ggatctatcc	gagagctaga	agaacttaca	150480
ggaactcaga	tcacagatat	tcataggcat	tttattgatg	atttgaacat	tgtcaaagat	150540
ggcaagccct	ttcatcgaat	tccttacgtt	tttgattgct	ggttcgactc	tggagcgatg	150600
ccttatgccc	aaaatcatta	tccttttgaa	aatcaaaaag	aaaccgaaga	ggcatttccct	150660
gcagacttta	ttgctgaagg	gttggatcag	acgcgaggat	ggttttatac	tctcacagtg	150720
atttctgcaa	ttttatttga	tcgtcctgca	tttcgtaagt	ccattgtgaa	tgggattatt	150780
cttgacagaag	accgcaataa	aatgtcaaaa	cgtctaaata	attaccctag	tcctaaatatac	150840
gttttagata	catttgaggc	tgacgcgctt	cgtctatatt	tgcttcatag	tggtgtcgta	150900
aaggctgaag	atcttcgctt	ttctgataaa	ggaatcgagg	gtgttttgaa	gcaaatcctt	150960
cttctcttaa	cgaacgtact	ttcctttttt	aatacctatg	ccgagctgta	tgggtttgat	151020
ccgaaatcac	aagatataga	accagcttat	acagagattg	atcaatggat	tttatccaat	151080
ttgtatagtg	ttgtaggtaa	agttcgtgag	agcatgagtc	agtatcattt	aaactttgct	151140
gtagaacctt	ttgtgacctt	tattgatgat	ctgactaact	ggtatatacg	tcgctgtcgt	151200
agacgttttt	gggaagctga	agatactcct	gaccgtagag	ctgcattttc	tcttaatatat	151260
gaagttctca	cagttttttg	taaggtaatt	gtccctctcg	ttccttttct	tgcgaagat	151320
atctatcaga	agttgaagtt	agaaaaggaa	cctgaatctg	ttcatctctg	tgattttcct	151380
caagtcgaga	tggataaaat	tctccctgat	ctagaaaagc	gtatgcacga	tattcgggaa	151440
atcgtaggtt	taggccattc	tttaagaaaa	gaacacaagt	taaaagtctg	tcagccttta	151500
gcaaaacttt	atggtgtcgg	gtctaaagat	agattgtcgc	ttctaaaaaac	atttgaaggg	151560
ttgattgctg	aagagctgaa	tgtgaaaaat	gtgattttct	atgaagaagc	tccgagtttc	151620
atttatacta	ccgtcaaacc	taattttcgt	atgcttggga	aaaaagtgg	atctaagatg	151680
aaagaggtcc	aaaaagctct	cagtgaactg	ccaaacaatg	ctatagataa	gctgattcag	151740
gaagaaacat	gggttttaac	cattgatgat	agagaaaatg	ctttggatgg	tgtgacgctc	151800
gtgatttgct	gtcacacaga	tcctggatat	attgcccgta	gttccgctct	atttagtgtg	151860
attttagatt	gccagttaag	agaacctctt	atagtcgaag	gtatagcaag	agagctagtc	151920
aataagatta	atactatgcg	tcgaaatcaa	caacttcatg	tttctgaccg	catcgcata	151980
agaataaaaa	ccacagaggc	tgttcatcgc	gctttcttgg	attatgaaaa	ctatatttgc	152040
gaagaaacgt	taattatagc	ctatgatttt	actcaggatt	ctgatttcca	aggggaaaaac	152100
tgggatatta	atggacatgc	aacgcaaatt	gaaattacag	ttagtctctat	agattcttag	152160
agattttcta	gaaacaactg	aaaaaccata	agaatgggta	tttcttgtgg	ttttctctct	152220
ctttcttagg	aaagagtctg	cgtcgttttt	gatagtagac	atatccaatg	agagagagac	152280
ccgtcgctaa	tgctatccca	ctaacaagat	aacctgagag	tggtgttggg	gcagaaactc	152340
cagttaaccg	tcccatgcgt	ccaataggcc	agaatgtaca	tagaggagat	cctaagagat	152400
tttccatagg	aacaaagcca	aattctcgac	tatccgcact	catagggtag	ttatctccca	152460
agacgagAAC	atgaccttta	ggaacttgaa	taccaaaaatt	atgtataaac	tccacgaatt	152520
ctttaaaaatc	ttctggaggg	agtcccttgt	caacaaaagc	tatatagggt	tgtgtctctg	152580
aagacccttc	ttgcttttcc	gtttcagaag	tcacaaaatt	ttgcagagtt	ggatcattct	152640
ttataaatac	aggagaatcc	atgatataaa	gattcccttg	gttaaagaat	gcataacggt	152700
taggtaaaag	tgcttgacgc	ggattcacag	gattataaat	agaactaaag	ttgatcccg	152760
agttaaaaag	ttcaatcact	tgcttatcat	tgagctgagt	aagggggtga	gaagatttta	152820
gcttataacg	aatctctcca	aagccaattt	gatacgcttc	gccttttagaa	tattcataac	152880



aaccatcagg	gaccttgggc	aggagaattg	cataggcttt	ggcaattcct	gaagtgttaa	152940
tcttgaattg	atgggtattta	tacgcacatc	cttgagcaac	aataaaacga	gaggtagtaa	153000
gattgttccg	aattaagtgc	aaatgttcct	tacgcaaagg	aagtaaagtc	ttcatagggt	153060
gaatcgagg	cgagagctga	tgctcatagt	gacgcaacag	aggctttggg	taggaaaggt	153120
tcgctgtatg	gcaaattttct	aagtagactt	tagttggact	tcctggattc	ggaagtagat	153180
gggatgttcg	tgccctgatgt	tctgttaaga	tgcgacccat	agcatagtta	cccataccaa	153240
aaagatcggc	atagctgact	ggcgaaagat	gaggatcttt	taatttatta	ggctcgtctt	153300
gatgccattc	tttatgggtca	aagaattgtc	catacatgga	ggtttgaggg	aaaatcagcc	153360
gaccataact	ttgattgaac	tgcttaaaat	ctataattgt	ttctgcccct	tctgtatggc	153420
tgctggtagt	gccatcaaag	gatataatag	ggacgtgata	taagttttct	aaaccatgga	153480
cagaaggaaa	ctctatgcgt	ttacctgcat	catcaagacc	ataaattttt	cctccataga	153540
aatataagaa	gtccccagggt	cttccccatgc	aacgtttaat	gtaacgcttt	tttcttgaa	153600
tcaatccgaa	gtactttgtg	tcagcatctg	ggatagggag	gtcgccctaca	gtgaaaacaa	153660
caagaccccc	gcgagttacg	gattcaggat	tgaaggcaag	tggtttctta	gcaaaagggc	153720
aatggagacc	aaatgttggt	ttggatacaa	gaatccgata	ctgttctaaa	attgtaggcc	153780
tcattggatcc	tgtaggcact	tcataaaagt	caaaccacaaa	ttgccgaact	aagaaggcta	153840
caacaccagc	aaaaagaagg	gccttgataa	gctcataggt	tttgcgtccg	aaggaattag	153900
gataacgggt	ggaaaatgct	aatgcttgct	gagctaagtc	gcttgagctt	tcttgatcat	153960
gttcaaagat	agcctcttct	agttgttcta	gtagttcttg	cagttgcttt	ttatctgcag	154020
gggaatgggc	gagtttttta	ctttttaaaa	gcttataagt	actgcggagg	atatgacgac	154080
ttttatttag	agaatagtgt	tgtttcataa	agatactggg	gtaagaaagt	cagattctat	154140
ctcttttagat	tgattataga	acggctgcat	tgataacttt	agagctaagt	gagactgaag	154200
acctaagtga	aaaatcaaaa	caatcctcga	gctaaattcg	taagtacatt	ctagcgtatt	154260
agatttttctg	atccaaaatt	attttgctat	attgttagat	cttttcattg	tgtcttagag	154320
tcaggaagag	aatagacata	gggagaagtt	gccccgtgtc	ctatatccac	agctcttact	154380
atagaagtcc	ctttaggagt	ctcgatactc	acccataaag	gaaacacaga	aatgtcaggt	154440
tggttgaaat	acataaggat	tcctgtttct	gataaggggc	ctcgatcttt	aggccagagc	154500
ccctgccatg	cattcacaga	gattgacgtg	agtggagccc	cttcaaaaaga	aactttggga	154560
gaccagggtc	tgttttcttt	tccttttagt	ttgattacgt	ttgcgggagc	tgagataaaa	154620
ggaagatcaa	agatttgcaa	gaaggcagga	actgtatggg	attttcctac	aggctctagg	154680
ctcttggttc	gagtgtttaa	agagaaaaac	tgagaacctt	cagaagagag	cgaaacaaca	154740
aagacttgtg	aaggtgattc	cagttgatga	atgacctgtt	tccaagaagc	ttgttctaaa	154800
gaagggcggt	ctttatgggc	gatacagggg	aaatggatga	tctctatcca	aacggtttta	154860
gggttggttg	atttgactaa	aacaaacgtt	ctttgagacc	ctcgacttaa	aacagtatat	154920
tctccagtct	tagcaagaaa	aatattttct	tgaattgttc	gtaaagaact	agtttgagag	154980
gcaaaaagac	cagaaaaagc	cgtcgagaag	aggaaagata	gaaagaggaa	taagaagagt	155040
gtttttcctt	gctttttcat	aagatatctc	tctgaagata	tgtcgagcta	tgtagagcta	155100
tcatttgcca	taataggata	gcgatttttg	agttgtcaat	atgaaaaaaa	ataccacccc	155160
tgaatataga	caggttttat	ttgtagattn	ttcaacaggg	tataaatttg	tttgtggatn	155220
tacctatcaa	agtgaaaaaa	ctgaagtttt	tgaaggtaaa	gagtatcctg	tatgttatgt	155280
cagcgtatcc	tcttcttctc	atcctttttt	cactggaagt	aagaagtttg	ttgatgctga	155340
aggtagggta	gataagttct	taaaacgtta	tagtaatgta	agacagcctg	cacagcaacc	155400
tcagcctgaa	gaagacgcac	tacctgctgc	taaaggaaaag	aaaaaagttg	taactaagaa	155460
aaagaaataa	aacttctttt	agattttccca	tttataaaaac	ccattctcag	gctctcaagc	155520
ccgagaatgg	gtttttttgt	gagggctttc	tctcttgcaa	tagcttgat	ataacgttat	155580
gctttcctag	gtcacgataa	ttttgaaata	gataacgtta	gatgcctgta	tcagtatacc	155640
agggtgtttt	agagaatttt	ttatctgatt	ccatttgata	ctgatttttc	accacttttt	155700
agggtattcat	gaagaaaaaa	gttgccgagt	atttaaaccg	tttagcagaa	gtcgaaataa	155760
aaatttcaaa	tcctgaaatt	ttttctaatt	ctaaagaata	tagcgctctt	agcaagggaac	155820
attcttatct	tctagaattg	aaaaacgcct	acgataaaaat	cttaaattta	gaaaaagtc	155880
ttgctgatga	taagcaagct	ttagctattg	agaaagatcc	agagatgggc	gttatgcttg	155940
aagaggggat	taacgaaaaat	aaagtagagc	tagagaaatt	aaataaaaata	ttagaaagct	156000
tattagtccc	cccagatcct	gatgatgac	ttaatgtcat	tatggaacta	cgagccggtg	156060
caggaggcga	ggaagccgct	ctctttgttg	gagattgtgt	ccgcatgtat	cacctgtacg	156120
cctcctctaa	gggatggaaa	tacgaggtac	tctctgcgtc	agaatccgat	cttaagggat	156180
ataaggaata	cgatcatggg	atctcaggaa	ctggggtgaa	gcgtttactt	cagtatgagg	156240
ctggtacaca	tcgagttcag	agagttcctg	aaacagaaac	tcaaggacgt	gtacatacat	156300
ctgcaattac	aatcgctgtc	cttcagaaac	cttcagaaga	agatacacag	cttcttatta	156360
atgagaagga	tttaaaaaat	gatacattca	gagcctctgg	tgctggagga	cagcacgtaa	156420
acgttactga	ttctgcgggtg	agaatcacac	acctgcctac	aggtgttgta	gttacatgcc	156480
aggatgagcg	cagtcacacat	aaaaataaag	ataaggccat	gcggattctt	aaagcccgga	156540
ttcgtgatgc	agaaatgcaa	aaacgccata	acgagggcgt	tgctatgcgt	tctgctcagg	156600
taggaagtgg	ggatcggtcc	gagagaattc	gcacctataa	tttttctcaa	aatcgctgga	156660
ctgatcatag	aatcggtatta	actttatata	acttagataa	agttatggaa	ggagacctag	156720

atccaattac	gactgcaatg	gtgagtcacg	cctaccacca	gttactcgaa	catggaaatt	156780
aaaaaggcga	ttcaagaggg	aaccgcttac	ctagattatt	atgggggtgcc	tctttctgat	156840
tgcgaaagccc	tgtatattct	catggattta	ttagaagtca	gttcaagggc	aaagttattc	156900
gatcttggtg	gaattagcga	aacgatgctt	atggagtatc	gaaagaggct	agctttaagg	156960
gggcaacggg	gtcctactgc	atatctcaat	ggtgccgtga	gttttttggg	attaagattg	157020
agagtggatt	ctagggtttt	aattcccagg	acagagactg	agctgcttgc	tgagtatatt	157080
atcaactatc	ttttatctca	ttctgagatt	caaacttttt	atgatatttg	ttgtggtagc	157140
gggtggttag	ggctagctat	caagaaatcc	tgctctcatg	tggaagtggg	gctttcagat	157200
gtttgtccgc	aagcagttgc	cgctcgcaat	gaaaatgcta	aaagtaatgg	tttggatgta	157260
aagattcttc	taggcgattt	gtcagccccc	tacactcgtc	ctgcagatgc	ttttgtttgt	157320
aatccccctt	atttgtcttt	taatgaaatt	attcatatag	atcccgaagt	gcgttggtac	157380
gagccttgga	aggctcttgt	tggaggttct	acgggttttg	agttttatca	gcgtatcgcc	157440
caagaattgc	ctaagattgt	aacttctaca	ggagtcgggt	ggttggagat	tggatccagt	157500
caaggagaaa	gtataaagaa	tatttttttcg	aagcacggaa	tttatggccg	tctccatcaa	157560
gatttgctcg	gacgcgatag	aattttttttt	cttgaaatgg	atgggagaga	tctctatcc	157620
tcgggggctt	attccttgatt	ttttctggat	aaatgattaa	ttctttatcg	caaaagctat	157680
cttctatttt	ttctttttttg	gtttcttctc	gtagaattaa	tgaagaaaat	atttccgaat	157740
ctattagaga	agttcgtctg	gctctcttgg	atgccgatgt	aaattatcat	gtagttaagg	157800
attttatttc	taaagttaaa	ganaaaatcc	ttggagaaga	gatctggaag	catgtttccc	157860
cagggaacaa	gtttatacgt	tgtttgcatg	aggaattagt	agcattttta	agcgatggaa	157920
gagaagagtt	tactattcag	aagacgcctt	cgatcatcct	tctttgcgga	ctccaggggg	157980
caggaaaaac	aacaacagct	gctaagcttg	ctgattatgt	aattaagaat	aagaaagcaa	158040
aaaaagtcct	tgtggttcct	tgtgatctca	aaagattcgc	tgctgtagat	caattaaaaa	158100
ttttggttgc	tcaaacgaaa	gctgaatttt	accaaagtc	agagaacaag	cctattgatg	158160
ttgttggttaa	agcgcttgca	tatgctaaag	aaaatgggtc	tgattttgtg	attctggata	158220
ctgcagggcg	tctcaatata	gataacgagc	ttatggaaga	gctgacggcg	atacaaaaag	158280
tttctcaagc	taatgagcgt	ctttttgtga	tgaatgtagc	tatggggcaa	gatgttttag	158340
caacagtgc	agcttttgat	cagtcctttg	atcttacagg	cgtagattctt	tccatgactg	158400
atggagatgc	tcgagcaggc	gctgttttct	caattaagca	cgctcctggg	aagcccatta	158460
aatttgagg	atgcggagaa	cgcatctcaag	atcttcggtt	attcgatcct	caatctatgg	158520
cggaacgcgt	tcttggaatg	ggggatacca	taaattttgt	taaagaaatg	cgcgagtata	158580
tttctgagga	agaagacgct	gagctaggta	aaaaactagt	tactgcggct	tttacttatg	158640
aagactatta	taaacagatg	aaagcatttc	gtcgcatggg	acctctaaga	aaacttttgg	158700
gaatgatgcc	tggtttttaat	aatgcgaaac	ctagccaaaa	ggaaatcgag	gattctgaac	158760
aacagatgaa	aagaacggag	gcgattatcc	tgtccatgac	tcttgaagag	agaaaggagt	158820
tggtggaatt	ggatattgagc	cgatgaaga	ggattgcttc	tggttggtgg	ttaactttag	158880
gcgacgtgaa	ccagtttctga	aaacagatgt	cgcaatcgaa	aaaatttttt	aaaggaatgt	158940
ctaaaggcaa	gatggaacaa	gttaggaaaa	aaatgtcagg	aggaaatcag	tggcggttaa	159000
aattcgttta	agacagcaag	ggcgtagaaa	tcatgttgtt	tatagattag	tgctcgacaga	159060
tgctcgagtct	cctcgtgatg	gtaaatacat	agaattatta	ggttggtacg	atccacatag	159120
ctctataaat	tatcagctga	aaagtgaacg	aattttttat	tggttagaga	ggggagccca	159180
actttctctg	aaagctgaag	cttttagtaaa	gcagggagct	ccaggagtgt	atagtgcgct	159240
attgtctaaa	caagaagctc	gtaagttagt	tgctcgtaag	aagcgacgtg	cttatagaca	159300
gcgtcgggtct	acacaaagag	aagaggctgc	aaaagatgca	actaagtagg	tagtgaactg	159360
ggatgaagat	cgatatactt	tctttatccc	caggttattt	tgatgggtcca	ttgcaaacga	159420
gtattcttgg	tagggccata	aagcagagac	tcttagatgt	ccagcttaca	aatcttcgtg	159480
actttggact	cggaaagtgg	aaacaagtgt	atgatactcc	gtttagtggg	ggtgggatgc	159540
ttttaatggc	agagcctgtc	acttcagcta	ttaggagtgt	aagaaaggag	aattctaagg	159600
taattttacct	ctctcctcaa	ggagctttgt	tgacagctga	aaagagtcga	gaattggctg	159660
ctgcttcgca	tttgatatta	ctttgcgggtc	actacgaagg	tattgatgag	cggtgctatag	159720
agagcgaagt	ggatgaagag	attagtatat	gggactatgt	cctgactaat	ggtggaattg	159780
ctgctctggt	ccttatcgat	gcagtttctc	gttttattcc	cggtgtattg	gggaatcaag	159840
agagtgcgtg	gagagattct	ttagaaaaatg	gtttgctaga	aggacctcag	tatacacgcc	159900
ctagagagtt	tgaagggaaa	gaagttccag	aagtatttgt	gcaaggggat	cacaaagcca	159960
tttcatcagt	ggagattgga	gcaaagttag	cgtagaactt	atgagagacg	tcttgatttg	160020
tatctgaact	atctctataa	acgctcgatt	gatcacaaat	ttgatgagga	gactacaaca	160080
aatagggatc	atttcaagtg	tgacaagatc	tctgtagtac	tagaggtaaa	taagttaaag	160140
cgcgcaaaaa	atttttactg	taaggtattc	ggtctggatg	ccatgagctg	cgagaataaa	160200
ttttgtcttc	ctcatgaagg	caaaaaccata	ttctggttac	gagaagttca	agctgagaaa	160260
aaaaacatag	tgactctctc	cctttcctta	gattgtgcat	gcgaagagga	cttttggttat	160320
cttcttagaa	gatgggagtt	atttggtgga	aagttgtag	aaaagcaagc	tgatgagcat	160380
gctgtatggg	ccttagcaca	agatttagat	ggcatgcat	ggatattctc	gtggcatagg	160440
atgaaataga	agaaagagaa	ttttaggtgg	tatattatgg	tgaatttact	caaagaatta	160500
gaacaagaac	agtgtaggaa	tgatcttccc	gagtttcatg	ttggcgatac	aattcgggta	160560

gctacaaaga	tttcagaagg	cggtaaagaa	cgagttcagg	tatttcaagg	tactgtgatg	160620
gctcgtcgag	gcggcggctc	tggagagact	gtatccttgc	atcgtgttgc	ttatgggtgaa	160680
ggcatggaaa	agagtttctt	gcttaatagt	cctaggattg	taagtattga	aattgttaag	160740
cgcggtaaaag	ttgctcgagc	tcgtctgtat	tatctgagag	gaaaaactgg	taaggctgct	160800
aaagttaaaag	agtttgtagg	acctagatct	tcaaagaaat	agtctgtagc	aagacttcat	160860
attgtcttat	tttgattttt	ataatctata	gtagcttatg	aatacttcta	tttctgaaat	160920
tcagcgtttt	ctttctatga	ttgcttttga	gaaaagagctc	gtctcagaag	attttagtgt	160980
cgctcgctgga	atagatgaag	ctggaagagg	gccactggca	gggtcccgtag	ttgctagtgc	161040
ctgtattttta	cctaagggaa	aggtatttcc	tggagtaaat	gatagtaaga	agctatctcc	161100
taaacaacga	gccccagttc	gggatgcttt	gatgcaagat	cctgaggtct	gttttggtat	161160
aggcgtaatt	tctgtagaga	ggatagatca	agttaacatt	ttagaagcca	ctaaagaggc	161220
tatgcttcaa	gcaatatctt	ctttaccgat	atctccagat	attcttcttg	tggatgggtct	161280
ttatttacc	catgacattc	cttctaagaa	aatcattcaa	ggagatgcta	aactctgcac	161340
catagcggcg	gcttctattt	tagcaaaaga	acatcgtgat	gatttgatgt	tacaactaca	161400
caggctctat	cctgaatatg	gatttgatag	acataagggg	tacggaactt	ccttgcatgt	161460
agaagcaata	cgacgttatg	gtcccagttc	ctgccatagg	aagagctttt	ctccaataaa	161520
gcaaatgtgt	gctattgtat	gaataagatc	ctagttgact	ctcctttttc	tccagatcac	161580
cagaagtgtc	gtcctaagct	ttttacaatt	agtgtcctcg	ctggagttgg	aaagacaaca	161640
cttgctccgta	tgtagagca	agagttttct	tctgcttttg	ctgagactat	atcggttaaca	161700
acaaggaaaac	ctcgagaggg	tgaagtccca	ggtaaagatt	atcattttgt	ttcccacgaa	161760
gaatttcaaa	gacttttggg	tcgtcaggct	ctcttagaatt	gggtgttctt	atccggagag	161820
tggtacggaa	caagtatgtt	agagattgaa	agaattttga	gcctagggaa	gcacgctgtt	161880
gctgttatgt	atatccaagg	agccttggtt	attcgctctc	ggatgcctag	tgtatctatt	161940
tttattgtct	caccttcaca	ggaggagtta	gaaagaaggt	tagcttcacg	gggatctgaa	162000
gagggctctc	aaagaaaaga	acggctggag	cacagtctta	ttgagctagc	agctgcaaat	162060
cagtttgatt	atgtcattat	taacgacgac	ttaaatcaag	cgtacagggg	tttaaaaagc	162120
atttttatag	ctgaagaaca	taggaacata	ttatgattaa	aaaagatcgt	ttcactaatg	162180
aaaagttaaa	taagcttttc	gatagtcctt	ttagcctagt	gaactacgcg	attaaacaag	162240
caaagatcaa	aattgccaaa	ggcgatgttc	gctcctctaa	tggtgcgac	gaaacactcg	162300
tcttgtttag	tagagaaggg	atacagcctg	agtttactga	agagattgta	gtaactgcta	162360
gccctactgt	ggaaagaaaag	agatcagaac	atacaaatc	tagaaaaaaa	gatccctcag	162420
catatacttg	gagtgtatga	aagtaatgcc	acaaaaagtc	ctgattactt	cagctttacc	162480
ctatgcta	ggtccgctac	attttggaca	tattgcagga	gtctatcttc	ctgcagatgt	162540
gtatgcaaga	ttccgtagat	tgtaggaga	cgatgtcctt	tatattttgtg	gttccgatga	162600
atttggcata	gcgatcacct	taaatgcgga	tcgtgagggg	ttgggggtatc	aagagtacgt	162660
ggatattgtac	cataagttac	ataaagatac	ttttgagaag	ttagggtttg	ctttggattt	162720
cttttctagg	acgacgaacc	cttttcatgc	tgagcttgtc	caagattttt	attcccaact	162780
taaagcgtct	ggattgtattg	aaaatcgcat	atctgaacaa	ctgtattcag	aacaagaaca	162840
acgttttctt	gcggatcggt	atgtagaagg	gacgtgtcct	cggtgcggtt	ttgatcatgc	162900
tcgaggagac	gagtgtcaga	gctgtggtgc	ggattatgag	gctatagatt	taatcgaccc	162960
taagtctaag	atttctgggg	ttgagttagt	aaaaaaagag	actgagcact	catattttct	163020
tttggaaccgt	atgaaagacg	ctctactttc	ttttattcag	ggatgctatt	tacctgatca	163080
tgctccgtaaa	tttggtgttg	attacataga	acatgtcagg	tctcgagcca	ttactcgaga	163140
tttatcttgg	gggattcctg	ttccagactt	tcctggaaaag	gtgttttatg	tatggtttga	163200
cgctcctata	ggatatatca	gtggaactat	ggaatgggca	gcttctcaag	gaaaccctga	163260
cgaatggaag	cgtttctggc	ttgaagacgg	tgtagagtat	gtccagttta	taggtaaaga	163320
taatcttctt	ttccattctg	tagttttccc	agctatggaa	ttgggtcaga	aacttgacta	163380
taaaaaagtt	gatgccctcg	tagtttcaga	gttttatctt	ttagaaggac	ggcaattcag	163440
taaatccgag	ggcaattatg	tggatatgga	caagtttttg	agttcctatt	ccttagacaa	163500
attgcgctat	gtattggcgg	ctacagctcc	tgaaacttcg	gatagttagt	ttactttcct	163560
tgatttttaag	actcgttgta	attctgagtt	ggtaggaaaag	tttgggaatt	ttataaaccg	163620
agttcttggct	tttgcaaaaa	agaatcacta	tgacaagctt	tcttatcatt	ctgtgggtttt	163680
agaagatagt	gacagggcat	ttcttgaaga	agtcgctcaa	ctgttctcag	atgctgagaa	163740
gtgctacaga	gagtatagtt	tacgtaaggc	tacgagtgtg	attatgtcac	tggcagcttt	163800
agggaatgtc	tattttaacc	aacaagcacc	ttggaagcta	ttgaaagaag	ggactcgtga	163860
gcgtgttgag	gccattttat	tctgcgcag	ttattgtcag	aagttgttag	ctttaatttc	163920
ttatcctatt	attcccga	gcgctgtagc	tatttgggag	atgatctcac	caaaatcttt	163980
agaaaattgc	aatttgata	cgatgtatgc	tagggatcta	tggaaagaag	aaattcttga	164040
tgttataaac	gaagaatttc	atttgaagtc	ccccagggtta	ttatttacta	ctgtagagta	164100
gagctcgagg	tcttttcttt	ttagaatcct	gatctgtagg	tgtaattaca	gattctgcata	164160
atttttctta	gtatcgagct	ctttaagaac	ttctgtagt	cctgtacatc	gggtgtgcac	164220
tcgatttttt	cttgttgcaa	tagcaaatgg	ctttttttgt	cccaactaga	atcaccaatt	164280
ttttccccc	cgtaatagca	gtatagagaa	gatttctata	gagcatcata	aagtgcgagg	164340
tatgaatagg	aatgataatg	caggggcttt	cacttccctg	gtacttatgt	actgaggtag	164400

cataggctaa	gactagatcg	tcaagctctg	agaaagaata	gccgacatgc	tttccttcca	164460
tacggacaac	aacagcttta	tcttcgaagt	tgattgtaga	gacatagcct	atatcgccgt	164520
taaagacttc	tttattatag	ttgttgcgga	tttgctattac	cttatcgcca	acggcatagg	164580
attgaaatct	accgtgaaga	tttgcttttt	tagggtttaa	tgcatgtttg	agtgtcttat	164640
ttagattata	gattcctagg	gttccttttt	tcattgggagc	tagtacttgg	atatcttgag	164700
gatagatatg	gtatttttgt	gggacgaatt	ttgtcacaaag	atgaatgata	tgattgagag	164760
cctcttcttg	atcatccttt	tggaaaaata	agaaatcacg	acgccctgtt	tctgaatata	164820
atatggggag	ttcccttca	ttaccctat	gggcattcgt	aacgattccc	gaatcatgaa	164880
cttggcgga	gatcttattt	aatctgatga	ctgtcatttt	attcgaagta	atcaagtctt	164940
taaggatatt	tcctgggccc	acgctgggta	gctgggtgaat	gtctccaata	aagacaagag	165000
ttgtgtagtc	aggaagtgtc	ttcaggaagt	ggtgcagcaa	gtgcgtgtcc	atcattccgg	165060
attcgtcaac	aatgatcaga	tcacagtcta	taggattgtc	atggttcttg	cggaaaagatt	165120
tcgttttaaa	atcatactgt	agcagagcat	gaattggtgac	ggagtgtttt	tgtgttaattt	165180
cgggtcatccg	tttagcggct	tttctgttag	gagctgcgag	gatgatttta	tgagtacact	165240
gttcacaaat	tttcagtatt	gcttgggttaa	tggtactttt	tccagtcca	gggccccag	165300
taatgatgag	aagtttttca	gaaaaacagg	ctttaattgc	ttctcgttgt	tgttctgcga	165360
gatctatact	tagtttttct	ctacccaagc	aattgtcttt	tctcgtcta	tagaacggat	165420
tctcctcgaa	gaaaataaaa	tgcgcttgag	atcagaaaca	atagttttct	ctgcgagatg	165480
gagataacgt	gtccagacat	ggagtgtccc	agaaatgtct	tgaatatgta	aaagttagcg	165540
ttttgcatat	tgaggatttg	cgtatcgatt	tcttcgagag	taataggagt	atcaaagaca	165600
tcttgattta	atagtttggc	gacgacatct	atcaggagct	ctatcggata	gcaagtatga	165660
ccttcttctt	gaagttcttc	taaggagtgc	tggtataccg	cacataggcg	actttcagaa	165720
ttttcgggga	cgcctagtgt	catagctatg	aaatcagcag	ttttgaatcc	gatgccctcc	165780
atttctctgg	ctagaaggaa	gggatcttcg	caaatttttt	ctatggattt	ctcttggtat	165840
tttttaaaaa	ttctcactcc	ataatgaatc	gggatattgt	attcttggag	aaagagaaga	165900
gttttcttta	acattttttg	ctcgcagagt	tgtttgcaaa	tagagacaca	tcgtgtttcg	165960
ctaattccag	aaacctcact	taagcgttct	ggagtgatat	cgaggacata	acatgttttc	166020
tcttgaaatt	tctcgtatgat	cttttctgcg	attttagggc	cgattccttt	gatgagtttt	166080
gaggtgaggt	actggaatac	gccacgatat	tcataaagaa	gaggagagtc	gtaactatgg	166140
atttgaaat	aattagtatt	tgaaggggaa	tggtctcaga	caccatagat	ttggatcggg	166200
gattcctagt	ccaaagggtg	gggaaggttg	cctttaatta	ggataggagt	cgttttattg	166260
ggtattttga	tataagcagt	aatgtcccca	gagtctttgt	tttcaacaag	tatttgcctc	166320
aagtatccgc	agattttctc	catagaattc	taaaatcttg	ttttcctgga	agatgaagta	166380
gcttaaggaa	tctttataaa	aagcttctaa	aaagtatgga	ttataaaact	tttgagataa	166440
aaacgagaca	tcccaaggct	tttaattttg	ggataaaact	atcaaagaat	tattttatat	166500
agtaattatt	tcctcgtata	ttgttttttg	ccataggaca	caaaatctat	cctaccgaag	166560
aacctttggt	attacaacaa	tttttataac	aatagattga	ttaggaaaga	tcgatgttcc	166620
cttgtgcaat	aggttcagt	tttatcagaa	cacgagtttc	ttttttaatt	ctttttcttc	166680
ttgctattgc	attcagctcc	atgaggagag	cttgagtacg	attttataca	aactgggata	166740
gggattgcct	ctatccgtgt	tggacaaaata	cctaagaaga	ttttgattcc	ggctttccga	166800
ctatatagag	aagaaattcc	taaggcactt	taattaaaag	gtttattgcc	atattcttgc	166860
cttgaaaatt	tttgattata	gatttttggt	ttgaacaatg	actagtgcag	taaaaacctc	166920
atcactcatc	caagtgactc	aaccttaaat	cagaagtaaa	caacgtacag	ttgcaattac	166980
gctccttggt	cttggcatte	ttttgattgc	ttctgggatt	atttttctag	ctgtcgctat	167040
tcctggattg	agttcagcag	ttgccttagg	attgggctgt	ggtatgactg	ctttaggaac	167100
tgtttttggt	attacaggac	ttgtcttgct	gatcaggagt	gagaagctcg	ctctagaaca	167160
agtagaaaata	aagcaagcta	ggaccagggt	gaataatgag	ttagatcaac	tcagtcagta	167220
tgttttctac	acagaaaatg	ttttagataa	tttgaagcgt	tggtcgtatc	gagatttagg	167280
ttttgtgaga	caggcgcaag	aggagggttac	aaatttagag	caagacattg	aagaaatttt	167340
cttgacgttg	cgagatatta	gaaatgctct	tgataacgaa	gagtttttta	tgactcatgc	167400
gaaacagtgt	ttagcccaag	tcggagaaag	cttatttcag	gatgctagta	tagatgagtt	167460
tattaatttg	gctcatctat	ccgaaatacg	tcagcatttg	gatatcaatg	atccgagatg	167520
gtctatgatt	acaaagaaag	ttaaaggcac	tgtggttcgg	tttatctatg	tctctacaat	167580
gtataaacaa	ataaaatcta	attttgaaaa	aagtgacttc	ggacaactta	ggaaagagct	167640
actgaacaat	tacaaaacaa	tagaagaggt	cttgatcatg	agttttcaaa	ggggctacaa	167700
tagagccgct	ttgttgagtg	aaaagacaag	aattattcat	acgagttctc	ttttgcattg	167760
ggaaaaggac	gaagataagc	atcttaatat	taagaacgag	tgtgcaagtc	gtcttgagaa	167820
tttcaagaag	tttagaacac	tatttcttgg	attatcagag	gaagacgtta	ttgactttac	167880
tggagcgtct	ggttgggatt	gttccaaact	gcctcggaaa	gaggtcccgc	ttgatggtgg	167940
caagaagaaa	ctgaggttta	aaagaacctt	tcagatgaa	caagtccggag	attgggatcg	168000
cactacgtct	cttgagcata	tgacacctca	agaggaagat	ccttttagaca	ggttaattgga	168060
tcaggttgaa	caagaggcta	cttcagctct	aaaagatcag	gatcggtatt	ggaaagagat	168120
cgagacaagc	gaagcaaagt	ttaggtccct	gccacgggaa	gatgattttg	aaaagcagtc	168180
acagattgat	agtttatattc	gggattttgga	cgaccattta	tcggtttggg	cgaatcagtt	168240

atctgctgca	gaagatgctt	tgatagaggt	tacagatgtg	caggaacatg	gaaatagaga	168300
aatgcttaag	aatatacaac	agggactgga	gcttattgaa	gatgctgtaa	aagctactct	168360
acctagagtt	gacttttatac	aagagctttt	agagaaggaa	gagcttccgt	tggttgctgc	168420
taggatgagt	ttagagaata	gttagaagat	aagcagctgt	gcagagatta	tgtcagaagt	168480
gaagcctttg	tttttaaaga	atgactcttt	tgatttggca	actcagagat	tccagaatct	168540
aattaacatg	ctacaagagc	aagccgagat	atataacgag	tatgaagaaa	agaatgctag	168600
ggttcagaat	gagattaagg	agcaaaagga	ctttgtgaaa	agatgcatag	aggactttga	168660
agccagagga	ctgggggtgc	taaaagaaga	gcttgcattct	ttgacgcgtg	atttccatga	168720
taaagcaaaa	gcagagactt	ctatgctcat	tgaatgtcct	tgtattggtt	tttattatag	168780
tattcatcag	gaggaacaaa	ggcaaaggca	agaaaggctt	caaaagatgg	ctgagcgcta	168840
tagggactgt	aaacaagtct	tggaggctgt	ccagggtggag	caaaaagata	tgatatcttc	168900
tagagtcggt	gtcgaatgaca	gctactttga	agaagaaaaa	gaagaacaaa	aggtggataa	168960
cagaaagaaa	gaacaggact	aggtctattt	ttctacagct	tttcccgtag	ggggagggga	169020
gttctagaat	tttttctgtc	gcctatncaa	gataacactg	ttgttttgtg	gtatcaaatt	169080
tagacattac	actagcttta	aagtttgagc	cctcccccgc	tttaagatcg	ctttctgaag	169140
ctgagtcctaa	ggtacaaaact	tttgctatag	gattattagt	tattggtatt	ctcatactat	169200
tgcattgggat	tatttttttt	ctctggagct	atttctagtt	gtggtctttt	agtgtctcta	169260
ggagttgggt	taggacttag	tgtttttagga	gtactttttac	ttctcttagc	aggtcttttg	169320
ctttttaaga	tccaaagtat	gcttcgagag	gtgcctaagg	ctcctgatct	attagattta	169380
gaagatgcaa	gtgaacggct	tagagtaaag	gctagccgtt	ctttagcaag	cctcccgaag	169440
aaatcagtc	gctagagagc	tacattcggt	ctgcagctaa	tgatctaaat	acaattaaaga	169500
cttgcccgca	taaagatcaa	agactcgtcg	agaccgtgtc	acgaaaatta	gagcgtctgg	169560
cagctgctca	aaactatatg	atttctgaac	tctgcgagat	tagtgagatt	cttgaggaag	169620
aggagctatca	tctaattttt	gctcaggaat	ctctagaatg	gataggtaag	agtctatttt	169680
ctacctttct	ggacatggaa	tcttttttaa	atttgagcca	tctatctgaa	gtgcgtccgt	169740
acttagctgt	aaatgatcct	agattattag	aaattaccga	agaatcttgg	gaagtagtga	169800
gtcatttcat	aaatgtaacg	tctgctttta	agaaagctca	gattcttttt	aagaacaacg	169860
aacattctcg	gatgaagaag	aagttagaaa	gtgttcaaga	gttactggaa	acattttatt	169920
ataagagttt	aaagagaagt	tatcgagaat	taggatgctt	aagtgaagaag	atgagaatca	169980
ttcacgacaa	tctctcttct	ccttggggtgc	aagatcagca	gaagtatgct	catgctaaga	170040
atgaatttgg	agagattgct	cggtgttttg	aggagtttga	aaagacgttc	ttctgggttg	170100
atgaggagt	tgctatttct	tacatggact	gttgggattt	tctaaatgag	tctattcaga	170160
ataagaagtc	cagagtagat	cgagattata	tatccacgaa	gaaaattgca	ttaaaggata	170220
gagcccgac	ttatgctaag	gttcttttag	aagagaatcc	gactacagag	ggtaaaatag	170280
atttgcaaga	cgctcaaaga	gcctttgagc	gtcaaagtca	ggagttttat	acactagagc	170340
atacggaaac	aaaggtgaga	ctagaagcac	ttcaacagtg	cttctcggat	cttagggagg	170400
cgacgaacgt	aaggcaagtt	aggtttacaa	attctgaaaa	tgcgaaatgat	ttaaaggaga	170460
gtttcgagaa	gatagataaa	gagcgtgtgc	gatatcaaaa	agagcaaagg	ctctattggg	170520
aaacaatag	tcgcaatgag	caagagctta	gggaagagat	tggggagtcg	cttcgtttac	170580
aaaatcggag	aaaagggtat	agggctggat	atgatgctgg	gcgtttaaaa	gggttgttgc	170640
gtcagtggaa	gaaaaatctc	cgcgatgtgg	aagcccacct	tgaagatgca	actatggatt	170700
ttgagcatga	agtaagcaag	agcgaattgt	gcagtgttcg	ggcgaggctc	gaggttctag	170760
aagaagagct	gatggatatg	tctcctaaag	ttgcggatat	agaagagttg	ttgtcctatg	170820
aagagcgttg	tattcttctc	attagggaaa	atttagaaaag	ggcataacct	caatataata	170880
agtgttctga	aatttttatcc	aaggcaaagt	ttcttcttct	cggaagacga	gcaattgtca	170940
gtttcggaag	cgaatctaag	agaggtgggt	gcccagttaa	aacaagtaca	gggaaaatgt	171000
caagagaggg	cccaaaagtt	cgcaatatatt	gaaaagcata	ttcaggagca	gaaaagcctt	171060
attaaagagc	aagtgcggag	ttttgatcta	gcgggagttg	ggttttttaa	gagtgaagct	171120
cttagtattg	cttgtaacct	ttatataaag	gcggttggtta	aggagtctat	accagttgat	171180
gtgccttgta	tgcaattata	ttatagttat	tacgaagata	atgaagctgt	agtgcgaaac	171240
cgctttttta	atatgacgga	gaggtatcaa	aatttttaaaa	ggagtttgaa	ttccatacaa	171300
tttaattggt	acgttctttt	acgggatccg	gtctatcaac	ctgaagggtca	tgagaccagg	171360
ctaaaggaac	gggagctaca	agaaacaact	ttgtcttgta	agaaattaaa	agtggctcaa	171420
gatcgtcttt	ctgaattaga	gtcaaggctg	tctaggagat	agtaaaaaag	ttgagttctt	171480
tgcgtagtgt	ttttgatgga	ttattcggtta	gaagacgata	cttgagagtt	ttccaaactt	171540
ttctgtactt	ttcttccgaa	gagaactagg	cagaggaggc	ttcctcctaa	cattagaaag	171600
attcctatac	cttctttag	agaagggaaga	ctttgtgagt	agagataggt	aagcacaagg	171660
ccaaaaattg	gttcaaagat	taatatcgcc	cctagcaatg	ctggtgagag	attcaaacta	171720
gctttattcc	aggctattaa	agcttttgct	gaggaaaata	ttcccatagc	actacatagc	171780
aacaagaaga	gcagtcgctc	ggatccccgt	gtatgcgaga	taagattgtg	tgttactgtg	171840
gtaattccac	agagatcgag	aataataatc	atagggaggc	agatgatcaa	agcgtgatt	171900
ccgatgaggt	agctccaggt	aatctggagt	taggttgggg	tgtttttcga	gtagcgattg	171960
attcggtatc	acatagatta	cccaaagact	tggtgagagt	atgactgcaa	tgactcccaa	172020
gatagagtag	agaggagagg	cggctgttgg	caagttgagt	gcggagaggt	gtgtcagaat	172080

cactcctgtg	atgatcacac	tgctgatagc	aaagagtaga	gaatagggga	gttctttttg	172140
ctttgtattg	gagtggtaga	gtacggcggt	tggagccagg	ctggcgatga	ctacagtgat	172200
tgcgatcca	acatagcgga	tgccaagggg	gattccgaag	taatacacgg	ggttaatcag	172260
cagtgtccag	aggaggcttt	ttctccaaat	atataaagga	gttttttttaa	ttacggagggg	172320
atTTTTtata	gcgcaagcaa	tcagggagaa	aataccaaaa	atggtataac	gggtaagtac	172380
aatatcaaga	tcgccaacag	aaccgaggaa	gtttggtagt	acaaagacga	ttccccagta	172440
taggcaggca	acgagcccat	ggaagatgcc	taggggtaca	ttacgggttc	tggattcttg	172500
atTTgcgctg	gggaacataa	agctctctta	aggggtatgag	caatagaatt	gcctacaatt	172560
ttaacatggg	agggattttt	gttgggtattg	agacttttaa	taatacgaat	tgtttttctg	172620
ttcgagagga	aaataagaag	ataggggaag	aatgttaagg	aatcaggtac	ttgtttactg	172680
tagtgagggt	gtttctcctt	attattttacg	gcatacgata	cgtttttctca	agtactatag	172740
cactcaagaa	ggtgcttttcg	atattcttag	ggtnacggg	aatttttttga	ttaagaatcc	172800
tttttgggaa	gaaacgacgc	gcttattggg	attcccagg	ggtgcggacc	gccccatca	172860
tcgtgtactt	catgggttag	gcactgcccc	tattttccaa	tatgtttctg	agggagggaa	172920
ttttctaggg	atTTgtgctg	gggcatattt	tgggtctaa	atgatttatt	tttatgagcc	172980
tgagggagcg	ccgttgcaag	gggctcgaga	tctagggttt	ttcccgggga	ctgccaaagg	173040
tcctgcttat	agggggaatt	tttcttatgt	gagtccttct	ggtgtaagg	tttcacctca	173100
gttatttttca	gattttggct	tggggtagtc	gatgtttaat	ggggggtgtt	ttttcgagg	173160
ctcggaagga	tatcctgggg	tgaatatcga	atctcggtat	gacgatcttc	cagggaagcc	173220
tgcgagcata	gtgtctagga	ttgtcagtaa	gggcttagcg	gttctttcag	gacctcatat	173280
agagtatctt	cctcattact	gtcgtatggt	taaggagaac	gtccagaaaa	cacgtgaatt	173340
cctccaaagg	gagcgtacaa	ctttggaccg	ctattgtcag	aatcttgtag	agcgtttgag	173400
tcagcctgca	ttttcgaaag	cggactgctg	aagatctaaa	ttaggcaatc	gaaatcatca	173460
gcgtgtattt	ttgtcgtatc	gaactcggtg	ataagctgat	ataggattgg	gctgcaaaga	173520
actatggagt	gcgttaggac	atTTcggtatg	ttattggagg	cataagacat	ctcttcatag	173580
ccgtggagta	gtccaaacga	ttgaatttgt	ggagctgnt	ggctgntntt	atatacaaa	173640
cgattgaaat	agtctctagg	ttctatagtg	tactcatctt	cattatagtc	taattgctcg	173700
aatacacaca	gaaaagcgag	tagttccatt	tgtcttgcta	tgggatttga	gcttctctgtg	173760
ttaaggctat	ctatgagtag	tattttgattt	ctttctaattg	ctgttgaaaa	taggttatgg	173820
tagtggataa	agaatttttt	gaaaattaga	tagagtgggt	tcgagatagg	atccccatca	173880
gatcttagaa	tgtcaggatt	atgtactaca	gggaagttag	aggtgatttc	atTTgtgtg	173940
gtttcgtatg	gggtattttt	atactgcgtt	tgttctgca	agtcggtcaa	tgaacttga	174000
gaggctatcc	ctaagtgtgt	tacatgtttt	tcttgtaatt	tttgataggt	tttttgtaaa	174060
ggttcggagg	tgacaaagat	tctcggatcc	atatggatat	gagaaaggat	atactgttca	174120
tcttgttcta	atattttcca	attggcgaga	gcacttttaa	ttaggaaatc	tggatcttta	174180
agaaagattt	ttttccattc	ttcgaaggat	ggaaaaaaga	gctcattttt	taggtttatg	174240
gatgttggat	ctaggagtag	tgtttcggag	gattgtattt	tatttttgag	aggatttagg	174300
agccaggggt	ctaaagaagg	tgtttcttta	ggaaaaatag	atTTtggttt	tgttctgctc	174360
ttttgaacac	ttttcgagca	ctgtgttcca	atgagcagg	agattcctgt	acttaggacg	174420
attatactga	ttagggacaa	tgctattatc	aaaagagtat	ttgggagaag	tcgggagagg	174480
gctatgagta	tgcatgctgc	aatccccaa	aatagggaaa	gtatggcgag	agaaagtttc	174540
gttatagcag	cgaatttggg	ttctggcagc	agttgagcgg	gttttttatt	ttcgtgtata	174600
attgaagaac	acttgaccat	agaagactat	caaagaaaat	gcaaataata	aattgaaaaa	174660
tcgttgaaag	aaggagtcga	agagaaaaaa	tactccggag	gatgggttcg	aaccaacgac	174720
caatggatta	acagtccact	gctctaccgc	tgagctactc	cggacacagt	tttactccct	174780
acatatctta	tgaccaaagg	gtaaaaagtc	aatgattttt	gtctctgaaa	aaagaaagat	174840
ttctcttaag	tcttgcaatt	ttccttatat	ttttcttcac	tagtgcgtag	gtttttccat	174900
cgatatgctt	tctggagtgt	tttatggaga	atgctatgtc	atcatcggtt	gtgtataatg	174960
ggccttcgtg	gatttttaaaa	acgtcagtag	ctcaggagg	atttaaaaag	cacggtaagg	175020
ggattcaggt	tctcttaagt	acttcagtag	tgttttttat	aggtcttgga	gtctgtgcct	175080
ttatatntcc	tcaatnnctg	attgtntttg	ttttgactat	agatttgctt	atgctcgcta	175140
taagcttggg	attgtttctc	ttaaaagttc	tgtacgctcc	ttcaatggta	gatcgtttgt	175200
ggtgttctga	aaaaggatat	gctcttcac	aacatagaaa	cgggcctttt	ttggatgtga	175260
agcgtgtaca	gcaaattctt	ctaagatcac	cctatattaa	agttcgggct	ttatggcgtg	175320
ctggagatat	ccttaggat	ccttcacaag	ctgcggttct	attactttct	ccttggactt	175380
tcttttcac	cgtggatgta	gaggctttat	taccgagtc	tcaagaaaag	gagggttaagt	175440
atatagatcc	tgtgctgcct	aagttgtcta	ggatagagag	agttctcact	ttagtgtttt	175500
tgagtgcatt	tactttggat	gacttaaacg	aacagggagt	caatcctttg	atgaataatg	175560
aggaattttt	atTTTTtata	aataagaaa	cgcgtagcat	gggattcagg	atttaaaaca	175620
cgagattatg	tcttcggttag	agaaaacagg	agtgccatta	gacccctcaa	tgagttttca	175680
agtttcacaa	gcgatgtttt	ctgtatatcg	ctacttgaga	caaagggtat	taacgacttc	175740
agaattaaga	tgttttccac	tcttaagttg	ttttaagggt	gatgtgggtc	attgtttagc	175800
ttcatttgaa	aaccctaaag	tcttagcaga	ttctgacttt	ttagaagctt	gtaagaacgt	175860
ggaatggggg	gagtttattt	cggcatgtga	gaaggctctt	ttaaagaatc	cgcaagggaat	175920

ttccattaag	gatctaaaac	aatttttagt	gaggtaatct	atgatcgagt	ttgcttttgt	175980
tcctcatacc	tcctgtacag	cggatcggat	tgaggatcgc	atggcctgtc	gcatgaacaa	176040
gttgctact	ttagcaatta	caagtctttg	tgtattgata	agttcagttt	gtattatgat	176100
tgggatttta	tgcatctctg	gaacggttgg	gacctatgca	tttggttag	gaattatttt	176160
ttctgtgctt	gctttggtag	catgtgtttt	ctttctttat	ttcttttatt	tttcttctga	176220
ggaatttaag	tgtgtctctt	cgcaggagtt	tcgttttttg	ctataaccag	ctgtggtttc	176280
tgcatcgct	tcctatgaat	acatttctca	ggacgctata	aatgacgtta	taaaagatac	176340
gatgcagttg	tctacccttt	cttctctttt	agatcccga	gcttttttct	tagaatttcc	176400
ttattttaac	tctttgatag	tgaatcattc	gatgaaggaa	gcggatcggt	tgtctcgaga	176460
ggcttttttg	attttattag	gtgagattac	ttggaaggat	tgtgaaacaa	aaattttgcc	176520
atgggtgaaa	gactcctaata	tcactcctga	tgatttctgg	aagctattaa	aagaccattt	176580
cgatttaaaag	gactttaaga	agaggatcgc	cacttggtata	cggaaggcct	atccagaaat	176640
tagattaccg	aagaagcatt	gttttagata	gtctatctat	aagggtgtgt	gtaagttttt	176700
attacttgct	gagaatgatg	tgcaatatca	gaggttatta	cataaggctc	gttatttctc	176760
tggggagttt	tctgccatgg	tttttaggtt	gggaagtga	gtgcctatgg	tgtaggact	176820
ccctaagggt	cccaaggatc	ttacctggga	gatgtttatg	gaaaatatgc	ctgttcttct	176880
gcaaagcaaa	agagaggggc	attggaaaat	ctccttgga	gacgtagcct	ctctttaatg	176940
aaagaagagt	cctcggatga	agcctatgat	ttcttctgta	ggtgttccag	gggtattgat	177000
atcgtaaga	cggctcttga	attgtggata	cgatgagtag	aagtgtttat	gagcttggtg	177060
ggataggggt	ttaataatat	ctccagggag	gttcagggtg	tagaggcttt	cttctagagc	177120
taggtagagc	aaggaaggga	gagcctctga	gagttttggt	aattctttag	ctgagctagt	177180
atggctatgg	aattccaagg	atggcacaga	aagatgggga	atgtctttat	ggttagctct	177240
gagtcctgac	aaccgtgtgt	ttagaaatag	gcatcttcgg	atgagcacgg	gagcacggtc	177300
tatccataag	tttgaggggg	tttctttttg	tggatggaag	tttttccata	ctaaagacca	177360
gtttgttttt	gtgcctgtac	tgtcgtaggg	gaatatggtg	aagtttgccc	catggataat	177420
gagctcggag	atttccaact	gtttcgtag	tagcatagat	atggaagaaa	atcgtagatc	177480
tgcgtactcg	atttcggcgg	cgtaaggaaa	gcgttcagaa	gctagagggt	tatgaatgca	177540
gatatgacgg	attttaattc	cagaagttct	tatggagact	cttctacag	tgacttgggt	177600
gtggaggcgg	ttagatagcc	attgctcaac	gatactttct	ttgcgcatcc	agaaatatcc	177660
aacgatgac	cacctataa	gaaatagatt	tttagcagt	ttaaacatat	aggcagagga	177720
gttttatatc	tttaataatta	agatagatta	agaaatgaat	attcccaaag	aaaaaggctc	177780
cttttcttta	gttagaaaag	agacctcatg	gaaaattgtt	aatactagct	taagagacta	177840
gtagtccatt	cctgcgcttg	gcatcgctgg	agctgaagaa	gatttctctt	ctgggatatc	177900
agcgattaag	gcttctgttg	tgaggagtaa	tcctgcgata	gaagctgcgc	tttctagagc	177960
tgagcgagtc	acttttagttg	gatctaaaat	tcctgcgtca	atcatatctg	tataagcgtc	178020
acgtaaagca	tcatagcctt	catttgcaga	tcttgctaga	acttgctgac	aaatgatagc	178080
gccttcttta	cctgcgttac	ttgcaatttg	ctttaatgga	cggtttaatg	cttttagaat	178140
aatacgagta	ccaatagctt	cgtcttcggt	tgctagcata	ggaaggaaaag	cttctagtgt	178200
agggatacac	cgaactaagg	cagttccacc	accaggggag	attccttctt	cgacagctgc	178260
aatgggttgcg	tggtgtgcat	catctactct	gtcttttttc	tctttcatct	ctatttcggt	178320
agcagctcct	acgcggatta	cggcgacacc	accggagagt	ttagctaaac	gctcttgagg	178380
tttttctttg	tcgtaatctg	aagtgcctatc	ttcgatttgt	tttttaatat	tgctgcctcg	178440
agcttggtata	tcaggtttgt	ttcctaagcc	ttcgacgatt	gtggtatctt	ctttagttag	178500
gataactttc	ttagcttttc	ctaacttgct	tagagttgta	ttctctagtt	tcattgccaag	178560
ttcttcgcta	actagtggc	caccagtaag	gatagcgatg	tcttctaaca	tagcttttct	178620
tctgtcaccg	aaaccaggag	ctttcactgc	acagactctg	aatcctgcac	ggagtctatt	178680
gactactaga	gttgctaaag	cttctccttc	aatttcttct	gcaatgatta	aaagaggggc	178740
tccagattct	gctacttgtt	gtaaaactgg	aagggaagtct	ttaattccag	agattttttt	178800
atcgtagatt	agaatcagag	cgtcttctaa	aacgcattct	tgagtttctg	gatttgtgga	178860
gaagtagctg	gagaggtatc	cacggttgaa	gttcattcct	tctacaacgt	cgagaacagt	178920
ttcgaagcct	ttagcttctt	caacagtaat	ggatccgttt	ttaccaactt	tttccatagc	178980
ttctgcaata	agatttccga	tttcgggaatc	attatttgc	gagatagtag	ctacttgagc	179040
gatttctttg	tgatgttgta	caggtttact	aatttttttg	agttcatcaa	caacaacttt	179100
tacggctttg	tcgatacctc	tttttaggtc	cataggattg	gcaccggcag	tgacatttct	179160
tagaccttcg	ctatagattg	cttctgcaag	aacagttgct	gttgtagttc	cgctgcctgc	179220
tttgctagca	gttttgctgg	cgacttcttt	taccatctga	gcgcccattg	tttcatgttt	179280
gtcttcgagc	tcgatttctt	tagctacagt	aacaccatct	ttagtcactt	ggggagagcc	179340
aaagctctta	tctataacta	cgtgacgtcc	tttaggacct	agagtaactt	ttactgcttc	179400
tgcaagagtt	tttaccctct	tatgtatttt	ttntctggct	tcttcattat	atttaatat	179460
tttcgctgcc	atcggtgttc	tccttaactt	tctataatct	gcaaactagt	attttatttt	179520
aggacggcca	tgatttctact	ggactgtaga	atgacatact	cttcgctatc	cattgtgatt	179580
tcttgacctg	catatttctc	cattaaaaatg	atatcgccaa	cttgaacttc	gaaaggaagt	179640
agagtaccgt	catcagttcg	tttgctgtg	cctaaaaacaa	ggacctcagc	acgatcttgc	179700
ttcctttttg	ctgtatcggg	taagatgatt	cctccacgag	cagtggcttc	ttcttcttcc	179760



ctttttacca	agattctatc	gcccaaaggt	ttaattcggg	gggtcgttgc	ttgatcagac	179820
atttatatgc	tccttatgtt	ttacgttcta	agagactttg	ctatttctgc	aatcacgata	179880
acaaagcggt	tttttttgtg	caataatttt	agcactcaat	aatttttaagt	gctaaaaact	179940
caatcttctg	aaagcaagga	agagagtagg	tctatctttt	tcgtaatgaa	tgcaaaaggct	180000
ttatctaata	gagcagaggt	ggcatatccc	aatccccgatt	tctttaatat	attgagtggg	180060
aagtcagacc	ttccgctttt	caaaaatttt	aaataaagtt	cgagagcccc	tggttcttgt	180120
gtaaganttt	tttcagcaaa	ggagagggca	gctatgatac	ctgtcgcata	ttgataaaca	180180
tagaaattat	agtagaagtg	agggattcta	gccatttcta	atgcagatag	ggaatccgag	180240
gttacaacac	ctccgtagaa	ttctttttgt	aaattaccgt	aagttgcgga	gaggaactct	180300
tcagtaagag	gagttccttg	ttctgctgca	gaatgaattt	cgtattcgaa	ggcagcgaaa	180360
aagggtttgac	ggaacagagt	cgcaaataatg	gtgtctagag	ttttagtgat	aattacgatt	180420
ttgtcttctt	tactttgatc	tgatttgctg	agagcttcca	tgaggagcat	ctcattgaat	180480
gttgaggcaa	tttcagcaag	aaacagaggg	tattgggcat	catgataggg	ctgtgcttct	180540
ctactgaagt	aggagtgcac	gctatgtcca	gcttcatggg	caatgacgga	aacgtcatag	180600
agtgtattcg	tgtagtttag	aagaataata	ggagcgctat	catagcatcc	tgaggagtag	180660
gctcccgaac	gcttgtgctt	attttcgtat	ctgtctaccc	aacgatttga	aagaagacca	180720
tttcttagaa	tttcaacata	atgagtccct	aaggggaagga	ggcttttgca	aactagggtca	180780
acgccttctt	cataactata	attcttactt	gtagtttggg	aaataggagc	ataaacatca	180840
taaaagtggg	attctttttag	atttagagct	tcttttttta	ggttaaaata	ccgattgata	180900
agagaagtgt	gtttctttgt	ttcgtttata	agattgatata	aaacagttgt	agggatgtta	180960
tggtggaata	gggatgcctc	taggcacgaa	gggtaatttc	ttgctttggc	ttcaaagaga	181020
tgcgcttgga	ctttcccat	gagaagattc	gcgaaggtgt	tacggtaatc	atagtaacgt	181080
tggaattgag	ctaagtaggc	agtacggcgc	aattcctgat	ctggggattg	catatacagc	181140
gaagccaggg	catgggatag	cggatgttct	tctccgttcg	aatcttttagc	tataccaaaa	181200
ggaatttctg	catcgcttaa	ggaagagaaa	gctttatttg	agacattaag	ggctgcaaac	181260
gaggaggcta	agatcttttc	ttcgtttgct	gttcctgtgt	ggggagaaaag	acggaaaatt	181320
ttttctaggt	aaaatctata	gggagcgagc	actgagctgg	atagcaaggc	agcgactttt	181380
tcttcagaaa	gagcaattan	agctggttgg	atccaagaaa	tttcttgaga	aaagagagtg	181440
tagagataga	caatggattg	gtagtcgctt	tccccttcgg	gatttghtaat	atcttgatcg	181500
tggtatgagg	gagcgtatat	gtagagttgg	tctaattttc	gttctacaga	gaattttttt	181560
gataaaagtt	cgagtaaaga	ttcgggggta	tcgatttgat	aatgagaggg	agagaattcg	181620
ggccatatgg	gagaacgac	ttttccagag	ctacaaagat	cgaaatcttt	tttccactcc	181680
tctctatttg	cgtacatgag	agttgtgtcc	caacaatgct	ttggatctac	ttgagttctt	181740
gttgggagtg	cttcgggttt	cagttcagta	gtcatgaggg	aaggaaactcc	tttttaagag	181800
tcaggatgaa	tgagaaaagct	cattataaga	caatctttaa	gaaaaagcca	agaacaaatc	181860
ttgggtttaa	gattagaagg	ggttggccgc	atctataaaag	gttgtggaaa	taggaaattc	181920
gctttttaga	tgctctgcaa	gagatttttg	acctactttt	tctgtggctg	tatgtccaaa	181980
tgctaggaag	ttgatattgc	tttctagagc	tgctcgaccat	gcaggttcat	caaaatttcc	182040
tgtgatgaag	caatcgactt	gggacgtggc	tgccgaagag	agttctctat	aagctcctcc	182100
tgagatcaga	gctgctgagg	agactctaga	ggggccgccc	aaggcagatc	cttttagggg	182160
agcttggtaa	tatcgagata	acagggtcaat	gaaagaatct	atatcgatag	gagagaaaga	182220
gccttgacac	cctaaataag	ggaggggaaga	accaaagggc	ttcaagtcac	gccaatttag	182280
atccagggca	actctccagt	tatttcctaa	ggtagggtga	gcatccaaag	gaagggtggt	182340
ggcaatgagt	tggatattgt	gttctattag	taattggatg	cgcttatgga	tcatgccggt	182400
aataggatag	ggcataccct	tccaaaaaat	tccgtgggtg	acaatgagaa	cgtttgcttc	182460
ggccgcaaca	gcttgtttta	tggtttctag	atctgcggta	actgcaacag	cgatttttct	182520
taccggaggt	tggggatctc	caacttgaag	tccgttgggt	ccataatcct	gaaatatttt	182580
tgatgagaga	agagtcctcaa	gatgagaaaag	gagatccgca	acattcatag	aacagactta	182640
tttaaaaaat	agcatttagt	acacaagtgc	ccattattgt	aaagggtttg	ttataaaaaac	182700
aagtaagtat	tcttagctca	tcaaactatt	ctatatgtaa	gatattagct	agttccatgt	182760
ttagtaatta	taaatgcatt	tagagtcttt	ctgtactttt	agaattttac	atggcttgat	182820
gttttccttt	agaaatnncc	aaaaaaatgg	gggttgtaat	tccgctgata	tatctgtggt	182880
agagaggatt	acattttcata	ttctataaac	ttcggcgagta	tttttagagt	ttagtatttg	182940
gaatgtttta	gtttcttagg	ggaaaccatc	cgcagatgag	attttttcca	acgtattaag	183000
ttttatcatc	tctatctaata	tttcagaaaag	agtatgaaga	tgagccctgg	catgtgaaaa	183060
gcagagacta	ttaganaaat	ctttgagcgg	aagagtcaaa	gattttaatc	aggctatcga	183120
taatgatgtt	ctgtgcgtaa	gttaggtttt	cttcgggtatg	tgccggagcta	atgaagtttg	183180
cttcgagggg	agatggagaa	aggtagactc	cattatcaaa	tacttcagag	tagaagggtt	183240
gaaatttctc	tacatcgga	ttttttgctt	catcaaaatt	tgtgggtgca	gattctgtaa	183300
aaaagaggct	gaacatcggt	ccctgatgta	ctagagatac	tggggaatcct	tgagatcgga	183360
tttctctctc	aattggagaa	taaaagagag	cctctaattg	gctgagatgg	tcatagaatc	183420
cttcgggattg	gcataattga	atggcggcgt	gtcctgtagc	catagcgagg	aagttcccag	183480
acatggtacc	tgcttggaat	atggtgcctt	cgggcatgag	gtgatcgaga	attgagcggt	183540
gtcctacaag	ggctgcagca	ggtaggcctc	ctcctaagat	ttttccatag	atggtaatat	183600



cggggggagag	attgaaaata	tcttgagctc	cttggaaatgc	cactcgaaat	cctgtgacga	183660
cttcatccat	aatagaaaaga	cttccgaagc	gtttgcagag	ttctatgata	tcgtctagaa	183720
attcggtctt	gggaaggacg	ataccatcat	ttgcacatat	agggtcaaag	ataattcctg	183780
ctacttgagg	tcctagagct	tccatgacat	ggtgtaggat	ttggctattg	ttataaggca	183840
gggatatcaa	taaagaatgt	ggagagggcg	tgtgtatcaa	tgaagttagg	ttgtctatag	183900
tttcttcagt	tgttgagatg	cctccaagaa	gagtatctgc	atgaccgtga	tatcccccta	183960
taaatttgat	aataatagag	cggtttgtga	ttctccagac	gagacgtact	gcagtcattg	184020
ttgcttccgt	ccccgaggat	acaaaacgga	ttttatgttc	tttgagtttg	agcgaggaga	184080
ggagcattgt	tgcaaataga	atttctctct	cagaggttaa	gccataggag	gttctcttta	184140
gagctgtttt	ttggatagcc	ttgacaattt	tgggatgact	gtggccgtga	attaaagctc	184200
cccagcctcc	acaaaaatca	ataaaactctc	gtccgtgagt	atctaggaaa	atatctcctt	184260
gtgctgagct	cactataggg	ggtgtgactc	ctacagaacg	gcaggcccga	acgggagagt	184320
tcacgcctcc	tgggaagact	tggcatgcct	cttcaaaagt	aacggtatgc	ttttgatttg	184380
agcagttcaa	catggaattt	cttttagtga	gtttccagac	attttggaga	agctgactct	184440
taatggctag	aaaaagccgt	gagttagttt	agcaatagat	tgtcagggac	tgtagaaagc	184500
gaggcatatt	ttcctccaag	atctttaaga	actaaagccc	agagatcttc	tggttctgag	184560
taaaagacgt	agtctttgtt	ccctggagct	agaaaccagt	cattgcttag	gaattctttt	184620
tcaagttgtc	ctgcttgcca	tccgctatag	ccaaaacata	ggttgatttc	tggcccagat	184680
tcgctagagg	cgatttcttg	gaggaaggga	agatctcctc	ctaagtagac	tgatggacaa	184740
atttctaacg	tttgttcagg	aatttcggag	catgaatgaa	gtaacatcat	ttggtttgct	184800
tgtagggggc	ctcccntaca	aaagcggata	ttatgattgg	agactttttc	aaaggtaaaag	184860
atgtcatctg	agatttcaaa	tcccagggtt	ttatttaaga	tgagaccgaa	agaagcattg	184920
aggctatgtt	cacaaagtag	gatgacacta	cgagcaaaga	ctccttggtt	tatattcagg	184980
agaagcgact	aacaaagatc	ctttttctag	gcgtgcataa	ggaattttca	taatatctct	185040
gagtttattc	ttcgtagggg	actacagcat	caaatactga	tttaacacac	aagatgggat	185100
tttatgagtt	aaggcgagag	ggatctatcg	ctaggacggg	catcgacatc	aacgacgtat	185160
agaaattcgc	gatctttttg	ttctaaaaag	agtcttgtgt	agaaaacggt	atctttatag	185220
tcattaatta	ctacacgtaa	cacttggtata	tcgaaacctg	aaaagacaaa	gttcagtaga	185280
tcatgagcaa	aagggtcttg	aggagagtgt	ccttcagtat	cagcaccttg	aaatgcttgc	185340
cccattgaaa	cgtgcccata	tatagcgaac	ttttttctct	cagtacctaa	gatcatgcct	185400
gcataattac	aaaaactgac	aagtttgtaa	aaattgagaa	gtactaaggg	ggtttcttct	185460
aggagtctct	tttctaagct	catacagaat	attttttgct	gattagacct	tggctattgc	185520
tagaccacac	ttcgactttc	tctataacaa	accgcacttc	aataacacca	tgaatttgta	185580
ttacttttaa	taaatccttt	tcaggatttg	ggtagggagt	gggggaaaaa	atatcgtaaa	185640
tgtagttgct	gctgtctgta	ataaataggt	caccagtatc	ttgtaggcgc	cattctcctt	185700
catatccaag	atggcgggatt	tcttcaataa	ttgctgagcg	accgaatcga	ctgatttcta	185760
aaggaacacg	aaattttctt	aggactggaa	ccagtttact	ttcatcaaca	aggataatgc	185820
tgcgttttgc	tgctcttaaa	agaatctttt	ctctgaaaaa	ggtccgccac	cacctttgat	185880
catccgcaat	tgagggtcga	cttcatcagc	accgtctacc	gtaagatcta	gggaagagaa	185940
tttttctggg	tttaagaggg	ggatggcaag	ctgctttgct	agagcataag	aattttgaga	186000
agaagctata	gcatgaactg	ctaaggactc	tgtttgaatt	ctatgggcga	gtgcaaagat	186060
aaattcctta	gctgtagatc	cactgcctaa	gccaaagaatc	atgcctgaag	ttacttgtgt	186120
agcagcctca	tgggccaggc	attttttctc	atgaagatga	agatcttttt	ccacagcgct	186180
actactatgt	tacaaaatat	tcccacagct	tatgcaaagg	gattcttcca	atactataca	186240
aaaatcgaaa	ccttttggac	gagtcttttag	ggtaatcgat	ttcagatctc	ttaaattgaaa	186300
gcgtattgat	cctattttct	gctatagggt	tttagtggta	ggaacggatc	ttttgtattg	186360
cattgtcatg	ggatactcta	gaaatctcga	agtgcgaaca	aaaattaaga	atggaattct	186420
tagtagacaa	tagttggagt	attttgaagt	gaaatttttc	caaagtcccc	ttcgatttag	186480
aataggagtg	actttaaaat	taagatagaa	aacgaacctta	gataacgtac	ataaagggaa	186540
gagctgggtg	gatctataga	ggttccaacc	agctctgggt	tcattatttc	caaacttctt	186600
cggaaatttc	ttttactaga	gcaacttttag	cccattgctc	ttcttctggt	aattttatttc	186660
ctatttcaca	tgaagcaaaa	ccacactgtg	gacttagaga	gagtccttcc	aagggcagggt	186720
agtctgtcgc	ttgatgtatg	cgagcaatga	cctcatcctt	attttcaagt	gtaggggttt	186780
tgctggtaag	aagacctaa	cagacagttt	tttctccaga	aatgaagggtg	agaggagaga	186840
agtctccaga	acgctcatga	tcaaactcta	aatagtagcc	gtctacattt	gtttgttcga	186900
ataggggctt	tgcaataaag	tcataactac	cactagcaaa	gaattttgag	tggtagttcc	186960
cacggcatac	atgtaaatta	acgactagat	catcgggacg	atctgcaatt	acaagattat	187020
taatcagaag	atattgttga	atcagatctt	gaagaccttt	ttcatcgata	ccataaccacg	187080
aacagactcg	agggtctact	aaacctcccc	gagtacagtc	atctaatttg	agatagcggc	187140
agccagcatt	ataaagatcg	cgaatgactt	tacgataacc	tgcaacaata	tcttcaattta	187200
gctcctgatt	tgtaggatag	aattttacgtg	tgacctctat	attattaggg	aagatcatct	187260
gctttaaaaa	ctgtgcccgt	gcaggaagag	tttgctttgc	agtcgtaaat	tcattcttcta	187320
gagctttttac	aaattttaag	tgatccacaa	atgggtgggtg	agatacacag	atcttgtctg	187380
tcagataggt	atcatcgatc	atagcgcgtt	ctccatcaaa	gaaaactcct	tctgtagctc	187440

tgtggtgacc	tacgccatga	aaacccccaca	tgaagtcgta	atgccacgta	gctctgcgga	187500
attctccatc	agtaataaaa	gaaagacctg	ctgctttttg	ttttttgatc	aaatcttgga	187560
tagcgatata	ctcaatttgc	atgagttgat	ctagagaaat	agagccttct	ttaaggcttt	187620
ctctagtttt	ttttaaatgc	tcaggacgca	aaaaactacc	gacaacatca	aaatgagatt	187680
tcagaggtct	tttttagtgaa	gtattcatga	ttgtcctcct	tcagactagt	gaaatggaaa	187740
gagctaagta	gaaaaacgtc	gaatttttcta	taggattaaa	aataagaata	aacaagttat	187800
aggcgtttct	gaaagacaga	atcgttactt	aatactttcc	acaatgttct	agcatttaag	187860
aacataggtat	atattttgtc	caactataac	tagatcattt	aaaaatattt	gtaatttagt	187920
tggaatatata	aaaatcatta	gcatttaagca	aactgttttt	cttttcttag	tttttagatg	187980
cgaataattt	gataatttct	caggtaatta	aaaatctttt	aattgttttt	tctgtttatg	188040
tttgacaagc	acaaggtgga	tgccactcta	tagtcacgat	ctttaagtcc	ttgatttggtg	188100
aagaaattgg	tccttaggag	ttgccgcttt	cttcagacag	ttcaagagat	cacttcctaa	188160
tgtattttta	gaaaggggaa	agagatcctc	ttaggttaga	cgtttaggtt	tggtagtatt	188220
tcgatagggg	ttgataaagt	tgccctcttct	acattctcag	aggaaagttt	atagattttt	188280
tattattcct	atgtaataag	aaaaaccttt	ttaaaaagt	cttggggtga	attttatgga	188340
gaaattttcc	gatgtgtct	ctgaagcttt	agagaaggct	ttcgaacttg	ctaaatcttc	188400
gaaacatacc	tatgtcacag	aaaatcacct	attactggct	ttattagaaa	atacagagtc	188460
tctcttttat	ttggtaatta	aggacattca	tggaaccctt	ggtttgctca	atacggcagt	188520
taaagatgcg	ctctcacgag	agccgactgt	agttgaagga	gaggtggatc	ctaaaccttc	188580
tccgggttta	caaacccttc	ttagggatgc	caaacaagag	gcaaagacat	taggagatga	188640
atacatttct	ggagatcatc	tgctgcttgc	tttttgaggt	tcaaacaaag	agccttttaa	188700
ttcttggaag	caaacaacaa	aagttagttt	taaagatcct	aagaatctga	ttactaaaaa	188760
acgacgagga	aatcgtatgg	attcgccaag	cgctgaaagt	aattttcagg	gttttagaaaa	188820
gtattgtaaa	aatttaacag	cattagctcg	tgaaggtaaa	ctggatctcg	tgatcggtag	188880
agatgaagaa	attcgtagaa	ccatccaagt	gctttcccg	agaactaaaa	ataaccctat	188940
gcttattggg	gagccgggtg	tagggaaaaac	tgctatagca	gaaggattag	ctcttaggct	189000
tatccagggg	gatgttctct	aatctctcaa	aggtaaacag	ctttatgtct	tagatatggg	189060
agctttgatt	gcaggagcta	agtatcgagg	tgagtttgaa	gaaagactaa	agagtgtttt	189120
aaaagatgta	gaatctggag	atggcgagca	cattatcttt	attgatgagg	tgcatactct	189180
tgttggagca	ggagctactg	atggagctat	ggatgctgcg	aatcttttaa	agcctgcatt	189240
agcaagaggg	acgctacact	gtattggcgc	gacgactttg	aatgagtatc	agaagtatat	189300
tgaaaaagat	gctgcttttg	aacgtcgatt	tcagcctatt	tttgtagacag	agccttcttt	189360
ggaggtagct	gtctttatc	ttcgtggact	aagagaaaaa	tatgaaattt	tccatggagt	189420
caggattaca	gagggggctt	tgaatgccgc	agtcctactt	tcctatcggt	atatcccaga	189480
tcgcttttct	ccagataagg	ctatcgattt	gatagatgaa	gcggcaagtt	taattcgcat	189540
gcaaattggg	agtcttctct	ttcctattga	tgaaaaggag	agagagcttg	ctgctttgat	189600
cgtaagcaa	gaggctataa	aacgcgagca	atctccttcc	tatcaagaag	aggcggatgc	189660
tatgcagaag	tctatagatg	ctttgagaga	ggaattagca	tctctacgtt	tgggttgga	189720
tgaagagaag	aagttgattt	cggggctcaa	ggaaaaaaag	aattccttgg	aaagtatgaa	189780
attttctgaa	gaggaggcgg	agcgtgttgc	agactataat	cgtgtagctg	agcttcggta	189840
tagtttaatt	ccccacttg	aagaagaaat	caaacaggat	gaagcctctt	taaatcaaag	189900
agataaccgt	ctccttcaag	aagaagttga	cgagcgattg	attgcgcaag	tggtagctaa	189960
ttggacaggg	attcctgtgc	aaaaaatgct	agaaggggaa	gctgagaaac	tgtaatttct	190020
tgaagaatcc	ttagaagaac	gtgtggtagg	acagcctttt	gcagtctctg	cggttagtga	190080
ttctattcgt	gctgcacgtg	taggtttaaa	tgatcctcaa	cgctcccttag	gagtcctttt	190140
attttttaggg	ccaacagggg	taggaaaaac	cgagcttgca	aaagctcttg	cagatcttct	190200
tttcaataaa	gaggaagcta	tggctccgct	cgatatgtca	gagtatatgg	aaaagcattc	190260
catttccaag	cttataggat	cttctccagg	gtatgtgggt	tatgaggaag	gtgggagtct	190320
ttctgaggct	cttcgacgac	gtccctattc	agtagttctc	tttgatgaga	tagagaaagc	190380
agataaggaa	gttctaaata	tcctttttaca	ggtttttgat	gatgggattc	ttacggatgg	190440
gaaaaaacgc	aaagtaaatt	gtaaaaatgc	cttgtttatc	atgacatcaa	atatagggttc	190500
tccagaactt	gcagattatt	gttcaaaaaa	aggaagtggg	cttacgaaag	aagcgattct	190560
ttctgtagtc	tctccagtat	tgaaaagata	cttgagccct	gaatttatga	accgaattga	190620
tgagatactt	ccttttgttc	cattaacgaa	agaagatata	gtgaaaatag	ttggcattca	190680
aatgcgaagg	attgcccgag	gattaaaggc	acggcggatc	aatttatctt	gggagatttc	190740
tgtaatatata	tttcttagtg	aacagggtta	tgacagtgct	ttcggagccc	gccctttaaa	190800
acgtttgatc	caacaaaaag	ttgtgatctt	gcttttctaag	gctttgctta	aaggagatat	190860
taaacctgat	acatcgattg	agttgacgat	ggcaaaaagag	gtgctcgat	ttaaaaaagt	190920
ggaaactcct	tcttagagag	ttttctatgg	gtgcggaatt	ttagatacta	ggaaaagccc	190980
tctttgttaa	gagaatggat	aggtttttag	attctatgtc	ttcttgctac	gctttcttgt	191040
ttccggggat	cataaaaaaa	ctaggacgat	aaagtgtgtg	taggattaga	attgtgcggc	191100
aagcttcatt	tggctaaaca	agagcagtc	cagaaattta	agaagtccta	tgtttaagag	191160
ctttatagta	aggtatatgt	ttgtagggtg	ccttggttca	ttcttgcttc	ctatccccga	191220
cttggaaatg	gcgaataatg	taacaaaaac	ttatgataag	aaagcttctg	ttatatccag	191280

agatcttaag	ctacaggaag	actgccagaa	gtttttggaat	cttgatccgt	ataaactaga	191340
aagtctttgt	gcttatcaag	tgctttacca	tgatgactat	agttccaaga	gaatacagaga	191400
gctttttcct	caaataccaaa	aagacgaagt	ccccatattt	gcaacaatga	ttcttacttt	191460
agggaaagta	gaccgtggct	tttctcctga	agaaatttca	ttgatccaaa	aactttctta	191520
cccaggcctc	tcattggctt	ctttgagagg	gtctacagaa	attagaccgg	aatacagatt	191580
tggctcgtgc	tttagtagtg	tcggagtttt	ctggagattt	agggagaagac	cgagctgact	191640
actatagcaa	tgcccttgat	attttggtgt	tcgtatttca	tgagaaacgt	caaaggtatt	191700
tagatcagtc	tccttggtgt	cctggaacct	ccgagtttca	taaggcaact	atagaagcta	191760
ttaatacgat	actcttctat	gaagaagcag	ttcgttatcc	ttcgaagaaa	gaaatgtttt	191820
ctgatgaatt	ttcttttctt	tccttcagtta	cagatagaaa	attcggcgta	tgtttagggg	191880
tctcttctct	ttatttctct	ttgtcacagc	gcttagattt	accttttagag	gctgtgacgc	191940
ctcctgggca	tatctactta	cgttatcagg	gtggtgaggt	gaacattgag	actacagctg	192000
gagggcgcca	tcttcttaca	gcaagttact	gtgattgtct	agatttagaa	gaccttcagg	192060
tgcgtactcc	tgaagaaatg	atagggctta	cttttatgaa	ccagggtctc	tttgccttgc	192120
agaagaaaaa	gtataaggaa	gcggaagagg	cttataaaaa	ggctcaagag	tatttgggag	192180
acgaggaact	acaagagctt	ttgggggtttg	ttcaaactct	aggaggaaaag	aaaaaagagg	192240
ggaaatcttt	gattggtaaa	agtcctcgcg	cttcccagaa	aggatcggtg	gcttatgact	192300
accttaaagg	tagaatcaac	attccaacac	tagctctttt	attttcttat	ccaggatcca	192360
attatgaaga	gatagcttct	tatgaagaag	aactcaaaaa	ggctatgaaa	agctcgatgc	192420
catgttggtga	aggacagcgt	cgtcttgctt	cagtagcatt	tcatttgggg	aagacagcgg	192480
aggcggttgc	tcttttagaa	aaatgcgttg	aggatatccc	taatgatctt	tctcttcatt	192540
taaggttatg	aaaaatccta	tgtgatcgac	atgagtatac	aaaggctttg	aaataacttca	192600
taattgcgga	aagacttatg	gaggatcagg	gatttcttaa	aaaagacaat	cgttcgttgc	192660
ctttatttta	tgaggtgaaa	aaaatcatat	ccaaagtggc	tcctcaaaaa	gctaacacct	192720
tgcttttaat	ggagtctgaa	agataaactg	atcagttctt	tctgtattgc	tcttatattat	192780
aacatgttat	aacattgcaa	gtgttaattt	ttaacagatc	tttatattgt	gcaatatttt	192840
tttaaataag	aattgagcta	ttttttagcc	tcatatgtga	gatgtcatga	aagatttgaa	192900
tcaaagtaag	tcttgctttc	caagcttttg	taggattaaa	gtgtttgaga	tgaattcgca	192960
ttttttaaat	tattgttgga	attagtatga	gcagttcgga	agttgttttc	cagacagttc	193020
atggccttgg	ctttggtgga	ttgtcttcaa	aaagtgttgt	cccttttaag	aaaagctctt	193080
cggatgcgcc	ccgtgttgtg	tgctcgattt	tagttttgac	tctgggggtg	ggagcgcttg	193140
tttgtggtat	tgccattact	tgttggtgtg	tcccgggagt	tattttaatg	gggggaattt	193200
gcgctatagt	tttaggtgca	atctcttttag	ctttaagtct	attttggttg	tgggggttat	193260
tttctaattg	ttgtggttct	aagagagttt	taccgggtga	gggattgcta	cgggataagc	193320
tttagatgg	tggattttca	agagcggcac	cttcaggaat	gggacttccg	ggtgatggat	193380
ctccaagagc	gtcaacgcca	tcttgccctag	aggaacttca	agcagagata	caggcagtta	193440
ctcaagctat	cgatcagatg	tcagatgatt	gactctaaag	cgtagaggta	cttaaggagg	193500
aggctttgct	aatcagtaaa	gaaactttaa	tacaagtaag	atctaagttg	aataacttaa	193560
aaagataatg	aataaaaaaca	aaatagcatg	ggggaccaat	ggctgttcaa	tctataaaag	193620
aagccgtaac	atcagccgca	acatcagtag	gatgtgtaaa	ctgttctaga	gaggctatac	193680
cagcatttaa	tacagaggag	agagcaacga	gtattgctag	atctgttata	gcagctatca	193740
ttgctgttgt	agctatctcc	ttactcggac	taggtcttgt	agttcttgct	ggttgctgtc	193800
ctttaggaat	ggctgcgggt	gctataacaa	tgctgctggg	tgtagcatta	ttagcttggg	193860
caatactgat	tactttgaga	ctgcttaata	tacctaaagg	tgaataaccg	agtcaggga	193920
acaacggtga	gcctaataaa	agaaattcag	caactcctcc	cttagagggt	ggtgttcag	193980
gagaagccgg	tcgcggcggg	gggtcacctt	taacccaact	tgatctcaat	tcagggcgcg	194040
gaagttagat	tttttatcta	acctaactaag	ttagtatttt	aactgtaggt	ttttccttcc	194100
gttggttttaa	aagaacctca	agaataacta	gaggttcttg	tttgtttatt	gcaatcttcg	194160
tttttgctat	ctatagttaa	cttatataaa	tataaggcaa	atggtggaga	gttagctcta	194220
tggaaagtga	gaaagatata	ggagctaagt	tttttaggtga	ctataggatt	ctctatcgca	194280
aggggcagag	cctatggagc	gaagatcttt	tagccgaaca	tcgatttata	aaaaaacgtt	194340
accttattcg	attacttctt	cctgatctag	gaagttctca	accattcatg	gaagcttttc	194400
atgatgttgt	tgttaaacta	gcaaaattaa	accatccagg	catcctcagt	atagaaaatg	194460
ttctgaatg	tgaggggaaga	tgtttcttgg	taacacaaga	gcaagacatc	cccatccttt	194520
cactaacgca	atatttaaaa	agtattcccc	gcaaacttac	agagctagaa	attgtagata	194580
ttgtaagcca	actcgcttct	cttttagatt	atgtgcattc	agaaggactg	gctcaagaag	194640
agtggaaatct	tgattctgtc	tatattcata	ttttgaatgg	tgttcctaaa	gtcatactcc	194700
ctgatctggg	gtttgcttca	ttgataaaaag	aacgtatttt	ggacgggttt	atttcagatg	194760
aggagaatcg	agaatctaaa	ataaaagaaa	gggtactact	tcacacttca	gaaggaaaac	194820
aaggtagaga	agatacgtat	gcttttggtg	ctatcaccta	ttattttact	tttggttttc	194880
ttcctcaagg	cattttccct	atgccttcga	aaagtttttc	tgattttatc	tattgtggg	194940
atttttaaat	tagctcttgt	ttaagtttgt	ttatggaaga	aagggaacaaa	gaacttttcc	195000
ccttaataag	aaaaaaaaact	ttaggagaag	agctgcaaaa	tggtgtcact	aactgtatag	195060
aaagctcttt	aagggaagtg	ccagatcctt	tggaatcttc	tcagaatctt	cctcaagcgg	195120

tccttaaagt	aggggaaacg	aaggtaagtc	accagcagaa	ggaatctgcg	gaacatttag	195180
aatttgtgtt	agtggaaagca	tgctccatag	atgaagccat	ggataccgct	atagaatccg	195240
aaagtagttc	tggagttgag	gaggaagggt	attccctagc	tctacagtct	ttattagttc	195300
gggaaccagt	agtgaagtcgt	tatgtagaag	ctgagaaaga	agaacccaaa	ccgcaaccga	195360
tacttacaga	aatggtttta	atagagggag	gagaattctc	ccgaggaagt	gtcgaagggc	195420
aacgtgatga	gcttcctgta	cataaggtaa	ttttacatag	cttttctcta	gatgttcac	195480
ctgtgacgaa	cgaacagttt	aatcgttatt	tagaatgttg	tggtagtgaa	caggataagt	195540
attataatga	gttaatccga	ttgcgagatt	ctcgtatata	gcgtcggtcg	ggtaggcttg	195600
ttatagagcc	aggttatgct	aagcaccctg	tcgttggggt	tacttggtat	ggagcctcag	195660
ggtaggcaga	atggatagga	aaacgcctgc	ctacagaagc	tgaatgggaa	atagctgctt	195720
ctggcggggt	ggcttgctac	gctatccctg	tggggaggaa	atcgaaaaaa	gccgggcaaa	195780
ttttttcact	gcggatacga	caacagtcac	gagttatcca	cccaatcctt	atggcctcta	195840
tgatatggca	gggaatgtct	acgagtgggt	ccaagattgg	tatgggtatg	atttttatga	195900
aattttctgct	caagagccag	agagtcctca	aggctcgtct	caaggagtct	atcgggtgct	195960
aagagggggg	tgttggaaaga	gcttaaaaga	tgatcttcgc	tgtgctcatc	gccatcgtaa	196020
taatcctggg	gctgtaaata	gtacgtatgg	tttttaggtgc	gctaaaaata	tcaattaaga	196080
gaggttcatg	aaggaagaga	attcacaagc	acactactta	gctttatgtc	gtgaattaga	196140
agaccatgat	tattcttatt	atgtgttgca	tcgtcctaga	atctctgatt	atgaatatga	196200
catgaaatta	cggagagcttc	ttgaaataga	gagaagtcac	cccgaatgga	aagtcttatg	196260
gtctccctca	acacgtctcg	gagatcgctc	ctctggaact	ttttctgtgg	tttcccataa	196320
ggaaccgatg	ctttccattg	ccaatagcta	ttctaaagaa	gaactaagtg	agtttttttc	196380
tagggtagaa	aaatccctag	gtacaagtc	acgttatata	gtagaactta	aaatcgatgg	196440
gattgcagta	gcaatacgtt	atgaagatcg	tgtgttgggt	caagcactca	gccgaggaaa	196500
tggaaagcag	ggagaggata	tcacatcgaa	tattcgaaac	atacgctcct	tgcttttaag	196560
acttccagaa	gatgctccag	agtttattga	agtacgtggc	gaggtcttct	tctcttatct	196620
tacgtttcaa	attatcaatg	agaagcagca	acaattagag	aaaactattt	ttgccaaccc	196680
gagaaatgct	gcaggaggta	ccttaaagtt	actttctcct	caagaaaagtc	gcaaacgtaa	196740
attagaaatt	tctatctata	atctcattgc	tccaggagat	aacgattctc	attatgaaaa	196800
tcttcagcgc	tgctttgaat	ggggattttcc	tgtatctggg	aaaccaagat	tgtgctctac	196860
cccagaggaa	gtgatctcag	ttttaaaagc	tatagaactt	gagagagctt	ccttgccctat	196920
ggaaattcgat	ggtgctgtca	tcaaggtaga	cagtttggca	agtcagagag	ttcttggagc	196980
cacagggaaa	cactatagat	gggccttagc	ttataaatat	gccccagagg	aagcagagac	197040
ccttcttgag	gatattctag	ttcaagtagg	aagaacggga	gttctgactc	ctgtagctaa	197100
actcactcct	gtactgttgt	cagggtcttt	agtatctaga	gcgtctctat	acaatgaaga	197160
tgagattcat	agaaaagaca	tccgtattgg	tgataccggt	tgtgttgcta	aagggtggaga	197220
ggtgattcca	aaagtagttc	gggtatgcag	agaaaaacgt	cctgaagggt	ctgaagtttg	197280
gaatatgcct	gaattctgcc	ctgtctgcca	tagtcacgta	gttcgggaag	aagatagagt	197340
ttctgtgctg	tgtgtcaatc	ctgagtggtg	tgaggagct	attgaaaaaa	tctggttttt	197400
tgttggctcg	ggagctttaa	atatcgatca	tttaggggtg	aaggtaatca	caaagctggt	197460
tgaattaggg	ttagtgcaca	cgtgtgcgga	cctatttcag	ctgactactg	aagatttaat	197520
gcaaattccc	gggatacggg	aacgctctgc	aagaaatatt	ctagagagta	tcgagcaagc	197580
taaacatgtg	gatctagatc	gttttcttgt	tgctctgggg	attcctctca	ttggaattgg	197640
tgttgctact	gtactagctg	gccacttcga	gacttttagat	cgggtaattt	ccgcgacttt	197700
tgaagaactt	ctttcactag	agggtattgg	agagaagggt	gctcatgcta	ttgctgagta	197760
tttttcagac	tctacgcac	ttaacgaaat	caagaaaaat	caggatttag	gagtggtgat	197820
atctccttat	cataaatcag	gatctacgtg	ttttggcaag	gcttttgtag	tcacaggagc	197880
gttagaggga	atgtctcggt	tagatgcaga	aactgctatc	cgggaatttg	ggggtaagggt	197940
aggctcctct	gtctcgaaac	agaccgatta	cgtagttatg	gggaataacc	caggatctaa	198000
attagagaag	gctaggaaat	tgggagtcct	tatcttagat	caagaagcct	ttacaaatct	198060
aattcattta	gaataattta	ttttaaaatt	ttcttaatac	attaattctt	atttgtaaaa	198120
gttttattta	aattatttat	tataaattct	tttacagcta	taattgtccg	tattttataa	198180
gtttttttgt	tcttttggga	gtaaacatgg	cttcttcttc	aaacaattcg	actaaacagg	198240
acggcatacc	atcttgggta	aacccaaatg	tccagtggaa	tcgagcgctc	cagggtgggtg	198300
atcaagaagc	gaattctcta	actccagagg	ctcaaacttc	acgtagctgg	ttttccgatac	198360
gcaagcattt	tcttgaagtc	ttagacgcta	gtctagagga	gatggagaac	aatgacctta	198420
agaaatactc	tagatataag	acgattatcc	tgattgccac	gctggctact	gttgcgatta	198480
cctgtatcgt	tcctatctct	atgggtgttg	gtatcccgat	gtgggtgccc	tgtcttattt	198540
tatttgagagc	gggtctttct	tcggcttttc	tttctcatcg	tcttcaatct	aagtgcgaagg	198600
agatccattt	aagataccga	gcgtaccaga	tttatcgcca	gcagctgttg	agtcagttacc	198660
ctgacttgag	aaagtctact	ctctataaat	atagtattac	ccatgtcaaa	ccgaaaaagg	198720
gatttggttg	taaaactcgta	gaaaatttgc	gccctgattt	gcataaaaaat	aaggacgatg	198780
gggggtgctg	tgacagactcc	agatttagatt	ttgcgggata	tggagtaaaag	cattatcaga	198840
cggatgctct	acttggagtt	tcagggtgta	atagtgtaga	atggcaacgt	cttgcctctc	198900
tgattatgag	tgtaagaac	gacattttta	atgatgtggg	aagcagagag	cccattgata	198960

aagcgcaaaag	gtctgcttta	gtagtcagtg	gtaaggatat	tggaggggag	attcagcctg	199020
gaggtatttt	agatatattcc	agagatatcc	tagcgatctg	tggctacggt	atgaatgtag	199080
gtgttgaggc	gaagaaagct	atagaccagt	ataagaagtg	gtatctcaat	agtagtacat	199140
ttattgcttg	gaatccgcag	cttcctgcta	ttgccagtc	ctatttacta	gaacaacaac	199200
gacatctaga	ttatgctgct	aagattttcc	aagatctttc	cgcattgacg	acagcccatg	199260
gtacagggca	ggctcttgaa	gatttagata	gtttgctttg	ttattatgat	cagttaattg	199320
aatctaaagg	tgtcggtgaa	aagataatag	catcgattca	ccagaaagca	tctcgactta	199380
gcaatgcaag	attcctgcga	tcaggaacat	ttaaagaaat	ggtcgaatct	ataccacgtg	199440
ttttcaatta	ctattaaaga	attcactgaa	ggtaagctag	aacaaaatga	ggtagtatct	199500
agaatacaaaa	ggcttcgagg	taagttagaa	aaaagtaaat	gcagcattct	tggaaattgt	199560
cgaaccaacg	cagaatatgc	aacaaagtct	gaaaaaaaac	tcgcagatta	tttgctgcag	199620
attggggata	gagaaccttt	ccttactgga	atgcataagg	cgatagccac	cggaaaagct	199680
attcaaggaa	aaagtggaag	agtcatttca	caacatcctg	aaaagcaaat	tatgatgctt	199740
cgggtgttcta	tagagagact	cgaagggatg	ttgcgtcgag	aggattgggg	agcaatccta	199800
caaaaaaacg	aagacgaagt	ccttgcatg	aagagtacaa	tgggaagctca	gcttcaagga	199860
tttaaggacc	ttgtaggtag	ctgggaagga	aaatatcagg	aatttaagaa	aaacaagctt	199920
tccaaagttt	tagttttacga	cttcacaaaa	tcctattcta	accttctaaa	tcgtttggag	199980
gtactccatg	ccgagagctc	cacggatgat	ttggttattac	atgtcgatag	aatgtcggaa	200040
gatctgaaga	aaacaatcga	ggagattgac	ggcaatttat	ttcaggtaac	tcctgaagag	200100
ctctctttgt	tagctcggga	atatcaggga	ctcatgaatg	aacttctctt	gatcgttcaa	200160
gaggggaatc	ggctccaaga	agcaatctct	agtgaagggg	tttctcaagg	attgatgttg	200220
ttgaactctt	tattgaatag	agatgaaaaa	ataaataaaa	acatagaaa	cagtaggaaa	200280
aacttagtag	ctatcgcgaa	acaagcacgt	agcgatgcga	gaaatataga	cagtcaggga	200340
ttggctcctt	tgatccaaag	gaatagagct	agcctggaca	acattctcca	gaatatgtat	200400
ttgtttaacg	gcagtatacg	taatatccat	gctctagata	cggaaacgtt	agtggcaact	200460
tcctctaata	tgttttctgc	gatgcatacc	ttcgactgga	atatctatac	gaatttgctt	200520
gatgttttag	aaatccaaag	caaaccagct	cctgcccta	tggagaatcc	tgaccttctt	200580
ggagctcttc	ctgaagaggt	ccaggatgcg	gttgctgaag	atgtttctgg	gactcacagg	200640
ctacatcacc	aggtgttaaa	gagacgctgt	gctgacttaa	aaaatatgat	cagtcaattg	200700
cagaagtcga	taaacaaatg	gggaatggct	aaggccattg	tcctgggaat	tgttgcggtg	200760
ctcttctgtg	ttcttagtgc	tatttttatt	ggtcagaaca	ttttatcctt	actcattctc	200820
tcttgtgtag	ggttactttt	gactcaggtta	tgtcctttta	tctttgatcg	tatatctaag	200880
agcaaggagt	ttgagaagca	agtgcctgag	acagcgcagt	ccttgattcc	tgccactaag	200940
attcttccct	cagaattcaa	taataaggat	cttaatcggt	tagctaagct	ccaggataat	201000
ttaaatcttg	agggtttttg	tcctacatgg	gcgcgcaata	ttgtgagtga	tctagagggc	201060
attccgacta	aagaaaagag	cttgaaggat	cttactaaag	agttccgtaa	ggattctaaa	201120
aacttaaaata	agcgtataaa	aagacgtttc	aaggaggggt	taggacaaga	agcgctgtg	201180
gttcgtccta	ctatcccca	agatatctgt	ggagctgagg	tttttgcaga	gttacatcgc	201240
gagttagagc	accttcaaaa	gcaaaaagaa	gagattagta	ttcggggaga	tgctctgggt	201300
caagagcgca	tgggtctgtg	cttagaaaag	tctaagtacg	acaatgaaaa	ggctcatgct	201360
gccgctatga	ctaagaaggt	tggaaaatta	caaaacatag	ataggcttca	aaaaaataat	201420
gaaacgtatg	taaggattca	gaattttttt	agaactttga	ttcaagagaa	attagggcgt	201480
gacacagtcc	aagagataga	cgtagtcaaa	gaggctaagg	aattacacga	attagcagca	201540
atcattttacg	gcaataccag	tgggaaatct	cagaagcaaa	gagcaaaaaa	gcagtttaaa	201600
gagaatgttt	tacacatagc	agggaaagggt	caattagaac	tttttagaggc	ttacttgaat	201660
gtgacagctt	ctcaagggtc	ctgtcgccat	caaatgcagg	cttcatttag	agaaagaatc	201720
ttgctaaatc	ccgatggagc	aaaacatgga	gaagccgaga	ggacgcttgc	ttctagggaa	201780
gaaatgttga	aaactctagg	gctttcttat	ttgacgcctt	ttgtaagatt	ttcttctcca	201840
gaaagtacgc	agtctggata	taaccaaatt	ctgaaagtcc	gtgagcagct	cttcgatatt	201900
gagcagaggc	ttcagaatca	ggagactgtg	agtcctcgagg	actatgcggc	tgtacaagct	201960
gcttttagcag	cttatgtccg	caagcatgaa	tctcttatag	tttctactta	tggattgggt	202020
gctcaagaag	gacaaaacgag	ttctaaaagt	accactttta	tgcgagattt	gcatgctgta	202080
gaagagcttg	ttgagatggg	tgtcgaaacg	tatcgattga	atcgagcga	tcagattctg	202140
catcgctgtg	attctgtttt	acacagccat	ctgcgagata	gcgattcttc	aggaaatgga	202200
attattgtatg	tagttaagaa	attgttttag	cttctgaaca	ataatgggaa	caatccta	202260
gatcccgaat	gccaaaagta	tatgcagata	cttttagatg	caccagtcag	tctattgtat	202320
gggtgcattta	aaagtttcaa	aaacgaattt	ttacttaatt	tcacgggaat	gaatattgct	202380
aattcaacaa	aagctgctga	ggaagaagct	aaaaggtag	ttgaagagaa	aggtagagg	202440
tttgagactt	attgggagga	ggctaagcaa	cgattggaag	caattgctgc	tgagttggac	202500
gacttaagga	atcaagagac	tctattggaa	caagaaattc	gtttggcgaa	tttaaagata	202560
agtatcttta	gtgattttaa	tttaagagag	aaggtttcag	tagaaaaagc	agctttagaa	202620
gaagaaatcc	aaggaataca	agagcaatat	gcagagatgc	aggggattga	agatctagag	202680
ttaaaacaaa	aattcgaaga	tttgcaaaa	aaacttgaag	ctctagaaga	aagattgttg	202740
caaataggtc	gaaggataga	ttcctctgta	gacaagcaga	aagaactgtt	gggtctcttg	202800

ggtagagaag	aggctgctta	gagaaatcat	tgcgttttga	gatctcattg	atgggtcagag	202860
attctttttc	tcatcaactg	caatgaaaac	catagaggac	taggaaaggc	tctctatggg	202920
ttttttttcac	aattttccact	aaatgcccac	aaacgatagg	tagaccttcc	aataggatag	202980
cgtcctaaaa	aggagtttagc	tgggtcttttc	gctggcaaaa	attctaagta	gatatgagat	203040
cagctcgtgc	agcttaaagg	tatgtgtttct	atatccgata	taacgatcgg	ggcggataat	203100
aaatagcgaa	tttggatttg	cgtgatagag	gttaaggatt	cgaggttcct	taacattgca	203160
aatctctatc	cattcgccat	attcttcttg	tagagcttcc	tttaagtcgg	ggatatcttt	203220
aaaaaagata	agaagggtgct	tactactttt	taaaggatct	aagaggaaaag	aaccgttttc	203280
taggcgagca	tctatagctc	tcattcctgg	accaggacca	tggatttcct	tatcttgagg	203340
agacattttg	ataatatcgc	tagaacggta	tttcagtgtc	tggtgagggg	ggtagtaata	203400
ctctttctcct	gtagtattaa	acttttcgaca	tcccttttaa	aagtagtaca	tcaaagcagg	203460
tgtatagaag	cgagaaaatg	ggagttttct	cgcgcgcttt	tccgtagtag	gactaatata	203520
aggtaggata	ttgccatctt	cctgtttctt	tgtaatcacc	aaatgtttta	atgcagcttt	203580
tttcaataca	ggaagttagct	tccaagcgag	attaaaggct	gcgtgaatat	tggatattaat	203640
accgttgaga	taagaaagaa	gcagagtatt	agagaggcta	cctaaaaata	atcacatttc	203700
atgttcagga	gggaatgcgt	ggtgacttgt	ttttatatgg	aaattttcat	cagagatgac	203760
gagattgtaa	gtataaagta	gcttctgttt	aagtttcggg	gatatggaat	gcgttccttg	203820
gggtagacag	agctgttttcg	ttttttcctg	gggattatag	aaaacgaaat	ttaagaagtt	203880
ctttgtgatg	ggaagaagat	ggatatgata	ttcttcaaag	ggctcgccct	catcgcaatt	203940
gataaaaaata	acttctcgat	ttattctacg	tgctctcagc	tggcttttga	caagatccct	204000
gatgtctagg	ttgttgtcag	cctcacaggc	tataatccac	tttggattgt	agatctcacg	204060
attttcaaaa	ttttgtgata	cttttagtact	ttcaataaag	atactgttat	caactagagt	204120
tacggggcggt	gtcggaccaat	ctatgacgcc	tccgcgtttt	agaaactcgt	caattaggtg	204180
ctgttctaaa	ctttgatata	ttgttgatag	agaaaaagga	actggagagt	ccgttgcttg	204240
gctgaactta	aataataagg	ttctcttttt	ccaatggtaa	cgcgcaccaa	agatcttatg	204300
gttggccttg	ataaaatcgc	ctagcatttc	actattgtga	agaagctcca	aggaagagca	204360
agacaagatt	acagggagct	tacgacaatc	taagaagcta	ggatcctcag	gagaagctct	204420
gtggtcgata	actttttacag	agatcccatg	ttgtattagc	atatttgcca	aaatgagacc	204480
tgtaggatta	gcacctatga	ctaaaatgtc	tgccatactt	gccctcggat	agtgaaaaag	204540
attttcatata	cattatagga	taaaatccta	ggaggaatca	agaaacgaat	tccaagagct	204600
atgaatatag	gtgcttccat	ctagaagttg	tattttaaata	tgtagtgttc	tagaaccgtt	204660
gtaccttgaa	ttaagggtaca	actgaaattt	aaagtgttcg	ttggaagtgg	ctcacaattt	204720
gatctaagat	catatctaaa	tcaggagctg	tggctaagtt	gtgtcctgtg	ttagggttaag	204780
agatgaaagt	cattcttccg	ggagctgtgt	ttttaaatag	tgtctgttgt	gtcctagaaa	204840
caagagtgtc	atcaatgcct	tgttgatgca	aaatataggg	ttttgtgggt	aggggaatttg	204900
ctgtaacgtg	atcttggatg	cgtatgagga	gatcaacatc	gccagagcaa	acaattatag	204960
gaggaggacc	aaatccaaaag	tccttcccaa	cagagataat	atctccttcg	ccgtgttttg	205020
agaaattctc	atagagctct	tttaataaga	tgcccccatc	tgcaattgga	gcccatacac	205080
tcaggggcttt	gatatttaag	tctcttgggt	tatagatttt	agccaactcg	aagcgtatgt	205140
ggcatcctaa	agaaaaacct	gaaattccta	aacgatatgc	attgagatct	gggtgttctt	205200
ggacagtttc	aagtatgggt	tgtgcatcac	gtaaataggt	ctctatagga	acttcttcag	205260
caactccttc	actatctcca	catccggcca	tgtcgacacg	taaagtggca	attccagctg	205320
cagcgaattt	tcttccctaat	tttcgatagg	ctccagttaa	acctccgaat	tttgttcctc	205380
ggaagccgtg	aaacaacacg	actgtaggga	acctccttc	cggtgtggga	gtgttaggaa	205440
gatgtaaaaac	accaataaga	ttgtgatcgt	cacatttgat	agtaactgtc	aaacatactt	205500
cttgcttctcg	acatacttct	gtcttgattt	gaacganatc	ttctggaatt	tgaggaaatc	205560
ccggaacacg	gactggagct	gccgaagccc	ctatagctac	tgaaaatagg	caagaaacta	205620
aaaaagcaac	tttacgcatc	ttgattaact	aattaaaaaa	ggaacacata	tagagtaggg	205680
gggcgctcct	gtttttgtca	atgtcatgga	agtttttgaa	ggaaaaacgg	acaagactct	205740
tgttttttcc	tctggggaga	cgtacactaa	gccttttttaa	tttttatata	tataaaagtt	205800
tagaatatgc	gatatgaccc	caacttaata	gaaaaaaaat	ggcaacaatt	ttggaaagaa	205860
catcgaaagt	ttcaagcaaa	tgaagacgag	gataaagtaa	aatattatgt	tttagacatg	205920
ttcccttatc	cttcaggagc	aggtctacat	gtaggccacc	ttattggcta	tacagcgaca	205980
gatattgttg	cgagatataa	aagagcacgg	ggattctcag	ttcttcatcc	tatgggctgg	206040
gatagctttg	gtttgcccg	agaacaatat	gcgattcggg	caggaaccca	tcctaagatc	206100
acgacccaga	agaatatcgc	taatttttaa	aaacagctct	ccgctatggg	attttcgtat	206160
gatgaaggac	gagaattttgc	tacgagtgat	ccgactattt	atcattggac	tcagaaactt	206220
ttcctttttc	tttatgatca	aggactcgcc	tatatggccg	acatggcagt	gaactactgt	206280
ccagaacttg	gtaccgtatt	atcgaatgaa	gaagttgaaa	atggattctc	aatagaaggg	206340
ggatatcctg	tagagcggaa	aatgcttcgt	cagtggattc	tcaaaatcac	agcatatgcc	206400
gataagttat	tagaaggctc	cgatgcccta	gattggcccg	aaaatgtaaa	gcagttacag	206460
aaaaattgga	tagggaaatc	tgaaggggct	ctcgtaacan	ttcatttgac	gcaagagggc	206520
agcttagaag	ccttcactac	cgcctagac	actttattag	gggtgagttt	cttagtgatt	206580
gctcctgagc	accagattt	agattctata	gtgagtgaag	agcaaaagaga	cgaagtcaca	206640

gcctatgtac	aagagagtct	caggaaaagt	gaacgagatc	gcattagctc	tgtaaagaca	206700
aaaacagggg	tctttacagg	aaactatgcc	aagcacccca	ttacagggaa	ccttttacct	206760
gtttggattt	cagattatgt	cgtcttaggc	tatggcacag	gcgtagttat	gggagtccca	206820
gcgcatgacg	agagagatcg	agagtttgct	gaaatgtttt	ctcttccgat	tcatgaggtg	206880
attgatgata	acgggggtttg	tattcatagc	aattacaacg	acttttgtct	taatggcttg	206940
tctgggcaag	aagctaaaga	ttatgtaatc	aactacctgg	agatgcgttc	tctcggaaga	207000
gctaagacta	tgtacaggct	gcgagactgg	ctcttctcta	gacagagata	ttggggagag	207060
cctatcccca	tcattcatctt	tgaagatgga	acgcaccgtc	ctttagaaga	tgatgagctg	207120
cctcttctcc	ctccgaatat	tgatgactat	cgtcccgaag	gattcgggtca	gggtccttta	207180
gcgaaggctc	aagattgggt	gcatacttac	gacgagaaga	caggtagacc	aggatgtaga	207240
gagacttata	ctatgccaca	gtgggcaggc	tcttgctggt	attatcttcg	tttctgtgat	207300
gcacacaact	actcagttgc	cttgagtaga	agaaaaagaa	agctattgga	tgccgtgtaga	207360
tctttacatt	ggaggtgcag	aacacgctgt	tcttcatctt	ctttactcga	gattttggca	207420
tcgagtcttc	tatgacgcgg	gtcttgcttc	aacaccagaa	ccttttaaga	aactgatcaa	207480
ccagggactt	gtgttagcct	cttcataccg	aattcctggt	aagggtacag	taagcataga	207540
agacgttagg	gaagaaaatg	gaacgtggat	ctcaacttgt	ggagagattg	tggaagttag	207600
acaagagaaa	atgtctaaat	cgaaactcaa	tggtgtggat	cctcaggttt	tgattgaaga	207660
gtatgggtgca	gatgccttac	gtatgtacgc	tatgttttcg	ggacccttgg	ataaaaaataa	207720
aacctggtcc	aatgaagggtg	tttgggggggt	gccgtcgttt	cctaaatcgt	ttttatgatt	207780
tggtnccttcg	tcagagggttc	aagatataga	agaccgtgac	gggctgggtc	tcgctcacia	207840
attggtgttt	aggattacag	aacatattga	aaaaatgtct	ttgaatacca	taccgtcttc	207900
atztatggaa	tttctgaacg	atttttcaaa	gcttccagtc	tattctaaac	gtgccttgtc	207960
tatggctgtt	cgtgtattgg	agcctatanc	tccgcatact	agcgaagagt	tatgggttat	208020
attgggaaac	ccaccaggga	ttgatcaagc	agcatggcct	caaataagacg	agagttacct	208080
agttgctcaa	actgtgactt	ttgttggttca	ggttaatggg	aagttacgag	gacgtctcga	208140
ggtagccaaa	gaagctccta	aagaagaagt	tttatctttg	tctcgaagtg	tagttgcaaa	208200
gtatctagag	aacgctcaaa	tacgaaaaga	aatttatgtt	cctaataaac	tagtgaattt	208260
tgtcctatga	tgctacgagg	tgtccatcgt	atttttaagt	gtttctacga	tgttgtttta	208320
gtttgtgcat	ttgtaattgc	cttacctaag	cttctttata	agatgttagt	ttatggtaag	208380
tataagaaat	ctctagcagt	tcgttttggt	ctgaaaaagc	cgcattgtccc	tggaagagg	208440
cctttgggtg	ggtttcatgg	agcatctgta	ggggaagttc	gtttgcttct	acctgtactt	208500
gaaaaatttt	tggaagaatt	tccagggttg	cgttgtctag	tgacttcatg	tacagaactt	208560
ggagtgcagg	tggaagcca	agtgtttatt	cctatgggag	ccactgtttc	aatactgcct	208620
ttggatttta	gcataattat	caaatcggtg	gtcgtcaaac	tgcgtccctc	ccttgcagtc	208680
ttttctgaag	gggactgctg	gctaaatatt	attgaggaag	caaaacgtat	aggagcaact	208740
actctcgtca	ttaatggtag	aattttccata	gattcttcaa	agcgttttaa	atttttaaag	208800
cgcctaggta	aaaactatatt	ctctccagta	gatggatttt	tattacagga	cgaagtccaa	208860
aaacagcgtt	ttctttcttt	agggatacct	gaacataaat	tgcagggttac	agggaatatt	208920
aagacctatg	tagcagcaca	gacagcactg	cacttagaaa	gggaaacttg	gagagatcgt	208980
ttgagattgc	caacggactc	gaaattagta	atcctagggt	ctatgcatag	aagtgatgca	209040
ggaaaatggc	ttcctgtagt	gcagaaatta	ataaaagagg	gggtctcagt	tttatgggtg	209100
ccaagacacg	ttgaaaagac	caaggatgtt	gaagaatctt	tgcattcggtt	gcacattcct	209160
tatgggttgt	ggagccgcgg	cgccaatttt	tcttatgtac	cagttgtcgt	tggtgatgaa	209220
attggcttat	tgaacaact	ttatgttgct	ggtgatttag	catttggttg	aggtaacttc	209280
gacctaaga	tcggaggaca	taatttatta	gaacctctcc	aatgtgaagt	ccctttaatt	209340
tttgggtccac	atattacatc	gcaatcagag	cttgcgcaac	gcctgttgct	ttctgggtgca	209400
ggactttggt	tagacgaaat	agagcctata	atcgatacag	tttctttctt	actaaataat	209460
caagaagtgc	gtgaggctta	tgtacagaag	ggaaaagtgt	tcgtaaaagc	agaaacagct	209520
tcctttgacc	gtacatggag	agcattaaaa	agttatatct	ccttgtaaaa	aaatagttaa	209580
gtttgataaa	ttcatcgcca	tatcgcgagg	tagagttagt	gtcatctcgt	tggtgctcata	209640
acccaaaggt	cggagggttcg	aatccttctc	ccgctaattn	ccattttgca	tggtggtgata	209700
gctcagggtg	ttagagcagc	agaancataa	tctgcgtgtc	gttggttcaa	atccgactac	209760
cgctatccat	gctagaagac	attcattttt	taataaaaat	taaaaaaatc	ttcttagcca	209820
aaatttccca	cctatatattt	ttacataaca	ctttgttttt	caatttggtg	ttatgttttc	209880
tcgaagaaaa	taaagatctt	cataaccaag	taaatacagac	ttaaagtacg	tcctgatgcc	209940
tttttcttga	ttagagaatc	cgttagaact	cgaattgtgt	gttttcataa	acaattcatg	210000
ccgcatttct	tcaataggaa	ttagagaaat	ttttnatttt	tctaagaaag	gcactccaaa	210060
actcaaggag	ttttaactaa	ctaaaaagga	taaggaaaat	aaaatatagc	agataataact	210120
gtatttttga	atagctcttg	cttactcatc	tctaataaac	aagtgattct	ttaacacacc	210180
tttattggag	ccttcaaaaa	aaagagtaaa	gccagtggta	ttggactcac	gaagatcaca	210240
ataaaagaac	cctgcaccga	gctccttaag	cctttctatg	agaataaagc	cacatccgtc	210300
aggatgatca	gattgtggag	ttgcagctct	ataaaatagc	aaacagtacc	atatagtaaa	210360
gagattgcct	attgtagatg	gtattccaac	accaccctga	gctattggat	acttattagg	210420
gaaaaatgcc	gtcctaccaa	gaaaagcgct	tcgtccaggt	tcctcactaa	gaacaacaat	210480



attgtgcac	atatgtctag	ccagaagctt	tttgccttcc	aagctaaaat	atttgttgcc	210540
ttcttcttcc	agaagaatat	cttttatcag	tttttcttct	tcaggatgac	ctgtaaagtc	210600
aaaaggctga	tttttcaaga	ggagttctgt	aggccaatct	aacgttaaaa	gtaattttat	210660
aaaacttgcc	ttaaggagtt	tcaactttca	taagttgata	tttcttagga	agagaataga	210720
agagcggaga	aacagttaga	gccgcttctt	tcactagcgc	aggaattttt	ggcaatgatc	210780
agttcttcgg	ctttagtaat	ttctgtgggg	ataaaaaata	ctgctcgatc	caaactctta	210840
ttaaacttgt	tatataagag	gtagcgtatc	gctagagcta	tcaagactag	aggaacacag	210900
ataaaggaaa	ggatttttaa	aattttttct	gctgtagaaa	caacagcctt	ctctttttta	210960
gccaaagata	gtccggaggg	tcaagagaaa	ataatgcgcg	tcacagtctc	tcctcctaaa	211020
caaaaatagg	agttcagctg	agccatcaac	gaagcttgcc	aattagggga	agctccagga	211080
gaaaattggg	atatgttcat	aagggcttct	ttataagtga	caaagctaaa	ttataatcat	211140
ttttgtatta	agattaaaaa	cagaaatctc	aagggaaaac	agtacaattt	agattagatt	211200
tatccgcctg	agcaccatcc	gaactctaaa	cttttttagga	agtctagaat	agagagccat	211260
gcccttttta	attgtctttg	ataaatccat	gatccttcaa	cacagatcca	tagttttctt	211320
cccaaactat	aggaatcct	ataggtccat	atggacctcc	attacgcccg	tcattttgag	211380
cgcttgcttg	tggcttatat	tttaatccaa	ggtttaagag	cctattatgg	acttcgcagc	211440
ctgcttggtt	aaaatccttt	tctagtttgg	ggcgttaga	atggtagtaa	taaaaaataa	211500
tgaaggccca	tacagtgggt	tttttagttt	catgactgaa	ctcgattaag	aaagattctc	211560
tacctccatc	aatagtggat	gtaggaaagt	tcaatccggg	ttcgagctta	aagagttggt	211620
ctaagagata	acgtgccaa	attttcttgc	tttctaaaca	aaactcctcg	ccaggattat	211680
tcttttcaag	tttagcaact	gtatcaatta	tagccttgct	ttcaggataa	taggcaaaat	211740
caaaatcctc	actcaaatag	agtttaggcc	atggtataga	atctgtatct	aagtcctcta	211800
agagcaaatc	tatatattata	gagagggtaa	ttttaggagg	ctacccttta	gaagtttggg	211860
tgtaacatac	tgtgtatttt	gtaggtaggg	caaagaaacc	tgggtggacc	tctcgagctg	211920
ctttttcaac	taattgagga	tttgctgcaa	gaattagctc	cagttcttta	ggcgtgtctt	211980
gagggataac	gaagcatttt	ctatcgaatt	ttctatgtaa	gaagtagcgg	atagccagag	212040
cgattaaaat	gatcgggaag	aagatcagag	caaggatctt	tataactttt	tctgctgttg	212100
agacctgtac	tttttcttca	gtagctaaag	aaaaccacga	gggagtcacg	gagaaaaatc	212160
gagttgcagt	ttctcctcca	aaacaacact	aagagtcgag	tttactcata	agcccagctt	212220
gccagttcgg	gcagatgcct	ggagaaaaag	agtatatggt	gctcataaac	aatccctttt	212280
aaagaattag	ccatcttatt	ttataaattt	tctgattcta	taagtcttag	ttgagaattt	212340
taatttttaa	tatagatggt	tttttaaagc	ttaagaaatc	ttaacacaaa	agagccgttc	212400
ctttgcatct	agcttagaat	attcttatag	gaatggacag	gttgtcagag	tagaggcgaa	212460
tgcgtttgat	tttcccaaag	caggggtcaa	ggtcgttgat	ctataagctc	ctctttcccg	212520
aagtactgta	aagggcctgg	aaaacgggat	aaatcttcaa	ccaaacaaga	atcactttgt	212580
tgaagtaaat	gttgaacagc	aggggatttt	gggtctacag	aatctgtttt	aataacagga	212640
gtctctgtcc	cacaacgatt	ttctaagtgc	atcatcttat	ataatggagt	ggctccccct	212700
tgccattcag	tataagattg	agcaagatta	ttgattgtaa	tcataatacc	agtcctttgt	212760
cggaccagaa	ataacgcaga	aatgatccct	aaagcgtatc	cataattaca	atcaaagtgt	212820
gaagggaatc	atgctcgtgc	ttcataacca	aaaaaatgcg	atacagaatg	gaattccata	212880
tggggtttta	tcttttcgat	ttccttcttt	accattactg	caagcagctc	ttctgtagca	212940
atttttgana	ctctaacatt	tccatgagaa	tctcgagcta	gaagaagttg	gttcgcaata	213000
tccttaggaa	acaagtgaag	tgtttttatg	tctctggaga	gagcttggaa	agaatttttc	213060
atagaagaat	ctccattggc	gagtaaaaca	ttgagttcat	ctataagctt	gcgtgtatcg	213120
aaaatatgct	caatcagctc	ctctgggatt	aacacagtac	tatagttttt	tccagattta	213180
tagcggcgta	ccaaacctaa	agcaagctgt	tcactcagtt	gctttaaaga	gattttccta	213240
gtggcaataa	gttcgcta	taaagctata	ttagggaggg	tctgcaatcc	gcattctaaa	213300
tagtataaag	agggctgctg	ccccataagg	cggatgaaat	ggtggtattt	ttttgcagaa	213360
agagcatctt	tagcaagatt	cccaatcatt	tctgagtacg	tgcgacaaga	agtatgaaaa	213420
cctaacgagg	tttcaatcca	acagttctta	agatcaccat	ctatagtttt	agggactcca	213480
atcacggatg	ttttgcagtt	gtgagcaagg	aaatattctg	caagcatcgc	agtgctccgt	213540
ttggaattat	ttcctcctat	aatgagtagt	ccgtctaaat	ttagttgctt	gactgtgttg	213600
aggatgtttt	ttttctgctc	ttcagttttt	attttttctc	ggcttgagga	gagcatgtcg	213660
aaccttccca	tgttgtaata	atcatagatt	acggagatat	ccagatcttt	atagagccca	213720
cgtagtaagc	ctaaaggctc	tttgatgaat	ccaaataagc	gagtcctggg	attgaatact	213780
cgtaaagcat	caaaaagacc	aataacgaca	ttatgcccc	caggagcttg	tcctcctgat	213840
agtaaaaccc	caatctttta	tggttttgat	gacgtttcct	gttcagtata	aatagaaact	213900
tcagggatcc	gacatagatt	gggaatgtgt	ttttgcaact	ctggaggggg	tgaaggggga	213960
gacgaagttt	cttggaatag	tttcgaacgt	atcgtttcta	ataaagtaag	aatctcaggg	214020
cggtagcgaa	ggcgttggat	ttcaaaaata	cttttattta	acgagagaag	ttccacagtt	214080
tattccccag	aagttaattc	tcttttttaac	cattgcgtga	gatccgaaag	agccgaagat	214140
tcggcaaaaa	gaaacgcgtg	atcgacatcg	ggataagtaa	gaatagtaat	tggtttctct	214200
tgatttgcaa	atgcttcggg	aaacagtggt	ctgtggttga	tagaaaccag	aagatcttgt	214260
tcaccttgca	tataaagaat	tggagggaga	ttgcgagcac	taggcataag	ctctttcaca	214320



atatctat	ttt	taaagaattg	cgtataaaaa	tcaggattta	aagtcacccc	agcataagta	214380
atggcgcc	ttt	tgactcat	tgtgatcact	tcaggagcat	ttttttgtgc	ttccgcagcc	214440
attaattctc	ctgaaattgt	aggcgccccat	acagctaagg	ctttgat	ttt	attaaaaaaa	214500
ggaagagtct	gaagagcaag	agttcctccg	agtgatgaac	caaaaaatagc	gagcctttct		214560
tggtctatat	gaagtaggga	atgcgtatat	tcaatgattt	cacgaatg	ttgcttataa		214620
ttttcaagag	aaaaatccat	aagctcaccc	tcacagtctc	catgaccaag	gagcttact		214680
cttagagctg	cgatacctaa	ccgagtgagt	tcctgagcta	gcctgacatg	agagcgtttc		214740
gaaccggttt	tatctgaagc	taaaccatgg	agaaggatca	ctataggata	gggaggatta		214800
taatggagag	gagtatgtag	aaggccaaaa	gttgtaaaat	tattcagtag	ggtcagtgaa		214860
aacatgggtgc	gctgctcatg	cttttccaat	accacgcctg	taatcaaaaag	aggctcctgc		214920
tttctggatg	tgcttgacct	atgtcaatgt	agtttctaaa	gaaaaattag	tcgagaaaaat		214980
tcgttgcatg	gaatgcctct	aactaaagtt	ctcaaaaaaca	gccatcaaaa	atcgtgtaaa		215040
atagtatcag	aacaatccct	ggatgaatag	tttacaggaa	tgatttaaac	ctccttattg		215100
gggtgatagg	aatcttccca	atagatacga	atcccttgaa	aaccttgaaa	attaggattg		215160
tctggctcct	gagaggggca	aattggaaac	ctaactccta	actcttgtaa	ttgctctaag		215220
atctcaaatc	ctcctcctcg	atcttcatct	agaggacctt	gtctgaaaaa	gacttgccgc		215280
catattgtag	gattttgtgg	agtaaaatga	gaatagatat	aacgaacact	aggggaataga		215340
gtcagtcctc	cagatgtatt	gttaggaagg	gcttcagggt	tttcttggtg	gatcccatca		215400
ataaataggt	gctgtaacat	gaattttaaa	agctacgctt	tcctacagaa	tttatgtaag		215460
ttcctgtccg	cagattttgt	acattctgta	taacacggtt	atctgccttg	ctgcaaaaaat		215520
ccatagtaga	gttaagatac	tccgtaggcc	aggaaaccga	atctaaatta	atgtcatcag		215580
caagttgctc	aagatctaaa	gaaaagcgaa	tgccgtgact	tgaaattata	atctgacggt		215640
attttgccag	tacacagaaa	aaagaggggt	ttgtagttcg	aagagccgct	tcaactnta		215700
gaggatttga	tcccatagct	tgtagatttt	tttgggatac	tggaaccaat	gttggttaatt		215760
tataatgaga	cgccgtgtnt	cctgaacgac	caggaatagg	cacatactga	ggagctcttt		215820
ctaaaatntt	agatacaagt	aagtgtattg	catatttagc	atgtagaaaa	tagtgtaggg		215880
ctaaagcgat	taaaatcaga	gggaagatta	agaaggataa	aatctttaat	attttacta		215940
ttgtggagat	ccgaacgttt	tctacttttc	caataattaa	gttaggttct	tgcaatacta		216000
tagatacaac	cttgattcta	ttcccgccta	agaaaagata	agaactctacc	tttgacataa		216060
gctgaaatat	ccaaggtgta	tctacatctg	aagagatgct	ataaagtttc	ataattcgaa		216120
aaggcgattg	tatatgttat	aaagtgtaaa	caaattataa	aatgtatatc	gatcattcat		216180
acccttacac	cagcgacacc	tctttgcacg	gagggggaaa	tttttccagg	tcttgtagat		216240
tctgcaattc	agaatgatct	cgagagatta	ctcacagtaa	agaaaagacc	tgatatcatc		216300
cgggagtatt	tgccgagcagg	aggtagtctt	gttacaacat	accctaagga	aggctcagaga		216360
ttgcgctccc	cagaacagtt	aagagttctg	gatgatttag	tgcaaagcta	tccaaatcac		216420
ctacatgcga	ttgaacttga	ttgtggtgca	atccctcaag	atttgatcgg	agccacctat		216480
atcatcacgt	tcgccgattt	ttccacctat	attctctctt	taagaagcta	ccaagccaat		216540
tctccctcgg	atgatacatg	ggggatttgg	tttggatcta	ttgacgatcc	tggtcaagca		216600
gtcatatcat	ttttaaaaga	tcatggattt	gctcttccct	cgaccttagc	tcaagatcct		216660
ttgcttttga	ctaacaagta	atttattaag	tgaaataaat	aatataaatt	aaaaatttat		216720
cgcttaattg	tgttttaaat	gtatttatat	taaaataaatt	ttttcttttt	taaaacagct		216780
tatgactaga	agtactattg	aaagcagtg	ttcgctatgc	tcaaggtctt	tttctcaaaa		216840
attaagtgtc	cagacattaa	aaaatctctg	tgaaagtaga	ttaatgaaga	tcacttctct		216900
tgtgattgct	ttcctaactc	taattgtggg	gggtgctctt	atagcttttag	caggaggggg		216960
gggtctttct	ttccctcttg	ggctaactct	atgaagcgta	ctcgttttgt	tttcttctat		217020
ctatttagtc	tcttggttga	aattttttac	tttaaaagag	atgacaatga	cctgtagtgt		217080
caaatctaaa	atcaatatat	ggtttgaaaa	gcaacgaaac	aaagacatcg	aaaaggcatt		217140
agagaatcca	gatctctnng	gagaaaaata	gagaaatgtt	ggaaatcggt	cggcaagaaa		217200
tcaactagaa	atgatcttac	acgagactga	cggaattatt	ttgaaaagat	atatgaaagg		217260
agctaaaatg	tacttttatt	tatgaattgg	gttccaaaaa	caatagacca	tgtagatcca		217320
gaatcagaga	tagatatacg	taaagtcgtc	tcctgctata	agttgataaa	agaatgtcaa		217380
cctgaatttc	gatctcttat	aagtgaatta	ctaggagtga	ttcgggtggtg	cttaagacta		217440
ttaaaacggt	ctaagtatca	agaacaggct	agaactggtat	ctgatgaaga	tgacacctct		217500
ttctgcctga	ctcgttctta	ttatcaagat	ggttatctca	cgccattaag	agcaggacct		217560
cgtgatctta	taaatcacta	tatacacttg	cgtcgccgag	agaatcctaa	gcatttttttc		217620
agtcctaagc	atccatgtta	ttatgctcga	ttggctttta	atgagtcagt	gtgtgtctat		217680
agagaactct	ttgatataga	gcgacttaca	aaaatgtatg	tcgaggggtga	ttattctaaa		217740
gaacaagaga	aaaacctaca	ggctattctt	agttttgtga	aaactctaga	tgaaggaaag		217800
gactttctta	ttgaacataa	agataccgat	ctcattggga	gaggttttac	tgatgtgttc		217860
tgactttaaa	tcaatgaaat	tgtctcaaac	aatataataa	aagcgattct	attatgtctg		217920
aaagtattaa	cagaagcatt	catttagaag	ctctacacac	atttttttata	aaattaacga		217980
atctctgtga	aagtagatta	gttaagatca	cttctcttgt	tatttctcta	ttagcttttag		218040
tgggtgcggg	agtcactctt	gtggttttat	ttgtagctgg	gatccttctt	ttacttctctg		218100
tactcatctt	agaaattatt	ttaataaccg	tccttgctct	gcttttttgt	ttgggtattgg		218160

aaccttatttt	aatagaaaaa	cctagtaaaa	taaaggaact	acctaaagta	gacgagctat	218220
ctgtagtaga	aacggacagt	actcttttaa	atttatattta	atgtataggg	ctaatacggag	218280
tacgcatttg	aatatcagag	caattactaa	aggaattatg	agcaggtaag	ataggatcctt	218340
cagtgtacag	tgtacagttc	atagagcctg	gcttgaattt	cctatcttta	gcactcaatt	218400
cttccacagt	gattccttga	tcctgtttgc	ttaggaagac	tatttgagac	tgtcccagat	218460
caaaataaga	atctacgggt	gcagctaaac	gttctaagcc	gtaattctcg	ctatttaaaa	218520
aaggtttagc	aagaaggatg	gtagggcaaa	aagggagcat	aaaaaatcct	cttgggaaat	218580
gcgaccacaa	atcttcatc	atctgttcta	ttaatgctat	ttctatttta	cgaattcatg	218640
caacataata	acaattatca	gactttatat	ggagatccta	gtagactatc	gtaaggctta	218700
agaacaaaat	atctcggcgc	cacctctccc	aataaaagt	gtgtctttat	gtgtagcaag	218760
aaagtcgtca	aagccgtcct	tctcatctaa	aatttgcaca	aaactaagaa	tcgacttttag	218820
gttgtcttcg	ttttgctgct	cataatcacc	cgcgccatac	atctgtttta	gttccgctgt	218880
gttaaagagt	tttcgataga	tacgcactga	ctcattaaag	gccaatcgag	catagtaaca	218940
tggatgcccc	ggattaaaaa	aatgctcagg	attctcacgc	cgacgtaagt	ttatatagct	219000
ctattttata	tataacgcgg	tcctgtctcg	agtggtgtaa	gatagccatc	tcgataataa	219060
gaatgagtgc	ggcagaaaaa	aggtgcatct	ttatgggata	cagttttagc	tcgctcttga	219120
tacctagaac	aacggcttaa	taaccctaag	ccactctgca	tcgctcttag	taattcactt	219180
ataagagatc	gaaattcagg	tttcatgct	ttaatctaat	tataacagga	gatgactgta	219240
cgtatagagt	cttctgatac	tggatctaca	tcgtccattg	tttttggaac	ccagttcata	219300
aataaaaagta	catctagatt	cctctcatag	atctttttca	aaacattttcc	atcacatcgc	219360
cgtaaagtct	cttttacttg	acttcttgca	gacgattat	tgtcttccgc	cctattttct	219420
ccaaagagct	caggattttc	cgtagccttt	tcaagatctt	tatttcggtg	cttttgaaac	219480
cattgggtgga	tttgagagtc	ggattttag	acaaccctta	gctcttttat	agggcagaat	219540
ttatatgaaa	aaagtaagaa	taaagcaca	agcacaacga	gcacaattcc	caagactaac	219600
caaggaagaa	aagaaagaat	gcctgtctca	gctaaagccg	tgagagtaat	tcccccaact	219660
aaagctaaca	aagcgataac	aaaagaagtt	atcttcacta	atctactttc	acacagattt	219720
cttaatggct	gggtatttta	ttccataact	aatgggtgtg	aacactctga	accaacattt	219780
ttcatgttat	tttctccgat	agtgaattct	atatgaaaag	attaacactg	tactttcaaa	219840
taatttttta	aagattaagt	ttaatattta	tacaaatata	aactaattat	ttcgtttcgt	219900
gaatcttgta	aaataactaa	gaaaaagtat	cggtagagt	cacagatcaa	aaagagatat	219960
ttgtcatagc	atgtttttata	agaaattctt	ttctgtgatt	ttcttatcta	agctagacag	220020
gtctttcctc	ttgtttccaa	caaaaagtcg	agttatttta	tatttaagct	acgttaaaag	220080
gcaatcttaa	atcatcatat	caaaaattta	atgagacacc	ctccccctcg	agctctcttt	220140
tcttcccatc	gactctcttg	aaagcttctt	ctctggagac	gctttttttt	aacattactg	220200
ctttagaata	gaaataaagt	aagaagaaaa	gctataagtc	ttaggaactt	ataaaaaata	220260
aaaaggaaat	ttagtgggtc	gtatctatag	tttttctcct	ggaacttatc	ctaactggca	220320
agtaactctt	atgggtaaac	tagatggctg	ttttcgttta	agagacgaga	aagtcactcg	220380
ggttatctcg	atcaatccct	ctggattctc	cttagctgac	gaaaaaatag	tccgggtctc	220440
tatgccttct	ccagcatgag	ctgcacaacc	aaaccctgag	tcataagcat	ttctatatcc	220500
agaagctaat	cgcttaggac	aggctccggg	cgcagattct	gatectgcgg	attgtatccc	220560
tacaaataga	ccaggaaatg	tagaatcaac	ctcttgagac	cattgaacag	cttcttgggc	220620
aggttcttgt	gtgttttatt	gtggagcaaa	tgttttattg	aagcagttta	aaaatcgtaa	220680
agtaatcccg	tgttttgaaa	acgtttgcga	agcacgatac	aagatttgat	aaaacttcat	220740
acgcgcgtgc	ttttcaggta	atgaaggata	caaaacatgg	gcaaggcgga	tattttgttg	220800
tacttcagta	tacacgatag	tatcgctccg	acattgctgg	agatagttat	tgaaaatgag	220860
aagaaggtct	tcttcatatt	ggattctctc	aggaggaaa	cgatgtcctt	gtactgtagc	220920
catcactcta	tcaaagctat	taaaatcgta	atttaagata	ttatatgtga	atacacttaa	220980
atccggatcc	ttttcggtgac	agatatcttg	aaagtttcgg	aaaatattgg	agtattgttt	221040
atgaggattc	ttaggagaaa	gtaatcgatg	attgggtccaa	gaattataag	accattttta	221100
gaacccattt	ttcacaccta	aaatccaagc	taattgaggt	gttatgggtc	caggaagggtg	221160
tacatggata	tctgcttttg	ggaggttttt	gatgatagct	tcgggtgcaag	cgattgtatt	221220
gagtcgtggg	actaatgcaa	agatctcatt	gcatactcta	tgtacagaat	cttccctttc	221280
aagattcttg	aataacgtat	cataagacat	agaaagaacg	aacgctataa	ctgtgcaagt	221340
gttatacttt	tctcctctaa	tgatattgatt	tttacgaaca	ttctaattgat	gttactaaat	221400
aacgagctct	tgattttacc	ctatggtggc	tattcccat	ctatagttgc	tggtggcttg	221460
tcagaaatat	catagaccac	tcggcttacc	tcgggtattt	cattaataat	tcgcgatgag	221520
caagaactga	gaacatcgca	tggaaggtag	gcccatcgct	ctgtcatgaa	atctgtagat	221580
tctacagcac	gtaatgctat	ggtataacca	tagcttctac	aatctccttt	tacagatact	221640
gattttatag	gaagaaatag	agcaaaggct	tggtttattt	tatcgtagag	ttttgctttc	221700
ctaagctctt	ctataaagat	gaggtccgcc	cgctcgtaaaa	tggttagata	ttcaggaagg	221760
atctctccaa	tcacacgaat	tgtcaagcca	ggctcaggaa	aaggatgcct	gtccaagaga	221820
tagctagaaa	gtcctagggc	ttctcctaaa	attcgaactt	catctttaaa	taataaacgt	221880
aagggctcga	ctaacttcag	cttaagattt	tttggaagcc	cccctacatt	atgatgtgat	221940
tttattactt	cggaggcatg	tccagagcgt	gaggactcaa	taacatctga	gtagatgggtt	222000

ccttgagcta	accattgtac	gtctaattgac	tgagcgactt	catcaaatac	ttcaataacg	222060
gtatcttgaa	ttttacttac	aaggtcttgc	tgaatatata	agggaattcca	tagtgtggga	222120
gcagaacaga	tctcttgaa	aaaagtttct	agaatcttat	ttcccgttgg	agtggagtca	222180
gaaacctcgg	gatgaaattg	cagcccgtag	aaccgttgtt	tggtattttc	tattcctgag	222240
atcgagcatt	gtgaggtgga	tgcgattaca	ttaaactcct	caggaattgt	cgtaacatga	222300
tcccgatggc	tcatccgaat	ctctgtgtct	agagattcgc	agtcgacgat	gtgtttgaag	222360
agctcacaag	gatacagatg	gatgggctga	tatccaaatt	ctcctacacc	agggtctaca	222420
gtccctccaa	aatctctagc	cataagctgc	atgccatagc	aaatagctag	aattggaatg	222480
ccaagtttat	agatttcagg	atctaaatgt	ggagccttgt	tttcatagac	agagtggagga	222540
cctcctgaga	gaatgatccc	caaaggcgtc	ctttctttta	aacattgcac	agagatatct	222600
caggggaagaa	cttcgcaata	tacaaataac	ttccgcactt	gctttgctaa	tacataagta	222660
tattgagatc	caaaatctag	aataaaatag	gtgttcaaat	gtctccttgc	actctgcaac	222720
ttaataattt	aaggttgggt	gaacttttga	aataattatga	atatgacttt	cagctcttcc	222780
agattcagta	atctgaacaa	aggaagcctt	agtttttaaa	tctttgagag	tttcagctcc	222840
aacatacccc	atacctgagc	gtattcctcc	taaaatttga	tagaggacat	cgtggacaga	222900
gcctttataa	gcgactagtc	cttcaactcc	cccaggaacc	agctttttct	gtccctgtgt	222960
ttgaaaatac	cggtcagcac	ttccttgttt	catagcgcct	aaagatccca	tgccgcggta	223020
ccttttataa	agcttctcat	cgatagaaac	gatatcccca	ggagcttcat	cagtccttgc	223080
aagcaaactt	cctagcatga	cacagtctgc	tctgtctgct	aatgctttta	ccacatctcc	223140
agaatagcgg	attctcccat	cagcaattac	agtcacggca	gagtttttaa	gagcttttgc	223200
tacgtttgta	atggcagtaa	tttgtggata	accgaccctt	gaaacgattc	tagttgtaca	223260
gatattacct	gggccaatac	ctacctttac	agcgtcaact	ccaatctcag	ctaaggaaac	223320
tgcggttcca	gctgtaaaca	gattccctac	aactaaagaa	atttgtggga	actgggattt	223380
tattttctaaa	actgtttgga	atactccttt	agagtgtgca	tgagctgtgt	caatgactag	223440
aacatttgct	ccagcttcca	caagatgatg	cgctcttgaa	attcctaaag	gaccaatgcc	223500
tatagcggct	cctatgggag	cttaaggata	ggcttcttta	atttttctca	cagatgagct	223560
ttgttctact	tcgctcatat	ttttatgtaa	gattcccaaa	ccaccttctt	gagctaaagc	223620
tagtgccatg	gctgtttctg	tgacagaatc	catagcagct	gaaagaatcg	gtatatattag	223680
agagaggggt	tttgaatgg	ccgttttcaa	ggacacttca	gaagggaagta	tttcagaata	223740
ttggggggatt	aaaagaacat	catcaaaagt	taaggcttct	tccatgtatg	ctacaatagg	223800
acacttttaa	ggatagtcaa	tgatcccttg	ctatactgtc	aatgcttttt	tcatgattcg	223860
tgacattcct	tcgaatctta	agaagaaatt	tctttggaac	agaagtttct	tcttccgtgt	223920
ttaggcttct	tattgaactt	atagcttaga	aaagattgaa	ggaaggaaag	ataagactat	223980
attgattctc	ttgtcttaag	atatacgacg	acagcactcc	ctattcctac	actcgataat	224040
aagtagaacc	aatactataa	gagataagat	cccaaataca	agtgaagctg	tttctccaga	224100
agttccataa	acagaaaaac	aaatgatgat	gctaagtagg	gataaaaaaga	taaaagagaca	224160
tcgggaacag	taatgacaac	aattcgatac	caaagttttt	gcatctatat	cctcgattgg	224220
ggaggggctc	gttgattcaa	cgaatctatc	cggaaatacg	ctaaagtcca	taaaaccttg	224280
ttgatgtttg	taagaatcta	ttttgtagat	gagatcgaaa	atcgtctaac	gatctgattc	224340
ttctcaatac	tttatttgcc	tggaatcata	aaaccttcaa	cctcttcgat	gtcgttgtgt	224400
ggcgcaatct	attgcaaate	acgaaaatac	ttgattgagg	gcttcggaga	aatttgaagg	224460
ggtgatgcac	aataggtgcc	agttcttgcg	ttttttaaaa	aatttttata	tggtttgtgg	224520
agaaaattgt	tatactatca	atgattatga	ctactatatc	taactcacc	tcccctgcac	224580
tgaatcccca	actttccctt	attcctccac	caacacttgt	atcttcaggt	acgcaaaccat	224640
ctctagctta	tacgatcccc	gcacaaggac	gaagatccac	cctacgtatt	atattagata	224700
tattcattat	cattcttggg	ttagctacga	tcatttctac	ccttattgtt	attttctttt	224760
taaatgggct	gaacttgctc	tcgaccccat	ctattatctc	ttcgtcatgt	ttaatcattg	224820
ttggattgct	ttttttgatt	atgggggttat	atttcatgat	ctcgagtttg	gatcaggggc	224880
ttgtaggcct	tctgcaaaag	gaactctctc	aagccgaaga	aagagaagaa	gagtatatcc	224940
aggaaatcga	agctttaaga	ggagctccta	gagcagaatc	tcccacagag	tctcctagta	225000
cctggttatg	attttacagg	atgaagttct	tattttctaa	aatttgtcag	cagtttttct	225060
tttataagaa	tacttttttaa	ttcttgattt	taaattcctt	acgacaaaag	ggtgaaaaaac	225120
gtcttgtaga	acattctagc	ttctatttagc	ctgtttccaa	tttttattaa	ggagacgcga	225180
tatggagcaa	cccaattgtg	tgattcagga	tactacaact	gttttgtatg	ccttaaatag	225240
ctttgatcct	agaacttagt	atgacactca	cagacttggg	aagcaatcac	ctcttgaagc	225300
agaaaatgct	cttgagagaat	ttattgaagg	tttgatataca	aatagctttc	ctttagagga	225360
agttgccatt	cccatcctgc	cagggttatca	ccctaagttt	tatttatctt	tcatagatag	225420
ggacgatcaa	ggtgtccact	atgaagtttt	agatggcgta	tttttaaaga	cagtcgctgc	225480
ttgtattata	gagaactcct	tcttaactga	ttctatgagc	ccggagcttc	tcagcgaagt	225540
taaggaagct	ctgaaacgat	gatgatccta	tggatgaatc	cgatggagaa	gaagcttcaa	225600
aagattctgc	attttcagct	agtttttctc	atgagtttgt	aaaatcaagt	actcgagaat	225660
ctaaaaatac	agtcacacac	tcaacagcgt	ctcgtacatt	atatatttta	aggcaggatt	225720
gttcttatga	tccaagagct	ctcaaagtag	atgatgaatt	tcgttattgg	gtagaaaaaa	225780
ggttgagcgc	caagaatcca	gattcattaa	atgcgttcgt	taaagaggta	ggaactcatt	225840

atgtcgcgtc	agtgaacttac	ggtggcattg	gttttcaagt	gctaaagatg	tcttatctcc	225900
aagtcgagga	gttagagaaa	gaaaaaatct	cgatatctgt	agctgcagca	agttctttat	225960
taaaaagtaa	aacatcgaac	gcgacagaga	aagggttatc	ttcgtatcag	tcggaatcat	226020
cagctcaaac	agtattttctt	ggtggaacag	tattacctga	tctccagcaa	gacaagttgg	226080
atttcaaaga	ttggtctgaa	agcattccta	atgagcccat	tcctctagct	attagtgtat	226140
cttcaattac	agatctcata	attccagaac	ttttcccttc	tgaagatgct	caagtcttat	226200
cccagaagaa	atcagctcta	ggacaagtta	ttcttaatta	tctagagagt	cacaagccta	226260
aagaagaagg	cccaaaaacca	gtccaaatta	cttctggatt	caattcatcg	tcttcggtat	226320
ttacgcttca	agcagcaaaa	gctcctaaga	ctgtgtcttt	cccctatata	gattattggt	226380
ctacaattcc	ctatctttttc	cccactctta	aagaaacttc	aggtgctcaa	cctctctcgt	226440
tctacttgag	gtttgatgac	atctttgagc	aacaaaattt	agtccataat	acttcatata	226500
ttttagcttc	aacctcggtg	aggttaggat	atttcggaga	ttcatataga	gattatgatg	226560
ctctatcttt	ctatggtagt	tggcctcaag	catattttga	ctgggcaggc	tataaagata	226620
ggtgtacttg	gaccttagaa	aaactcaata	caactggaga	tcttttcata	cgttctggag	226680
accagataag	tttaaaacac	aatacctctg	ggaaatatct	tgctacaacg	agcatgtctg	226740
atggctatca	gacattaact	tgtacgacac	agacgagtga	ttctgtcttt	ataattactg	226800
tataaataga	gttaagacat	ccccttaagt	tttaagggga	tgtcttattt	gctttctaga	226860
gaactcatct	ctaagtaaac	ttcttttctt	agggctgagg	aggaactttc	ttatagcttt	226920
catgaacaca	gagtatagaa	gttccgtttg	ctaaaaacgt	gcttctgagg	tagtctctctg	226980
caaaggaatc	tccaaaagca	ttcagagaat	cagaggaaga	aacgctttcc	cagactaaag	227040
aatagtaccc	ttttacaggt	aggacctctt	ttgagcaagc	actctcatct	gcaatccagg	227100
cataagcaat	gacaaaagga	ttcccctgag	gtacgcagca	cacttcaacg	ggatacaggc	227160
tataaacacc	ttctcgcctt	ctagctatta	caaagtcttc	ttctgtcatc	tcaaggccta	227220
tagcattaca	gcgtcgtccc	gaagatttaa	tgagattcag	tacagctoga	tttttcggac	227280
catcgtgaga	agttctacgg	cgacttccgt	tttttaagta	ctttcctgtg	tctatattaa	227340
aagaacgctc	gtatccattt	atccaaatag	gatgtggacg	atacgttttt	aatgtaagag	227400
ctgctgattt	tgggtgcatc	agacttccat	aagtcgatat	gggaatgtaa	gaacctttga	227460
ttttgagatt	tttatggatt	tctctccaaa	ttttacgaga	ctcttcatca	gtcttagcta	227520
cgacataagg	atcattgtgc	tcttcagaaa	agatttgagt	cgtaacgaaat	gcagaggat	227580
aatgaggcag	ttgcgaaaca	ctcttatttc	catgaacaaa	gaattcttcg	ctcgttgag	227640
tgttgtgata	attccaagag	ggcttttgat	tacaggagga	aagagatcca	agacctaatc	227700
ctaaacatac	acttgaaaag	ataagagaca	tgggctgttt	catggattcc	tcggagatta	227760
agaaaaatgaa	ttttgatnng	tttgctctct	tttgctctac	ttaaaggagc	ttttcaacaa	227820
cgtttcggctc	tgaatttttg	ctaaacaaga	ccctgcccgtt	accctagctt	gtcccagctt	227880
ctctagcata	atttgaaaat	tgtaaaggaa	atatatgaaa	aaaggaatac	gaaaccacc	227940
ctatctaagg	nattcttaat	tctgaacgta	tagtatccag	aactaagaat	tctctatctt	228000
aggaagtcta	taatgaaagc	accccgagat	tccggagaga	acttttggtta	gtgcatgcct	228060
tgaacagttt	attccaagta	cacccacact	tctctttctc	tgttttcata	acctgtgata	228120
atgcctagcg	cgagcagttg	ttttaaaatg	ctctcaccta	aacaaagctt	accatgccca	228180
ggttcggtct	taccagctat	atggaaaagc	tgacctgtag	ttgttttagc	atctatagat	228240
tctcctccaa	atttctgaga	gaccgtacag	tgacgttttg	tttgaggatc	tctttcaaca	228300
ttccgttgca	ctagaaaatc	taagtattct	ttcactcaaa	tctaacttct	cctcataaga	228360
aagggttaggt	ttgccttcaa	agatgcatag	gagccggaga	gatctaaaag	caataactca	228420
acttagtgaa	aattaaggag	gacatgaact	ttctgtcttt	cttaagagat	cttggcaact	228480
tagcgatcaa	tccctttaag	aagtgatgag	gtactacctt	taaaatcttt	cgcactaacg	228540
cggcttgctg	gttggtgtgt	gcttcaagggt	cttgttcatt	aaagaaccct	atagattcaa	228600
aaatacagga	atagtttagga	gtttttgcgt	catttacatt	taagaggatc	gctttttttc	228660
ctggaatgat	tccagagcgg	cctgcttgca	aagtaaaatt	aaagaaatta	gcaacacatg	228720
cttttgatgg	acgcgagctt	cttcttgatt	tgtggaatga	tttacgaagt	cttctgttaa	228780
actttggaac	tgaggttgct	tcaattctag	tttcgaaatg	agtatcccag	atcttaggtc	228840
aagcccaaca	acccttgga	cctcaatatt	tccaatttta	cacgctgcaa	gtaggtttct	228900
tgcatgtgtt	ctacgtacca	tagcctctac	aagaacatta	tctagaggat	tagataagcc	228960
attcatctca	ttgttttttg	aagatacaaa	tgtaaagcgg	agattcggat	aattatctac	229020
acaaaaagta	aatcggaat	aatgattagt	atgataaaca	tctaataaac	agattttctt	229080
agcctcgaga	atctgattag	cccagcagg	atggcaatcc	gcttgattaa	aataggcatc	229140
acgtacttcc	ctctgagcgt	gcaatatctg	agaaggatac	gtttcagacg	ccacgggtatt	229200
ctggataaag	actggccttat	acttacaatc	cagaatctta	tgtaaagacg	tctaacacaa	229260
taaatctccc	tagaaatatc	gtctctagct	agaacatctg	ttgtatcccc	tccccaatag	229320
aaataagagt	cgagggcttg	cacagctttt	tctaaactgc	taggtttttc	atgatgagaa	229380
tttaaagaat	aattattata	aaatagcttc	ataaattttt	taaaaaaata	ataaacgccc	229440
tctatttttaa	acaattcatg	cacttattaa	gaagtattta	attcaacaac	agcttaataa	229500
atttaaaaat	catcttttta	taaaagaata	tttatataaa	aataattctt	agaccattgt	229560
aaattttaatt	agaaaagcct	ccgagcttca	agagccctaa	ggaagattct	taaattattt	229620
agaattcttt	aaaaaaagaa	tttccttgag	caagtaggtt	atcgatatag	ttaatatcgt	229680

aattagattc	tagaaacttc	ggattatcca	acataaactg	gtggaaaggt	attgtagact	229740
gcacaccacc	gatatgaaac	tctttcaaag	ctcgtttcat	gatagctata	gcttcttctc	229800
ggtttttgcc	cttagcaatt	acctttgcta	tcatagaatc	ataataagga	gggattgcat	229860
agccgctata	acaagctcca	tctacacgaa	ttgaaggacc	tgcaggagga	agataataat	229920
ctaaacgacc	tggagatggg	gagaaattat	tggtaggata	ctcagcgtaa	atgcgacatt	229980
ggatgatatg	acccgagaac	tcaatgttct	tttgtttcca	aggcagctta	tttcccatgg	230040
ctacatgaat	ctgttctttt	acaagatcta	tacctgtgac	ttcttcagta	atgggtatgct	230100
ctacctgaat	tccgggtattc	atttccataa	agtagaattt	tttgtcttta	tctaataaga	230160
attcgactgt	tccaacagaa	aaatatccgg	cgcttcttgc	tagatctaca	gcaacttttc	230220
ctactttgac	tccgattttcc	gcattgagaa	tgggactagg	agtctcttca	atcaactttt	230280
gacgtcgccg	ttgaatgggtg	cagtctcttt	ctcctaaatg	cacataattt	ccatgggtat	230340
ccccaatgac	ttggattttct	aaatgccttg	gattttctat	aaacttttca	atataaacat	230400
tgggggttatt	aaaaccggct	tccggttctg	cacgtgcggc	agaaaacgct	ctatgaatt	230460
cgtccttttc	tttaacaata	cgaattcctc	ttccccacc	tccagcaacg	gctttaataa	230520
caatagggaa	acctattttt	tcagctattt	ttaaaccttc	gctctcgtct	tcaataatgc	230580
cttcagaacc	tgggaataaca	ggacatttga	ttttctttgc	cagggaacttc	gcagcaatct	230640
tatcccccat	catagcaata	gactctgaac	tccggccctat	aaagggttaag	ccacagctct	230700
cgcataattga	agcaaagttt	gcgttttcac	ttaaaaaccc	atatccagga	tgcacagcat	230760
cagctcctgt	gatctcacag	gcagccaaga	tattggatat	ctttaataa	gactttgctg	230820
cttgagggtc	tccaatacaa	atagcctcgt	cagcaagaag	tacgtggaga	gcctcttgat	230880
ctgctaaaga	atatacagcc	actgtcgaca	atcctaaatc	atgacaggca	cgtataattc	230940
taacagcaat	ttccccctta	ttagcgatta	agactttttt	catgatgcat	cttttagctat	231000
acgaaacaac	ttagacccaa	attggacagg	atccccattg	gtaatcaata	cttcaagaac	231060
acgcccactc	attcctgctt	tcacttcatt	cattactttc	atagcctcaa	cgatacaaac	231120
aatagtatct	tccgaaacaa	tatcgccagg	ttttacaaaa	gaaggagaat	ctggggctgg	231180
agaaccatag	aaagttccca	ctaaaggaga	acttataaag	tctccggaac	ttgttgtagt	231240
agaagtttct	gaattttctg	tagtagtctc	tttaattgta	tcttttttag	ggtccgttgg	231300
gataggctgt	tcttgagaaa	atccactaaa	taacctgctg	tcataaaaac	caggctcttg	231360
tctattcccc	tccttagtat	ctctttccaa	ctccaattca	agcccttcac	gttttatagc	231420
aaaacgcttc	ataccattgc	gtcccatagc	aatcatgagc	ttttctattt	gttttaagtc	231480
cataccaagt	ctcttttaat	tgaatttaga	cgcgttgaat	atactcacia	gtccgcgtat	231540
ctatttttat	aacatcacca	atttctacaa	aagggtgggac	cataacttca	attcctgttt	231600
ccagcaaagc	tttcttaact	cctccggaaa	gagagagaga	atctccagga	aagtctgttt	231660
ttgataccat	aagctctaga	aaatgaggca	gctctacaga	aaaaaccaca	ttgtcataga	231720
ccattgcaga	gacagtcaca	cctgccttta	aaaacaaaaa	gttatccttc	atgatttctt	231780
gtggaatgaa	taacttttca	taatttccta	aatctaaaaa	aagataactt	tcactttcaa	231840
gatataaata	ttctaaagtg	cgggtttcaa	cttgagcctc	ttttacctct	tgagttgctt	231900
tgaattttct	ctcaataaca	acatcagaat	cgcgagcctg	caaagcgact	ttaatgaagg	231960
attcgccttt	gggcccctgcc	accttagaca	ctgaggttac	tttataaaga	ccgtcctttg	232020
tagaaataaa	catccctacg	gataattggc	tacttaacac	cataattttc	tcctcgcagc	232080
aacaaaattt	tatcttccat	tgctaattgaa	tctgcttcta	ataagtaaga	agctgtgact	232140
aaaatatctg	ctcctgcac	tcgacataac	ggcgcagatt	gctgatctat	gcctccatct	232200
acttctatta	aacaagaatc	ctttaaacct	aaagtcttta	tcgcatgacg	tgcaaaagca	232260
atctttttcta	ttgtatttgg	taaaaagctc	tgctctgtaa	atcccggata	aactgacatt	232320
agcacacga	catcacaaaa	cgggaaggaaa	gaagggaagaa	attcgattga	agtagcggga	232380
gaaaaagcta	gacccgcttg	aacccccacat	ttttttatat	aagatagaag	ctctttttata	232440
tccctctgaag	cttcaaaagt	tactataatt	ctatccgcac	cagaacgaac	gaaactttct	232500
ataaattcaa	aaggattgta	aatcatagcg	tggacttcta	aaaatagatc	cgtagatcta	232560
ttaatggcag	caatgatccc	tggaccaaaa	gtaaggttcg	gaacaaagt	gccatccatg	232620
atatctatgt	gtataaaatc	acttcccggc	tgctctagtt	tttttgcttc	tacacccaaa	232680
caggtaagat	ctgcccccat	aatcgaagg	ccaactaata	cggattcctg	tttcttcacc	232740
tcagcctatc	tcaacttcac	tacgctaaat	ttaaagttaga	gtgagcttta	actttctact	232800
attttatatt	actggttgat	gtattcatga	actcctactc	attgtatgaa	tagaaaatga	232860
atacggacta	ctaccataat	acagaacgaa	tatattttcaa	agaaccattg	aacattttct	232920
attaaaaaatt	cttttctttt	tatacaaaaa	tccaagatt	aatctttctg	tttactaat	232980
gaaaatgcat	ttggagataa	ggattatgat	atagcaaata	tattgtgatt	ctaacctcct	233040
ataccttcat	caaacatcaa	attagtgaat	taaagatgat	taaatatatt	ttggatcctc	233100
agcaagaaaag	gtataaaatt	cttgattttt	agatcgagaa	aaacaacaat	tcttatccaa	233160
gttaacctat	taaggataaa	attcttatgt	catctcctgt	aaataacaca	ccctcagcac	233220
caaacattcc	aataccagcg	cccacgactc	caggatatcc	tacaacaaaa	cctcgtttcta	233280
gtttcattga	aaaggttatc	attgtagcta	agtaataact	atttgcaatt	gcagccacat	233340
caggagcact	cgggaacaatt	ctaggtctat	ctggagcgct	aaccccgagg	atagggtattg	233400
cccttctgt	tatcttcttt	gtttctatgg	tgcttttagg	tttaatcctt	aaagattcta	233460
taagtggagg	agaagaacgc	aggctcagag	aagaggtctc	tcgatttaca	agtgagaatc	233520

aacggttgac	agtcataacc	acaacacttg	agactgaagt	aaaggattta	aaagcagcta	233580
aagatcaact	tacacttgaa	atcgaagcat	ttagaaatga	aaacggtaat	ttaaaaacaa	233640
ctgctgagga	cttagaagag	caggtttcta	aacttagcga	acaattagaa	gcactagagc	233700
gaattaatca	acttatccaa	gcaaacgctg	gagatgctca	agaaaatttcg	tctgaactaa	233760
agaaattaat	aagcggtttg	gattccaaag	ttgttgaaca	gataaatact	tctattcaag	233820
cattgaaagt	gttattgggt	caagagtggg	tgcaagaggg	tcaaacacac	gttaaagcaa	233880
tgcaagagca	aattcaagca	ttgcaagctg	aaattctagg	aatgcacaat	caatctacag	233940
cttgcaaaaa	gtcagttgag	aatctattag	tacaagatca	agctctaaca	agagtagtag	234000
gtgagttgtt	agagtctgag	aacaagctaa	gccaaagctt	ttctgcgcta	cgtcaagaaa	234060
tagaaaagtt	ggcccaacat	gaaacatctt	tgcaacaacg	tattgatgcg	atgctagccc	234120
aagagcaaaa	tttggcagag	caggtcacag	cccttgaaaa	aatgaaacaa	gaagctcaga	234180
aggctgagtc	cgagttcatt	gcttgtgtac	gtgatcgaac	tttcggacgt	cgtgaaacac	234240
ctccaccaac	aacacctgta	gttgaagggt	atgaaagtca	agaagaagac	gaaggaggtta	234300
ctccccaggt	atcacaacca	tcttcacccg	tagatagagc	aacaggagat	ggtcagtaat	234360
ctgccgtaaa	gtcttcaaa	acttccttag	aaaataagca	gtaaaagttt	aactttactg	234420
cttattnttt	tttgaaatga	actcactcat	taaagatatt	tgcaacaaat	tttctctcgt	234480
cttatgcttg	ttcttttagg	attgagtttt	tctcacttac	actagaaccc	tacctatgca	234540
ttcaaaaattt	ctttctcgaa	gaaaaaaaa	tagttctcat	aaggaggaaa	cctcttgagg	234600
ttgtatagcc	tcaagttaca	ataagatagt	ccaagataaa	gggcactact	atcatagaga	234660
aactatcctt	ccccaaactcc	tgcccttca	caccttaggt	tcaaaaagtt	ctgtattgga	234720
tattggctgc	ggccaagggt	ttttagaaa	ggcccttcc	aaggaatgtc	gttatctagg	234780
catagatatc	tcttctagat	tgattgctct	agcaaagaaa	atgcatcg	taaacctca	234840
tcagtttaag	gttgcatagc	ttagcaagtc	cttagagttc	gtagaaccga	cattattctc	234900
tcatgcatga	gcaatcctct	cccttcaaaa	tatggaattc	ccgggagagg	ctatacgtaa	234960
tacagctacg	ctcctcgaa	cactcgggca	attttttata	gttttaaac	atccttggtt	235020
tcgtattcct	agggcacat	cctggcacta	tgatgaaaat	aaaaaaagct	atctctcgtc	235080
atatagatcg	ttatctctcc	ccaatgaaaa	tcccaatcat	ggctcaccca	ggacaaaaag	235140
attcgccttc	taccctctcc	tttcactttc	ctctaagcta	ttggtttaaa	gaactgtctt	235200
ctcatggatt	cttagtttca	ggtccttgagg	aatggacatc	ttcaaaaacc	tcaacaggaa	235260
aacgagctaa	ggcagaaaac	ctttgtcgaa	aggaatttcc	attattcctt	atgatttcat	235320
gcattaaagt	aaaataaatt	tttaattatt	taattaggtt	ttttattaga	ataaataaaa	235380
aacacnaaat	tcttgcattha	tgtttcgaaa	acttttcccg	ttttctaaaa	aaaaaacagg	235440
tcagaagcaa	cgtcttcgaa	acaatggact	tctgcaagcg	atcattcaat	caataaaagt	235500
cttactacat	aacgaagctt	ccaaggaagc	ctgctgtgta	agctactatg	gtttgcttac	235560
ttgtgttctt	atttttagtat	tctttctaa	gctttcccaa	cacttattca	ctaacttgaa	235620
ttggaaagaa	tggttgatta	tcaaatcc	agattataaa	aagccaatcg	tagctattgt	235680
ggaagccgca	tatcatgcta	cagaaagcaa	tataggatta	gtcctagtgt	gaagcttttt	235740
tggtttctgt	tggttggtgca	ttttaatgct	cttatctcta	gaagatggcc	taataaagat	235800
cttcgcgacc	agctggactc	caatatcttt	aaagaggtta	gtctcttatt	ttgtgattac	235860
cttagtgagt	cccatgattt	ttattatcgt	ctgtggttcc	tggtttata	ttacacagat	235920
catgcctatc	caatacgtca	agttgttttc	tctcagccat	tccatgacag	cattgtactt	235980
tatttctagg	tttgccctt	acctgctgct	ctacctagct	ctattttgct	gttatgcttt	236040
tcttctctcg	gttgcaatcc	aaaaaacatc	agctcttctc	tctacgctaa	tcataggatc	236100
tgtatggata	gtctttcaaa	aggcattctt	tagccttcaa	gtctctattt	ttactatag	236160
cttcaacttat	ggcgccctcg	tagccctgcc	ttcattctct	ctcctgctat	atatctatac	236220
aatgatctac	ctattcggag	gagcactgac	atttattatc	cagaatcgag	ggtgcacttt	236280
catatttctt	ggggacaaaa	tcctgcccag	ctgttattta	caactcatta	cctcaacata	236340
tattctagct	ttgacaacac	gtcagttcaa	tgaaggcttc	tcccttttaa	ctgctcaatt	236400
catcgccaaa	caatcgaaag	tacctattgg	tgaggctctc	caatgtctag	atgtattaga	236460
aaaagaaggt	tttctttttc	cttataacaa	tgggtaccag	cctgtcttca	atttctctga	236520
acttacaatc	aaagatattg	ctgacaaact	cctgcacatg	gaaattttca	agaaattcaa	236580
tcccgacctt	gggattactt	tcatagaaaa	cagcttccag	aacatattta	accaagcttc	236640
taaaaataaa	gagaatctta	ctcttagcga	gattgctagg	cgaatcaaat	gaaacgaaga	236700
tcatggctta	aaattttggg	aatctgttta	ggcagcagca	ttgtcttggt	attccttata	236760
ttcttgcccc	aactactttc	aacagaatca	gggaaatacc	ttgtgttttc	cctgattcat	236820
aaagaatccg	gactctcgtg	ttctgctgaa	gaacttaaga	tttcatgggt	tggaaggcaa	236880
acagctagaa	aaataaaact	cactggagaa	gctaaagatg	aggtctnttc	tgctgagaaa	236940
ttcgaactcg	acggatctct	attacgtctt	ctgatttata	aaaagcctaa	agggattact	237000
ctatcaggat	ggtcttttaa	aattaatgag	cctgcctcta	tagaccatcc	ttctgtgagt	237060
cacttagatc	caggatcttt	acttacctac	ctaaatgact	gcaagattat	ttctgagcac	237120
ggatttatca	ctatgaagac	agtatcagga	tcttcattat	ctgtatcagg	gtnttatcta	237180
gaganatctt	cagaaaaggt	catgacgaaa	tgctgtgtct	ctgaagatca	gcaatccggg	237240
aacatcttta	tagagagtgt	actttctcct	gatgtcagta	tttccgctca	gttttcttca	237300
gttcccggtg	catttttttaa	aattttttata	gcttcccttc	tctgggacca	tcttctctct	237360

cataaatctc	aaagaaccct	gcaatccaaa	tctctaccta	tagcaagcgg	agctttctat	245100
cctaaaaata	tcaaacaaaa	acaatggata	aaactctcaa	aaaaccctca	ctactataat	245160
caaagtcagg	tggaaactaa	aacgattacg	attcacttca	ttcccgatgc	aaacacagca	245220
gcaaaaactat	ttaatcaggg	aaaactcaat	tggcaaggac	ctccttgggg	agaacgcatt	245280
cctcaagaaa	ccctatccaa	tttacagtct	aagggggcact	tacactcttt	tgatgtcgca	245340
ggaacctcat	ggctcacctt	caatatcaat	aaattccccc	tcaacaatat	gaagcttaga	245400
gaagccttag	catcagcctt	agataaggaa	gctcttgtct	caactatatt	cttaggccgt	245460
gcaaaaactg	ccgatcatct	cctacctaca	aatattcata	gctatcccga	acatcaaaaa	245520
caagagatgg	cacaacgcca	agcttacgct	aaaaaactct	ttaaagaagc	tttagaagaa	245580
ctccaaatca	ccgctaaaga	tctcgaacat	cttaacttta	tctttcccgt	ttcctcgtea	245640
gcaagttctt	tactagtcca	acttatacga	gaacagtggg	aagaaagttt	agggttcgct	245700
atccctattg	tgggaaagga	atttgctctt	ctccaagcag	acctatcttc	agggaaacttc	245760
tcttttagcta	caggaggatg	gttcgcagac	tttgctgate	ctatggcatt	tctaacgac	245820
tttgcttata	catcaggagt	tcctccttat	gcaatcaacc	ataaggactt	ctaaggactt	245880
ctacaaaaca	tagaacaaga	gcaagatcac	caaaaacgct	cgaatttagt	gtcgaagct	245940
tctctttacc	tagagacctt	tcatattatt	gagccgatct	accacgacgc	atttcaattt	246000
gctatgaata	aaaaactttc	ataatctagg	agtctcacca	acaggagttg	tggaacttcg	246060
ttatgctaag	gaaaatttagc	acctctttta	atctcgcaaa	cttgtaaga	actgaatctt	246120
atactaaact	gggtgccttt	gtggcacctc	gtttccttct	gactgctctt	ctctctctac	246180
tcaaccgcat	ccctaaaagt	tgaaatctta	ttctaaagaa	aggtctttta	tgctccgttt	246240
cttcgctgta	tttatatcaa	ctctttggct	cattacctca	ggatgttccc	catcccaatc	246300
ctctaaagga	atTTTTgtgg	taaatatgaa	aggaatatgcc	acgctccttg	gatccggaa	246360
aaactcgtct	cattgcagac	caaaactctaa	tgcgctatct	atatgaagga	ctcgtcgaag	246420
aacattccca	aaatggagag	attaaaccag	cccttgacga	aagctacacc	atctccgaag	246480
acgggactcg	gtacacattt	aaaatcaaaa	acatcctttg	gagtaacgga	gacctctga	246540
cagctcaaga	ctttgtctcc	tcttggaagg	aaatcctaaa	ggaagatgcg	tcctccgtat	246600
atctctatgc	gtttttacct	atcaaaaatg	ctcgggcaat	ctttgatgat	actgagtctc	246660
cagaaaatct	aggagtccga	gcttttagata	agcgctatct	cgaatattcag	ttagaaactc	246720
cctgcgcgca	tttctacat	ttcttgactc	ttctattttt	tttccctgtt	catgaaactc	246780
tgcgaaaacta	tagcacctct	tttgaagaga	tgcccattac	ctcggtgtct	ttccgccctg	246840
tgtctctaga	aaaaggcctg	agactccatc	tagagaaaaa	ccctatgtac	cataataaaa	246900
gccgtgtgaa	actacataaa	attattgtac	agtttatctc	aaacgctaac	actgcagcca	246960
ttctattcaa	acataagaaa	ttagattggc	aaggacctcc	ttggggagaa	cctatccctc	247020
cagaaatctc	agcttctcta	catcaagatg	accagctctt	ttctcttccg	ggcgcttcga	247080
ctacatgggt	actctttaat	atacaaaaaa	aaccttgga	caatgctaaa	ttacgcaagg	247140
cattgagcct	tgcaatagac	aaagatatgt	taaccaaagt	ggtataccaa	ggtcttgacg	247200
aacctacaga	tcatatccta	catccaagac	tttatccagg	gacctatccc	gaacggaaaa	247260
gacaaaacga	aagaattctt	gaggctcaac	aactctttga	agaagctcta	gacgaacttc	247320
aaatgacacg	cgaagatcta	gaaaaggaaa	ctttgacttt	ctcaaccttt	tctttttctt	247380
acggaaggat	ttgccaaatg	ctaagagaa	aatggaagaa	agtcttaaaa	tttactatcc	247440
ctatagtagg	ccaagagttt	ttcacaatac	aaaaaaactt	cctagagggg	aactattccc	247500
taaccgtgaa	ccaatggacc	gcagcattta	ttgatccgat	gtcttatctc	atgatctttg	247560
ccaatcctgg	aggaattttc	ccctatcacc	tccaagattc	acactttcaa	actcttctca	247620
taaagatcac	tcaagaacat	aaaaaacacc	tacgaaatca	gcttattatt	gaagcccttg	247680
actatttaga	acactgtcac	attctcgac	cactatgtca	tccaaatctt	cgaattgctt	247740
tgaacaaaaa	cattaaaaac	tttaatcttt	ttgttcgacg	aacttcagac	tttcttttta	247800
tagaaaaact	ataggagaaa	aagtttagac	ttaaaattcg	atagtaaat	tattaaagta	247860
atTTTTaaaa	tgTTTTcacg	atggatcacc	ctctttttat	tattcattag	ccttactgga	247920
tgctcctcct	actcttcaaa	acataaaaca	tctttaatta	ttcccataca	tgacgacctt	247980
gtagcttttt	ctcctgaaca	agcaaaacgg	gccatggacc	tttctattgc	ccaacttctt	248040
tttgatggtc	tgactagaga	aactcatcgc	gaatccaatg	atttggaatt	agcgattgcc	248100
agtcgtata	cagtctctga	agacttttgc	tcttatacgt	tctttatcaa	agacagcgct	248160
ttatggagcg	acggaacacc	aatcaccttc	gaagatatcc	gtaacgcttg	ggagtatgca	248220
caggagaact	ctccccacat	acagatcttc	caaggactta	acttctcaac	tccttcatca	248280
aatgcaatta	cgattcatct	cgactcgcgc	aaccccgatt	ttcctaagct	tcttgctttt	248340
cctgcatttg	ctatctttta	accagaaaac	ccgaagctct	ttagcggtcc	gtatactctt	248400
gtagagtatt	tcccagggca	taacattcat	ttaaagaaaa	accctaacta	ttacgactac	248460
cactgcgtct	ccatcaactc	catcaaaactg	ctcattatct	ctgatataata	tacagccatc	248520
cacctcctaa	acagaggcaa	ggtggactgg	gtaggacaac	cctggcatca	agggattcct	248580
tgggagctcc	ataaacaatc	gcaatatcac	tactacacct	atcctgtaga	aggtgccttc	248640
tggctttgtc	taaatacaaa	atccccacac	ttaaatgatc	ttcaaaacag	acatagactc	248700
gctacttgta	ttgataaacg	ttctatcatt	gaagaagctc	ttcaaggaac	ccaacaacca	248760
gcggaaacac	tgtcccgagg	agctccacaa	ccaaatcaat	ataaaaaaca	aaagcctcta	248820
actccacaag	aaaaactcgt	gcttacctat	ccctcagata	ttctaagatg	ccaacgcata	248880



gcagaaatct	taaaggaaca	atggaaagct	gctggaatag	atttaatcct	tgaaggactc	248940
gaataccatc	tgtttgtaa	caaacgaaaa	gtccaagact	acgccatagc	aacacagact	249000
ggagttgctt	attaccagc	agcaaactcta	atctctgaag	aagacaagct	cctgcaaaac	249060
tttgagatta	tcccgatcta	ctatctgagc	tatgactatc	tcactcaaga	ttttatagag	249120
ggagtaatct	ataatgcttc	tggagctgta	gatctcaaat	atacctattt	cccctagaca	249180
aaagaagtct	ttggtaaggg	gtttttttta	ttgaagagac	ctttcttcac	cagtatacta	249240
ttgtatcttt	ataagaagtt	tcttctgtat	ataaattgct	atatgaagaa	acagtaagta	249300
ataggagcat	taggatacgc	ctccttaagg	tatttctatc	ctgaaagata	caataatctc	249360
attcccccat	cgactaaatc	caccacggac	tccgacctcc	catgtcttca	atccatatga	249420
acgtaatat	aagtagcaaa	ttgagtacta	tataatgaag	atgcataggc	ttaaaccctac	249480
cttaaaaagt	ctgatcccta	atcttctttt	cttattgctc	actctttcaa	gctgctcaaa	249540
gcaaaaacaa	gaacccttag	gaaaacatct	cgttattgcg	atgagccatg	atctcgccga	249600
cctagatcct	cgcaatgcct	atttaagcag	agatgcttcc	ctagcaaaaag	ccctctatga	249660
aggactgaca	agagaaactg	atcaaggaat	cgcactggct	cttgcaagaa	gttataccct	249720
gtcaaaagat	cataaggtct	atacccttaa	actcagacct	tctgtgtgga	gcgatggcac	249780
tccactcact	gcttatgact	ttgaaaaatc	tataaaacaa	ctgtacttcg	aagaattttc	249840
accttccata	catactttac	tcggcgtgat	taaaaattct	tcggcaatcc	acaatgctca	249900
aaaatctctg	gaaactcttg	ggatacaggc	aaaagatgat	cttactttgg	tgattaccct	249960
agagcaacct	ttcccatact	ttctcacact	tatcgctcgc	cccgtattct	cccctgttca	250020
tcacaccctt	agggaaatcct	ataagaaagg	aacacccccca	tccacataca	tctccaatgg	250080
gccctttgtc	ttaaaaaaac	atgnacacca	aaactactta	atttttagaaa	aaaaactcca	250140
ctactatgat	catgaatcag	taaagttaga	ccgagtcacc	ttaaaaaatta	tcccagacgc	250200
ctccacagcc	acgaaccttt	tcaaaagtaa	atctatagat	tggattggct	caccttggag	250260
cgctccgata	tctaacgaag	acaaaaaagt	tctctcccaa	gaaaagattc	ttacctattc	250320
tgtttcaagc	accacccttc	ttatctataa	cctgcaaaaa	cctctaatac	aaaataaagc	250380
cctcaggaaa	gccattgctc	atgctattga	tagaaaatct	atcttaagac	tcgtgccttc	250440
aggacaagaa	gctgtaactc	tagttcccc	aaatctttca	caactcaatc	ttcaaaaaga	250500
gatctcaaca	gaagaacgac	aaacaaaagc	cagagcatat	tttcaagaag	ctaaagaaac	250560
actttctgaa	aaagaactcg	cagaactcag	catcctctat	cctatagatt	cctcgaattc	250620
ctccatcata	gctcaagaaa	tccaaagaca	acttaagat	accttaggat	tgaaaatcaa	250680
aatccaaggc	atggagtacc	actgcttttt	aaagaaacgt	cgtcaaggag	atttcttcat	250740
agcgacagga	ggatggattg	cggaatacgt	aagccccgta	gccttcctat	ctattctagg	250800
caaccccgaga	gacctcacac	aatggagaaa	cagtgtattac	gaaaagactt	tagagaaact	250860
ctatctccct	catgcctaca	aagagaattt	aaaacgcgca	gaaatgataa	tagaagaaga	250920
aaccccgatt	atccccctgt	atcacggcaa	atatattttac	gctatacatc	ctaaaatcca	250980
gaatacatte	ggatctcttc	taggccacac	agatctcaaa	aatatcgata	tcttaagtta	251040
gatccgaaat	ggaaaaatta	aaaattttat	agacaatctt	gaaaagagaa	ttaaaatctt	251100
ttaatttaaa	ttatagtgtg	aattgaaaa	gcccctaaga	atcggggcc	ctaactactg	251160
aatctacgtg	aaatgcaatt	gttaaaaaaa	taagagattt	atagaaaaat	aaaagtcttc	251220
cttccccacg	cattttttgt	attgaagatg	actaanantg	naagtataat	gacttaaaaa	251280
tttttagagct	gaggtctact	tcaaggtaga	aatgcttaat	agggttgtct	ctcgtgttct	251340
catacataaa	aaaccgaatt	cttttttaatt	tgctttctct	atggattggt	ttgacactca	251400
cgttccctagt	tatgaaaacc	atcccaggag	atcctttcaa	tgacgaaggc	tgcaatgttc	251460
tttccgaaga	ggtcttacaa	accctaaagt	ctcgatacgg	tttagataaa	cctctctatc	251520
aacaatacac	acaatacctc	cactccatcg	caaaactaga	ttttgggaac	tcgttagttt	251580
ataaagatcg	caaagtaacg	aacatcattt	cgactgcctt	tcctatatca	gcaatcctag	251640
gattgcaaa	tctttttctc	tccataggag	gggggatcgc	tctcggcacc	atagcagcat	251700
taaaaaaaaa	gaaacaaaga	cgctatatct	taggcgcctc	tatactccaa	atctcgattc	251760
ctgcttttat	attcgcaaca	ctcttacaat	atgtctttgc	tgtaaaaaatt	cctcttcttc	251820
ctatcgctg	ttgggggaagc	tttactcata	ctatactccc	gactctcgca	cttgctgtaa	251880
ctcccatggc	cttcatcata	cagcttacct	actcttcagt	atccgcagca	ttaaacaag	251940
actatgtcct	actagcctat	gcaaaaggac	tctccccact	taaagtcgtt	ataaaacata	252000
ttttacccta	cgccatatct	ccaaccattt	cttattccgc	attcctaact	actacagtga	252060
ttacaggaac	ctttgtctat	gaaaatatct	tctgtattcc	tggattaggt	aaatgggtta	252120
ttttagtagt	caaacaacga	gactaccag	tagcccttgg	cttatccgta	ttttatggaa	252180
cttattttatg	ctctcttctt	tactttctga	cctgattcaa	tccattatag	atccgcaaat	252240
ccgttatgcg	cacggaaagg	aaaaaaaaag	aaaataaaa	tcataagaaa	aaaagaagca	252300
taaacttatg	gaaaacctat	cctcagctcc	atcacgtagc	atttggaaat	ctataatcca	252360
gaataaaaatg	cttgttctag	gcctcacgac	cctcataatt	ctaattgctt	gagccctcct	252420
tttgccatgg	ttctatcaag	attatgaaca	gacttcatta	aaagacattc	ttgtctctcc	252480
atgctcgcgc	tttccctttg	gcacagacac	tctaggcagg	tgcatgtttg	cccgaactct	252540
acgaggtcta	cgactctcct	tactcatagc	gacgatcgct	acacttattg	atgtgtgtgt	252600
gggactttta	ttggccactg	ttgctatata	tggaggggaaa	aaaatagatt	tcttaatgat	252660
gcgaaccaca	gagattctct	tttctctacc	gagaatcccc	atcattattc	ttcttttagt	252720



tatgaagaca	taatcaatct	atcagcagag	gcaacacata	ccaatgatgg	taagatttct	237420
atgacagcct	ctggcgaggg	aaatcaaatt	caaatagaagc	ttcaaggcca	tattcataaa	237480
tccacatttt	atattgtaga	agggagttct	tctgtcatag	aacttaaacc	tgagctcgcc	237540
tcagctcttt	gcaaccagat	cattccgctg	tccacaccca	ttactagtaa	gcaaatacan	237600
tgctacggtc	tcttatgcta	aaattccctt	ggatattacg	aaatggaaac	atattgaaat	237660
tacctctcaa	gcacagctcc	ctgaagtcgc	aatacatccg	aaagacccta	atcttgctatt	237720
acagctgcgc	gacacaaaagc	taggaattaa	aaagacggag	aaattntcag	acatccgtta	237780
ctcctcatct	acagctcttag	gaggagcttc	tccctctcac	cttaatgggt	taatcagtat	237840
agataacaaa	aaacatctta	ctaaatttcg	tctacaacaa	gcacaactcc	cccacaccta	237900
tctaagagcc	attttccctc	aacctttcgt	gatcaatggt	cccctggatg	ttgcttatta	237960
ttcattaaat	atcgaaagga	cgtacaaaaa	tgctcactta	gaggcagatg	ctatcctaga	238020
taacccgcta	ttgaaattgt	catgctccat	gtctggagca	tggaataaatt	ttctttttta	238080
agggcaagga	acgtaccact	ttaataaaaa	atggcaggag	attctctctc	cccactctc	238140
ttacgctgaa	gctagattct	caggaaaagc	acaaattacc	gatacgaatc	tctttttccc	238200
taaatcttct	ggaaaaatta	ctgcaagaga	aaatgagctg	ctcatccatg	caaaaatttg	238260
ttccccta	gaacctataa	aaacctgaaac	tacctctata	ctcatccacg	gacaattttg	238320
ttctctgcca	actcagccta	gtttctaatc	acctagcccc	cttccatttg	aagaaaattga	238380
cattttcctt	ccatacggat	ggaggtaagt	ttgtaaccaa	aggaaaacctc	caagctctta	238440
ttgagaatcc	agactatccc	gacctaaata	atacgcgtat	cctaataccct	gatcttcttc	238500
tttctcttga	tgaatcctca	acttcacctt	cttcaaaaga	cttgaaaatc	cagggtcttg	238560
gagagatatt	ttctttgctc	ctggattcta	ttactaagac	ctatgggaaa	caagtgcgtc	238620
tctctcctta	ttttgggttc	tctggagact	tgaaactttg	agtaaaactac	aatcctaag	238680
atcagaataa	gtcacacta	ctatctanct	ttaagtcaga	agctctccta	ggagaactga	238740
agttagtc	ggacttttct	atgaagctat	cttcaggaac	tcagggaact	ctccagtggg	238800
aagtgaagcc	agaacgttat	gcaagtttct	ttaaaaacgc	atcatgctct	cccacctgtt	238860
tgcttcatag	aactgcaaat	gtacgcttag	acatctcaaa	actctcttgt	ccagaggaaa	238920
ccaaagggtt	atcttgtctc	acgcttcttg	ccgcagagga	cttgaagggt	cattagaagc	238980
aacaccgttg	atcttctatg	ataatgtgtc	taaagagact	tttattatta	atgactttan	239040
aggttctttg	cgagccaaca	atttagacgc	taaaaataga	tatgatctta	aaggctcgtg	239100
tctagctcct	aggcaagact	ctaaaactct	tgcaaatatt	tcattagaag	gacaggtaga	239160
tcctctgttc	tctccagagt	ctcgagaatt	taaacaaact	gcaaattgga	ttcacatacc	239220
ctcttcgttc	attgctggaa	tcattcccat	gtctccagga	ttgaaagctc	agatatcctc	239280
gcttgacggc	cctagaatca	acgtatcaat	taaaaatgcg	ttccgatttg	gagaaggccc	239340
tgctcgacatt	atggctcgact	ctgaaaacct	tcaagctcag	attccactga	tcttaaacga	239400
aaagtcacat	ttactgagag	agaatctaac	agcgcacctt	agtataaatg	aagatgtaaa	239460
taaggctttc	ctacaagagt	ttaatcccc	cttagcagg	ggagcctact	cacaataccc	239520
agtaacctta	gagatcgata	aacaaaactt	ctatctccct	atacgcccgt	attcttttga	239580
agaattccgc	atccaatccg	caacatttga	tatggggaaa	atctcaatag	caaatacagg	239640
aactatgtat	gctcttttcc	aattccttga	tattacggat	caaaagcaat	ttgtagaatc	239700
ttgggttca	ccaattttct	tttctgtaca	aaaaggctct	atcatttgta	agcgcctcga	239760
cgcccttata	gatcgtagaa	tccgccttgc	tctatggggg	aaaactgata	tcgctcatga	239820
tcgtctgttt	atgaccttgg	gtatcgatcc	tgaagttatt	aagaaatact	ttcataacac	239880
ctctttaaaa	actaaaaact	tcttcttatt	aaaaatccga	ggatccatct	cgtctcctga	239940
agtggactgg	tcttcagctt	acgctagaat	cgctctatta	aaaagctaca	gtcttgggaa	240000
cccgtttagt	agtcttgcg	ataagctatt	ctcttctctt	ggcgactcta	ccccccacc	240060
aacgtacac	cccttccctt	gggaaaaatc	taattttgat	tctatagaaa	ataaatagaa	240120
tcaatataaa	aacttaacag	ttctttttta	tttaattatt	ttataaatct	taaaaataaa	240180
attaaattaa	ttattagtaa	taaaactcat	gagaaaacgt	cactctttcg	actcaacctc	240240
tacaaaaaaa	gaagccgtca	gtaaagctat	ccaaaaaatc	atcaagatta	tggaacaac	240300
agacccttct	ttaaatgtag	aaacccccaa	tgcagaaatc	gaaagcattc	tccaagaaat	240360
caaagaaatt	aaacaaaagt	tatcgaaaca	agcagaagac	ctcgggtctt	tagaaaaata	240420
ctgttctcaa	gaaacctctt	ctaactctga	aaacactaac	gcacgcgtca	agctttccat	240480
aggcagtgtc	atagaagaac	tcgcttctct	caacaaactt	gtagaggaaa	gtattgaaga	240540
atccttaggg	caacaagacc	aactcatcca	atctgtactt	attgagatct	ctgataagtt	240600
tctttcctct	ataggggaga	ctctttcttg	aaatcttgat	atgaaccaga	acgtaattca	240660
aggactccta	atcaaagaaa	accctgaaaa	atctgaagca	gcttctgtag	gatatgtaca	240720
gactctacta	gagcctctaa	gtaaaaggat	cggcgagact	cataagaagg	tcgctactca	240780
tgatgtgaat	atctcctcct	tgcaatttca	tatgatgtca	gtggcaggag	gtaggttccg	240840
tggtcatatt	gatatgaatg	gctatcgctg	tttaggattg	ggagagccta	aaaatggaga	240900
agatgctgtc	tctaaggatt	atttagaagc	ttacgtaagc	tcgcagctca	ctatagacaa	240960
agttgaagac	aagcccatta	caaagccaaa	taagggaaaa	tactctatt	cccaaggac	241020
gagtcctaaa	cttgagggtc	ccttaccttt	agggcttctg	acatctggaa	tctcaggatt	241080
tacttgaaa	agtgaagca	aatctaacga	tggaagcttc	ccttttagtg	ctttaagaca	241140
caaggaaaca	gagtcggata	cagattgctt	ccagattact	tccacaacgc	tctcaggaaa	241200

tcaagcagga	acctacacct	ggtccttate	tttaaaagt	ttgggtgcctt	caatcttcca	241260
aatcgaaaaa	ccagaagtcc	agctctctct	tgtctactct	tatgaagact	ggcttcctat	241320
cgataatata	ttcaatatgt	ctcagcctag	gaccatacca	ctagctctcc	taggacaaac	241380
aatgcttgca	ggacaaaaat	atgatatacct	agagctcgcc	gcacatcaaa	caaaccaaac	241440
tctaatagatt	agccccgaact	gttctcgatt	ctctctacaa	ttaaaacaaa	ctaatacgtt	241500
tgaaaaactcc	cctgtcgatt	tctatatattgt	ccatgcccgt	cattcctgcc	actggtcagg	241560
attctaaagt	atcactacag	ctgctctagc	agctgtagtc	ctattgagca	gagtggtat	241620
atttcgataa	tggatgacca	gaatcgagct	ctccgtcacg	cttgtcatag	acccccgcaa	241680
cagttccttg	atctataaga	tagatacgat	ccaaacaact	atgaacaaat	tgcattgtcat	241740
gagtagttaa	ccctacagtc	agttcctggg	ctcgaagtgt	ttctaaaaga	tgtcggaaacg	241800
atgccgtagc	aaaaggatct	aaagccgatg	taggttcctc	aaaaagtaat	gtatgtttat	241860
ccatacataa	agaacgtaca	atagccacac	gttggtttttg	tccccagag	agctggtcag	241920
gataattctt	agcaacctct	tcaatatcca	acaaatgtaa	aagctcgaac	gccttttctc	241980
gagcttcttc	ggtactacga	cccttgatat	ggatttgtgg	atgggtgcaa	tttcctaata	242040
ctgtcatatg	ggaaaataac	tcgggttggt	ggaaaactag	agctggagcc	tccccctcaa	242100
tccaaatatc	tccttgagtg	ggctggacta	agccccgcaa	agcacgtaaa	atcattgttt	242160
ttcctgaacc	actcttccca	acaaacagtg	taatgtgccc	tcgctctaaa	gaaaaagtta	242220
caccatctag	aatctttttc	ttattttacag	agtaggcaag	gtttcggact	ctaattgtca	242280
taactccttc	tcttttctga	taacctagaa	atacaggaaa	atgatgttgt	cattaagaaa	242340
tatagcccag	cacaaataag	atacatttcc	atagggttca	actctctcga	gacaatatcc	242400
ttagttactt	tagttaactc	ggggacaccg	acaaccatta	aaatactact	ttccttgatc	242460
aaagaaacaa	attcattggg	taaggatggg	aaaatatttt	taaaaacttg	aggataaata	242520
atataaacga	aaatttgata	cttcttatat	cccaaaacca	ttgcggattc	ccactgccct	242580
atagaaagag	aattgtatac	tccacggata	ttttctgcaa	gatattgctgc	agaattcata	242640
cttaaagcaa	taattccagc	aactagaggt	gtgggttcta	tggggagaac	ttcaggcaat	242700
ccaaaatata	taatcaaaat	ttgaataaat	aaaggagtcc	cgcgataaac	agtcacataa	242760
ctattagcta	aaagtttcgt	taacttagaa	gggaagtata	gagaagtcac	cgttccaatc	242820
aaaagaccta	aaatagaacc	acatagaatg	ccgattccgc	tcacacataa	gggtgatccg	242880
catcctctta	acaacagtct	tgctatagct	agccaatgat	ccactccgac	ctcttatgca	242940
tattttattta	taattgaaatc	atatttatgc	aattaatcca	agaaaacttg	cagtaaattt	243000
gcaatcgaaa	ccatcaacaa	tgggagccct	ccttcactta	taggagtgc	aaaaatcgtg	243060
tcattctctg	ccaaagtctc	aagaatttca	tctttgagcc	cttgatctaa	caaagcagcg	243120
atccaagaag	ctgaaccagg	aaccgtacga	attacaataa	gagaggcgtt	atggcgataa	243180
gagagcacca	aatgacgggt	cgtggtcttc	tctgttgaa	agggttaaaga	ataacgagca	243240
ccacgctctc	cagcaacctt	tacagcctga	atctttcgt	gccaacgaga	tacagacgac	243300
tgggttgtag	caaaaacctg	agctaagagt	tttgcacata	attcctcctg	agttgcccgt	243360
ccttcaagac	gtaaaaatttc	ttttaaagcc	tcacttatag	ttactttttt	tttcaataaa	243420
atccccatga	acttttactt	gctcatattg	agaagtcccc	catactataa	aaggcaacctg	243480
ttctttttct	tgggtttttta	tgctcacctt	aggcttgga	agttcttgcg	atgagactgc	243540
ctgcgctata	gttaattgagg	ataagcagat	attagcaa	attattgcct	ctcaagatat	243600
ccatgcatcc	tatggcggag	tcgttctctga	acttgcttca	agagcacatc	tccatatctt	243660
cccacaagt	ataaataaag	ctctacaaca	ggccaactta	ttgatcgaag	atatggatct	243720
gattgcagta	acgcaaactc	cagggttgat	aggttctcta	tcagtaggag	tgcatttttg	243780
taaaggcatt	gccataggag	caaaaaaatc	cttgattgga	gtcaatcacg	tcgaagctca	243840
tctctatgct	gcctatatgg	cagcgcaaaa	cgtgcaattc	cctgctttag	gtcttgtggt	243900
ctctggagct	cataccgcag	cgttttttat	agaaaatcct	acatcctata	aactctatag	243960
aaaaactcga	gatgatgcta	taggagaaac	ttttgataaa	gtaggacgct	ttctaggatt	244020
accataccct	gcaggcccat	taattgaaaa	actcgcttta	gaaggctctg	aggacagtta	244080
tccttttagt	ccagctaaag	tcccaaacta	tgacttttca	ttcagcgggc	ttaaaacagc	244140
tggtctctac	gcaatcaaag	gaaataatag	tagccccgc	tctcctgctc	cagagatatc	244200
tttagaaaaa	caaagagata	tcgctgcttc	atttcaaaaa	gcggcctgca	ctactattgc	244260
acaaaaactt	cccactatta	taaaagaatt	ttcgtgccga	tctatactta	ttggaggtgg	244320
cgtagccatt	aatgaatact	ttagatccgc	atatacaact	gcgtgtaatc	tacgtgata	244380
cttccccctt	gctaaactat	gctcagataa	ttgtgctatg	attgcaggtc	tagggggaga	244440
aaattttcaa	aaaaactcta	gtattccgga	aattcgtata	tgcgcaagat	atcagtggga	244500
atctgtatca	ccattctcct	tagcctctcc	gtagtctctc	aaggctgcaa	ggagtccagt	244560
cactcctcta	catctcgggg	agaactcgct	attaatataa	gagatgaacc	ccgttcttta	244620
gatccaagac	aagtgcgact	tctttcagaa	atcagccttg	tcaaacatat	ctatgagggg	244680
ttagttcaag	aaaataatct	ttcaggaaat	atagagcctg	ctcttgacga	agactactct	244740
ctttctctcg	acggactcac	ttatactttt	aaactgaaat	cagctttttg	gagtaatggc	244800
gaccccttaa	cagctgaaga	ctttatagaa	tcttggaac	aagtagctac	tcaagaagtc	244860
tcaggaatct	atgctttttg	cttgaatcca	tttaaaaaatg	tacgaaagat	ccaagagggg	244920
cacctctcca	tagaccattt	tggagtgcac	tctcctaata	aatctacact	tgttggtacc	244980
ctggaatccc	caacctcgca	tttcttaaaa	cttttagctc	ttccagtctt	tttccccggt	245040

catcttccat	cacggactgc	tcccgtctaat	ccttgcaatg	acaattacag	gatggattcc	252780
tatatctcga	attatctacg	gtcagtttct	actcctgaaa	aataagccct	ttgtcctttc	252840
tgcaaaagcc	atgcatgcct	ccacgtttca	tattctaaag	aagcatcttc	ttcccaatac	252900
cctagctccc	atcatatcta	cattgatttt	tactattcct	aacgctatct	ataccgaagc	252960
cttcattagc	ttcctgggtc	taggaataca	gcctcctcaa	gcaaagcctc	ggcaccttag	253020
ttaaagaggg	aatcaatgct	atagattact	acccatgggt	atttttcttc	ccctctctaa	253080
ttatgattgc	cctctctata	agcttcaatc	tcacgcggca	gggggctaaa	acactatgtc	253140
tcgaagaggg	atctcatgga	taactactta	ctaaatatca	aggatctcac	aataacctct	253200
acaaacccta	agagaactct	aattgaaaat	ttatcactac	agctcaaaga	aaatcgaaat	253260
cttgctctag	tcggagagag	cggctcaggg	aaaactacaa	ttaccaaaagc	catcctaggg	253320
ttcctccccg	aaaattgtct	gatcaaaacc	ggaagtattt	tatttgaaga	tatagatatt	253380
accaagctct	caccaaaga	gtcccataag	atccgcgggtc	aaaagatcgc	cacaatacta	253440
caaaatgcta	tgggttctct	aaccccatcc	atgcgcatag	gaatgcaa	catagaaacc	253500
ttaagacaac	accacaaaa	gaataaagag	gaagcctata	ataaagctat	gcaactcctt	253560
accgatgttt	gcattcctaa	tccaaaatat	agcttctcac	aataccctct	tgaattgagt	253620
ggtggcatgc	gccaacgtgt	tgtaatcgcc	atagcactcg	caagccaacc	taagctcatt	253680
cttgccgatg	aacctacaac	agccctagac	tctatgtcac	aagctcaagt	ccttaggatt	253740
cttcgtaata	tccaacaaca	gaaacaagct	acaatccttc	ttgttaccca	taacctctct	253800
ctagtcaaag	agctctgtaa	tgatatctgt	attatcaaag	acggcaaact	catagaaaca	253860
ggaaccgttg	aagagatttt	cctctctcgc	aaacaccctt	atactctcaa	gctcctcaat	253920
gctgtctcta	aatccctat	taaaaaaacc	agctctccca	tccttaaaaa	taagttccaa	253980
cctctaatag	gtatgcaagg	tggtttatga	caactctact	aagtataaag	gacctttccc	254040
taaccatcag	aggaagaaa	attcttaatc	atattaacct	caacctaatc	aaaggaagct	254100
acttaacaat	cgtaggacc	agtggctcag	gaaaatcttc	cttagcactt	actattctgg	254160
atctcctaaa	acctaccaca	ggaacaatca	cgtttcatat	ggaccccaag	atccccagag	254220
cacgtaagg	ccaagtgtac	tggcaggata	tcgactcgag	tctaaatccc	tgcatgtcta	254280
taaaaggaat	tatttccgaa	cccctaaata	tcacgcggaac	ctattctaaa	gccgaacaaa	254340
ataaagagat	ttataacgtt	cttgatcttg	tgaacctccc	caagtctgtt	ctccacctta	254400
agccttataa	actcagtggg	ggacaaaaac	aacgcatagc	cattgcaaaa	gctctagtct	254460
caaaaccgga	gtcctttatc	tgtgatgaac	ccctctcttc	actagacacg	ctcaaccaat	254520
ccctaactct	agaccttttt	caaacaataa	aaaaagaata	ccaaaatacc	cttctcttta	254580
tcaccacga	tatgtccgca	gcgtattata	ttgcagacac	tatcgccgtc	atggatcaag	254640
gaagtcttgt	cgaacatgct	tgtagagaaa	aaattttctc	aactcccaag	catacaacta	254700
cacaagatct	tctcgacgcc	atccccatat	tttccctgat	ctccacagaa	atggaaccct	254760
cggaagaata	cgaattacaa	gtcgcctcaa	agtanataga	tttagaaata	acgaattctt	254820
atagaaaaat	taggattttt	gacgtctctc	aatagaaaaa	tgaaagtctg	atatgatgaa	254880
tcaaaaaaac	caatagttaa	tttgattttt	gaattgtttt	ttctcagaaa	gttccctgac	254940
tccactaaaa	actcgtatc	tagttataaa	atagagtcaa	cgctccttac	ggcgcgccaa	255000
tctagggtta	gatcaaaaaa	acttaacact	agaatcagac	gccaattatt	tctaaactat	255060
tgtattacaa	tcattcctat	ttgaattaaa	cactttgaat	ccccataatg	ttcttgcttc	255120
aacaaacgca	accattctaa	agaaccctc	gccttctcta	ttgcgacgtg	taccttaatt	255180
tattgaaata	taaagcatcc	gaaaactgta	gttctattaa	gagctgggcg	cttaggaacc	255240
ttaagttatt	cctataaatc	gtccccctcc	cccaaaaaaa	caataaagag	accagttgta	255300
tgaataccta	taccttctct	cctacacttc	agaaaagctt	cagcctattt	cttttagaaa	255360
aattagactc	ttactttttc	tttggaggga	ctcgtacaca	aatccttagtc	atcacaccaa	255420
ccaatattag	attagcagct	aaaaaaaagag	ggtgtaaggt	ttctactata	gaaaagataa	255480
tcaagatcct	ctctttttatc	ctgctgcccc	tagttatcat	tgccctttata	cttcgctatt	255540
tcttacataa	gaaattcgat	aaacagttct	tgtgtatccc	aaaagtcatt	tctaacgaag	255600
acgaagctct	tcttggtatct	agaccacaag	cagttgaaaa	agcagttcga	gaaatatctc	255660
cagccttctt	ctctatacca	agaaaatacc	aacttattag	aatcgacact	cctaaagatg	255720
acgctccctc	aatccttttc	cctataggca	tagagatcat	tctcaaagat	ttatgtattg	255780
atacactcaa	gcaatcta	cttttccctta	aaagagaaat	ggatttctta	ggtcattccag	255840
aagaaaaagc	attattcgac	tcgatatggt	ctatagaaaa	agatcaagaa	tggatgagct	255900
tggaaagtaa	aaaactttta	atcacgcact	tcctaaagta	tctctttgtc	tctggaatcg	255960
aacaactaaa	tccaggcttt	aacccagaga	atgggcgtgg	gtatttttca	gaaataagta	256020
cagcaaagat	ccattttcat	cagcacgggtc	gatatgggccc	aatccgttct	tcgggaccca	256080
tcatgaagga	aatataaaaa	taaaaggcat	gggctaccaa	atcttcacaa	gacttaaaaa	256140
acttggaatc	tcattctcct	cttataattc	cattaatcct	aatccttact	tcttcgatga	256200
aggctgtttt	gtctactggg	aatcccaatt	taaatccgca	ctgcaagatc	acgggattct	256260
ccagaaacag	acagaaacat	tctatagaaa	tacttaataa	catttctaag	aagtctgtct	256320
aagagaactc	caaaccctata	aaaaaacctt	taaatatttc	ctaaatagaa	gactctataa	256380
aaggctatgg	tcccgctagt	gccttttagaa	atccccctca	gctattgcta	aagttctttc	256440
tagtatgtga	agagttatgt	atacttactg	ttgctacaca	tagagctctc	ttagaaactc	256500
ctttagctct	atcatttttt	aaagaactta	aagacaaaat	atgtctacag	ggcgaagagc	256560

atactacaac	tacataaacct	ataaaggatt	tactatcctt	aatacatcac	cgttatgttc	256620
ttaattttctc	tatctgtaaa	tcgttgacag	aagaagccct	gcatgctacg	actcaattaa	256680
cagtgatgca	attggagtat	ctttgctaata	ggatatttcc	catatcctgg	aagatcttgc	256740
ctatgacgaa	gggatccctc	caaggggaagc	tatagaagcg	gctattgtta	aacaaatgca	256800
aattacgcct	tattttactgc	atatttttaca	cgacgctact	cagcgcgctcc	ctgagattgt	256860
aatgatggg	agttatcaag	gtcacctcta	tgccatgtat	ctcctcgcac	aattcagaga	256920
aagtcgcgca	ctccctctca	tcattaaact	ctttgcatth	gaagatgata	ctccacacgc	256980
aatagcaggt	gatgtcctaa	ccgaagatct	gcctaggatc	ctagctagcg	tctgcaatga	257040
tgactcgcta	attaaagagc	tcatagaaac	tccaaaaatc	aatccttatg	tgaaggcagc	257100
ngcaatctct	ggtcttgtaa	ctcttgtagg	agccgggaaa	attcctaggg	ataaagtatt	257160
ccgttanttt	gcagaacttc	taaaactatag	attagaaaaa	cagccctcgt	tgcgttgagg	257220
taacctaatc	gcagggatct	gtactcttta	ccccggagag	ctcttctatc	caataagcaa	257280
agcctttgac	ggaggacttg	ttgatacatc	tttcatcagc	atggaagatg	tcgaaaaatat	257340
tatccacgaa	gaaaccgtgg	aatcttgat	ccataccctc	tgttcttcta	cagaactcat	257400
taatgacact	ctagaagaaa	tggaaaaatg	gttagaagac	ttccccatag	aaccgtgaca	257460
tcgatcaatc	aatattttcta	accactacac	cgaggtccta	agtgaacaaa	aaaaaacggt	257520
tcttatctct	cctctttctg	actgcagtac	ttttaggcat	ttggttctct	ccccatcccg	257580
catctataaa	ttctaattgct	tggcaactct	tcgctatatt	cacaactact	atcatgggaa	257640
tcattttcca	gcccgtcccc	atgggagcta	ttgccattat	tggaaatctcc	acactactac	257700
tcacacaaac	gttaactcta	gaacaaggat	tgtcaggatt	ccataatcct	atagcgtggg	257760
tagtcttcc	ctccttctca	atagcaaaaag	gaatcataaa	aacaggactc	ggtgaacgaa	257820
tcgcataact	ctttgtcagt	gctttgggga	aaagtcctct	aggactcagc	tatggactgg	257880
taatcacaga	ttttttcctt	gcacctgcaa	tccccagcgt	gactgctcga	gctggaggga	257940
ttctctatcc	cgttagtcacg	agcttatcag	attcctttgg	aagttccgca	gaaaaaggaa	258000
ctcaagatct	tatcggatcc	ttcctcatta	aagttgccta	tcaaagctca	gtgatcacca	258060
gcgctatgtt	cctcactgct	atggcaggaa	accctctggg	ggcagctcta	gcaggccacg	258120
tcgggggttt	tttatcttgg	gttctatggg	caaaaagccgc	aatcattcca	ggactcctca	258180
gtctattcct	catgccgatc	atactctaca	aactctaccc	acaaaaaaat	cacatcttgt	258240
gaagaggcta	tccgatcggc	aaaacttcga	ctcaaagaaa	tggggccgct	aaaaaaaagaa	258300
gaaaaaacia	tattgatgat	ctttttcctc	cttgtagtcc	tctggacttt	tgggactctc	258360
ttaggaactc	cagcaacaac	agcagccctt	ataggactgt	ctctcctcat	ctccactaat	258420
attctagatt	ggcaaaaaga	tgtcatagca	aatacaacag	catgggaaac	attcatctgg	258480
ttcggagcct	taatcatgat	ggcttccctc	ttaaaccaac	tcgggtttat	cccactcgta	258540
ggagactcag	cagcagcact	ggtcagtggc	ctctcttggg	aaattggctt	ccctctactc	258600
ttcctgatct	acttctactc	ccactacctt	tttgctagca	ataccgcgca	tatcggagcc	258660
atgtatccca	tattcctcgc	agtctccata	tcgttaggga	ctaatectat	attecgcagca	258720
ctcaccctag	cattcgcaag	caaccttttt	ggaggactca	ctcattacgg	atccggaccc	258780
gcacccctct	acttcgggtc	acatctcgtt	actgtccaag	agtgggtggc	gtcaggattc	258840
gctcttagca	ttgtcaatat	tgttatctgg	ataggaaatc	gaagcttgtg	gtggaaagcc	258900
ctcggactca	tttagaaacc	aagtctttta	tatagaaaaat	attcttttagc	aagttttatat	258960
tttgtgaaat	atganagctn	aatcatagga	ccacctgtga	tttagccttc	tgtcataagc	259020
tctcttttta	tagcctaaag	ttgaagaaag	cttagccgta	aaaggctctg	ttgtattctt	259080
ccaacgagtt	acaacgaaat	acactaaagt	tcattctcaa	agtagaatca	ttccttaaaa	259140
taagaccttt	ttaaaaaaac	ctgatgttct	tatgcacaaa	agaatccca	ttgactttag	259200
ccttggggatg	atgcaaaaag	caaaatttaga	gtgtagccgt	tatccttatg	catcctttat	259260
acgttgatct	tgatactatt	atcagctcct	actctcctcc	cttacctaata	gaatttcaag	259320
aagcagcctc	tttaattgct	gttccagata	cttcacattc	taagcctgtc	gttccaggag	259380
tgaaaaccct	ctttccacaa	acctaccacc	ttccctatct	aaagtttgct	caaggagaaa	259440
atgtcgttca	cactcctcta	aaagtaggag	taatgttctc	aggaggacct	gtcaccaggag	259500
gacataatgt	catccaagga	ctcttcaata	gtctaaaaga	tttccatccc	gattcctccc	259560
tcgtgggggt	cgtaaatat	ggagacgggc	ttacaacaaa	taaaagcata	gacattactg	259620
aagagtttct	ctccaaatc	cgaaattccg	gaggttcaa	ctgtatagga	acaggaagga	259680
aaaaaattgt	aactccagaa	gctaaagagg	cttgcttaaa	gaccgcagag	gctctggatc	259740
tcgacggact	agtcattatt	ggcgggtgat	gtcccaatc	agcaaccgct	attcttgag	259800
agtattttgc	aaaacgagc	ccaaaaccct	ctattgtcgg	agttcctaaa	actatagatg	259860
gggatctaca	acacaccttc	ttggatctgg	ccttcggatt	tgatactgca	acaaaattct	259920
actcttcaat	cattagcaat	atttcaagag	atgctctttc	ctgtaaagct	cattaccact	259980
tcattaaact	tatgggacgc	tcagcatccc	atattgcttt	ggaatgtgct	ctccaaactc	260040
atccaaatat	tgcccttatc	ggcgaagaaa	ttgccgaaaa	aatctacca	ctaaaaacca	260100
tcacccataa	aatctgctcc	gtaattgcag	atagagccgc	tatggaaaaa	tactatggcg	260160
tcacccctcat	cccagaaggc	attatcgagt	tcacccagaa	aatcatcaac	ttaattacag	260220
aaatcgaaag	cctatcagaa	tacgaagata	aaatctccag	gctctctcca	gaaatcccaac	260280
gcctactgaa	agcttccca	gcacctatca	tcgagcaaat	cctcaatgac	cgcgatgctc	260340
acggtaaatgt	ctatgtttct	aaaattagtg	tcgataaact	actcatccac	ctggctcagca	260400

atcatctcca	acaatatattc	cctaacgtcc	ctttcaatgc	gatctcacat	tttctaggat	260460
atgaaggacg	ctcgggattg	cctacaaaat	tcgataatac	ctacggctat	agcctcggat	260520
acggcgccgg	tattctcgtc	cgcaatcact	gcaacggcta	tctctctact	atagaatccc	260580
tagcatgccc	tttcatgaaa	tggaaattac	gggcaattcc	cgtagtgaaa	atgttcacag	260640
taaaacaaca	ggcagatgga	actctacaac	ctaaaattaa	aaaatacctc	gtagatatag	260700
gaagcacggc	atttcgtaaa	tttaagctct	ataggaaaaat	ttgggccctc	gaagactcct	260760
accgattcct	agggcctcta	caaatagaaa	ctcctccaga	aatgcactct	gataatttcc	260820
ctcctcttac	ctttttgctt	aatcataact	tttggcaacg	tcaccagggt	tgcatagaaa	260880
tccttgatac	tacgtattaa	ttacgttcta	atacgttctt	aattcctgaa	aatctaagat	260940
gcttccacgc	aagcttatcc	gcatactaaa	cttagcagaa	gtaatggatc	tgattcggat	261000
acagtaagac	tgttacaagc	cacaactggg	gcactgaatc	ctgtacatgc	catgcaactc	261060
ggtacgaatg	ccacgccatg	acgaatcaaa	gggaaactag	atacaaacgt	ggcaataaga	261120
aaagagagcg	tcgatcaacc	aaggactttt	gataagctac	ctgcctatag	aatcctctcc	261180
ccacttaaca	aagtttttta	taaaganact	ttcattctta	tttaataagag	ataattcaat	261240
cgttactatt	taaaaataag	caacttagaa	tcaactatag	agagaaaaca	attattatat	261300
taaaattcat	cgaacaacat	taggttgaag	atggaaactt	atagcttttc	tacagaacta	261360
cagaaaaata	cttctctcta	tatcatggaa	aagttagatt	cctatttttc	ctttcaaggc	261420
aaacgcacac	gggtaattgc	aataaccctt	gcagggttag	ccatcgccct	cgagcagaat	261480
atccacctct	ctatgaccgt	gaaaatatta	aaagtcctct	cctttccacg	gtctctcctc	261540
aggacaacta	gtttgtggta	tcgcccttga	taatacgaat	atcgataaac	aaaaacaact	261600
atccgaagaa	ctcaaagact	ctcccaacca	acattttgtc	tatatagaac	tccaaaaatgc	261660
cttcttctcc	tataccgaga	tctaataaag	tttcatagac	atcgatatga	agattttgta	261720
atcattcctg	cttattctgt	gtctttccgc	ggcgacttca	cagtttcttc	ttcgaacata	261780
gaatctaaac	tatgttttagc	ggcanttcat	acttctctcat	aactaaacag	ccccgttcta	261840
acttactttt	agcaattgca	aactcaagct	cttttagtttg	ttttattccc	ttttcgagct	261900
ctagaaggct	gaatttctcc	ctaatagaact	cctcttttagc	cctagcctgc	tcttgaaaat	261960
ctgtggatgt	cttacataac	aatgtatact	catacagcaa	caataagtac	ctcaatcgtg	262020
attgatacaa	acaatccttt	tgatactcct	cttgactggg	agtcttagaa	aaacaaaaaa	262080
gagaaacatc	atgcaattca	ataataatgt	cgtaaatgtt	cctttgcaga	tcttgaaatcg	262140
agcatttctc	catcgcatgc	tcctctctaa	gaaggctctc	attgagctcc	ttgggttctt	262200
tttcaaaagt	gcatagcttc	ctctttgcta	tttcaacaca	atcattcccc	caatccacaa	262260
actcttctat	cttgcaaaga	ggccatctaa	aatctaacag	gtaatatgca	ttcaaactctc	262320
ggattgctgt	ttttagaaaa	tgtatctccg	aagcaatata	aaaagccctc	cgattcactt	262380
ttgataaata	ggcaccacaag	aattctatag	tctgatagat	agcacctatg	tccccaagac	262440
ctaaaacatc	tctggctttt	gtcagtaaaag	cattccacgc	atcgattgct	ttttgagact	262500
caaaaagcac	atcttcatct	tccgtagcct	ttaaaaattt	gtcctggccc	agcccagata	262560
aaacgaattc	aagatgatcc	aaacattgat	aaagtgaagt	gatctcttgg	tcacttgtcg	262620
gcttctgggc	ttttaaatgc	gcaaactctc	ttttaagagc	ctctaactct	actagcatag	262680
tgctaatagt	agcatgctct	ttctctctaa	ttgtcttgaa	atactctctt	tctctttccc	262740
aaagtttctg	gtactataat	aaagattttg	cctcctcaac	taaaagtccg	actcctccag	262800
ctaataaaaag	aagtcccaga	acaatcccaa	gaaccccaaa	aactaatgaa	aggactccat	262860
gagaaaatac	tgtgagtatg	gcaaccccag	caagaagaaa	aagagaacct	ataataacta	262920
agctcacagc	taagatcaca	aaagtacttt	gtttaaagca	cctcttctgt	tgtatctggg	262980
cagaagtctt	atgaagcaaa	gcagattgaa	tagaagaggc	ctgtacattg	gaaatatcag	263040
gataagacat	aacacattct	caacaaaact	tatgggaaaa	gaataaaaatc	ttctttaagg	263100
cattttatatt	ttaagcaatg	ccttataaaa	agaaattgta	taactttgaa	tggcttaaaa	263160
aataaaaatat	ttatttgttt	atgcctctag	aaggatatcc	acataaaagt	gagcaatctc	263220
gagttctaaa	gtctttgtat	gtactacgca	catttgtagc	tcttcaaagg	tctcaataca	263280
atcctccaca	gccatccgag	cccttaccct	gtcaagagta	tctattgggt	tcctagatac	263340
tacctcatcg	ttgtatatcg	cccataaagc	atgtaacata	gtcacacgta	tacagtggat	263400
ttgggtattct	tccaaaacat	cctcagaatc	actcgtaaaa	agattcgttt	catttttctaa	263460
gtctgtttca	atctcagtag	aacaacacag	aagttctgaa	accgatagct	gttttgctct	263520
tttctttttc	tcattcactc	tcatactctc	cacacagact	ttacataat	tacgcaaat	263580
ttttgctgtg	cggcacatag	catatgcttc	cataagaaaa	tggggagcag	ttccttcaaa	263640
aacatcacca	atataaagat	tactcagtag	tttctttgaa	acatgaattt	ctgaatagca	263700
ccaaagggtct	tctctgtagg	atctccaaaa	agcagctttc	ctatcataga	gcttcttgaa	263760
gatctcctga	gcagattttc	ttcgaaataa	tagtgccctct	ttacactgct	ctaaaataga	263820
gttttgctct	tgggctctct	cctgaatttc	acttagattt	cgaggaacac	ctatcttttag	263880
aatctgtttt	ttctctgttt	tagaaccttc	caaaacatcg	agtcgtgcag	aaaacccacg	263940
aatcaatgta	tcctttttct	gctctaagtc	caactccctt	gctaaatcag	caatctgtatc	264000
ctgcatctgt	ataatctcac	taggaagctt	cttatcgaaac	cctccctcaa	caccaaatag	264060
ctctttaggc	tctaattccat	agcgctcctt	aaatttaaga	agcgccaatc	ctatacttat	264120
taagagcagc	cctaaaatca	tgctgctcat	ccctaaaagg	tacgtagaga	aaactcccaa	264180
gaataccatc	cccaggcata	cgaaaagagt	ccctaaaata	ataagacaaa	cgatcacgac	264240

attaagacg	tggtgaatgc	gaatactcgc	cgtttctata	ggcccaaaag	ggaaaagact	264300
gtgtttacaa	gaagtaagtt	ctgaaaaact	taatatctcc	gaataaatag	acacaaccac	264360
tccatacgac	agctctcaga	gagattttat	aaaataattd	ctcantttta	atattttttt	264420
acaaaccgtt	cttctaattc	aataattctt	gaaattcgcc	tcttgaagta	tggtgtaata	264480
ctatttgata	ttaaggatga	ttaacgtacc	ctcaactctc	gaaaacagaa	aacagaaaac	264540
agaaaggatc	gttctctttc	ttccacaaag	gaaggataag	ctctaactcg	ggaattccta	264600
tctgattggt	attagaaaaa	attaccctag	agaaaactac	caaaatctat	aaaccttgaa	264660
tgtgtagaac	tgctaagaga	ggcaactatg	gtcatcatag	tttagaaacg	ctctcttctg	264720
tgcttttagt	ggagatctgt	aaactaagtt	tcttctgtca	ctatatcttt	tatcttatgg	264780
atcagttcta	gttccaatga	cnntattacg	tcttgaagtg	atcgtaactc	tttttcaatc	264840
tctgtgagtt	tttcaaaaata	cgcagatttt	atagcacctc	tgaactggag	cttacgcacc	264900
agaagggcgt	tcaaccctag	agaagccgcc	ctcattcgat	tttcacattc	ttcaagagtt	264960
aggccagaag	ttactgttcc	agaaataagg	aactcataat	gatgcagaac	tatttcgcta	265020
tttaaataat	tcaaaattaa	aagctgttga	tacggactaa	aaagttcagg	atgggaaaga	265080
ttttcaggat	ctagcccctg	attttttaagg	gcttcttcat	tttttttcat	ttctaaagaga	265140
gactcagttc	taccctatgaa	aagacgtgcc	ggactttctt	tcttggtctt	atccataagc	265200
ttttttgttg	ccctatcgac	aatatcaaaa	gctttctcta	cttcttttaa	ttccctactc	265260
atttcattaa	tgaacttctt	acgttctctga	gctttcacat	caagcttatc	taatctagag	265320
gttaatctta	ttaacagacc	tttgatagcc	tcaatttcat	cataatctac	cttgagtata	265380
cctgggggga	gcagaaaaaa	atttaataga	acttggaggt	ctttcctaag	cctatacaat	265440
tctaaatata	atgaagactt	ttctctatgc	aaatcaaaaa	tattgctttg	gatcccttta	265500
acctgttctc	caaaagtggg	aaaatttctt	ctggtttcta	aaaatctatc	tgaacaataa	265560
agaaatttag	ctacttcgtc	ttctaagggt	agccatttct	ccatgcaatt	tgtaaattta	265620
ccctgaagct	cttggcttag	atcagagaaa	tctttcgtat	ggaactgaaa	cagattttgc	265680
aacttttcaa	atgttaccgc	caactcagag	atgtcattgg	ggatctcttt	cttatgaatc	265740
accaaagaat	ctaaatcttg	atcataataa	tctaaatctt	gacgagtctt	gtgtttgtga	265800
cataagaaaa	caataagagc	tacagccaat	aaaacaagac	ctatgcaaag	tatgggaagc	265860
gccgctccta	aaagaactcc	gcaagacgta	tgaacaagga	atgcaagaga	accagataaa	265920
aagaaaatcc	caaggataaa	taaagcgaca	accaccacag	tagaaacgtg	cgaaaaatac	265980
atccttttaga	atctacacgt	tgaggatgtg	gagcaggagg	tatgtttaca	taggtgggac	266040
gctcatagtc	ttcttttaat	ccaagaaatc	atcgtgagca	tcttcaaaac	cactatcatt	266100
acctctaat	gattcgctct	cactcaacaa	atccgtcgta	gatgcaacaa	atgccacatt	266160
tgctctgact	tgatccaatt	taactctaag	agtcttgcta	atacgtgctt	ttaaggcctc	266220
atactcctct	aagactttct	cttggtccga	agagaaagtt	tgagttaaaa	actgctcaac	266280
aatacgacat	tgaacttcat	aaaggcgcaa	taaatgatac	tgaataagag	ttggttcaca	266340
actcagatct	tctactaccg	atttcctgac	ttgaatatca	agaagttctg	cttttagcttt	266400
atctagtgt	tcttgcagct	cttcttcaga	aaagacggtt	ctgtgtaaa	atgctaattt	266460
ttcttcaaat	gcactcacia	cttcttcgaa	aaagtgaatc	tctttttcaa	cggaaagcct	266520
tggttttagg	acttctaata	gttccctcct	ataacttcgg	gaaacacctc	cagtttctct	266580
actttccttt	tgtctcgata	acattcctgt	tctatcttta	cgtcttttta	agcagattta	266640
aaacttagtca	actcacaagc	aaagcttcaat	ccagatttcc	ctactttcat	gacttctttt	266700
cgaagcttat	ctatttcaca	ttgaaggcga	tctccttttt	tccttaaaaa	ttcaagaggc	266760
ccccagatat	tctttaactc	agtaagtaac	gctacatccc	ttccgtctag	ttccttccaa	266820
atcgtctcgt	atttttcgac	ttcacgtcca	aacagaagaa	gatccccctc	aaatgtagcg	266880
aactgactct	tatgttgagc	gacaacctct	ttaaagtctt	cccactcctc	taatagaaaa	266940
ttgctccatt	cctgaacttc	attaagctct	tttctaagat	ctgcccacgg	ttgatattct	267000
aaagtaattt	tttgttctaa	tgatctcgtg	gcttctgaaa	gtttccggtg	ataagagaca	267060
aagaaaaatca	gccccaaaat	caagagtaaa	cttcctaaga	aaacacctgc	gcccccgagt	267120
cctacagtca	agacagaaaa	actaaaaata	gcattttaca	gcaagagcat	ccccacacat	267180
aacaggagaa	caccaagac	aatcaaagat	acagaaagga	tcagagactt	atatttaggt	267240
ggatgaactc	ctaaagttag	agagggttg	ggggacggag	acgggaaaca	atcacgggca	267300
atagcgctag	acataacttg	ctttttactt	gaagtttaact	acttaatttc	catacactta	267360
tatgaatgaa	gtttcttttt	gtcaacaaac	cagtaataca	aacattttta	taaaaattta	267420
taatatattgt	attaaaacca	aataaatcaa	taaacaaatag	ccccgtttat	taaacaaaaga	267480
cactatcgct	ataacgaaat	ttctccgcta	ctctcagctt	ttcttcaata	attcctagac	267540
gctcagaaat	cgcactcatg	tctctctcag	attcaagatc	ctcttttatat	aagggagttt	267600
catattgagg	aacctctttt	tcaagataga	gagaaagtac	atcaggaaca	cgtttctctt	267660
gagataagag	caaaatcagg	ctaaaagaga	aaagaaaaag	agcaaaaatc	aagcagccga	267720
gtcctagagt	aaaagcagcc	cccgcagaaa	gtccaaccag	acctatatcc	aaacaaatga	267780
cagataaaat	ggataagaca	actccaagaa	taagtaagcc	ccccgccact	atataggagt	267840
tgattctcaa	agaagtgtct	tcaggaataa	aatcaacttg	aatacgatca	aatgtcacag	267900
gattcatggt	gcgtgccttg	ttctagattt	ttcgcaccaa	agatgttatc	aattattttat	267960
tttaaatagc	atgcaaaaata	atacaatttt	gattttgatgc	tatccccctaa	gacatatcca	268020
cgaaactctt	taaccatgca	cgcacaagct	tcatatagcg	ttgtgcgatt	tacacctcga	268080

gacatctatg	actgggaagg	atttccaagc	atcatctaca	aataaaatcc	tacatatctt	268140
aaactaaaac	gaaatgtatc	tgatctatga	tttcaactaac	caaaatgctg	caaattgaaa	268200
ggatTTTTat	ctgtgaatga	attaatTTTT	ggattccaga	ctttctctgt	tgtagtTTta	268260
ggagTTTTct	ttgcctctag	aggaaaaggct	tggcttacag	gatggctatc	gctgctctca	268320
agcatcatga	atgtctttgt	tctaaaacaa	atccatctct	ggggTTTTga	agttacgtct	268380
gctgatgtct	atgtgattgg	tttgcttact	tgtctaaatt	atgcccga	gcactacgaa	268440
aaaaacgata	tcaatgatgc	tatgctatgc	tcctgggtca	tctccatagc	gtttttgggt	268500
ctcaccagc	tacacctatt	tttaatcccc	tcacctaacg	actcttctca	agagcatttc	268560
ttagctcttt	tttcttctac	tccaagaatc	gtagtagcct	ctctgggtcac	tttaattttc	268620
gttcagatcg	tggatataaa	actctttacc	ttccttcaac	gagttttttc	aaagaaatat	268680
tttgcaatgc	gctcaacaat	ttccctgctc	ttttctcaac	tcattgatac	cataatatTT	268740
tcatttttag	gattgtatgg	attgggtcagc	aatctttgtg	acgttatgat	ctttgcaatg	268800
ctagtcaaag	gcattgtaat	tacactagct	ataccgactc	taacagtaac	ttaagccgtt	268860
ttagatcgct	gttctcttta	agctaagaaa	ttaacagctt	cacctatacc	ctctaaccatc	268920
ctttcggtaa	aggagagggt	ctgcacacaa	gtaaagggtg	aattacaata	gagaagtagg	268980
cttagaatta	ttgcgacaag	gaaagcaagg	aagcacccta	taatatacaa	gacaagaatc	269040
agaaccctta	aacctaaaat	ctcaataaca	gcttgaagca	cctcgaatct	gtacttcatt	269100
ttatctctag	gatggatcgg	ccctgaatgc	gcttctatca	atcgaatgat	tccaccaatg	269160
gtagaaatga	taggaagggt	acgatatagc	ctatgggtga	ttggagtctt	cttaaagtca	269220
tgaatacga	aaggagtctc	tttaagttct	gaatcaacaa	aataccttcc	ctggaccaaa	269280
gctcttaaag	acttaggcca	ggaggaagct	acatttgcaa	aatcttcata	agattcgaaa	269340
aactcttttt	tagacaaaaa	aattaaaaaa	caaaacaaat	atacattatt	attcattaaa	269400
ataaaaagttt	taaaaagatt	aattttcttta	aaacaaaata	tccccaataa	aatattgtac	269460
ctaccagcgc	ctatccgtat	taagaccag	gaattcagaa	agctcctttg	gagtaaaaga	269520
ccctacttta	aatctaagaa	atcccaagct	agggtcagat	aaaacaaacc	ctattttactt	269580
aaaaattttg	tcattgtaaa	cttctctctc	cctaaaagac	acatccacct	tgttctttat	269640
agttaaggat	ctagtttggc	actcaaattc	catctcatcc	atcaatctaa	gaaatcccaa	269700
gctagggctg	gacaaaataga	gaccagccat	ggagtgatcg	atacaccgcg	atttgtcccc	269760
gtagcaactc	accgagcttt	aaaaggagtg	attgatcaca	cgcataattcc	ctctgtcttc	269820
tgtaataacct	accaccttct	tcttcattcca	ggcccagaag	cagtagctaa	acttggggggg	269880
ctgcaccagt	ttatgggacg	tcaagcacca	atcattacag	attccggggg	atttcaaatt	269940
tttagcctag	cctatgggtc	tgtagctgaa	gaaatcaaaa	gttgtggcaa	aaaaaaaggc	270000
atgtcctctc	tagttaaaat	tactgatgaa	ggcgcaggtg	tcaaataccta	tagagacggg	270060
agaaagctat	tcctctctcc	agaactctca	gtacaagccc	aaaaagatct	cggagctgat	270120
attattatcc	ctctagacga	gcttctcccc	ttccatacag	accaagaata	cttcttaact	270180
tcgtgttccc	gtacgtatgt	ctgggaaaaa	cgttcttttg	aatatcatcg	aaagatcctc	270240
agacaccaat	ccatgtatgg	ggtaatccac	ggaggcctcg	atccagaaca	acgtcgtatt	270300
ggcgttcgtt	ttgttgaggc	tgagccattc	gatggctctg	ctatcggagg	cagcctagga	270360
agaaaccttc	aagaaatgtc	tgaagtgggt	aaaatcacca	cttcatttct	atcaaaagaa	270420
cgtcccgtac	acctattagg	aatcggcgat	cttccctcca	tatacgctat	ggtcggcttt	270480
ggcatagact	ctttcgacag	ttcttaccgg	actaaagctg	cccgtcatgg	tcttatctta	270540
tcaaaagcag	gacccatcaa	aatcgggtcag	caaaaatata	gtcaggactc	ttccactata	270600
gacccctcgt	gctcttgttt	gacctgcttg	tcaggaatct	ctagggcata	cctgagacac	270660
ctttttaaag	taagagaacc	taacgctgct	atctgggctt	ctatacataa	tctacatcac	270720
atgcaacaag	tgatgaaaga	gattcgtgaa	gccatcttaa	aagatgaaat	ctaagtctcc	270780
tttctaaaga	ttccacatct	aaaaaactct	aattttttcca	tttatatttca	aaaaaatctg	270840
taaagatttc	tttattttaga	tcacaaaata	ctctcttatt	tataagaata	aaaaaaatta	270900
atttttatta	aaaaataatt	aattttatcgg	atttttaaacc	aactttttat	aaaattgatt	270960
ctatagtttt	ttaaaaaaaa	agggaatttt	ttatatgtcg	aaggaaagca	ttagaagtta	271020
ttctgaaatt	tctactccaa	cgccgatatt	cagagaaacg	ccctcgaaag	aaggcgtggc	271080
atataaactt	cagcttagat	caccagctaa	agactgcata	ctcaggaata	gagtatctct	271140
aaaaggagct	ctattaagat	ccattccatt	ttacggatca	tctttaggtg	ctaaaaagaat	271200
ccatagtgcc	tggtctgcaa	aagatgcccc	ctgcacaact	agagtgtatc	actacctagt	271260
cgggtgggctt	gagttatttg	gactcggggg	ttgttgttct	agcgtgtaaa	gtactcgcca	271320
ccgctctaaa	gttttttattc	tctaaagcct	cctcgaagat	aaaacaaatg	aaatggcgag	271380
agaaagcgcg	caacctagca	gccaaagata	cggtacaatc	aataaaagag	ttctgttccg	271440
ttgatcttac	atcttgcttt	acaagatggt	tcaggcttcg	aaatagagtg	gtagaggaag	271500
gtgcatctga	aaaccaaaaca	gtaagagaga	tcattgtata	atctcatagt	tttctatgta	271560
ttcttaaaca	aggatatacg	cctataaaaat	cgcaagaaaa	ctttctcata	cttcaataaa	271620
gaaacgaagt	acctatacgt	agcagctact	aagaaaaaag	gaatccccac	ttctcttagt	271680
agctgctatt	attataaaac	acgtaattta	ataacgtaga	ccgcctaacc	ccatagcatt	271740
gtcttccctc	ccacaatagc	gcacagaatc	cgaaaatttat	aaaagtctta	attatgaaga	271800
atttttaata	aatgattgaa	aaactcgtac	tatttcaaag	atcttagcat	tttataaaac	271860
aagcgtatc	ttcataatcc	gctttatata	aacatttttat	tttatctaaa	attagattag	271920



gatgcactac	gttacaagta	tgaaataggg	atccaaatgg	taaacagata	caagagctct	271980
gcagaatfff	ccgctgatca	ttactatgat	gacaacctgg	ttcggatggg	gtataaaaaga	272040
aacttaagag	gactagctcc	tgtggagaat	gaagctctgtc	tttttgagga	gaataaccta	272100
ctcgaatctg	tcattggcgtc	tataccaatt	atgggatcga	tacttggtct	aggcagactt	272160
catagtgttt	gggtctacaca	ggaccctaaa	gatagtaaaa	tctctataat	tttccatact	272220
gcacttgga	ttctagaaac	cctaggtcta	ggaatcattg	ttctccttat	taaaataacg	272280
attactattc	tccttattct	atttactcca	tgtctctctc	gttatttcat	gtattcctgc	272340
tgcttatagt	gattttcatc	ctatttagtt	aggttctaac	attctctatt	taaaaaaagc	272400
tttgaatggt	cctttgacaa	gtagacgagc	aacctaaagt	ttccttcgga	gaatcacgag	272460
ttttttcttc	aggttacatc	tcagtttttag	aggaaactaa	gacgtagaac	gtttgtgttg	272520
cgaatccatc	ttaatcatga	atgattctca	tatggcacia	gcagttctcc	aagctctcta	272580
ccagtaagaa	gttgggtata	ggagcttttg	ctaccgtagg	ctccaatctc	acacacgatc	272640
cttcggacaa	cttgtaaaac	tcggcatact	agcattaggg	tctgaaacat	cctggcatag	272700
aaagcttctc	tctcgcattg	aaacaagtcg	tttcagaatt	catgattcta	gctgttttat	272760
cgagccaatt	ctgtaagggtg	aaaagtffff	aaaaccttgg	gagaagttgc	gagaattaaa	272820
tgcttttgaa	ttaaactcaac	ctgaagagta	tcgaaaccgt	tgggttttga	tgcttgtct	272880
taagtgtcgt	ttttgtagaa	cgcaacatgc	aaaagtctgg	tcttatcgtt	gtgtccatga	272940
agcttctttg	tatgagaaaa	attgttttct	tactttgact	tatgatgata	agcatttacc	273000
tcagtatggt	tcgttggttaa	agctgcattt	acagctgttt	cttaagagat	taagaaaagt	273060
gatttctcct	cataaaattc	gttattttga	atgtgggtcg	tatggaacca	aattacaaaag	273120
acctcattat	catctacttt	tatcatgaca	taaagatttt	tttaaaaatc	ttaaaaagaa	273180
atgacctaa	gactgttaat	tatatggaat	ttttattacg	agtttcatta	aaatgtctcg	273240
ctaaaaagtt	aaagtacgat	gctaataagg	agatacagta	gtgatgacca	attcactgaa	273300
gcaacaaaaa	acaccccaac	cataattaag	ctaggttttg	ttagagataa	tctcgaggga	273360
ttaacgaacc	ctatctctga	aatcgtctcg	gaaacctcct	cttctattaa	agattccgtt	273420
cttcgctctc	ttcctatttt	agggtccatt	ttaggatgcg	cccgaactta	cagcacactc	273480
tctacaaatg	atcctcttga	cgaaactcaa	gaaaagattt	ggcacactat	atttgagacc	273540
ttagaaacct	taggcttagg	gattctcatc	ctcttattta	aaattatttt	tgttatatta	273600
cactgcatat	ttcatctagt	tattgggttc	tgcaataaac	aacaattaat	ccacgcctac	273660
ggcgtaatta	aattgtatct	ttttagaaaa	agacaagcgt	ataatataca	tttaaaaatc	273720
ctaaaaaaaa	taagaaaaatg	aagccaaata	gtattatttt	tttagaaaat	actaagcatt	273780
atccccgacat	ctttcgagaa	ggatttgttc	gtgatcgta	tggactaatg	gaagcctcgg	273840
attggttact	ttctacggaa	attacgatca	ttcgtctccat	tctgggagct	atccctattt	273900
taggaaatat	tcttgagacc	ggacgactct	atagcgtttg	gtatacaagt	gacgaagatt	273960
ggaaaaaaca	agtgggttga	cacacgatat	ttggaatcct	agaagttctt	ggccttgagg	274020
ttcttgcttt	agcattaaag	attctcctaa	ccaccattta	ttacttgcta	cgaggcctct	274080
ggaacgtttc	ctttatgctt	atagagatct	tttccgcact	ggtccctaata	tatccagtac	274140
ttgtttaaaa	ctctttcaca	ataaaaattt	tacttatgac	taaaaatgct	ataaaattcac	274200
aaacaacaac	cccacaaccc	aatttaacag	acgcagaacc	tatcgctagc	cgtgcgcaat	274260
gtaaatcaat	agcggtaatc	attagtttgt	ttgctctggg	aatgctccta	ctctgtctgg	274320
ggataatcct	tatttccata	cctattcctg	gacttgctgc	acaagttgct	ctcggcctcg	274380
gaatagtaag	tttaattctta	ggaattgctt	tagccaacat	aggtttccta	tgttttattac	274440
ttagatgcaa	gcagttcccc	aaaaacccga	tacattgccc	tctgaaagct	ctaaacagcc	274500
ttccgaggga	agcactccca	ccgcactccc	atggcaagct	ggagaatttt	tagaaaaagt	274560
acaagtatct	gcaaccccta	tactccttcc	caagaacaaa	gatgaagagt	tatcagcaaa	274620
agttatgaaa	gaaggagccg	aagcagcctt	cttcaattaa	acaagctgtt	ctagaatcta	274680
cagagaaatt	aatcgatgct	agaaaaacaag	aggagagccg	acgagaggct	aggaaaaaaa	274740
tcgtggcgga	ggaggctgaa	gcattctagaa	aacgtattca	acagcaaatg	gcagccgacc	274800
aagaagcgtt	aagaaaacga	aaagaagaag	tagctaaaag	aaagtaagct	atttttaata	274860
gaaaaagaat	gccatactat	gcaaacaccc	tggagttcat	ccagggaact	caaagtctat	274920
gtcctttaat	tcaaatatgg	gtttgtaaga	caccattata	aaggacaact	agaaatcgaa	274980
gatgcttctc	acgactggga	tttcttagaa	cccccttcta	catggaaacg	cactctcctt	275040
cctgcaattc	ctattctagg	atccgtcata	ggcttaggaa	gaccctttag	caatctgggtc	275100
gattagagaa	ccccaggact	ctcaagaata	caagctcata	ttctggcaca	ctctatgtgc	275160
tgctcctagaa	atttttaggac	tcgggattgt	agctcttatt	ctaaagatct	tagcaacctt	275220
tattatggca	atgccagggt	taaagagagt	tgcaactttc	ctattttatt	cttaagagtt	275280
acaaattctt	taggcctaga	atcgtctacc	ctatcctcta	taattttttg	taagaactaa	275340
gagacatata	atggcaccga	aagcaacaac	agacgccata	gggatcgta	cgtagctaaa	275400
aagaaagatc	tttggttgagc	aggagactct	accgcagata	tccaattgca	tccctggaat	275460
ttcttgcaag	aaaacttggt	agatagaaat	ccctaagcct	aggactgcct	gaggaaggat	275520
atacagtttg	attgaagagt	cctcgcgata	agctgaaatt	cctaaaatta	cagttagtgg	275580
gaacagacag	attctctgat	agtagcaaac	ataacaaggg	tctacgttaa	gaatagagct	275640
ataaaaaatg	ctaatacaag	tgccagcaca	agaaatagcc	caagcaaaat	ataaagcata	275700
gctacggata	aaattaatca	tcatgatctc	cttcaacagc	ttgcagctga	cgaatatggt	275760



gaatcgctct	ttctatttca	tgaaacgtag	gatcttcgat	taagtagtct	ccgactacag	275820
ccgttggtgt	tgctaactgt	cctcctaaaa	cctgagaccc	gtatagatta	ttcttcttaa	275880
tctgctcgtt	atactgtcct	gaagcgatac	actgttccaa	gccttttagga	ttaacactac	275940
gtccagaatt	tattttttaa	ccctcagcca	actttgttaag	aaacccagga	gtcaccagg	276000
ccgggagcat	tcctcttttag	gataagtcaa	aatacgaatgg	aaatattcca	tataagcgtc	276060
tatatctgcc	tgacgtggaa	tcgtgatgat	aaatacatag	caatgcttga	gctgcagggt	276120
tagaccgcg	aataaagcag	acaggaatca	aagtaaaaga	aatctctcca	gtatcaatat	276180
agtgtctctt	taacaagggg	aacacttcag	tagtgaattc	tgcaacaagca	gaacaagaag	276240
gctcctcaaa	tactgttatg	tttataggag	cataaggatt	ccctatggta	ggaaagtgtt	276300
ttgcatattgt	aggaatatga	gcttttagggg	gtagaatcgt	atgtttttta	tgtattagaa	276360
agccaaagca	aacgataaaa	aacatcgcag	tgacacagaac	taggancttt	ttattcaaag	276420
gactcgtaaa	gagaatttgt	taattgctta	atagaacaaa	aaacataaaa	ttcaaaagcg	276480
ttttcttttt	tganaattga	acagggaaaac	ttttcttcta	agtttaagaa	atccgctcta	276540
tcttttacct	ataacaccgc	aaatctcact	aaaagtactt	tcacttttat	tctactgctt	276600
ttattaagga	aaaaagatca	gggcctaaga	tttatggata	aagaaacact	agaaaaatct	276660
tatcgacatt	ttcgataaccg	tttttttaaaa	ctcaatatcc	tccttgcatt	tcttgggtctc	276720
cttcttctat	gtttctcaaa	taccctaaat	tatacacaag	tcgatgtcat	cttctctgat	276780
cgtcttttga	gttggtttact	tattttctta	gctattgctt	ccctaaccac	acgttctctt	276840
ctctgggttag	gagccccact	aggcatctgg	gttacccttt	tcgcctgcgt	tgacagcgat	276900
ctcctactat	ttttgcaaat	gatactctaa	ttggattcgc	aattcttgcc	gtagtgtgta	276960
tttcccctac	acgacccgaa	gcccttgaag	tagggcccgac	attacctgaa	ggtttttctt	277020
acaatccttc	tgacaggagga	cgcagagctg	cagactattt	cctaagctta	ctgggggtggc	277080
tagaagctcg	gtatcttact	gcttccagct	tggggaattac	atcgagtcag	tcttcgaact	277140
tcttactatt	gtactcatct	ataatgactg	tatactctct	gctcgtgggt	ctctctctag	277200
caggaagtga	gcgcgcgtgg	cacacaagac	caaaaatcgt	aatagcgaca	gcttagcttt	277260
aacaggcgctc	attatttttaa	ctcttctccc	tatcatccta	caccaactgc	gctatgattg	277320
ctggctatgc	tttgccctaac	tatagaacct	gctcttgccg	tggtctttgc	ttacgatgaa	277380
accaggggcca	ctttgcgcta	tattttctcaa	tttttaggag	ataaacgagc	tcttactaga	277440
gcctcgtttct	ttggatcaga	atactataaa	cacactctgt	cttgggaaga	aagaacagta	277500
cgtcctctac	gaaaggcata	taaacaggca	tttgagggga	tctccttccc	aatcaaccag	277560
ttattggcta	tcctagttgc	tagtttttgt	aaaagtcaat	agcagtatgg	gccttctctac	277620
ctttcctagn	natttccctca	atatatgttg	ttgggtttatt	atcgctctgt	tcactcttagc	277680
ttttgcagaa	agccttcgtc	atttgcgttg	gatgaatctg	atcttctctg	cagcgatttt	277740
attctctcca	gtactctttc	atattcccgt	agaatctccc	atgttcttgc	cgatcatcgt	277800
tacaggactc	attctaatta	ttctatctat	aggaagaga	cgaagaacta	aacgcaaact	277860
ctaaaagaga	agcttacgtg	cctaaccctt	cccataaggg	attgggtttt	gaggcgtttt	277920
ttgcttcttt	cttagcttcg	cgttcgtcac	gcttttctct	ttgggtcttg	ttcatgtaga	277980
tattctctct	agcagctctt	aaagcttttt	gtatcagctc	atcatgtttt	aaagattcag	278040
gagaatcctt	ttttgggaatg	attttaagcg	tcttacctaa	gatcatagaa	gagaatcttt	278100
tgctatactc	aggtactagc	acctgagatt	ctatgtagag	agaaagagct	ttcttattag	278160
gagttttctt	ttcttttttca	cagtgggtcat	agatttcttt	gtaattgctc	tgtgtaatcc	278220
tctcatggag	agccaacact	tgcttatggg	gggaataagc	atagatattc	aaaggcaaaa	278280
caagaagaac	aaaaacgaga	atcgagggtta	atagccaggg	aagaatcaca	tcataaagaa	278340
tagatgcacc	ttccagagga	gcacccaaaa	gtatagatcc	taaaaacaaa	ccaaaataac	278400
aaaacatgag	aagtgtgct	gctaaaatta	tagcaggagc	cccatgccaa	atatgattaa	278460
aggctttctt	gtagcaagct	actttctcct	ccccagtaag	tacaacataa	cggcttaaaag	278520
aagagggaagt	ggtgaccaga	ggctgtgaac	tcatgtatat	aagtgttttt	ttaaatcttt	278580
aatgaaacat	agccccattat	ttaaaggtct	cattgaagga	tccagaggaa	caggagttag	278640
tgttttgttc	ttaataacgt	acaagacatc	ccctaaacag	gaaacgtcat	gaaagtctgt	278700
agtgacaaga	agcaccgtct	tattttcctt	ctttgctaaa	gcaacaatat	cttggtagag	278760
ctgttcttta	agcaatacgt	ccaaagacga	aaaagggtta	tctaaaagga	gaataggctt	278820
taaagacaag	cactgagctg	caagagcgat	gcgctgcctt	tgccctccag	aaagtctgtc	278880
tggaatacga	tcaagaagct	gtccgagatc	aaaattgtgt	ataatctctt	caaggcggtc	278940
attggataag	gcgttggtgac	ttgtattgat	gccaagctcc	gttgacaacg	tcatgttttt	279000
taaagccgta	gcgaaggaa	gcagggtctt	tttttgctgc	atataggcaa	cgtctttgcg	279060
atttagaggg	ctcccatttc	atagaagttc	gccttcttgc	aaaggtagga	aacccgcaag	279120
caaacgaaac	aaagttgtct	ttccaactcc	agaacttctt	aaaataatcg	taattgtccc	279180
tggaagacgt	tggaagaag	catcctttta	aatgacttga	ttgtcacaag	aatagcatag	279240
acgatgagct	tgtaacatgg	aaaagcctct	atcttgaata	gaaacgaagg	cttgcgggtta	279300
ccaagacttg	aacttgggac	ctcgacatta	tcagtgctgc	gctctaacca	actgagctat	279360
aaccgcgatt	tggaagactag	gagattcgaa	ctcctgacct	tctgaatgca	aatcagacgc	279420
tctaccaact	aaagctaagtc	ccgggccatc	ccaataaggg	aaaagtaaaag	aatcatctta	279480
cctatcaaga	gatttaagct	caacaaagaa	agtataggaa	aatctcacct	taatgagaag	279540
aacagagttc	ttttaataca	ctcttgagca	aggatatccat	ataaatttta	cttgcctcac	279600

tttgaagatg	cttccaatcc	tcgttactcc	gtgattctaa	aggatgaggg	agaaggatat	279660
tcacacctaa	acaaggaatg	ctatatctcat	agcatacctg	agaaacagcg	ccgctgacac	279720
tatcaaaacc	atgaatctct	ggatacaatt	tttgtaagga	aagaaaatag	tttcgcgaca	279780
tcgcgaaaaga	ctcgctgtga	gcaaccaaac	cttccattaa	gggtgtgctcc	gttttggttg	279840
ttgatttcaa	atacccatga	gtcttcaaaa	gctcttcgat	ttcttggtta	tgggtagaaa	279900
taaactcttc	gcctccacga	agaattgcct	cccgatgaac	ctcactgggt	gcaaaaacac	279960
tctttttaat	gtctggaatc	tcaaatcttt	caaagaaagg	cctcacatct	gcatcataat	280020
taatgtagcc	tttagaaact	aagacgctgc	caaaacggct	atcttgagac	ctagagtaac	280080
acgagcctat	aattagaata	agatccactc	gatgtttaag	aatcatatta	caagccacaa	280140
cagctgaaga	aactttatta	ggccaaagag	cagaaactac	aaagtatttc	ccaaaggagt	280200
cgccagagta	ataaattctc	tgtccctcta	gagtcttttt	actatgagaa	aaccaaggaa	280260
tagaacaatt	accatcaaaa	gaaacggggag	taaccccgag	taaagcaaaa	ataatactta	280320
cacgacttaa	aggactctgt	ttttcttcta	gaatagtga	attatcagca	gagaatgcga	280380
ccaaaggaag	agagctaaga	ataagaaaca	aaaaacgacg	cataagaaat	ttcttctaag	280440
ttaaagatac	tgttttcgca	ttgtataaga	aaaagatctg	ttaaatagaa	ttaaaaaacg	280500
aaagtacgct	tctttttaag	ctctagatac	tcccttaaac	tcttcttaac	tctgtccttt	280560
gttctttaat	gacacatcca	tttctactac	tataaaagta	ctgacaaaag	cacagagtac	280620
gattttcaaa	tcgggagctc	caagatgaaa	gaagatccca	atctcttgaa	cgtaagacct	280680
tcgagaaatt	cttagcaaaa	agagaagaac	tttgcccaaa	aacatagtc	ttgctttttc	280740
tcaagaatta	gagctttcag	atgcctagta	tattgagaat	ataaataaaa	aaaccattgc	280800
caacccggca	atgggtctta	aaacacaaat	ccaaaatata	gaatcttaca	gactcacttt	280860
ctttttcact	gaagaaggaa	tcgttcttgg	ttctcgtatt	ttagtaattt	taaaagactg	280920
agaaaaacgc	tctattcttt	tatccaaggc	ctgaggattc	ttattcttat	aaaccataaa	280980
gacttgataa	agagtgtgat	ttacggaaat	caacatccct	ctgaaataaa	catcttcgca	281040
aacaatccaa	aattccaaag	ccttatggcc	ttgaatctgc	cttgcttgca	tgaaaagaac	281100
ctgggattca	gggagagcct	gcatcatgcc	tgaaaacccc	tcttgagat	tgagctctgg	281160
acgacttata	tctacttttt	caggatactc	ccaaacagag	actacatata	cagtgttgct	281220
tggatgagtc	tctgtttacat	aggtatcata	acgtatggta	atctctgatt	gagggacttc	281280
tacaatttgc	cccgaatgat	caggctcccc	aggaaattcc	acagaaaacc	cagaacttga	281340
tgtatagtca	tagcgtttcc	atgaaagact	gtctttaattc	ggtaaaattc	tagcctcttc	281400
ctgaatctct	ttttttgaga	accatctctt	gactttccct	aaaaaaccag	atttagcttc	281460
gactcccata	ccagggatag	gggtgaaaagc	taaaatcgat	actactatgg	ataataaggc	281520
ctttttgcaa	ctctgcaaca	taataaacta	aaaaacaaaa	caagataact	aacttaataa	281580
tatcccttcg	agatttttat	tttgtaaaat	aaaatacttt	tttttcagaa	aaataaaaaa	281640
aatattgcgt	tttataaaaat	gcatcacaat	aatcctggta	gtcttaaaaa	cataagtttt	281700
tgtttaggtat	ctccttatga	agccgggaaga	gtctgagtg	ctgtgtattg	gagttttgcc	281760
cgcacgctgg	aatagcagtc	gctatccagg	aaagcctttg	gctaaaattc	atgggaaaaag	281820
cttaatacaa	agaacttatg	agaatgcttc	ccaaagtctc	ctattagata	aaattgttgt	281880
tgctactgac	gatacagcata	ttatcgacca	cgtgactgat	tttggtgggt	atgcagtgat	281940
gactttctct	acatgttcca	atggtacaga	acgcacaggt	gaagtagcta	gaaagtactt	282000
ccctaaagct	gagattattg	taaatattca	aggtgatgag	ccttgtctaa	attctgaggt	282060
tgctgacgct	ttgggttcaga	agttgagaag	ttctcctgaa	gcagaactgg	tgactcctgt	282120
ggcactcacg	acagatcgtg	aagagatctt	aacagaaaaa	aaagtaaaat	gtgtttttga	282180
ctctgagggg	agggctctgt	atttttagtcg	cagtcctatt	ccttttattc	ttaaaaaagc	282240
aacccacagta	tatctccata	ttggagtata	tgcttttaaa	agagaggctc	ttttccgcta	282300
ccttacagca	tanctcannt	cctcgtaagc	gatgccgaag	atcttgagca	attacgtttc	282360
ctagaacatg	gaggcaagat	ccatgtgtgt	atcgtagatg	caaaaagtcc	ctctgttgat	282420
tatccagaag	acatagctaa	agtagaacia	tatatcacat	gcctttcaaa	tgcatatttt	282480
taacaggagg	agttgtctcc	tctttaggaa	aagggttaac	agcagcatcc	ctagccctaa	282540
ttttagaacg	tcaacgggctt	aacgttgcta	tgttaaaatt	ggatccatat	ctaaatgtag	282600
atccagggaac	tatgaatccc	tttgagcatg	gagaaatcta	tgttacagat	gatgggggtg	282660
agacagatct	tgatctcggt	cactatcata	gattctcttc	tgctgcactt	tctagacatt	282720
caagtgccac	ttcagggtcaa	atttatgctc	gtgtcattaa	aagagagcgt	gaggggtgatt	282780
atctaggaag	cacgggtacaa	gtcatccac	acattaccaa	tgaaatcatt	caagtcattt	282840
tagacgcagc	taaagagcac	tctccagatg	ttcttattgt	cgagattgga	gggaccatag	282900
gagatattga	atctcttccc	ttcctagaag	caattcgaca	atttcgggtat	gaccattccg	282960
aagattgtct	aaatattcat	atgacttatg	tcccctattt	acaggctgct	gacgaagtta	283020
aaagtaagcc	aacgcaacac	tccgtacaaa	ctctacgtgg	tattggcatc	attcccagcg	283080
cgattctatg	tcgttctgaa	aaacctttta	ctcaagaagt	taaatctaaa	atcagtctct	283140
tttgcaatgt	tcccaaccgg	gcagtgttta	acgttataga	tgtaaaacat	accatttatg	283200
aaatgccttt	gatgcttgct	caagagaaaa	ttgccaattt	cataggggaa	aagttaaagt	283260
tagtctacggt	tccagaaaaat	cttgatgact	ggagggtact	ggtaaatcag	ctatctcaag	283320
atcttccgaa	ggtaaaaaat	ggagtcgttg	ggaagtatgt	tcaaacaccga	gatgcctata	283380
agtccatatt	cgaagcactc	actcatgcag	ctttaagatt	aggtcatgct	gctgaaatta	283440

tccctattga	tgctgaagat	gaaaatctta	ctatggaact	ctctcaatgc	gacgcatgtt	283500
tagttcctgg	aggcttcggc	gttcgtgggt	gggaaggaaa	aatcgctgca	gctaaattct	283560
gtcgagaaca	aggcattcct	tatttttggt	tttgcctagg	aatgcaagt	cttgtttag	283620
agtatgctcg	caatgtctta	aatctggatc	aggcaaattc	cctagaaatg	gaccccaaca	283680
cccctcatcc	tattgtatat	gtcatggagg	ggcaagatcc	cttagtagct	acgggaggca	283740
ccatgcgctt	aggagcggtat	ccttgtctat	taaagccagg	gagcaaagcc	cataaagcat	283800
ataacgaatc	ttctctgatt	caggagcgcc	accgccatcg	ctatgaagta	aatccggatt	283860
acatacagag	tttagaagac	cacggccttac	ggatcggttg	gacttgtcct	ccacaagggc	283920
tttgtgaaat	tattgaagtt	tcggatcatc	cttggatgat	tggtgtgcaa	ttccatccag	283980
aatttgtatc	taaactcatc	tctcccatc	ctctatttat	cgcatttata	gaagcagctc	284040
tagtctattc	taaggatgca	agccatgtct	aagccatcta	gttgcaaagc	ataccttggc	284100
atagactacg	ggaaaaaacg	gatcggcctt	gcctatgcag	ccgaaccctt	cctattgaca	284160
ctaccgattg	gaaatataga	agcaggtaaa	aatcttaagt	tgtagcagca	agctcttcat	284220
aagattattt	taagtagaaa	tataacttgt	gtagttctag	ggaatccctt	tcctatgcaa	284280
aaaggtcttt	actcatctct	gcaagaggaa	gtttccttac	ttgctgagga	gcttaagaag	284340
ctttctacgg	tagaaatcat	cctatgggat	gaacggcttt	cttcagtaca	agcggaaacgt	284400
atgttaaagc	aagattgtgg	actaagcaga	aaagatcgga	aaggaaaaac	agattccctg	284460
gctgcaacat	taatcttaac	aagttttcta	gatagcttac	ctaaaaaact	aaccttgtaa	284520
tcatcaaaaa	ctacgggatt	ttaatttttag	aaacttttta	ctttttgtta	ttttcgcaag	284580
tgcggggaca	aaaaaggaga	taaaaatgac	gaatgttggt	caggaaacta	taggtggatt	284640
gaattcccca	cgaacgtgcc	ctccttgtat	tttagttatc	tttgagcgca	ctggagatct	284700
gacggcaagg	aaacttttac	ccgctctata	tcacctact	aaagaaggac	gcctttcaga	284760
ccagtttgtt	tgcgtaggat	ttgcacgtcg	agagaaatcg	aatgaactgt	tcgcgcaaga	284820
gatgaaacaa	cgtgtcatat	aattttctcc	ttccgaatta	gatattaagg	tatgggaaga	284880
tttccaacag	cgctcttttt	atcatcgctc	agaattcgat	aacaatatgg	gatatacatc	284940
tctcaaggac	tccttagaag	atttagataa	aacgtacgga	acacgtggaa	atcgtctttt	285000
ttatctttct	actccccccc	aatatttttc	tagaatcatt	gaaaatttaa	ataaacataa	285060
gcttttctat	aaaaatcaag	accaagggaa	accctgggtc	cgtgtcatta	tagaaaaacc	285120
ttttggaaga	gacttagata	gtgctaagca	acttcagcaa	tgtatcaatg	agaacttaa	285180
tgaaaattcg	gtctatcata	tagatcacta	tttagggaa	gaaacgggtc	aaaacattct	285240
aacaacacgt	ttcgccaata	cgattttcga	atcgtgttg	aattcacaat	atatcgatca	285300
tgtccaaatc	agtttgagt	aaacgattgg	cataggatct	cgcggcaatt	tctttgagaa	285360
atctgggatg	cttcggggata	tggtacagaa	ccatatgatg	cagctactct	gtttactcac	285420
tatggagcct	cctacaactt	ttgatgctga	tgaaatcaga	aaaganaaaa	tcaaaattct	285480
tcaacgtatc	tcaccatttt	cagaagggtc	ttcgattgtc	cgaggacaat	atggtccagg	285540
aacggttcaa	ggagtctcgg	tccttgggta	tcgtgaagaa	gagaatgttg	acaaagattc	285600
ccgagtagag	acctacgtag	ctttaaaaca	gtcattaata	atccccgttg	gcttggagtt	285660
cctttctatt	tacgtgcagg	aaaacgactc	gccaaaaaat	ctacagacat	ttctattatt	285720
tttaaaaaat	caccctacaa	tttatttgca	gccgaagaat	gttcacgttg	tccgatagaa	285780
aatgatttgc	taatcatcag	aattcaaccg	gacgaagggt	tcgctttgaa	attcaactgt	285840
aaggttccag	gaactaataa	tattgtccgt	cctgttaaga	tggacttccg	ttacgacagc	285900
tattttccaaa	ctacaactcc	agaagcatat	gagcgtttat	tatgtgattg	cattataggg	285960
gatcgtacgt	ttatttacgg	gggggggatag	aagttatggc	ttcttggaa	ctttttactc	286020
ctgtattaga	ggagtgggac	caagattcct	cacctcgtt	tccaaactat	cctgcaggat	286080
cttcagggtc	taaagaagct	gatgctctca	ttgaaagaga	cggaagaagc	tggagacctt	286140
ctatagacaat	cttatacagc	atctagaaat	cgataaacat	gacaaaacata	gggattgaga	286200
tatggcaac	actgataaat	ttcaatgata	cgaacaaact	tttgcttaca	aagcaacctt	286260
ctctatttat	agatctagct	agtaaagatt	ggatagcttc	tgcaaccag	gcaattaagc	286320
aacggggagc	attttatgta	gcattatctg	gaggcaaaac	tccttttagaa	atctataaag	286380
atatcgttat	caataaagac	aaacttatag	atcctagtaa	gatttttcta	ttttggggag	286440
atgaaagact	agctccgata	acatcgtcag	aaagtaatta	cggccaggct	atgagcattc	286500
tccgtgattt	gaatatccct	gatgagcaga	tctttcgaat	ggaaacagaa	aatcccgatg	286560
gagcgaaaaa	ataccaagaa	cttatagaaa	ataaaattcc	tgtatgtagc	tttgatagta	286620
ttatgttagg	actaggagaa	gatgggtcac	ccctttctct	tttttccaat	acctcggtt	286680
tggaggaga	aaatgacctt	gtgggtctta	attctgttcc	acatctagaa	acagaaagaa	286740
tgaccttaac	ctttccttgc	gtacataaag	gcaagcatgt	tgttgtttat	gttcaggggg	286800
aaaataaaaa	gcctatcctt	aaaagtgtct	tcttttctga	aggtagagaa	gaaaaactct	286860
atcctataga	gcgtgtaggt	agggaccgct	cacctctatt	ttggattatt	tctccagaat	286920
cttatgatat	agcagacttc	gataatatct	cttcgatata	taaaatggac	atcctctaaa	286980
aaagataggg	gttgcgattt	agccgtagat	agtatcgtaa	gccggcggtg	gaaaaggagg	287040
aggagcacta	ggcatggtag	gagccgtagg	gtatcctgct	ccaaaatggg	atcctgcaaa	287100
gccccctccc	ccaccaaaagt	gacttctctc	aaaattaccg	tttctctctc	ttctattctg	287160
ataatcagag	gagcctccat	aatgctgaga	tggtcgagaa	cctccaccag	gagctcctcc	287220
ttgaactaac	tgagcaactt	cttcgttaga	gaagaggtgt	ccataatgag	acagacagtc	287280

tgtgagaaat	aggctctcttg	ccaatgcatt	tgtttgga	tgagagggat	catgtagcag	287340
agcctcacta	acggcagtat	gcaaaaacaac	attcgttagg	tgaccacgc	atgcctcttg	287400
gtgctttgcc	ttacgaacta	tagcaatcca	tagtcctagc	agagaaatta	acagagcgcc	287460
tccacctgca	gcgcagaccc	catcattgcc	gcagtaatta	cgggagcagc	tccaggagct	287520
acaaaaata	atactaagac	aatgccagct	gttaaggcta	ttaaagctaa	agaagctatt	287580
aagctaacga	ctaaggaccc	tatcatagca	ctcttataca	acttacacgc	ttttacagcc	287640
tcttctgatg	accttatggt	tgcaacacct	gcagctcgat	ggaagacatt	ttgagcagga	287700
tgacgtaata	cttttgccct	cgcccttattc	agagagtaaa	tcatcttccc	aagcgtataa	287760
actttataag	cacaataaac	cagggcacct	aatgtcggtc	ctaggataag	agcaattacg	287820
aagaaaagta	gtgtagctcc	taaaacgatc	gctgatgtct	cttttctcgg	agtttgacag	287880
ctcttacatt	gcgaaaagca	cataatcaat	attccgaagc	tattgaacaa	attcccccac	287940
ttctgcgcac	tttaaaccct	gtcatcatca	tgctggttgg	tctatcaaat	agagattcaa	288000
tatcaggaac	tcgtcccttc	atgatctcac	taaacattac	ttctgtactc	tcggaaggag	288060
atacaaattt	gttttctaga	aaataacaga	agttactcgc	caccactgaa	ttagctttaa	288120
caacagattt	tgaggaagg	gaaaacacca	taaaataaac	caattactaa	caatacatta	288180
cttactaacg	ataagtattt	agctaagggc	tctcagcctt	aagtaagttc	tttgtttatt	288240
aacagaagta	ttttatctta	atgatttaaa	aacttcaact	ctcgagactg	attttagaat	288300
cgtattttaa	ataatttaag	aatttttaata	accgattggt	tgaacgaaaa	acttaaaaaac	288360
ttaaaaattt	aaattttataa	tttagataaa	aattaaaaaac	tacagcttgc	ctatttgctaa	288420
aataaataat	tcataaacac	aatgcgaaac	ttcgtttataa	aaagcacatg	caatctagtc	288480
ttaaaacggg	gattataaaa	attagcgata	ataaggagga	ggagaagaag	aggggaaaagg	288540
agaattcgag	gagctatcgc	tagaataggc	cgggtggagat	tctctaggaa	tcacgttgct	288600
gctaccatcg	ctcccctcct	catgaaacag	agctctcgtaa	cttggagggtg	gcgctcgtctg	288660
acggttcaag	gggacttcgc	tctcgatatac	tctatactcg	tcatcactga	agaactgttg	288720
gtatcttcgt	atagactgag	taagcacttt	tttagttcct	ggagtgatag	gaaggtaggg	288780
catctgaata	attgtgttac	tcactataca	acgcaatagt	gcggtatgca	tatgatgaac	288840
accttcttgg	cttttctgca	cgctatacac	agaagcaagt	aaaaagccta	ttacagagag	288900
gaggattcct	gttcctcctg	cagcacagca	tcctatcatt	gctgcgggtca	ttacagcagg	288960
agctccagga	tctaaaaaaa	atagagcaaa	aacaaggcct	acaattaaag	ctgctaaaga	289020
tatcgttaata	attaagccaa	gcacaaagaa	aattaatgtg	gattgtctaa	atactttaca	289080
agccttgatt	gtagattgtg	aggcggcagc	ggcggtctga	gccccgaac	gatgtataaa	289140
aggatctgat	ttctgtacgg	aatttatgac	ctcagtgtgg	gttcttgata	aagaggatat	289200
tttcttggta	agttgataaa	ttttatatgc	agagtagcac	aaaatgccta	gtgtaggccc	289260
gaacacaata	gctaagactg	taaagaggac	agctgcgaaa	ataccgggta	tgagtgtctc	289320
acagggatca	gtgtgatgag	aatctgtcac	taacaacagg	ggacaacacc	ctattccaaa	289380
tatttttttca	aaaaatctct	gataaatcat	tttcaagctg	atattagaat	acacttgaaa	289440
gtgatgttcg	ccttctgtct	ctactacatc	tttcaaatca	tctataatag	cagttgacga	289500
aagtgttctc	cgggctagga	atactttaat	cgggaagaatc	tctgtgttat	gttcaacaaa	289560
ttcgtccata	gctaaagata	ctaggacgtc	gcggacctgt	gtattagaag	caatgcttgc	289620
ctcatgtgaa	gaagaaagag	aaatcatggc	agacataaat	tttaccagaa	aaatttatca	289680
cgccctcttg	tttaaaaaata	gtcatttttt	atttaatgca	aggaagaaga	gtttccttgg	289740
tctattttaa	aagacttctc	tttctaacga	agcgagctca	tttccttaag	gtttgattaa	289800
tccagacatt	cctgccaat	gaagaatcgg	ggcttgcata	aagactattg	cggatgagag	289860
tctagecgtc	tcactagtc	tatgtgaaat	tataaatccg	tgaattgcgg	ttcctatgac	289920
tgggacgatt	aacaagcacg	caagtagata	aggaaggcca	ccaccataga	ggcattttaa	289980
atgtgatccc	agacttactc	tttccccagg	taaagcactc	gatgcactac	ataacttaaa	290040
cggaaatgag	agaagtagaa	atagaacctt	taaaatcaac	aaaactacac	ttacaactgc	290100
acaaactaca	gcaattacag	gataacaacat	agtatctaca	actaaacaag	ccgtttttct	290160
tactcaaggg	ttcatcatca	taatctcctt	gagacattct	aaaaaaaata	gaacaagcca	290220
taagaataac	cgttgggttc	tgagaaaatt	gatataaaga	acaatatatt	aaagattttt	290280
agtttttaatt	ggaataaaaa	ttctaaccct	tccccctcta	attacgatgt	agttgtttta	290340
aatatttttta	attattagaa	actacttggt	attgggtccat	gaatataaaa	atagaggtct	290400
ttctagctta	gaaaaacccc	tatctatagt	tattaccaat	ttataatagc	agttgatccc	290460
acttgataag	caggagatat	aataaagtat	cttaaacgat	tagtatccga	ttgtactgta	290520
ataatcgtgc	cataaattag	ggtccctatg	atcggaataa	gtactaggca	tcctaaccac	290580
tctgatggac	ctgggtttatc	ctttgggtcca	aacaagcatt	gaaaattctc	tttacacgag	290640
ggcagaggcc	ttgatttaca	agctgcaata	caggtattaa	caagggaattt	tatagctaaa	290700
aacagtagtt	ttactaccat	caagacggca	aaaacaactg	cacaaatgac	cgccataaaa	290760
gggtagagaa	gaatatctgc	aactagagct	actttcgacg	caacgaatct	gtcgggctcg	290820
tttgacattac	acacatgata	accaatagaa	caagccatta	ttatcctccc	tttaacaaat	290880
tttaataaaa	aaactaaata	attatagttt	attttattaa	aaaaataaag	ttatattctt	290940
tactattttcc	ccgttcaagc	caaagagacc	tctttttctt	ttaattttctt	gtttttctat	291000
atttacagta	ttttgaaaag	atatatagta	gtcctaggga	aaatcttggg	actcataacg	291060
atccaattct	atcagaatct	aggtggaatg	tcttcggagc	gctatagtgc	tttgacattct	291120

aggaaaagtc	tctctgtttt	accccatgtc	gtacgaaaag	tattgttaag	tttccctgat	291180
tttaggggta	atgggtgacgt	caattttaagg	aacatttcgaa	gtgactaagg	gctctgtttt	291240
tattattatg	gggcctccag	gctcaggcaa	aggaacccaa	tctcaatata	ttgccaatag	291300
aataggctta	ccccacatca	gtactgggga	tttattaaga	gcgattattc	cgagaaggaa	291360
ctcctaattg	attgaaggct	aaagcctacc	tagataaggg	tgcttttgtt	cctagtgtat	291420
ttgtatggga	aatactgaaa	gaaaaactgc	aaagccaagc	ctgctctaaa	ggatgcatta	291480
tcgatggggt	cccagaaacc	ttagatcagg	cgcattctct	ggatagtttt	cttatggacg	291540
tccattctaa	ctacacggtg	attttcttag	agattttctga	agacgagatc	ttaaaaagag	291600
tgtgttcaag	atttctttgc	ccctcctgtt	cgcgtatcta	caacacaagt	cagggcacata	291660
ccgaatgtcc	agactgtcat	gtgcctttga	tacggcggtc	tgacgatacc	ccggaaatca	291720
ttaaagaaag	attaacaaaa	tatcaagaac	gcacagctcc	tgttattgcc	tattatgaca	291780
gcttagggaa	gctatgtagg	gtttcttctg	aaaacaaaga	ggatcttgtt	tttgaagaca	291840
ttttgaaatg	catttataaa	tagtttttct	tccttccaaa	gaaaagtacc	gaattcacc	291900
gaaaaaaatt	cactcagaac	cttgtcttaa	acttgtcaga	aggaaattat	gaaacactac	291960
ctatcatttt	ctccttctgc	tgattttttc	tctaaacaag	gtgctattga	aactcaagtc	292020
ctttttggag	agcgcgtctt	agtcaaagg	agcacctgct	atgcatattc	ccaattattc	292080
cacaatgagc	tgttatggaa	gccctatcca	ggtcatagct	ttcgttctac	cctagtcccc	292140
tgactctctg	aatttcatat	ccatccaaat	gtttctgtgg	tttctgtgga	tgcattttta	292200
gatccttggg	ggatccctct	tccttttgga	actttactcc	atgtgaattc	tcaaaaatacc	292260
gttattttcc	ctaaggatat	tctcaatcat	atgaacacca	tctggggctc	cggcacacct	292320
caatgcgac	ctagacatct	acgtcgtcta	aattataact	acttttctga	acttttaatt	292380
aaagacgcag	accttttact	gaactttccc	tatgtatggg	gaggacgggc	tgtacacgaa	292440
agtcctgaaa	agccgggtgt	tgattgttcg	ggatttatca	atatccttta	ccaggcacag	292500
ggatacaacg	tccctagaaa	cgctgcagat	caatatgcgg	attgtcattg	gatctctagc	292560
tttgagaacc	ttccttctgg	tggtttaata	tttctttacc	ctaaagaaga	aaagcgtatt	292620
tctcatgtta	tggtgaaaca	ggatagttcc	accctcattc	atgcttctgg	tgaggggaaa	292680
aaagtggagt	atttcatttt	agaacaagat	gggaagtttt	tagattcgac	ttatctattt	292740
tttagaaata	atcagagggg	acgggcattt	tttgggatcc	ctagaaaaag	aaaagccttt	292800
ctgtaataag	aaaggctttt	tccaaaaacg	attcgaaaaa	cggtaaataat	cttaacgctt	292860
agagaattgg	aaagcttttt	gagctttttt	atgtccgtat	tttttacgtt	ctttccttct	292920
aggatctcta	gtaagaaccc	gcaactcttt	aggtcttgtc	tattctcttc	attttctttt	292980
aagagagctc	gtgcaaggcc	taatcttgta	gcaattacct	gcccttgaat	ccctccaccg	293040
ctcacacgaa	taattaaatc	gtattgactt	tggtcttctg	taattttttt	caaaggagaa	293100
agaattgtag	ttctttgaat	ttccaaagga	aaataatctt	caaaagactt	accgtttaca	293160
tcaattttac	cacttccagg	tcgtaaaccg	acgctagaga	cagcctgttt	tcttctacct	293220
gtagctacag	attcttgtat	tgtaactttt	gccacaactc	atcctaaatt	aaatatctaa	293280
taaaattggc	ttttgagatt	caaaagtttc	gtatgaatcc	ccttttacia	tccttaagga	293340
cttcaattgt	ttctttccta	agcgagttct	gggcatcatt	cccttgatcg	catgctcaat	293400
aatgtaatta	ggttttctcg	ccatcatatt	ttcaaaagga	atttctcgca	ttccagagat	293460
atatectgtg	tagtagcgat	agattttttg	gcctttctta	gtccagttta	ggcgaacctt	293520
ctctgcatta	ataacaataa	caccgtctcc	catagccaca	tgaggagtat	aggtgacttt	293580
atgcttgcc	cttaaaattt	ttgccacttc	tgaagaaagc	cttcctaagg	ttttcccagc	293640
agcatcaaca	acataccatg	acttcgtagt	ttcactggac	tttactatag	ttgtttttgt	293700
gtcttttctt	ttttccataa	taatgtaact	gtcttactag	agagggcgat	tataagctg	293760
ttcaaatatt	tttccaaaca	aaaacagccg	aaaaatacaa	gtctcttagt	ttaaaaatat	293820
ttccataaat	ttcttttctg	acaattagca	gttttttctt	aacggctgct	gatataaaag	293880
cattcagaca	ccgtctaaag	ctagatctca	aaaatatgga	tttatcttga	aatcagaggg	293940
agtgttttct	taagagttat	gaaaaaatag	cttgccattg	gataagactc	cttccctaga	294000
acacctagag	gcgagggtgt	tattatgtgt	cacaataaga	attccacata	atgcggatgc	294060
ttgttctaac	agaaggttat	gaatctgttc	tgaagtctct	tcacgcagat	ttcccgaagg	294120
ctcgtctgcc	aaaaggatgg	ccggttcggt	gattaacgct	ctagcaatag	cgactcgctg	294180
tttttccctt	cctgataatt	tagagcagcg	agtcctgact	ttgtcttcaa	gattcactaa	294240
atccaagagc	tctagagccc	tggtatatac	aggagatcct	ttagatatgt	tttttcgagc	294300
aattagagct	ggcattaaga	cattttttta	tactgtgtcg	tcttctagca	aataaaaaatt	294360
ttggaagaca	aagccgatat	gctggtttct	aaaattcgca	agatcctggg	tttttagatc	294420
cttatcaaaa	aagcgtgaagc	ttccagaaga	aggaacatcc	aaagtctcta	agagatgcaa	294480
tagcgtgggt	ttaccattac	ctgaggctcc	tgtaatcgat	atagtttctc	ctgcatgcag	294540
tgataacgat	acatcggtca	aaatagaaat	attttgggtc	tggttgctgga	tagtttttaga	294600
aagggttttta	gcttctataa	gtaaggacat	agctaactctg	cttttataat	ttctgagaca	294660
tgcatttttg	cgacttttct	tgagggcagg	gctcctgaaa	ctgaggctaa	aagtagcgta	294720
cctaacccta	gaaataaaat	agcctggggg	tgaacgctat	tggaagattt	tgggccaaag	294780
aaagcagtat	taaatgtttc	tcttccctgt	aaatagttca	gtgctttttac	aatgaattgt	294840
aaatttttta	atgtaattat	agcgaatatc	gttctctata	ccactccaca	agctcctgaa	294900
aatgctccac	aacaagcaaa	gatgatcttt	aaacttcgtg	atgatgtccc	catagcttta	294960

agaatgccta	tttccttttt	cttattattt	acaaggagca	tcgacatagt	cacgatgttg	295020
gagcaagcaa	caataagaat	aagtatgcac	acaaaaagaa	agagaacttg	atcactttga	295080
agttgatcta	ggataggctg	gaaataatcg	taatcgtgta	gggaagaaat	ctcccaatag	295140
tcatcgacac	ctaaggaagt	tagaatattt	tctatttgtt	tttttacaaa	gacaatgcgt	295200
ttggtattgg	ggaaaaatag	atggaagccg	ttactcatcc	ccaagccctc	ggattgagaa	295260
cgaatggatc	tagcaagatc	tgggtctata	aatacagttc	ttccccctaa	cggagagagc	295320
ccgggattat	aaaatccgat	gacatgaact	gtatattgag	tttctttttc	attctctatg	295380
gagtaggtac	taaaaactcc	tgtatcccct	actttataac	cagagtcttt	ataagtacta	295440
gggagtatga	tcgaagctcc	tcggtagagt	tcttctaaat	gatggaaatc	ttgttgccat	295500
cccagggggc	ttctattaaa	tggattcaat	tccgcagagg	tatagtctgt	ttcatcgtag	295560
ggtaaaacct	tatcttcata	ggaaagctta	gagggatagc	ttaaaaaatg	cgtgagattt	295620
ctaggctgag	gtttttgtaa	ttttagagag	gttttgatat	cgaggtaacc	cactccctgc	295680
tcaaattcga	tcactttccc	gtgttgggat	tgaaggtagg	gtcctaaaga	ttctagagtc	295740
atctttacag	gatctttttg	ctgccctcct	agatcacagt	cttttaatgg	aaatgtttcc	295800
ggaagaaggt	agtctgattc	aggatcataa	gggtcgaact	ctggagaagc	tattttttct	295860
cctaaagtgt	tcgtagtgtg	gttagaaaaga	ctggagtgtt	tgtctatttg	atagtagtac	295920
gaagaataat	atgtgtcggg	gggaagaata	gtaattggag	aatggagtgt	ggaaagatcc	295980
tctatccatc	tttgttctaa	accgtgaatg	actgaaataa	aaactataga	aagccagaca	296040
acaagagaaa	tgatacccac	agaaaatagg	gagactatag	ctgaatatag	ccttccccct	296100
cctggaatca	aatactttta	agctactgaa	aattcgaact	tcatgacttc	taactaagaa	296160
tacgatttta	gaagcagagta	gttaagtacg	atgaaatcct	tttacctagc	ttctttgaaa	296220
attacgtgcc	tacgcagttt	tctatcatat	tttttgagtt	ctagtcgacc	tgttgatttt	296280
cttttgtttt	ttacagtcca	gtacatatca	gaactttccg	agctttttta	tttaataatc	296340
tcccgaattct	tgcttgccat	ggatgagtc	ttttaagaaa	atagtaaate	gcttactatg	296400
ctatatttct	tttcaaaaag	aatcaagaac	tctcccaatc	attattagag	aacctaggat	296460
gacaacaaaa	agttaggat	ctttcaattc	agttatttcc	aaaaataaaa	ttcattttat	296520
tagtttgagg	tgctctcgga	accttgtaga	tagcgaagtc	atgctaggca	ttcttcttaa	296580
ggcagggtac	gagtcacta	atgaaattga	agatgctgac	tatttaattt	taaataacctg	296640
tgcggtttta	aaaagtgtca	gagatgaagc	taaagattat	ctagaccatc	taattgatgt	296700
aaaaaaaagag	aacgctaaaa	ttattgtaac	tggatgcagt	acttccaacc	acaaagatga	296760
gcttaaacc	tggatgtcac	acatccatta	cctactaggt	tctggggatg	ttgagaatat	296820
tctttctgct	attgagtctc	gtgaatctgg	agaaaaaatc	tctgcaaaga	gttacattga	296880
gatgggagaa	gttccaagac	agctttccac	acaaaaacac	tatgcctatt	taaaagttgc	296940
tgagggctgt	agaaaacggt	gtgctttttg	tattattcct	tccattaaag	gaaagctccg	297000
cagcaaacct	ctggatcaaa	ttcttaaaga	attccgcata	cttgtaaaca	agagtgtgaa	297060
agagattata	ttgatagctc	aagacctagg	agattatgga	aaggatctct	ctacagaccg	297120
cagtctcgag	ctagaatcac	tattacatga	gttactgaaa	gagcctgggtg	attattggct	297180
gcggatgttg	tatttatatc	ctgatgaagt	gagtgatggc	attatagatc	ttatgcaatc	297240
taatcccaaa	attgttcctc	atgtagatat	tcccttacag	cacattaacg	accgtatttt	297300
aaagcaaatg	cgaagaacga	cttctaggga	gcaaactcta	ggattcctag	aaaaattacg	297360
tgccaagggt	cctcagggtc	atatccgttc	ttctgttatt	gtgggtttcc	ctgggtgaaac	297420
tcaggaagaa	ttccaggagt	tagctgattt	tattggtgag	ggttggtattg	ataatctcgg	297480
aattttcttg	tactctcaag	aagcgaatac	cccggcagca	gaactccctg	accagatacc	297540
agaaaaagtt	aaagaatcga	ggttgaaaaa	tctatctcaa	attcagaaac	gcaatgtgga	297600
taaacataat	cagaagctca	ttggggaaaa	aatagaagca	gttattgata	actatcatcc	297660
tgaaacgaat	cttttactca	ctgcaagggt	ctatggacaa	gctccctgaag	tggacccttg	297720
tattattgta	aatgaggcga	agcttggttc	tcattttgga	gaaagatgct	ttatagaaat	297780
cacagggact	gctgggttacg	accttgtagg	gcgtgttgta	aaaaaatctc	agaaccaagc	297840
tttgctaaaa	actagcaaa	cttaggggtcc	tgtgggttagt	taacaaaagg	caaagtcgct	297900
atattccaag	aaaaactttg	cactctaaag	ctataacttc	gattttccaa	aacaaagtat	297960
ccagggtctca	cagcataata	tgttgagcaa	agccactgca	ttggctcgtgc	acggtaataa	298020
cttggtccag	aacacgtcga	catagctaat	tcaattctta	tgtcaggaaa	taacgggttt	298080
tgatttgctt	catatgctac	caaaaagaagc	tcccctcctg	taccattatc	aatccaactc	298140
ccatgcttgg	tcataaaaa	tgaaatacga	aagagcctag	gaatagaagc	acttgcttga	298200
aatcgcatca	tccaagtctg	acttgagtcg	atataaatag	cgggaattgat	cactgtactt	298260
tgtgttgacg	tttgattgaa	cttattccaa	ggtacattga	ctccccccaa	ccaatatctc	298320
ccgaacctac	atgccctcct	gaaagagcag	ctcgtgcat	catcatgact	ctggtaagtt	298380
tgtagtatcc	ataaggcaca	tactgttgag	gttgctcagt	attaatattt	gcatagtctt	298440
gacgcttatt	ccccaggag	tcttgataag	aaaaaggaga	attcgataga	ttcaccgcgac	298500
cggtgaaaa	catagtattg	aagggtttgtg	gagtgatatt	gatatttcc	ccaacggaaa	298560
gacggttctg	gcatatcagt	cctccatctg	catcaacaaa	atttccctaaa	acttgagtat	298620
tctctgtagc	aatattctga	ccaatatgtg	gtgctgtttt	cttttgctca	tcagtaaggt	298680
tgattgattc	gatgttaaat	cgaacaaaag	taggaatcga	tattgttatt	ttttgtgttg	298740
tgggtatcga	actcgacatt	aatctacctc	cacaaaatta	gatggaaatg	gaaaccaaat	298800

gaccacatgt	ggatagagac	ataaggttca	tccatategt	gctctctaag	ttaatccaag	298860
gatagtcata	aggaggacta	gaaaccagct	ctgttacact	gaagattgca	gttacagcga	298920
cactcgtacg	gtcactcgaa	taacctcctc	tagtatctga	agtacaaagc	aacgttttat	298980
tatttccaga	gacaaaatta	agaattagag	tggcagaatt	atctccgtca	tgttgctccg	299040
tccaccgtgt	gagctgcata	gtgacttgat	agatcccgcg	ttgtttgagt	ttaaccacag	299100
gctcaatatc	tgcataatct	ctgaagtcag	gggtcgcgtt	acgactcaca	cttttagagg	299160
tgatagctgc	aacatgagtt	tcaattgtag	tgttaggggc	aacgtaataa	ccattcccag	299220
gataatcagc	atagagattc	gcagcctgac	atccagtttt	tctataataa	ctaaatgtaa	299280
gcgcactctg	agcagactga	ggatcactaa	tattattgca	tactggagtt	tgcgatacgt	299340
ctgtcttaga	atagatatta	aaaccgtcag	agagtgtagt	agcattaagt	tgagaacctt	299400
ccgcagacac	attacccttc	acaataaatt	cacatggaga	agtcgtggta	tctaagactt	299460
tgagatcccc	agtcctctaa	ttatttttcta	ttcttacatt	cctttcgaca	ctgagagtgt	299520
cttgatctat	aaataaattc	tgatctttga	ccccagagt	tttcattggg	attttatagg	299580
ggagtcgtcg	gtccaaatat	gtttccctgt	tgttttatnt	tttccataac	tacctctat	299640
cgtccggata	atagagaaga	gaaaaggagt	aattccctat	acctgcacta	gaaccaccgt	299700
tactgagata	gaaaataccc	gctctatagc	gatccgaagc	attcggatca	ttaggattag	299760
gagctacatc	tacagaggct	ctatatattg	aggtccccag	tgtacctatt	gttgcatacc	299820
ctccaccact	ataaatcgtg	ctttcacatt	ggacttgtcc	taaaccatta	ttgatataaa	299880
tggctcctcc	ccaaccatta	ttccatcccc	accgtttacc	aacagtaaat	gaaacgatat	299940
aggttcctgc	tgcaagaaat	tgtatcgcag	tatttccccc	tacagttaat	tctcgtgtac	300000
tttgcttcca	tcctataaaa	cgaaatatac	tattttacatt	acgtgactga	tatagagtat	300060
attccgaacc	agtcagaggg	aaataagatt	ccccagagt	aaaatcaaaa	tctccgatca	300120
gaggcttggg	acagaaaaaa	tattcgggag	aacgaacata	attcgcgtgg	accggatcgc	300180
agtcttcttt	tggcaatgca	caattactca	gacgattatt	tttaaaatct	atagagattt	300240
gggaggaagt	aaagttttgt	gcattttaaat	tataagtagt	tcctgaagtt	aatccagttg	300300
ctgaaacttg	atcttttaaat	gttgcatctc	cctgaacaga	aaatgtttca	gtcgatgaga	300360
ttccttgggc	ctgtgtatca	aaggtcttga	gattggctgc	taacaaatca	ccatctacag	300420
ttgagtctaa	tttaaaatag	cactcattat	tattaatatt	gtttttcatg	ataactttta	300480
ataaagttta	atztatcaac	tcaaaatcaa	attaataata	ttaagtcaaa	ttattaaatt	300540
taaaaataga	aaaagataag	aatcagaaaa	tattcaaact	taagaaaagg	gattcaataa	300600
aaatgagtgt	gaataaccgt	aagaaataga	agccaagtga	tataaggaaa	tcgaactcca	300660
agcatcgtta	gttttctaaca	atacttggag	ttcgatgatt	attcaacgta	aggcaaggca	300720
actatgttcc	aagaaaagaa	agagactctt	aacctccac	cagctctatt	ctggaaaagta	300780
aagtaaccat	tattttgagc	atagtatgta	acgcaaacta	cctgtaaagg	acgtgtttca	300840
taataactgg	accctctaga	ggtcgtcatt	gcaagatctg	tgacatttat	cctccctccg	300900
ccttgctcat	attcattcgc	cgctaagaga	atatctgctc	ctggtccgtt	atccaaccaa	300960
gaaccatggt	tagccataat	aacactaata	cgaaaaagtt	ttggcacctt	attattttact	301020
tcgaaaacca	atttagtga	gtcatttggg	tcaatataaa	tctctgttcc	tgatgttttt	301080
tgagttgacg	tttgatcgaa	cttattccaa	gggacataac	ttccagatgg	aacacttcca	301140
ccacctacat	accctgatga	atgagcagct	cgctgtgcca	tcataatttg	cgtacgttta	301200
taatacccga	aaggaacata	ttcttgaggt	ttccctgagc	tcattttttc	atagtcggta	301260
atgtcttgtc	cttgagaatt	tttataagac	aaaggtgaat	tagataaatt	taagcgacca	301320
tcaaaaacca	tgctattggg	gcttgtaggt	ctgatattta	tatctttttg	tattgtaaga	301380
tccgattgac	aagtcagtc	gccgtctgta	caggtgagat	ctcctctaac	tacagtattt	301440
tctgtagtta	cttttccccc	aacagtaaat	gtcgtttttt	tttgatcttc	agtcaaaattg	301500
atagattgaa	tattaaatct	aacaaaagtc	ggaattgaaa	tttttgtttt	cggtgtagga	301560
tttgacatta	atctacctcc	gcaaaattag	cttgaaatgg	aaaccaataa	acacatgttg	301620
acatggattt	aatatctaaa	ccaatagtag	tttctaagaa	taaccaaggg	taatcatgag	301680
ggggggtagc	aacaatttct	gttaaagtaa	acgtgcctgt	tacagcaata	ctagtcctat	301740
gtcctcctga	gtaacctctc	gtatctgaag	cacaaaagcag	cgtcttatta	ttcccaatca	301800
ttaagttcag	atataaatta	ggattatcaa	gtccactatg	ttgcccgtc	tcgagacgta	301860
tttgatttgt	gacttgatag	attccaggtg	ccttgaactg	aatatagggg	aatctcgtta	301920
cagcatcata	aatttttagct	gaagcgctaa	tgcgatacgt	ctctggattc	gggttttgac	301980
acaccgtttc	gatttggttta	cctacagttag	taggctgaga	tgaactatag	taggtataca	302040
gattaagggc	ctggcatcca	gtgttcctat	aatagttata	tgtaaagca	tctcttgagg	302100
attggggatc	gctaacattt	gtaaacttag	gaactcggcc	atcctgatct	tcagaagtga	302160
tctccaaacc	tttagaaaagt	gttgctcgctt	taaattgaga	actttctgct	gataatccgc	302220
ccccgacagt	aaattcacat	ggagaagtga	ttgtatctgc	aacttttaaa	tctcgagtct	302280
ctaaaaagtt	ttctatatcg	acattgccat	ccacattaag	agtcgcttga	tcaagaaata	302340
agttctgatc	ttttattcca	gtattttcgg	ctacatttgc	agacggagta	gaagaaatag	302400
gtagaatttt	ttgtagggtt	cttcttttca	taactacacc	ttatcccccg	caaaataaag	302460
aaagtgtaaag	gaatagttcc	ctattaccgc	gctgtgatct	ccattgcgaa	caaacaaaaa	302520
attattcata	tatttgtcac	ttggattgtt	cgggtcagga	tctatatcac	tatgatctct	302580
atatactgcg	gtacttaaat	accctatcgt	tgaataccct	ccgccactat	acactgtgct	302640



cccgcacaac	attgttccat	cgccagtgtg	tttcccttca	aatagacgaa	tcgacccctc	302700
ccaaccattg	ttccatcccc	agcgcttacc	aatagtaaaa	gttaggatat	aggttccctgc	302760
agcaagaagt	tgtatggctg	tgttcccccc	aagtgttaatt	ttttcgaatt	ttgatcccaa	302820
tctacaaaac	gaaaaacatc	accagccttg	cttgactgat	acaaagtata	gtttgatcca	302880
tctccagtta	taggtaagta	tcgactactt	ccatcaaaca	taaaagtccc	ttctattggc	302940
ttggcacaga	aaaaatattg	gggagaacgg	acatagtctg	cggaacagg	atcgcatggg	303000
tttttcggta	atgcgggatt	actaagacga	ttattcttca	tatcgattgt	tattgaggaa	303060
ggcgccgggc	ctgtagcatt	taacttatag	gtagatgccg	aagtcaaac	tgttgctgaa	303120
actttctctt	taaatgtcgc	gttcccttga	acagaaaatg	tttcagtcga	tgagattcct	303180
ttagcttgct	tatcaaaagt	ctgaatatct	gaagctaata	agtctccatc	tactgttgaa	303240
tcgagtttaa	aataacactc	attgttatct	tgattatttg	ttgttgctat	ttcaataaaa	303300
tagttataag	tttttctttt	aaaaacaaaa	tagatctatt	tagtcaataa	attaactaat	303360
aataattctc	ttacgaaaca	agataataaa	taaaattcac	aaaaaatagg	aactgttcgc	303420
aatcaaaaac	ctttgattat	cgattgagat	ttggaacttt	taattcaaaa	gttctctccc	303480
cgaatccaaa	taatttttta	cattttctga	gcgaattgat	tagatagaaa	ctatgagatg	303540
acaattcatg	aaatgcattc	ccaatagtta	taagttttat	ataagatcct	tgagaattca	303600
agatattgaa	gaaaaagaag	tgggggtggc	tggatttgaa	ccaacgtatc	cgtaaggagc	303660
cggattttaca	gtccgatgca	attgaccact	atgcgacacc	cccaaaaatg	ctggagaaa	303720
gaattgaacc	ctcaaccgtt	cgattacaaa	tcgaatgctc	tgccaattga	gctactccag	303780
cagaaataga	agtgcgatta	tctcaaaaag	aaagttttat	tctcaatcag	aaagtaactt	303840
atctgaaatt	aatcttctct	aactggaggt	ttttgagagt	tttcagatat	gcgaaaactt	303900
tcttgtgtag	ggataaaaatc	ctcacaacaa	aaattagtgt	cttgattcaa	agtagctgta	303960
ctctccatag	gtggagctag	attctctcca	gtattttgaa	tctcaaaatt	atgctgctga	304020
agtttctctg	taaccaattt	ctcttctttt	gcctgagctt	tcttaagagc	ttttttactc	304080
attacttctt	tgttcttagt	aatctgatga	aacttaccaa	cagccgcttt	ctgttctgaa	304140
gttaaagatt	gagataaacg	ctggaacaac	ttcgtacaat	tatctcctgc	ttctccctgc	304200
tcggatgcag	agagaacttc	agcagaaaat	ttaaattttc	cttcagttgt	ataccgagct	304260
gtttgttctt	cttttttttaa	acaacattgc	ttgtactttt	tattagaacc	acaagggcat	304320
aaatcatttc	tattaatttt	ttttgacacg	tgatcctctt	ccacacaaga	tcttttagaa	304380
aagtctaaat	aagctcaaaa	taaaatccaa	agtcacaaatg	aaaaacctat	tgcttttttc	304440
tttaaccttg	gaacctagta	ctcgtttaata	aaaagaagaa	aaacttaatg	aataattaaa	304500
ggtaacaaat	ttatgccagc	ctattcacct	gaactataag	tttctggatt	tttaacagcg	304560
attttcttaag	aataatatct	ctttaaccat	ccattcattg	ttttcatgtc	cactttactt	304620
ttaaatctct	cgtggatgaa	agcgggaaaa	cgtatagaaa	gcttggtccg	aaaagcactc	304680
tatacccata	ccatgttagc	aaatcatcgt	aaaattgtag	ttgctctcag	tggtgggaaa	304740
gatagtctta	cacttctttt	aatgctcaaa	gcaatttctg	gaagaggatt	cccagattta	304800
gatctccaag	cgttcaatat	cggaggaaaa	tactcttggt	gagcagaagt	taataaacct	304860
tatttaaccc	gcattctgtg	tcaactgtgc	attccgttta	gaacaattcc	ctctccttat	304920
gcaccgaaa	cccagaatg	ttatccatgc	tctcaagcaa	ggagacgttt	acttttccaa	304980
gcccgtaaa	aaataggagc	ttcggctatc	gcttttggtc	atcaccgaga	tgacctcgtc	305040
caaaccgcct	tattaaatct	tctacataaa	gcagagtgtg	ctggaatgct	tcccgttttg	305100
gatatgggtc	atttcggagt	taccattttg	cgccctttaa	ttttcactcc	cgaattctgg	305160
attcgcaagt	tcgctaagga	aaacgcttcg	caagagtcac	ttgccgttgt	cccgtgggtt	305220
cattaagaag	caaagcggaa	caaagtttaa	agttattaga	agaggtattc	ccttttagcac	305280
gtcataatat	cgctttggca	attcaagaac	atgggtcatc	caaatacaca	aaaatttgag	305340
agacactttg	ttattaatta	attttttaata	taaataaggn	agtaaaagtt	tacttggttc	305400
tcatgaataa	aagattaaag	ataattctaa	ctaattgatga	tggaaatcaca	gctaaaggna	305460
tgagttgcct	agtctctgct	ctattggaag	caaataattgg	tgatatttat	attgcagctc	305520
cccaagccga	acagtcgggg	aaaagcatgg	caatctctct	gaaccaagta	gtctgcgcct	305580
ctccgtatgc	ataccgcaa	cccgttaaag	aagcatgggc	agtaggaggc	tctcctacag	305640
attgcgttag	actcggcctt	agaacacttt	ttgaatcggg	ttcccttgat	ttagtgattt	305700
caggaattaa	ctgtgggaac	aacatagtca	agaatgcttg	gtattcagga	accataggcg	305760
ctgcaaaaaca	agccttggtc	gatggcattc	catcgatggc	actttctcag	gataaccata	305820
tttctttctt	tcaacaagac	aaggctcctg	aaattttaaa	agcatttagt	atttatctct	305880
tgtctcaacc	ctttccttgt	ttaactgggt	taaatattaa	ctttcctacc	agtcctgggg	305940
gttctctctg	ggaaggtatg	cgacttggtc	ctccaggaga	tgaatttttt	tacgaggaac	306000
ctcaatacct	aggctctgta	aacaaaaatc	aatattatgt	agggaaaatt	tctggagtac	306060
ggattggaga	gcatccatca	gaagaactcg	cttgcatgct	agaaaacccat	atcagcgtgt	306120
ctcctatatt	ttcacaaaac	tctcctatcg	gcttaatgac	tctagaggaa	tttcaaaaaga	306180
cacaagaaaa	tttcaatgca	tcgcttttaa	gctctgagct	gaccactaaa	attttctaaa	306240
agccccctag	tctttgggtat	cagaggctct	tttttacaaa	agatctcttg	tttaactcgag	306300
atttaatcac	ttaaattgaa	agaaaaataa	ttgtgattaa	actatttctt	ctggtaaggt	306360
tatgctccta	tcttattgga	tgcgtagctc	agcgggttaga	gcacctgtct	tacacacagg	306420
gggtcatagg	ttcaaatcct	gtcgtgtcca	tttgcgggag	tagttcaatt	ggttagagca	306480



ccgccctgtc	aaggcggaag	ttgcgggttc	gacccccgtc	tctcggaag	tatgctttca	306540
gaggtttcag	gatgtctcac	ggtccacgtc	caacaaaatt	cagtttccct	ctgtatttct	306600
ccaaaacatt	aagtgtggtt	atttttaggtg	gctttcttgc	tgcttgcgga	gttcagatgg	306660
tattagtgcc	taatgaactt	atcgatgggtg	gtattgttgg	cctctccatt	atagcctcgc	306720
atTTTTtagg	tcacaaagcc	cttctttttt	gcttagttct	cttcaatctt	ccttttgtat	306780
tcctagcatt	taagcaaatt	gggaaatact	ttgtgattca	aatgttgaca	gccgtgatta	306840
tttttctgtg	ttctctctgg	cttattgatc	aactcccttc	ttggctcggc	atgagccctt	306900
ttgtttttaa	aggatcagaa	atggaaaccg	ttgtgctagg	cggtgctatt	attggcgtgg	306960
gttgtggatt	gattatccgc	cacggagggt	ctacagatgg	cacagagatt	ctaggaatca	307020
ttatcaataa	aaagaaaggc	tacactgttg	gccaaatcat	tttatttgta	aacttcttta	307080
tctttgcttt	atctggtatt	gtctacaaaa	attggcacac	tgctttcggt	tcatttctaa	307140
cctatggaat	tgcaacaaaa	gtcatggata	tggtgatttt	aggcctcgaa	gatacgaagt	307200
ctgtcactat	tattacctct	tctccaagaa	agctaggcca	tattctcatg	gaaaccttag	307260
ggattggctt	aacctatatt	catgcagaag	gaggatactc	cggagaacct	agaaaccttc	307320
tttatgttgt	tgtcgaacgt	cttcaacttt	cacaactaaa	agaaatcggt	catagagaag	307380
atccctcagc	atttatcgcc	attgagaacc	tccatgaggt	aatcaatggt	agacgaactt	307440
aatccttgaa	agaatcactc	tggattcgac	cattgtttcg	ttaggtcgct	agggatattt	307500
agataagcaa	ggatttttcc	tactaaagca	ttttcaagat	cttcaaccga	ttgaggctta	307560
aagtaccaca	taggcacg	cggaaaaatc	gttgccccac	tcttgcttaa	ttttaagaga	307620
ttttctaaat	ggatcgtatg	caaaggggtc	tctctaggga	caagaatcaa	gggtcgcctt	307680
tctttaagag	ccacatcagc	aacacgtcgc	agtaaattat	ctgctaaacc	tatggaaata	307740
gctgcaactg	tagtcatact	gcaaggataa	atgatcgtag	cttctacagg	acaagatcct	307800
gacgctaaag	agctctctat	agcttgaatg	ctatgagtat	gaatatactc	taagttttct	307860
tctgaaaata	atgcttcaaa	agactgacac	cctagttcat	aatacaacgt	ctttcttctt	307920
gaaggagaaa	taattacttc	aacttgatgt	tttgcattta	cgagttcctt	aataagctta	307980
acagctagta	ttaccccgag	ggcacctgaa	atgccacaaa	cataacgctt	catctactca	308040
aactccaaaa	caaagtcata	cttacaagaa	acgatagagc	aatcgcaata	ttcgctaaaa	308100
agaatttggc	tctctccttc	ttgatctttt	ttactgtagt	tagaatacat	tctaactacc	308160
ttaagaatca	caactagagg	aatgatagct	gtgaaataga	actctttatc	taaagaacca	308220
acaaaacctg	aaaaaatata	agcaagataa	cttaccata	agtttacttt	tgcaatttca	308280
acggctttct	tttcaccgta	atgtgcagga	acactacgca	atccttcttc	cctatcaaat	308340
tcggatatctt	caattgcata	tatgatataca	tttgacgcta	ttaccatacc	cacactccct	308400
ccccataaaa	gagcaagaaa	gcataaacgc	atggaaagcc	ccgactcagc	aaaagcacaa	308460
aaattcataa	gaatcgctac	agtgtacacc	aaccctaata	cccaatggca	gaaaaaagtc	308520
acccttttca	tatagggata	gacgatcata	agagtcagtg	aagcgatgcc	caaactaaaa	308580
atacggagaa	tcttgacagag	aaaaagaaaa	agaaaactac	aaaatagaga	gagtacccaa	308640
gcaaaattta	aagaacaag	attcgcagga	aggactcttt	tcgatgttct	tgtatttttt	308700
ttatcaatga	accggtcgat	acactgatct	actacaattc	ccgtagtcct	tgcaaaaaca	308760
aaggctatgg	ctccaaaaac	tgaaatcttg	aacccttctt	taaatgataa	atTTTgggaa	308820
atctcattta	tagaaagagc	aaagactgtg	gatgctgata	aaaaaagtat	tgaaaatatt	308880
gaatacttaa	aattaactaa	atttaaaaaa	taatttaata	tcacaattat	tatcttctat	308940
ataattatTT	TTTTatttat	aaaaaaaaata	tactcctctc	tattcatcgg	gggtgatccc	309000
cccaatcttt	ttagaacccc	ctatgttagg	gggttcgtct	ttttatgcct	ctactgtgta	309060
catttcaggc	attagtgcga	tacatttttt	ttaaatccaa	aaagttccat	gttctttcgt	309120
atagagggtg	gttcttgtgc	atcagaaatg	gtcctttaac	aaaactccta	acgccaagac	309180
aacaagctga	ttatgaagtg	cttgtcaaaa	caaaaactct	tttaaatata	ttgctcttta	309240
aagaaaaata	atgacaagaa	attcgtaaaa	aagcgctgtt	ttattaacaa	aaaggaagag	309300
actttatact	tatgattcta	gtacaaaatt	gcagaatcag	atgaaaagaa	ctgtactagg	309360
gttttttaaaa	tttagttatt	atatcaagaa	ataaaattaa	aaataccttt	aacctaaaaa	309420
gattaatctt	gatttaattg	attttttctaa	taaaattatt	cgatctcaaa	aataaaacga	309480
gtagataatg	gcgttagatg	aaattaataa	tcagaacaac	ccatcgcaac	agatagcctc	309540
ctcgacttct	caaacttcta	aaatcaacca	agatcgaaaa	actttcgcac	gcactgttac	309600
cctacttggt	gtagcaactt	tgatgatcct	atccgggatt	gttttgctat	ttactatagg	309660
ttccctaggga	ctcagcggtt	ctttatctgg	aattctaggg	acttttgcag	tgacagtagg	309720
agctgttctc	tttatcacag	gtctaaactat	tctagttaga	aaatccctag	gaatcgaaca	309780
gaaaaacgaa	gacttgaatt	ttttaaaagat	taagacccca	actccccag	cacgccccct	309840
aatgtcaaaag	tttagtggtta	cctgctccac	tacaagtatt	gttttaggaa	tggtcttctt	309900
tatcggtgct	gtcgtctccg	tattttttct	cacaggatat	ctacaactag	gcttgtgtgc	309960
aggacttgta	ggtcttgga	ccgccctatt	tggtgcagga	ttagcaagga	tgccccctcg	310020
tagcctagca	gaccaagaag	gctccggctc	cgcgattctt	caatcaaata	ttggtggaga	310080
aggtgagcca	aaagcagctc	aggaacaaaa	atggtataaa	atggcagtg	taaggggaga	310140
agatgggtata	ccaacagcaa	ttcgccctaac	accagagaaa	taaactatta	ttttaagaac	310200
aaaaaagggt	tttaaagtag	gtaaatgaga	aaacttactc	actataaaac	tcttaaaact	310260
ataaaaaattc	cgaactttta	tactatatcg	aaagcaattc	atccaggaat	tacagaaaat	310320

tgaaaaacta	tttaataatc	tacctaataatt	ttctgattta	aagaactata	agatgtaact	310380
ttaacgattt	tttttagtaa	ctaattcgga	ttaaaaatga	aatgagtgtc	aataatgtca	310440
ttgaataaaa	ccaatgccct	tctcaatcaa	ccagagcctg	ctgtttgcct	taatgcttgg	310500
gaccctaaat	atatcaacca	agatcgaaaa	actttcgcat	gcactgttac	cctacttggt	310560
atagcaactc	tgatgatcct	aacaacagga	gttatcgat	tacttgctat	gggctctcct	310620
ggattaagcg	ttcttgtatc	aacaattata	ggaacctctg	taacaacttt	agggactgct	310680
ctcttcataa	ttgggttagt	taaactaatt	aaaaaatcat	tagcatggat	acagtatcag	310740
aaatactttc	aagaagtcgt	aaaacagaaa	tatgaaccct	ttagcattcc	taaaaatgat	310800
aacgtacaca	aactcacttc	gtgcttacca	tcacctttag	atattgagag	tccgtctcca	310860
gaagcaagta	ccccagtctc	taagttacgc	attgcatgtt	caggagtcgc	tattgtttta	310920
ggagtgactc	ttcttattgg	tgctgtcgtc	tccgtatttt	tctgcaactg	atacctacaa	310980
ctagctctat	gtgtaggatt	cgcttgtcct	ggaactgccc	tctttgttgg	gggattggca	311040
gggttgcgga	cccacagctt	aatcgctcag	ggcatcatgt	atctttacct	gacttactat	311100
ctatcatcgg	ctctggaaga	aagaaacgaa	acagtcgaag	atcagcgtaa	cgaatcaat	311160
acatatttta	ccgaggaatg	caggcagcaa	aaaagggaag	aggcaactgt	ggaatagaaa	311220
caatgggcac	tatctctcat	gtctcaatgt	cagagtagca	gtacatctac	ctgggaatgg	311280
atgaaatctt	ttgtgccaaa	ctggaagaat	ccaactcccc	ccttatctcc	tataccttct	311340
gaggacgaat	ttatattagc	atacgagcca	tttgttctac	cgaaaacaga	tccagaaaac	311400
gcacaagcta	atcctccagg	cacatctaca	ccgaatgtag	aaaacgggat	cgatgatctc	311460
aaccctcttc	tggggcaacc	caacgaacaa	aacaatgcc	acaatccagg	aacttctgga	311520
tctaattcta	catctctacc	cgccccgaa	cgactccctg	aaactgaaga	gaacagccaa	311580
gaagaagaac	aaggatctca	aaataatgag	gatcttatag	gataaaaaca	gtgcgaatga	311640
gttccgcccc	gttataact	gtgttaagaa	agagcagcaa	ttcagataaa	tgtccagcta	311700
aagcaagaag	gacaaagact	cttgcttctc	ctttgataca	agaaatgact	cctatctttc	311760
atagtttata	gcaatactat	aatttcacgt	ctgttatctt	tggattcact	tgttctacaa	311820
tgacttgctt	taaaaatttc	tcagcccag	aagaaagtat	ggactctgct	ttccctttag	311880
aaaaaatacg	atgaatcaac	tgatttagaa	cgggatgggc	ttccgcagaa	ctacactcat	311940
taaaaaagaa	attttcgtct	tcatttgc	aaaagaaatc	cgacccaaga	acaatacttg	312000
ataaaattcc	gagattctcc	gcattggagga	catgcttctc	caaatacccc	aaggaatctc	312060
ctacataaga	cctcactaga	ttcaaacc	taacaccttt	tcttctcaca	atctccttgg	312120
catgggcatc	tacaagggtc	cttcgatgat	caagaacaga	tcgaaaatta	gaatgactgg	312180
caatcactgc	gagattgggc	aatttatcgg	cagtataatc	taaaatatct	tcagctaact	312240
tatcactaca	atgggctaaga	tctattggaa	ctccaagtcc	gtacatgata	tctaaaagaa	312300
ccttaccatc	attagaaagt	ctcttaggag	cttctgtgcc	gcctccaaaa	cggttatccc	312360
ctttccatac	gattcctaga	taggcaagag	gccccgtgtt	agttaaatgt	ataagctttg	312420
ctaataagag	cccaaggggg	gcgggtatcat	ctcccaaagc	tgaggcattt	tctatactac	312480
gaataagact	tagtgatttt	ttttgagaag	aggatccgtt	ctcttcttct	tcataagata	312540
ataaccaat	atccggatat	tgggttaggaa	gagaaaaaaa	cagagagtgt	tgatttatcac	312600
aattagggtc	cccccgactg	tgggggacaa	aaatagcaca	cacctgctga	cgtagcctc	312660
cagataggag	ttgttctgga	gaacacctca	ccgcaggatc	tttccgacaa	aaatgcggat	312720
gcgaaagtaa	gtcacaaatgc	atatcgatag	tcataacaca	cctaaatgct	actcaatata	312780
ataaggggaa	agaaagggga	aaagttcggg	ataatccgat	gtatttatat	cataaataaa	312840
gactatagaa	ggagttttct	tttttaaagc	ttcccgtaat	ctggtataaa	aattcttagg	312900
tttaggatgt	tcacaaacca	caccttttaa	atctaaagat	ccgctcaaaa	aagatactaa	312960
ttgctcttga	tttttctactg	tatagatctt	gatatgcttc	gaaaaggcat	gtgacgttct	313020
atgaaaaatc	ttagcttcag	tccttgcaat	gttttctata	acactgagag	aaatcagccc	313080
ctcacgataa	atataaagag	gatctgaggc	aactactgtg	gactctaaac	catgggaaca	313140
agggccatca	aaaatacaga	gatcatgatc	agcaaagtct	gcgaatatct	cttgagctgt	313200
aagagctgaa	ggaaactctg	aaagattcgc	agatgttccg	attaagggtc	cacagtgate	313260
cacaatttcc	cgaactacag	agtgatctac	aatgcgaaac	gctagtgttt	ctttagggaa	313320
tctaggattg	cggtgcttaa	ctactaaagt	aattgctcct	gggaaaagtt	gagctaattt	313380
cttagctgta	ggagataagg	gataaccaga	aatgttttcg	attcttcaat	agaatttaca	313440
taaagggcaa	aagctttact	aggttctcta	tcttttaaag	catagagtct	ttcttcagct	313500
tcagaggcat	acaagctaag	aacaaacc	tagacagtgt	cagtaggaag	atcgacaatt	313560
ttcccttgat	gataagctga	cataacctct	ggaagcgaaa	aagtaatctg	tgttttttta	313620
tcaggcacaa	taactccaaa	aatagattaa	agaaggtcta	tgttttttag	aatccgcaca	313680
aaaccgctta	tacatataat	ttgtacgctc	tttatcaaaa	agagaattcc	ttagattaac	313740
gcaaaaagtt	aatctaaatc	cataattttt	attcagaaaa	tagatttttt	attaacttat	313800
acaaactaaa	cattcaaaaa	tccaaaacta	catcttaaaa	tattgactac	gccacttgaa	313860
gacaaaaaag	aaattattga	tccctaattc	ccttcgatat	aacgtggtaa	cttcttatta	313920
ttaaaaataa	aaacttatga	cagactactc	tttctttcgt	cgcaaaattg	gcaatattga	313980
agccatagag	tgccctggaa	atcctcaaga	tcctatcatt	attctgtgtc	atgggttacgg	314040
atcacttgct	gataatctca	ccttctttcc	ttcgatatgt	tccttttcaa	aattacgccc	314100
cacatggatt	tttccaaatg	gaatccttcc	cttgagagaa	gacttccgag	gctctcgtgc	314160

atgcttttcc	cttaaatgttc	ttttattaca	agaactctct	aggctctatg	ccaatggagt	314220
agggaacctt	caagaaaaat	atgatgaact	atgtgatgta	gatctagaga	caccgaaaga	314280
agctttggaa	gaacttatcc	tcaatctcaa	tgcaccctat	aatgaaatta	tcattggtgg	314340
athtagtcaa	ggagccatcc	tggctaccca	ccttgtctta	acttctcaga	atccttatgc	314400
tggagcctta	atctttgctg	gcgcaagact	gttcaatcaa	ggctgggaag	aaggacttaa	314460
acaatgtgct	caagtgccat	ttttacaaag	ccacggttat	gaagacgaaa	ttcttcctta	314520
tcacttagga	gcacacctta	atgatcttct	attaacaaag	ttgaacgggc	aatttgtttc	314580
tttccatgga	ggacatgaaa	ttccctctgt	agtattccaa	aaaatgcaag	ttacagttcc	314640
taattggata	gatcctgccc	ggggctgaca	gaaacgagtt	ccttttcttt	atactggaga	314700
gataccaact	gaatagctac	ccattctaaa	acagatgctg	ccgatgagga	gttattcaat	314760
gaccgaccag	gcagattcca	caattaaaag	caccttatct	aaaggcagta	atggcaattg	314820
taggatctcc	ttaacatgct	caggatagtt	taaagctgaa	gcctttaatc	ctaaattcag	314880
agtataacga	tctcgatata	gctctaggag	cacttccatg	aatcggtgca	ccttgtctct	314940
taacacctgt	tatatctgtct	ctgaagattc	ttttataaatt	tgagacactt	cagtaacggg	315000
aatttcacat	tgggcatagc	gaataaaata	agaaaacgtc	tctttggaac	ataagatttt	315060
ttctcccttc	tcaataaaaa	tagagagact	ccgagaaatg	atagtctttg	gcaatctctg	315120
aacttttgct	gttgtaata	tgataacagc	atgtttcggg	ggttcttcga	agacttttaa	315180
aaatgcggaa	atcgagctta	aagtcattcg	atctgcttcg	tgaataatgt	agatcttata	315240
gtttgcttca	aaaggagata	tataaatctg	cttcttaatt	cccctaggaa	gatctataga	315300
gtgcagtctt	ccctttcctt	ctggaaagaa	ttgataaata	tcgggatgaa	tcttttagaga	315360
aactttatgt	tcggaacctg	gagatgacga	tagcaaaatc	tccgatgcta	actgttctgc	315420
tttatcctgt	aaaacaggaa	gggtaaaatc	atgcagcagt	atagctggag	gcacttctctg	315480
atgataaaat	ttcctaagta	aagcttccca	gccttgattc	tcttcttcta	ggtgcataac	315540
ccaagttagc	tatgtagcat	cactttgtct	attaaactag	ctagtgatcc	acgagcatca	315600
agaaccaagt	aacgactagg	atcggcacta	gcaagagata	aaaatccttc	tcggatcctg	315660
ttatgatagc	tcaaaggctt	tttttcaaac	ttgtcaaaaa	ccttttgctg	gtgcttccct	315720
tgtgaagcaa	tgtctgcagg	aatatccaag	agtaaaacaa	aattaggaag	gaaagggtga	315780
ggtcctacaa	ccttagaaca	aaggctcgga	acaaaatcag	cacccaaacc	ttcggctatt	315840
ccctgatata	caatcgtaga	atcgtggaat	ctctcacaaa	tgacaatata	gccatcacgc	315900
aatgcgggaa	tgtactcttc	ctgaatatgt	tgagcacgtg	atccaagaaa	caaaaagagt	315960
tcacaacagc	gagagagttc	taagttagga	ggttccaaaa	ttaaatctcg	gagtctttcg	316020
cctataaggc	accctccagg	ttcccttggt	aacaaaacct	tccgatcttg	agctactagc	316080
tgatctccta	aagcctttgc	taaagaactt	ttgccagacc	cttcgcccc	ctcaatcacg	316140
ataaacacaa	tactacctta	ggcttactgt	atcagaacat	tcttcttcgg	accctgatag	316200
tacttcatca	tcattttcat	tagaagagag	tttttccata	gaaacaagag	catccccttc	316260
tttcaagtga	actaaacgca	ccccttgagt	cgactctccc	atcactctaa	catcttgcat	316320
gttaatgcga	attgcctgtc	cctgactcga	cattaataaa	atactgtcgt	gatccgtaac	316380
aggaatagct	cctaggacat	tgcctgttct	ttcattgata	aggatagaac	gtacgcccac	316440
gcctccacga	ttgggtttgc	ggaaatcttc	aactaaagat	ctcttaccaa	aaccttgatc	316500
acatacaatt	aaaaccgact	ggttctcagt	cacaatttga	caactgacaa	ctttatcttc	316560
ttcatttttc	aaagagacac	cgcgaaaccc	acgtgcagtt	ctacccatag	gacgaacttt	316620
ttcatggggg	aagcgaactg	ccataccaag	atgagtaaat	aacattacct	tctcttcac	316680
actaacaatg	tgacaagctg	ctatgagttc	gtctccctca	tctatctcta	aagcacgtat	316740
tccctttttc	ctagggttgc	taaaggcgct	taaggaaact	tttttcacaa	caccacgttt	316800
ggtggctaaa	aataagaagc	cggcattatc	aaaattctta	atattcaata	tagctgcgag	316860
ctcctcacca	ggacgaattc	cctctaggaa	gttgatgatg	ggcttacctt	tcgcccctcg	316920
ctcccccttc	gggagctgcc	ataccttcaa	ccaataacat	tggccaaaat	tggtgaagat	316980
taggagatag	tcttttagtaa	aggcagagta	tacagcttta	aggaaccctg	ctcccttctt	317040
catatcaaat	cccgttaactc	catgcccgcc	acgacgttgt	tctttgaaca	cttttacagg	317100
cattctcttt	acgtaatcat	ctccggatat	cgtgataata	acagactcat	tggtaatgat	317160
gtcttcaata	tcacgaatat	catcagcatc	gaattctata	gtagtgcgtc	gagctacctt	317220
atgatgcttc	aaaagatctt	gtaactcatt	tctgatgata	tcttttacta	aaccttcac	317280
cgataaaaact	tggtttataat	aagctatctt	atttaataac	tcttcgtact	ctttttgaat	317340
cttttcagct	tctaaaccag	taagttgata	taaacgcagt	tctaaaatcg	caagagcttg	317400
aggttcggta	aaacccaaaag	attcaataat	ccgttcttta	gcatgctctt	tattcccact	317460
ctcgcggatc	gtttttacta	atgcatctaa	gcaagataaa	gccttaagg	atccttctaa	317520
aacatgagct	cgtgtttctg	ctttatttaa	ttcataacga	gtcctacgac	ggatgacttc	317580
tttacgatgg	cgtatccaag	cggaaatcat	cctatgaata	ctcatcggtc	taggtaagtt	317640
cttatccagg	gcaagcatat	ttgccccaaa	agttacctga	acatcggtga	acttgtagag	317700
cctattgata	atgatttccg	aagattctcc	ttttttgatt	tcaaggacaa	cacggattcc	317760
atctttatca	gactcatcgc	gaacatctga	aatgcctgcg	agagtctttt	cattcacaa	317820
atttgcaatt	tgctcaatca	aacgtgattt	attcacatta	taaggcatct	ctgtgatgat	317880
gatgctctca	cgatgtttat	cttcattctc	ttctacatgc	agacgagctc	gaactttaat	317940
ctttcctcgt	cctgtagtat	acgtggagcg	aattccttca	gaaccgcaga	taattcctcc	318000

tgtagggaaa	tcagggcctg	gcatgacttg	taaaatctca	tccacagaag	cctgtggatt	318060
tgcaagcaga	agaagtgtag	cttctataag	ttcccctaaa	ttgtgtgggg	ggatattcgt	318120
tgccatccca	acagcaattc	ctgaagaacc	attgcaaaga	agattcggaa	atttagaagg	318180
aaaaactaca	ggctcgtggt	ttgtttcatc	atagtttgga	acaatatcca	cagtatcttt	318240
gtccaagtct	tccataagat	acatagcact	atgggtaaga	cgagcttctg	tgtatcgcac	318300
agcagcaggt	ggatctccgt	ctatggagcc	gaagtttctc	tgtccgtcca	ccaaaggata	318360
acgcacgcgc	cagttctgag	ccatacggac	aagcgttaga	taaatgacgc	tctcaccatg	318420
tggatggtag	tctccagagg	tatccccaca	aatttttgca	catttacgat	gcttagctcc	318480
tggagaaaga	cttagctgct	tcatggcata	aagaactctt	ctttgtgaag	gcttgagtcc	318540
atccccgata	tctggaagag	cccagagata	aatcacagac	atcgaataac	gaaggtaact	318600
ttccttcatc	tcttcttcaa	gatttttagg	gactataatt	tcatctttat	tgaacatagg	318660
gattgtggac	tcctaaatat	ctaaattatt	tatcctaatt	gacaaagcat	gactttctat	318720
gaattctctt	cttggaggga	cttcttcccc	catcaacata	gtgaaaatat	ggtctgcttc	318780
tacggcatcc	ttcaatgaca	catgaatgag	tgttctctgc	tcaggattca	tagtagtctc	318840
ccaaagctgg	tgggcattca	tctctccaa	acctttatgc	ctctgaattt	ctatgccttt	318900
tcttccaaga	tttttaagat	agttaatgac	ttcttccaag	gtatagcagc	tatatgtaca	318960
gcttggggaa	tcttcatttc	caatcacaa	ctcgtttttc	tgagggataa	gatagctaga	319020
aatatctaaa	ccatattctt	tgagttgatt	ttgaatatct	acgaacacag	caactttata	319080
aagctctatg	attttaaact	tatgagtttc	ttcttgagct	aaagcttctt	ctttttcttc	319140
atcagaataa	agatagcgcc	ctccctgcat	tccagttgcc	ggagcaagat	agtacaaagg	319200
atagcctatc	ccctctttat	acatctctaa	aaattcagag	aagggaatcg	ctttttcttc	319260
aagagtgttt	ataaagctct	ctacatctaa	aatgacgttg	ataaaaactct	ctaaaagctc	319320
tccacgtaat	tctctttccg	tagattttaa	gagaatggag	ctctcattcg	tgcctaaccat	319380
gagcaaatag	ctgtccattt	ctttctctga	aagaatataa	cggaagtctt	ttttcttact	319440
caccttgat	aaaggaggtt	gagcaatata	aacacattca	ttttcaataa	gcgctgtcat	319500
atgacgatag	aagaatgtga	gaagtagggt	acgaatatga	gaaccgtcca	cgtcagcatc	319560
tgtcatgata	atgatacgtc	tatagcgtaa	tttactgaga	ttaaaattat	cagcacctat	319620
gccacagcct	aaagctgcta	tgatggttcc	tatctcttgg	ttttggaaaa	ttttctgtag	319680
acgagctttt	tctacgttca	gaattttacc	tcgaatagcc	agaattgctt	gaaatcttgc	319740
atctctacct	tgtttcgcag	atcctccagc	agaattcccc	tccacaatgt	acatctcaca	319800
cttttcggga	tgtttttcta	aacaatcaat	tagttttcca	ggtaagcgtg	cgctatctaa	319860
agcacttttc	cttaaagtca	attctcgagc	tttttttgca	gcttctctag	cttgcgctgc	319920
aacaaaaacc	ttatcaacaa	tcctcttagc	aatttgagga	ttctcttcaa	aaaagattgt	319980
cagagcttcc	cctacaacct	gttgagccac	tgagctaaca	tcactgtttc	ctaatttctg	320040
ttttgtttgc	ccttcaaatt	gtggatttgg	gacctttaca	gaaatcacag	ctgtcagacc	320100
ttctcgaata	tcttctccgg	ttaatgcaag	cttattattc	ttcgcaagg	tatgagcttt	320160
aatatacgta	ttgattaccc	tagtaagcgc	ggtagaaaa	cctgtaagat	gcgttctctc	320220
ttggcggtga	ggaatattat	tggtcatagga	ataaacaagt	tcagaatacc	ctgaattcca	320280
ttgtaaggct	gcttttcaact	cgattttctc	atcatctcct	actcgagttc	cacaaatata	320340
aatcggttca	gagaaaaggc	tttctttatt	ttgattcagg	taacttacaa	aagattgaat	320400
ccctccctca	taaaagaagg	taacctgtgc	aaagctaaca	tctcgatcat	cttcaaagac	320460
tattgtgatc	ccacgattta	agaaagcaag	ctctcgcaag	cgtttcatta	aaatagagcg	320520
atcaaaagta	caagtcgaaa	atatttttagg	atcagggtag	aaaacgattt	ctgttccctg	320580
ccgatcacta	acacttacat	actgcaatgg	agttacagga	attcccctag	agaactccat	320640
ttgataacac	ttcttatctt	taaagaccgt	ggcaactaat	ttctccgaaa	gagcataaac	320700
gcaagaaacc	ccaactccgt	gcaagcctcc	ggatacttta	tagctatcct	tatcgaattt	320760
tctccagca	tgaaggactg	ttaaaaccac	ttctaaagca	gagacctctc	taccttgttt	320820
tgacagactc	ctttcgtgaa	cttctatagg	gattcctcgg	ccattatcta	cgatgacaat	320880
acccccgtcc	tctaaaatgc	gaacatcaat	cctagagcaa	taacctgcca	tggcttcgtc	320940
aatgctgttg	tctacaacct	catagactag	atggatgaag	acccgtgatt	cccgtatctc	321000
caatgtacat	cccggggcgc	tcacgaacag	cttgtagccc	ttctaaaaca	gtaatagcgg	321060
atgcatcgta	atttttttct	tttgggtcca	taaactatcc	taacaaaaac	tgtatttccc	321120
taatctgcac	gtgagaagcc	acctgataca	aactcataat	taaatcattt	tgaggcgtct	321180
gttttaacaa	agcatataac	gaggaattgt	aaacttttat	taacaaaata	tgactctctga	321240
accctatagc	tttagacatc	cccttatatt	tgtctctaaa	aacctgattc	caagcgtcaa	321300
tagcgtcatg	aggcctagct	gccataattt	tttgaagtgc	ctgcaataaa	ttatggagat	321360
agtgttttagc	gtgtttttata	ggggaagctg	ttcctttatt	ttgaacttga	gatcctcccc	321420
ttttttttcg	ctttaagaac	atatcctacc	tgaagaataa	cacagcgcac	atcacaaaaa	321480
cacagattta	tcaaattgag	agacctttat	gtctcgtctt	ttctctgttt	ttctttatga	321540
tcagttttta	aataaagttt	taataacatg	ctgcatcaaa	agaaacttct	tatatccaca	321600
gaaacgaaaa	aagtcaataa	gacgaagagg	aattcttatg	ataaaaaatcc	ctttttaggg	321660
gctgtaagaa	tgttaagaga	gcagtaaaaca	cacatgtcgt	tacatgctaa	acatatataa	321720
cggtaggata	aggcttatct	ggagaaataa	gagtcttcac	ctctataggg	tctagctctt	321780
caccttgaga	gcaaaaaacct	aggtacttta	caaccaccac	cacgcagaat	gcaatcgctc	321840

ctataatagc	gactacacaa	actccaaggc	caaacaagca	aacgcataga	acatctatga	321900
ggcattttat	taattttaatg	attacttgga	gcactaaggc	tgtgatttct	aacgctagta	321960
taacgatccc	tccgccgaga	atctctacaa	ctccacgaac	ccgatgtgcc	caaagattta	322020
cagaagttga	ggatttacta	tgtgttgatt	tctctaattt	ttcctgcgca	acttcctcta	322080
tatcctcagc	ataagtgcta	ctaattctag	aacaacctat	aactatattc	aaaataggaa	322140
tagcagcttg	gaaattagtt	gaaaactgct	gaacagaagt	aataccaaaa	gctggggctc	322200
taacattaat	tatcattaga	attacaccgt	agaaaattag	ggggggtaga	ttctttatga	322260
gaacttcttt	tccttcaata	aaatatttctg	ggtaaaagat	cgaaatattt	tattgaagga	322320
aataagatca	aaaagagcgc	acaagtacaa	cgacttattg	ctctaaccat	tgtcttgagt	322380
cattgtcaaa	atattcccat	gatattttgt	atcaaaaaaa	tgttgtagag	aaggagattg	322440
aaacagcttc	tgtaatTTTA	tcatttttagg	agaacctacg	tcttcagaac	gaatgacaac	322500
aaggtttgta	tacttagata	ccgaaagatc	ctctaaacaa	agactatctt	tcttttgaga	322560
aaggtttgct	gctatagcaa	aatttccagg	aatgacagca	gcatcaacgt	caggaagaga	322620
tccgacaaga	agaggagctg	acacctctaa	tatgttgata	cttctatttt	ctttcccaca	322680
gacatcttta	gctgtcatat	ttaaatttagc	aggccctttg	caaacaatga	gtccgcactc	322740
ttctaacaag	tgtagagcac	gctgagcatt	cgtagcatcc	acaggaatcg	ctatagttag	322800
tttcttctgg	ctttttaagc	gctctaaaga	agaatgtttc	ttagaataaa	ttgcttgagg	322860
ttccaaatga	acttttagcga	taacaactaa	ttcaccctta	caatcataac	gctcgcattc	322920
gtcatcaaga	aaagcttgat	gttgaaagta	atltgcatct	acttgtttat	ccaaaagcaa	322980
acgatttagga	atacgataat	catctactgg	aagtattttc	agcttgattc	caagatcttt	323040
agcctcttcc	tgtaaactct	ccaataattc	cgcatgaggt	gtcggactgg	ctacaatacg	323100
tattttattc	tgagcatctt	ccttatggca	agaactcaaa	aacctacaag	ccccagaaa	323160
taatgataat	ttttttttca	tagaattccct	ctatacttta	atacacgacg	ccccagaaa	323220
tctcctagaa	tacgcactga	ctcgataaga	actaaagtga	tgacaagtac	tgatgtttgt	323280
acagaccatt	caaaacggta	gtaaccatac	tgcaataata	actgtcctag	ccctccgcct	323340
ccaacaaatc	ctgcaagagt	cgaacatgaa	atgagatgaa	caacaagaga	cttaagagaa	323400
aatatgagct	gtggatagct	ttcaggtaga	agtataccaa	aaagaatatt	ccttttagga	323460
attcccaaag	caacggcaga	ttcaagatag	ttaagggtcg	aattacgaaa	agcatcaacc	323520
actatagtaa	caacaaaagg	aatggctccg	atagtgagag	gaacaataga	agccgtaggg	323580
cctaagaagc	tccttacaat	ccatcgcggt	atcggaaaaa	gaataacaat	aagaatcgca	323640
aatggaatcg	cggtaagaaa	acttagaatc	attgagattg	ttgcgtaaag	gcttttctta	323700
ggattaagac	tcttagggca	cgtgcagaaa	agccccaac	ctagcatccc	tccaatagca	323760
caagagaaga	aaaaagcagt	cgacaccata	taaagtgtat	tgactgtttc	ttttaataaa	323820
atctgaataa	gatcggtattg	cataatcttt	ttctaataaa	attctttaat	aacgacgcct	323880
agctcaatta	aaagctcttt	tgctttttta	cgttgctcaa	cttccccttc	caaaaacaata	323940
attagaaatc	ccattggggga	ttttctaaat	aaattaatgt	tgccggaaag	aatattgata	324000
gagaccagtc	cagtctgaat	caccttacta	atgatccctt	gtatagcgag	ttctttggaa	324060
aaatttaatc	taagaacttc	ttccctgtct	tctgcaaaat	aacacgaact	caaagcagca	324120
atattttat	cttcatggaa	caattcattt	gtaattgagt	tctcagaatt	taaaaaaagt	324180
tcttctgtag	ttcctagtct	ttcgacagca	ccttgatgca	ttaccaaaac	atgagagcat	324240
atTTTTTTT	ctacatcgat	ctcatgcgac	actaaaacta	aagtaattcc	cctttcctga	324300
ttcaattgaa	gcagcctttc	aataatattt	tcagtagatt	taggatccaa	agcagaggta	324360
atctcatcac	aaagcacaa	ttcagggttg	cacacaattg	ccctggcaat	ggcaacttct	324420
tgtttctgac	caccacttaa	atttccctga	taggcgtcat	gtctatgata	gagggtttaa	324480
aaattaagag	tatcgtatac	ctgttccctc	acttcacttc	tagacatttc	tgaatgatga	324540
atacgcaaa	gataggctat	gttttcaaat	acggttttctg	aagaaaacaa	cccataattt	324600
tgagaaatat	aggcaacttt	tttagaaaaa	ttacgacgtg	aaaacttctg	tggtggcaaa	324660
gagttatcaa	accagcttac	acttatagag	ccagatgtcg	gcatgtcaag	aaagtctaaa	324720
caacgcaaaa	gcgttgTTTT	cccagaaccg	ctatgaccaa	ctataccaaa	aacctctcca	324780
ggatagacag	aaaaggagac	tttgagagaga	agaatatggt	cgccctaactt	cttactaaca	324840
tcttgaacgg	aaatgatagg	agaatgttgt	tctgacacaa	gccacgcctc	tccttttatt	324900
tatgaatata	aaatagaata	caaagaatct	tgaagtattc	ttaaccatta	aactataata	324960
ctattatatt	tctgcaagca	agtttactgc	tgttaaaatt	ttgttatcaa	actatctant	325020
ataaacaata	agagggttga	atagatgtaa	gttctatttc	aaacgacaca	acatttgatc	325080
tactatacaa	caagatttca	tcgaaagcat	tttcaagacg	aacttcttgg	tgacgataca	325140
tcacaaaaaa	taaataagctg	cgatttttaa	cagacgcctc	aaaaatatat	agaactaaga	325200
acaacttgaa	attttaacat	aataaaaaaa	atactcctta	agtcttttat	aatacattaa	325260
aaaactaata	cttaacttaa	taaactcgtt	gataaagttc	cttgacaaat	ccctgggtta	325320
accccaaaact	gagctctgaa	taagcttaag	gagacacacc	ctcatgttga	atattcatga	325380
tattctagga	aatgatgacg	aaaacctatt	gtcatatcaa	tgtaaacaca	ttacaaaaga	325440
caaactaact	cttccctctc	atgattttgt	agacaaagga	tttggactct	ctgataggaa	325500
taatcgtgtt	ctcagatccc	tacaaaactat	gttttctcat	ggaagggttag	caaattcagg	325560
ttatctatct	atacttctctg	tagaccaagg	catagagcac	tcggcaggag	cctcttttgc	325620
tattaatcct	atatattttg	atccagaaaa	cattgtgaag	cttgccatag	aatctggatg	325680

tagtgctgtg	gcctctacct	atggaacact	gagcttactt	tctaggaaat	atgctcataa	325740
gattcccttt	atgctaaagc	taaaccacaa	cgaactcctc	tccatcccaa	caaaatatca	325800
tcaaattttc	tttactcaag	tagaagcagc	ttattcaatg	ggcgccgttg	ccgtaggagc	325860
tactgtttat	ttcggttctg	agacttctaa	tgaagaaatt	gtagcagttt	ctaattgcatt	325920
tgctaaagct	cgttccctag	gtcttgcaac	agtactttgg	tgctatctac	gcaatccagc	325980
ttttgttgct	aatggagtag	attatcatat	ggcagcagat	ctaaccaggac	aggctgatca	326040
tttaggcgct	accctaggag	ccgatattgt	gaaacaaaag	ctccccacat	gccagggagg	326100
atttaaggcc	atcaattttg	ggaaaacaga	cgaagagtg	tattctgaac	tctcttcaaa	326160
tcatcccat	gatctttgcc	gttatcaagt	cttaaatagc	tactgtggca	aggtaggcct	326220
aattaactcg	ggaggacctt	cagggaaaaa	tgattttaca	gaagcggcta	gaacagcagt	326280
gatcaacaaa	agagcagggg	gaatgggtct	cattcttggg	agaaaagctt	tccaacgtcc	326340
cctatccgaa	ggcatccaat	tattaaacct	ggttcaagat	atctatttag	atcctaatat	326400
tacaatcgct	taacttttca	aagaaggctt	ttatgcactc	ccactcaaaa	ccaacgaaac	326460
cggtgggaac	attcacggtc	ggcatgttat	cacttgctgt	agtgattagt	ttgcgtaatc	326520
tcccgttaac	agcaaaacat	ggcttttcca	ctctgttttt	ttatggacta	gcagtcatat	326580
gttttatgat	tccgtatgct	ctgattttctg	ctgagcttgc	ttctttcaag	cctcagggaa	326640
tttatatttg	ggcacgtgac	gctctaggca	aatgggtggg	attctttgct	atatggatgc	326700
aatgggtttca	caacatgacg	tggtatcctg	ccgtgttagc	ttttatagcg	agtaccattg	326760
tttataaaat	caatccagaa	ctcgttcaca	acaaagtgtg	cattgcaacc	gtgatccttg	326820
ctgggtttttg	gatacttaca	ttttttaatt	tttttaggaat	tacttcttcc	gcattattca	326880
gctctatttg	tgtaatcata	ggaacattaa	ttccaggagt	catcttagtt	agtttggtct	326940
tcttttggat	tttttctggc	aatcccattg	ctatttctct	ttcttgggga	aatcttcttc	327000
ctaatttcag	taactgtatc	tcactgttac	tactagctgg	aatgttactt	gcgttatgtg	327060
gtctagaggc	taatgcgaac	cttgcttctg	atatggtaaa	tcctagaaaa	aattatccaa	327120
aggcagtctt	cattgggtgca	atagcaacac	tcactatttt	agttctgggt	tctttatcca	327180
tagcaatagt	gattccgaaa	gaagaaatta	gtttagtctc	tggaactagta	aaaacgttta	327240
ccttggttctt	tgataaatat	aacctctcct	ggatgactgg	aatcgttgta	gtcatgacca	327300
ttgcaggatc	gctaggcgaa	cttaatgctt	ggatgtttgc	aggaacaaaag	gggcttttta	327360
tttccactca	gaatgactgt	cttccccgac	tctttaagaa	agtaaatagc	aaaaatgttc	327420
caacgaactt	aatgttatcc	caaggatttg	ttgtgacaat	attcacactt	ttatttctat	327480
gccttgatcc	agcagacctg	gtgtattgga	ttttaactgc	actgagcgtg	cagatgtatc	327540
ttgcgatgta	catctgtctg	tttcttgca	gaccgatctt	acgtatcaaa	gaaccaaggg	327600
ctcaacgcct	ctattctgta	ccaggaaaagt	ttttgggaat	ctgtacgatg	tctatcttag	327660
gaattctctc	ctgtgcgttt	gctctttggg	tgagcttctc	gcctcctaga	gaacttgctc	327720
agatatctga	aggcagcaaa	ataggatata	ctacattcct	gcttttagca	tttagcttga	327780
attgcttaat	tcctttcgga	atctatttca	cgcataaacg	cttatctaaa	aagagctaata	327840
ctaaaagcat	ttttgggaaa	agaaaagaaa	gaagccttcc	ttgttgtagt	gcagcctgga	327900
aagcttcttg	attcaaat	gctctcctgc	aaaaagtttc	aatctctcct	tgacaaaata	327960
gtcctgtttg	aaaatatcct	aaatatatcg	cgtgtaaaag	cttatcccat	aaatgtatag	328020
gcattaataa	ctttaggtat	ttacctacag	atatgctgaa	ttcctctgat	tccagtagag	328080
cctctaagaa	aatgaatggg	ttttgtttca	tcttctttct	atcgatagcc	attagaatct	328140
ctgccccctg	tttgaaccgt	cgagctcgca	aaagctgtgg	tatcgatgta	atagacaacg	328200
caggaagaac	aagttttttc	aatccttctc	tacaagcttc	cttggtctta	ttgaagtctt	328260
cttgctgate	ctcggcactc	ttggcacaat	cctcactatt	aatactttgc	caacagctgg	328320
gatctggctc	agggtataga	gcattcggtg	ctattaaatc	caaccttaat	gacagttggt	328380
ttatgcaagg	gaactcgtcc	ccttcaaaac	gatgatgtaa	aaatggagta	atatatttct	328440
ttgttctaca	aaatttttgc	cctcttcaga	agaaaattgg	ggacaaaatt	gctgaataat	328500
cttaactgcc	tgagacctat	catgactaga	tcgtaaacac	aaccctgaaa	gtaggagatt	328560
aatgcttatc	aggcccaaag	aacaagattc	tatggtttca	gctgtttcac	tggaattttc	328620
gatcccaagg	gtcgagtgtt	tcttcggatc	tagcatactt	ttcaatcaca	taggatctaa	328680
agaaaataat	acttctaata	tctcttctcc	tggaagcttc	aaaattttct	gtaaaacttc	328740
ataaagagga	gcaattgagg	aattctttta	atctttcttc	gcaaatttta	taagaagctt	328800
cactgggtta	gggggtgatt	ttcgaaagct	aataacttta	gcaacagcat	ttttataaag	328860
atcttggaag	tatgagagtc	ttcttcccta	ctctcattag	gccttccctg	ctcatctaga	328920
aaatttgaat	aagggaagcat	cttcggccta	cggaaatcat	cagctggaaa	gttcttaaga	328980
agttcatcaa	ttgcagacac	tgaatcttct	tctcgacctc	agagtaaatt	aagatcctca	329040
tcagagaaaa	atactgaagg	actggttata	gaaaagacct	tagtcttttc	tatagaagat	329100
tgctgataga	ataaataggc	aacgcaaaga	acagagcaga	ccgatagagg	gatcagcatg	329160
cccaaaaacaa	acgtcccaac	actaatgatg	ccacaaaagt	agagaacaga	catcagtggtg	329220
gctatagcta	agatagctaa	aatcaataaa	gtaatcggtc	ttaaactact	tttcaatgaa	329280
agaccatagc	tacttggtgt	gttcactaca	ggctcatcta	tgactgggtac	ttggggagcg	329340
ggatgtttca	tactcaaaaa	tcaataaagt	ggtgtaataa	aagatccaga	atttttccag	329400
aacctatcgc	ttgcgttatc	tctttgaaag	gaactcctaa	atgttctgct	ataatcttaa	329460
gttccttttt	tctagctatg	ccagaacaaa	gcattcccat	tagcatagga	cgaaaaagcg	329520

cagcccaatt	actcatcggc	attgctttct	ctaataaacc	ttttaagaaa	gtctgacact	329580
tgggattctc	gtgtagcaat	tctattaata	aaaatgggtt	ttgtaaaata	acagattgtt	329640
gatttgagaa	gaatgtaaat	aaaagggaga	agtccttgta	gtggctagct	acagaactag	329700
taaaattcca	actggagggt	gacggtatct	tctcacaana	tgctaggcgc	tcactcaaag	329760
actttttaag	aacgcttaga	tctttaaagt	catacatata	ctcagaagag	ttgattgccc	329820
gaacgtagtt	gtccccatct	ttagctgaag	gaagttcctg	agcatcgctt	gggaaaagag	329880
ctcgaaactc	cctttgcate	tcagaagact	ggaaaagataa	aagaaactgc	actatatctc	329940
ctgcttctaa	atgcgccttt	aactcgtcag	taagaagatt	agggtcgtat	gcaacgattt	330000
tttcaataca	cttttctctt	aatgaccatc	catagaacca	aaaattaata	gaaagtacca	330060
actttctgat	atgaggagtg	agctttcgtt	tttccgtttt	taaaagaattc	aggtgcgcaa	330120
tcaactgttg	ggtcaccata	tttaaaggct	ctgggtttgt	taaaagaaga	atgagtaggt	330180
cagagcttgc	atattcttct	actatagatc	ccagacgcct	taaaacaagcg	gtcaaagagt	330240
actttacctt	gcgactcaag	aaacgaggaa	gaaaaagatt	cttaatttca	gagatgactc	330300
ccctgagcaa	gctaccagaa	ctcttagagc	tttccctccag	agcgcgaggg	aagtcacaac	330360
ttaacgttgt	gatctctttt	tctagagact	gcattcgcctc	tgctatcgcc	ttagaataga	330420
ctttattctg	atgataaaat	gtacttttga	taacataggg	cttaaaatca	tcttctacta	330480
ttgatgggat	tttagcctta	aaagaaacgg	tcttacgcctc	tttgggaaga	ctttgacctt	330540
caaccggaac	aggcttaaga	ctttcagggt	cttttatctt	aaggtccttg	gtgggggtcta	330600
tcttttcttc	gttagagggc	tcaattaagg	gttttctctc	cttatacaaa	cacattaggg	330660
aaacaatggc	catcatggag	catactgaag	cggcacaccc	ccaaacaaga	agacctagag	330720
gagcggcaag	tacatgacac	cctaccaaa	cgaaaacaac	accagcaat	aaaagaaccg	330780
aaatggctaa	aagacagaga	atagtcacag	gagacaatga	gaaggactga	ttcttctgt	330840
aaattattctg	gtgacttgct	gtgggtctctt	tatttgcagt	gaaaaaaaat	aaattaaaca	330900
attcttttta	aaaaagttag	ttaagcaaaa	tcgacgaaaa	tattatacaa	aactaattaa	330960
aaaagagaaa	gtttatacct	ccggctatca	gaaaaaagat	tatcattgac	ataatatcat	331020
ttagggctgt	gacaatgggc	ccggaggcta	aagccgggtc	tactcctagc	ttagcaaaga	331080
aaaatgggga	taaaaccctt	agagtcgtag	ctgtgagaga	agctcccaga	accccgtag	331140
ccaccgtaac	gcctagttga	atacctctc	cggagaagat	atttaagcct	agaaagccca	331200
ttaaatagac	aacaagacca	catagaatcc	ctaaaacgac	tctgtgaagc	agcccgatac	331260
tccattcttt	aaaaatgggt	tctcgacgcc	gtccgaaaga	aagcgtccct	gtagccatac	331320
tccgcataaa	aatagtgtga	cattgaacac	ctacatttcc	tgacattccg	ttaatcaaag	331380
gaataaagaa	gataatcaga	gctaaaagg	cgggggaaat	tttttggaag	tatgccatga	331440
cggaggcgct	aatcaaacct	gcaaataag	tcaccaaag	ccaggagct	cttagtaaaa	331500
atctttgcac	aacatgacag	gtctgataac	ccacatcttc	cgtagtacct	gccatcctag	331560
ctatagtctc	atcagcgatg	tctcgtatag	cttcaacaac	atcttcataa	gtaatagccc	331620
caatcaagaa	attttctctc	tcaacaaccg	gaagagcgcc	aattttatac	ctctctacaa	331680
gatcgacgac	ctcttcacgg	gtagcatcag	gaagcacctt	atgttcaatc	tgattcataa	331740
tttgctttta	agacatctcg	ggagggttaa	tgatcaaaact	tctatcggtg	acgacacctt	331800
gcaactcgcc	tttaaaatcc	aaaacaaaga	ccaaacgagt	taaatcaatc	ccaggattac	331860
ttcgaataca	agcagaaacg	tctttcaccc	ttgtttccat	caaaaaggca	aaaaactcat	331920
tggtcatcag	ccttcttgca	gtatttcttc	cgtgtttctg	caaatcacga	attttttagtg	331980
cttttttaga	atctataagc	tcaagaatcc	tccgatacct	acgatcgggg	atatcatcta	332040
aaaccatac	cgcttcatct	ggaggcatct	gttcaattaa	agcgcagacc	tcagaatccg	332100
acaacctacg	aaaaatcgcc	caccgcgaag	cagaatctgt	attgatgata	aacgcaactt	332160
tagcggtaat	acaagagagg	ttcttatata	aaatagcagc	cgattccgag	ggaagacagg	332220
aaacagcata	agcaagggtc	atcggtttat	actcaatcac	aatttttagaa	agatcatgag	332280
aatgtatatc	tgtagaaaaga	caagtaaatg	ctttttctaa	cttaaaactc	agctcgtcac	332340
ctagatgact	cgctctggaa	tccatcaagt	tcccagaact	aaaagctgta	tctagtttct	332400
cttcatttctg	gttttggtcc	ccaaccataa	tcttcccttt	tgattctcta	caacttcacg	332460
aaatgcatgg	atttccctga	ggttagctaa	ataaggatcg	tttaaccact	tggtctctgt	332520
aatacgaacg	ccatactgcg	cagagcgaat	gaccattccc	cacgccttgt	tcacatcttt	332580
gatcactgca	taaaactttc	ccaaagtata	atacgcctct	ggacacccca	aagaagttgc	332640
cttctctaaa	tatgttctag	caagcttacc	taaacacaca	tctttatttt	tccaaaatag	332700
gaataagtat	acttttctta	acagtagtaa	gaaattctca	tcttcaagat	aaacttcaac	332760
tagaggttct	aaaatctccc	gtgcttcttc	agccgggtct	gtatcttgta	gtaattcttc	332820
tttccccaac	aaaaccgcag	caagaatcaa	tttaacccta	gaggaggata	aagtaagatc	332880
taccttagtt	aaaagtgtgt	atgcctcatc	ataatgaaac	aaactttgtt	gcagttcgcc	332940
aagcaataaa	tgagattgtc	cccaaagttc	taggatttcc	agtcgaccac	ttaaattccca	333000
cgctctctga	taatgtaaca	gtgactctga	taagaaaatt	tctttataag	cttcatcgat	333060
tgtggcttct	gccaagcatt	ttaatgctaa	tcctcgatca	ctccaaaata	aaaaagcttc	333120
tggaagcaaa	gaacataacc	tacttgctac	atctacagct	tttcgtagca	actctagcact	333180
ttttttcttg	atcccccaag	aaaaatatgc	atcaataaat	ttttgccaca	ttctgtctgc	333240
atccaaatcc	cattctaaac	aagactgaaa	acaagaaata	gcagaagcaa	aatgcgagtc	333300
ctcattgaaa	taaagtgcgg	agcaaagctg	cacaacacca	agagcatgga	ctaacgcact	333360



attgccagga	aacatcctca	tagcagaaat	cagcctgtgc	cgactatctt	taaataaatt	333420
tggttcttct	aagtataacc	ctaaaatagc	aatccctgta	gctagtaaac	ctgaaagcgc	333480
aatgggatca	ttcgtctttt	tttgtaaaga	agccagtttt	tctaaaccaa	cttcaatata	333540
cttcataatta	ctattcaacc	atcccgaacg	aatgaggagc	tcaccccaaa	ccatccatag	333600
ccctgaaaaga	ttaggaaacg	cctgaacggt	ttggtaaagg	atgttcatag	cctgatcaaa	333660
atgctctttt	ttataagtca	gatcgaataa	cttcacagaa	gcaagagcat	agctataacg	333720
ataattttga	taggcaaggg	tgtcaccatc	cctgctgaaa	ctcagaaaaa	tggcttttaga	333780
aaaatgctcc	atccctcttt	ctatgagcaa	agactttccc	tgtctagtgc	ctaaaactac	333840
caggccctta	gcatagtcag	catggatatg	agcattatta	ggtgataaat	ctagagctaa	333900
ggccagacat	ttcatgccgc	aggccaaatc	actcaattct	aagtgcctgt	ggtataattc	333960
tataaaacta	cggcccacag	cctgatacac	agaagcactt	gctactaaag	aaacctcttc	334020
ttgcttagct	cctatacgga	agtgtcccca	tccaaaacga	ttcttcagtt	gaggatgcat	334080
tttcaaaagc	tggttctatta	aacggaaatt	atctacaact	tcagagagaa	atttcatctc	334140
tcccgtctga	gaataaagtt	caaaattgat	acaggttctt	gcagagcaca	aggaaagcct	334200
atcagaagca	ataattccta	atttttcaaa	aagaaaatct	atatagggtca	aaacatcaat	334260
gaaaatcgac	atacttttat	gttttaaaac	ataagagacc	ccatagaaaa	tcactctctt	334320
tacaacttta	gggtgattgt	gagtcacat	taatagagac	cgagacaaag	ctaagtagcc	334380
ctcgctcggt	tcgtcttggt	gtgccataaa	ttcaatttca	gagaaaagga	aatcaaccac	334440
atcttctgga	caactgaact	catcctgcaa	gccccacata	tttaaggctc	ttttagagga	334500
aataaaaggt	aatggtgatc	taatcataca	ccttctttta	ttatcatagc	taaatcacct	334560
tgaaattcat	attagaaggt	gttcttacc	actaataaaa	actagttttt	gaaaagaatt	334620
ctaaaaacct	tcttttaate	ttttcaaaaa	caagaacatc	tatttcttat	tgacaaagca	334680
cttcatctat	tcatagtctc	aaaactgaga	tcagtctatc	ctatttcatt	tttcaattaa	334740
aaatattttc	tatctctata	gtgacagtta	tccccttttag	aaaaggctgc	ccatcgtctt	334800
taaaacaaag	agcctgtcac	tataaatctt	gtttaaaact	cgcaaaagac	tctagggttaa	334860
attcttttga	tacttaaaca	ataaaatttt	tagcactgtc	attccccgaa	tcagggatca	334920
cacttatatg	tggatatcta	ccactagtgt	cgagccctcg	tctctcaggg	agctggattg	334980
agggatgggc	tccagaaaca	atttctcctt	tatcaaaaaag	gaagacagat	tgtggctggc	335040
aacacaacat	caaataaaaa	gcatgctgtc	ctaaaccttt	acgcccccca	cctccttcaa	335100
atcgggaata	ggaatgagcc	tcattggcta	aagatacaga	tcgcgcaagt	atcacgttat	335160
catccaatac	tctttctaca	ctccccatca	atacacggcc	tgcaagaggg	tccaacaaac	335220
tataaaaagc	tcctatcata	catgcagaag	cataaaaagg	agctttcaaa	aaagcagcaa	335280
gagaccgccc	catctctcga	gcaacatctt	tataaataaa	tctatcgtct	tcgggaagat	335340
gtttacagaa	aaaatgctcg	taaatcattc	ggaaaatgat	ataaaatgga	accactaaaa	335400
agcgtatcaa	attgtaaatac	attctaagca	aagctacaaa	aggcatcgca	cacggaattc	335460
caaaacaagg	gaatgcgcga	aataataatg	gtggacattg	ataaaccgca	gctattccag	335520
aaccgtcagc	actcagcgtc	gatatatcta	gataagagca	agcactcacg	tgcttttcat	335580
cgaattcttc	caaagtatgg	ctggaggata	taggaaccca	acaccgtctg	ctaaaagggtg	335640
gaataccacac	ccctgaaatt	acatctactt	tcttccccag	acgatgcaga	atgtacatgc	335700
ctccagtaag	caaaattggt	gggataagaa	ttgctgcagt	aaccaaaggc	caggaagtaa	335760
ttacaagtgt	accttgatg	ctcgctaaca	ttatactgaa	tagaatcaac	acaccacga	335820
cagcaagagc	gatcacctgt	agcctcacaa	aaagggttcgc	atcatattta	ttcactttac	335880
aaacagaaac	ggacagggta	tcagatctat	gctttcgcaa	tgctgaacga	aaatagcttt	335940
gccatccttg	tttggggaaa	gatgccttag	gactaattgg	tctttaaactt	tcgtttgtag	336000
atgtaagatt	aaaacaagac	ataattacat	tataaaattt	tgctcggcac	tcaaacccaa	336060
agaaaagaaa	ttcacgaatt	gttatactta	tttaccattt	aaaattttta	tcgacttatg	336120
aaaaaacaac	gctctcatta	tacaaaaaat	aatcttttat	tacttctttc	tatattgggt	336180
ggcctaggtt	taggaagtgt	gcaatcccca	tggattgttt	attctgccga	atgcatagca	336240
aatacttttc	taaaattctt	acgttttact	agcattcctt	tgggtattctg	cgctctcggc	336300
tccaccatta	cttctataca	aaatttcaat	actatggtga	ctctaggaaa	aagaatttta	336360
tattataccc	tgctgacaac	agttatcgct	gcttccattg	gaottctgct	gttcttttta	336420
ctccgtcccc	aaatgataac	tcaagatgcc	ctagccacaa	ctacaaagtg	taatccccca	336480
ggatacttgg	atgtccttag	cgacaccctc	ccagaaaata	cttttaagcc	attcctccaa	336540
ggaaatgtca	tttcagccgc	ttgcctagca	gtcctgctag	gaaccgcgtc	cctattttctt	336600
caagaaaaag	aaaaacattt	cgtaaataca	ttttttaatt	catttttttc	tatctttctc	336660
aacctggcta	gaggcggctt	aaaacttctc	ccaatagcaa	tgctcgggtt	ctctgtcatc	336720
ttgttcaaag	aattgaaaga	tcaaagcaac	cttacaatgt	ttgccgagta	tctgctttgc	336780
gttataggag	cgaacctcgc	ccaaggtttt	attgttctcc	ccatactact	taaaataaac	336840
aaagtctctc	ctttaaaagt	cgcaaaaagca	atgtctcctg	cactagtgc	agcttttttc	336900
tcaaaatcat	cggcagcaac	attacccttc	accatggaac	ttgctgaaga	tgatttaaaa	336960
ataaataaga	atctttctcg	atttagcttc	ccgctatgct	ctgtcattta	catgaacggg	337020
tgcgctgctt	ttattctaat	tactgttttg	tttgttgcca	cttccaatgg	tatgatcatt	337080
tcgectctaa	tgtcttttag	atggattttt	attgcgactc	tcgcagctat	aggaaatgcg	337140
ggcgtaccca	tgggatgcta	ctttcttact	ctttctcttc	tcacatctat	gaatgttctt	337200



ttatctatat	taggtctcat	cttacctttt	tatactgtaa	tagatatgat	agaaacttct	337260
cttaatgttt	ggtctgattg	ctgcgtagtc	agtttagcaa	actaacaact	ctcaaaaaaa	337320
ctctcactat	aaaggagtgc	tttaaccatg	aataaaaaac	acgccagttt	ttcatctcga	337380
ctaggattta	tattctctat	gatagggatt	gccgttgggg	caggaaacat	ctggcgcttc	337440
ccgagagttg	ctgctcagaa	cggaggtggg	gcattcctaa	ttctctgggt	atgtttttta	337500
tttttatggg	ccataccctt	aattattata	gaactctcta	ttgggaaact	aaccaagaaa	337560
gctcctatag	gggctttaat	taaaactgca	gggaaaaaat	ttgcttgggc	tgggggcttc	337620
attacccttg	ttaccacttg	tatactcgcc	tactactcta	caattgtagg	ttggggatta	337680
agctactttt	attatgcagt	ttcaggaaaa	attcacctgg	gaaatgactt	tgcaaaatta	337740
tggacatccc	actatcagag	ttctatccct	ctctgggcac	acctcacctc	attaggatta	337800
gcctatcttg	tcattcgtaa	aggcattgtc	catgggattg	aaaaatgtaa	taaaatcctg	337860
atccccgcat	tctttctatg	taccatcgct	ctacttttac	gagcagtgac	tcttcaggga	337920
gccgttcaag	gaatcaaaca	actcttttagt	tgtgataaaa	gttgcttttc	aaactacaaa	337980
gtatggatag	aagctcttac	gcaaaatgct	tgggatacgg	gagccggatg	gggcctactg	338040
cttgtgtatg	cgggctttgc	ctcaaaaaaa	acgggagtag	tgagcaatgg	agctctaaca	338100
gctatatgta	ataaccttgt	ttccttaatc	atgggggatc	attatctttt	ccacatgtgc	338160
ttcttttagac	atttttaggaa	ccacgcagct	acaagatgga	gcaggagcgt	caagcatagg	338220
gattaccttt	atctacctac	cagagttatt	taccctgttg	cctggaggaa	tttatctaac	338280
cacctgtgtt	agctctatgt	tcttcctagc	attttctatg	gcagcgcttt	cttccatgat	338340
ttccatgctt	ttccttctct	cacagactct	tgcagaattt	ggaatcaagc	cctacatttc	338400
tgaacccttg	gcaacaatca	ttgccttttg	cctagggatc	ccttctgcac	ttagtctcac	338460
atttttctct	aaccaagata	ccgtttgggg	agttgcactt	attgtaaagt	gcttgatctt	338520
tatttacgca	gcttttagtct	atggcttccc	taaaactaaag	aaagaagtca	ttaacgctgc	338580
tcctggagat	ctccgactca	acaaagcctt	tgattatata	atcaaatatt	tactcctaata	338640
tgagggaatt	cttcttttag	gatgggtatt	ctatgaagga	ctcttccctg	aaaatgggtca	338700
gtgggtggaat	cctattttctc	tctatagtct	gggcagttta	gtcctgcagt	ggtcttttagg	338760
actcataatc	ttatggaagt	tcaataaaca	actttattta	agattttccc	gttacaatca	338820
cgaaattcta	taaatccaat	cgataattct	actctgaata	ttcagggtag	aatcacagca	338880
ttttggaaag	aaaaaaatat	ttaaagattg	aaaataacgt	tttctctggc	ctagtatgtt	338940
tggcattaat	ctatttttag	ataggaaaaa	catatgtcag	cacctatacc	aaccccacaa	339000
gaattgtcag	accaaatac	ctgcttaaat	gtccaatacc	aacagggtatc	cgaactagca	339060
agagaaaaca	aaggagatat	tgaaggctta	aaaacactga	ctgcggctct	aaccgctgat	339120
gctggcatac	agccttcagc	tgatgaaatt	tactcattgc	aaacagccgc	agccctaatac	339180
ttatctgctt	ccgaaaaacc	tggaagcggg	ccctctggaa	gtactgaagg	atctgttact	339240
gttcaatctc	catgcaaatt	caaaaaagta	ctagcagtcg	tattaacgat	aattgcttta	339300
attgcaattg	ctgtacttat	agcttgtatt	attgctgctt	gcggagggtt	ccctctactt	339360
ctatcagctc	ttaacctata	taccataggt	gcttgcgat	cactaccaat	catagcttca	339420
acctcggttg	cgcttatttg	cttgtagaca	tttgtagcaa	actctctaata	taaaccgta	339480
attactgtcc	gtacaacaag	ataataagta	aaaaacacaa	aaaatagtga	ttttatgacc	339540
tcaccgatcc	cctttcagtc	tagtgggcat	gcctctttcc	ttgccgagca	gccacagcaa	339600
ctcccgctca	cttctgaatc	tcagctagta	actcaattgc	taaccatgat	gaagcatact	339660
caagcattat	ccgaaacggg	tcttcaacaa	caacgcgatc	gattacnaac	cgcattctatt	339720
atccttcaag	taggaggagc	tcctacagga	ggagcgggtg	cgctttttca	accaggaccg	339780
gcagatgatc	atcatcatcc	cataccgccg	cctgttgtag	cagctcaaat	agaaacagaa	339840
atcaccacta	taagatccga	gttacagctc	atgcatctca	ctctacaaca	aagcacaaaa	339900
ggagctcgta	caggagtctc	agtggttact	gcaatcttaa	tgacgatctc	cttattgggt	339960
attattatca	taataactagc	tgtgcttggg	tttacgggctg	tcttgcttca	agtagcttta	340020
ttgatgcagg	gtgaaacaaa	tctgatttgg	gctatggtga	gcggttctat	tatttgcttt	340080
attgcgctaa	ttggaactct	aggattaatt	ttacaaata	agaacacgcc	tctaccggct	340140
tcttaaaaaa	ataaattgaa	ttagaataag	taatagtaat	ttcttctata	cctcccttgc	340200
aattaatcac	tttggtctta	taaaatgtct	tcttttgctt	gggtagggtat	ggagtatgca	340260
gagagttttg	cgactgctgt	ttaacctaca	tcattgggaa	gaaaaaaggg	cttctctttt	340320
ttttctcttg	ggattggtct	gggggatagg	ttgttaccgc	actctctctc	tagctgaagg	340380
cttattcatt	gaaaaattag	gatcggcaga	attaccaaaa	atttatttag	gttcttctct	340440
gatcctttgc	gttctttcat	ccctaattct	ttacaatctt	tttaaaaaac	acatctcagc	340500
aacagctctt	ttcttaattc	ctgtttcttt	atctatcctt	tgtaattttt	atcttattct	340560
ctcttctatc	tttgctatcg	atcccccccg	gtctctctct	tttttctatc	ggattgtaat	340620
ttggagttta	acgattctct	cttacacgag	tttttgggga	tttgtagatc	aattttttta	340680
tttacaagat	ggaaaacgac	acttctgtat	ttttaatgct	atcatcttct	taggagatgc	340740
tatcggcagc	ggaatcatag	ctagcctggt	acacacataa	ggaatccagg	gcactcctgat	340800
tttatttaca	gcagccctgg	tcctgacatt	ccctatcgta	ttctatgttt	caaaactctct	340860
aaagtgcgct	tccgatgacc	atgacctttt	catagataca	ggccaccac	cacccttattc	340920
aaaagcattg	aaactctgtt	tttatgataa	atatactttt	tatctgcttt	gctttttattt	340980
tctcatgcaa	ttgctagcga	ttgctacaga	gtttaactat	ttaaaaatct	ttgaaattca	341040

atttgcctct	aaggaagaat	tcgaactcgt	cgcacacata	ggaaagtgtt	ccctgtggat	341100
ttcttttagga	aatatgtgct	ttgctctttt	cgcctacagt	agaatagtaa	agcgtcttgg	341160
agtcaataat	atcattttat	ttgctccgct	atgtttctta	agcctctttc	tatttttgga	341220
ctttaaaaca	accctaagca	ttgctgtcct	tgctatggta	gtacgtgaag	gcgttaccta	341280
cgctcttgat	gacaacaacc	tccaactact	catctatgga	gtccccaaca	aaatccgaaa	341340
ccaaattcgc	atcgtagtgg	aatcctttat	agaacctatc	gggatgttgg	tctggtcctt	341400
agtctgtttc	ttgtcttctc	aacaatatgt	gttctgccta	atcatctcac	taatcgccac	341460
tattctgggt	tgccctgtac	gctcttatta	tgcggaaggcg	attctcaaaa	atctatctgc	341520
acaagcccta	caacttacc	gctctatgca	agattggatc	aaatctatga	cagttaaaca	341580
aaagagacaa	gtcgaactct	tcttacttgc	tcatcttaaa	caccccagtg	agcgtcatca	341640
aacctttgct	tttcaacatc	tcttaaactc	agcaagccgc	agtgtccttc	caagcctcct	341700
tgcccatatg	aacaagctca	gcctccctaa	taaactcaag	actatagaaa	tggtaaaatc	341760
tagcttatgg	gccaaagatt	ttctaaccct	agagctcctg	aaacgttggg	caagtatttt	341820
cccccatcct	gccatcgcat	cagcaatata	tctttatttt	gcagaacacg	atctcctaca	341880
tatcactcat	attgctgaag	acctctatga	tactgttggg	gatagacttc	ttgccgcaat	341940
tcttacagta	agaagacagg	aagcttatgg	gccctatcga	gaccttgcag	acaagcgctt	342000
gaaagaacta	ctcaactcgg	atcaacctga	agatatagtc	atgggggtga	ccatactgaa	342060
attagaaaag	aatccacaga	acttcccaat	tcttttagac	ttcttgaaca	ccaaaaacga	342120
agatatctta	attgtcacct	gcaaagccct	acacacttct	gttagagcta	atcataaacc	342180
ttattgcccc	gaacttctga	aaagactacg	acaatgctcg	cataatgatg	aagcaagtca	342240
atatctatta	aaaacaatta	gcattgcttt	agatatctca	ttcgtaaaag	acttactgat	342300
gacaacatga	caactaaaaa	acacctctag	aaaatatgct	gaggctatga	ttggagagtt	342360
ggataaagaa	gtcgccccag	catttctcca	agtcctcacc	gatgagggaa	cacacaatcg	342420
ttgtcgtatc	cttgccgcca	aagccctctg	taaaatcgat	aattggctgc	tgaaaaaaca	342480
cgcgataaaa	attgtgaagt	ctaaagcaag	taaggctctg	ttctattcct	atcacggcca	342540
ttacattcaa	aagaaatacc	ccacatacaa	cctcagcttg	ctggcaaaca	cattaaattc	342600
taattattat	gcagaagtaa	acttcatgct	ctctctccta	gggattcttg	gttccatgga	342660
gcactctggg	gtactgattc	gagcattaac	tagtaaaaaa	caaaaaatca	aagcacaaagc	342720
actagaatct	ttagaaaaaa	actgcatag	ccacttattc	tctttactag	aaccttttgt	342780
taatcaacca	ggcatgtgct	atagcgaaaa	atactacttc	aaatgtgggtg	tgattcctct	342840
aactcttaaa	gaacttttaa	atatgatgga	aaactcccca	tcatctttaa	acaaactaac	342900
agcacagcaa	ctcaaagaag	aactttccta	ttgcgatcca	gactttccaa	tctgtaaata	342960
caatctataa	ccaagaacat	gaagacttca	ggacagagga	atcagaaacc	ctaatatctt	343020
tcttatctat	ctaaacttca	atgattccaa	tttagatatc	cacagaaaaa	ccttgggaaa	343080
ctgaagattt	aaaaaaacca	agattgatgt	ataagtttcg	actgcaagaa	aaatcaattt	343140
caacgggtcc	ttcttgaaac	tcttctatct	taaaggtaag	atctacgtat	caagtattac	343200
atctgtgggtg	atattaaaaa	ccttgatttt	aacaacactg	attcttctta	aacctattgtg	343260
gaggcttttt	tttaaactac	ctgcactgta	gttattgctt	ctatccttcc	caaaaataata	343320
caatccatct	caaggatagc	tctctgtgcc	tttacttttg	tcaaaaacta	aaactatggt	343380
gtgaataagg	aactttttta	tgaatttgat	cgatcgcgcc	tttctactaa	aaaaaacgat	343440
tatatcccaa	tcttttagaca	tggaccttct	tttaacaatt	gccgataaaa	ctgaaacgat	343500
aatatttaag	cctggcagca	atgtattctc	tataggacaa	cctggattca	gcttttatat	343560
cattgtagaa	ggatacatta	cgatctctaa	agaaaaacta	gagtctcctc	taaatttaaa	343620
acctttagat	tgttttgag	aggaaagctt	attcaataat	aagcccaggg	aatacaatgc	343680
ttctgcaaat	acacaagtcc	gcattgctagt	tcttagcaaa	ggacaaattc	taaactattgt	343740
ggaagagtgc	ccatccgtag	ctttatcttt	tttagagctc	tatgctaaac	aaatcaagtt	343800
cagagaacct	taaaaagaca	aaataaatct	ttctagatga	gctactctat	agaaaaaaag	343860
gcacgccgta	atcactattg	aaaaacaata	gctttaaaaa	agattacgac	gcacccagaa	343920
tataagaaag	tttattgttc	agcttgacgt	ttcttaatat	aagtaaatac	atccccgaca	343980
gtacgaagct	tctcagcatc	ttcttctgaa	atttcaaaaag	caaatttttc	ttctaaagtc	344040
ataatcaatt	ctgttaaate	taaactatca	gcattcaagt	cttcaataaa	agaagagttc	344100
tcattaactt	cttttgatc	cactcctaac	tgctcaacaa	taattgctat	tacatcatct	344160
tctaaactca	tgtcttatat	ccttttacta	tttaaactat	acaatacttc	actattccct	344220
agggacaaag	agaaagagaa	ttagtatcgc	aaaaaatcat	tttttattcg	acggttactt	344280
aattagtctt	cgaagagaaa	ttttcaaate	cctttcttct	attgtcttag	taagtcaatc	344340
ccccatcaac	aaccagtgtc	tgcgcgggtc	tatagctcga	taactgagag	gctaaaaaca	344400
acgccacacg	agcaacatct	tctggaggtc	cagccctacc	taaagggatc	gacttaagcc	344460
actcagcttt	taaattgtca	ttcaacacgc	ttgtcatgtc	tgtttcaata	aagcctggag	344520
caaggcagtt	gacacgaata	tttcttgcag	ctacttccct	agctaaagat	tttgtgaaag	344580
caataatccc	agcttttagca	gcagcatagt	tggtctggcc	cgactaccg	atcttagcaa	344640
caatagaagc	cacatttata	atagatccctg	aacgcgcctt	aatcatatgg	cgaatcactg	344700
aggaacatgt	ataatacaag	gaagtcaagt	tggtgctaat	caccgattgc	cagtcgtcct	344760
cagacatacg	atcaacaaaa	ttatccctgg	taatgcctgc	attattttacc	aaaatatcta	344820
ttttgttgtg	cttatctaaa	aatttctgca	cgcaatcttt	cactccacca	ttatgactca	344880

catccacacg	agcaaaagaa	acttcgccac	ccaagcctgt	taaactttct	ataacagcct	344940
gacctcgctc	ctcattcaat	ccccaaat	ctacatctgc	tccgtttctca	agaaaaagct	345000
taactatccc	gagtccaatt	cctcgagatc	ctccagttac	tataactttt	ttgcctacta	345060
atgttatatc	catacaaatc	atacctctga	taggaatttt	tcaatctgag	caaaagtacc	345120
aagacttgta	atcggtttag	aaatccctat	agagcgtatt	aaaccagcca	aaacttttcc	345180
tggaccta	tctaaaaaact	catccacctc	tgattcgata	tggttaacaac	tctgatacca	345240
taacgtagg	gatgtcattt	gccgagctaa	acactctcgc	atcttctcag	tatttactaa	345300
agattttcct	accacgtgtg	acactaaggg	aaggctagaa	tctttcatgc	ataaagcata	345360
aatgtctgga	gctaagccat	cttgagcaac	ttgcattaaa	ggagtatgaa	atgctccaga	345420
cacctttaaa	cgaactgctt	ttttacatcc	taaatcacga	aataactcaa	tcgcttggtc	345480
tactttttct	gctattccag	ccactacaag	ctgtttgggt	gcattataat	tagcaatcca	345540
aattccttga	ccaagacttg	ttatattttt	ctctataact	tcagagggaa	gccctataaa	345600
agccgccata	gcccctgggc	tctgattaca	agcttcattc	attaactgac	cacgctttct	345660
aacaagctca	agcccgctga	gcacggagat	tctatcgaa	gcaactaaag	cagtatactc	345720
ccctaaaact	aattccagaga	ctaaagaagg	ctgaatagaa	gaacgctggg	atagaacctt	345780
taccacagcc	atgctatgaa	gataaatagc	tagctgacta	tgtactgttt	ccatcaaaag	345840
atcctcagga	ccttcaaaca	taattgaagt	cagagaaaat	cctaaccttt	cattagcaaa	345900
atcaaaaagc	tctctaacct	caggatactc	catatatagg	tcttgtccca	tacctacata	345960
ttggctccct	tgctcctggga	acaaaaaagc	ataacgtttt	ttcatgaaat	tatcgctcct	346020
attagacctg	ctttaaaaact	actgcgcccc	aagacaaaac	gcccccaaag	gcaactaaaa	346080
gtaataaatc	atcaagctta	atggattctg	tattgaactaa	ttcatccaaa	gcaatgcccc	346140
cagacgagcg	cgcagtattt	ccatacttat	gtacactctt	aaacactcta	gactcatcaa	346200
tctcaaaaacg	cttcgctaaa	gcactctatta	ttctttccat	ttagcttgat	gaggtacaaa	346260
ccaatctata	tcctcttctt	gaatgcctgc	cagggctatc	gaatgtttag	ctgccgtttc	346320
catacgtctc	acagcatgct	taaaaacttc	ttttccctcc	agagcaataa	aatgtttgcc	346380
tgattgtaaa	gtctcttttag	aagcaggaca	acgactacct	ccagcaggaa	ggcttaatac	346440
tctcctagct	taccatctgc	gcctaaagac	aacctattaa	tctctaaaga	tcctggccga	346500
ctctccccta	tgacacaagc	agctcctcca	tctccaaaca	acacacaggt	attccgatct	346560
gtataatcta	caaaaagaaga	caacttatca	gcagcaatta	acaatacatg	gttatatgta	346620
cctgattcta	cataagcctt	agctacagac	aaaccataca	aataccaggt	acaagccgcc	346680
tggcaatcaa	atgtaggggac	atcctcaatg	cctaaatgtg	cttgagcaag	actccgcttg	346740
atgggaaaat	ataatctggg	gctgctgtcg	agaaaatgat	acagtcaatc	tgatccttgc	346800
ttaaacccgc	atgttgctata	gctttctctg	cagcgatggc	tcccataaga	gaagtgtact	346860
cctgaggtcc	agcaatacga	cgctctttga	tcccgtttct	ggtcacgatc	cactcatcag	346920
aggtatctac	cattttttct	aaatctgcgt	ttgaaagaac	tttctcaggc	aaataggaac	346980
ccgttgccca	aattgctgct	tttttgtttt	tattcacaga	gaaccacatg	taaagaaaaa	347040
agctagtata	ctattcagag	agtttatact	ctaacccttaa	tttaggcccc	agacccgaat	347100
gtaaaaataa	aattcacatc	actatgacaa	gatataccaga	ttacttatct	aaattaattt	347160
tcttttttacg	aaaactttcca	ggaattggat	ttaaaacagc	agaaaaactt	gcttttgaac	347220
tcactctcttg	ggacagcgaa	caattaaaaa	tattagggtaa	cgcttttcat	aatgttgcta	347280
gtgagcgtag	tcactgtccc	ctatgtttta	ctctcaaaga	atctaaagag	gcagactgtc	347340
acttttgtag	agaagaaaga	gataaccaaa	gtctatgtat	tgctcgttct	ccaaaagatg	347400
ttttctttct	agaacgttct	aaagtattca	agggacgtta	tcattgttct	ggttcactct	347460
tatcgcccat	tacagggaaa	catatagaaa	acgagcgtct	ctccatttta	aatcacgcga	347520
tagaaaacgct	atgccccaaa	gaaattatcc	tagccattga	tgcaacctta	gaaggagatg	347580
ctactgccct	ttttctaaaa	caagaattac	aacattttct	tgtaaatatt	tcccgtctag	347640
cttttaggtct	tcctataggc	ttatcttttg	attatgtaga	ttcaggggaca	ctggcaagag	347700
ctttttctgg	acgacactcc	tattagcagc	tctcttatcc	taaaagtaaa	caagttctct	347760
tctatgctag	tctttcttac	tttcccctag	gacacagtga	attatcgaat	ttgccttaaa	347820
accatgtaat	cagtagagtt	atgttgagcga	caaggtttat	taagcttttt	aaggaagcaa	347880
aaaacccgcc	gaaatattca	ggctctagtc	tgagcacagt	aataatcccg	gtgttaggac	347940
gggaaaaaat	caaacacaat	ttaaattttct	ttagaaaatac	aaaaataatc	taagttagtaa	348000
ggctctgtta	aaaaactttct	ttgtccctat	ttttgtgctt	acctcattat	ctgataaaaca	348060
agctttctat	ctagggaaga	ctcttgggaa	tgctcatcat	gcgaaataaa	gttatcttgc	348120
aaatatctat	tctagcggtta	atccaaaccc	ctttaacttt	atcttctact	gaaaaagtta	348180
aagaaggcca	tgtggtggta	gactctatca	caatcataac	ggaaggagaa	aatgcttcaa	348240
ataaacatcc	cttaccctaaa	ttaaagacca	gaagtggggc	tcttttttct	caattagatt	348300
ttgatgaaga	cttgagaatt	ctagctaaag	aatacgactc	tggttagcct	aaagttagaat	348360
tttctgaagg	gaaaactaac	atagcccttc	acctaatagc	taaacctcca	attcgaaata	348420
ttcatatctc	aggaaatcaa	gtcggttctg	aacataaaat	tcttaaaacc	ctacaaattt	348480
accgtaatga	tctctttgaa	cgagaaaaat	ttcttaaggg	tcttgatgat	ctaagaacgt	348540
attatctcaa	gcgaggatat	ttcgcattcca	gtgtagacta	cagtctggaa	cacaatcaag	348600
aaaaaggtca	catcgatgtt	ttaattaaaa	tcaatgaagg	tccttgccggg	aaaattaaac	348660
agcttacgtt	ctcaggaatc	tctcgatcag	aaaaatcaga	tatccaagaa	tttattcaaa	348720

ccaagcagca	ctctacaact	acaagttggt	ttactggagc	tggactctat	caccagata	348780
ttgttgaaca	agatagcttg	gcaattacga	attacctaca	taataacggg	tacgctgatg	348840
ctatagtcaa	ctctcactat	gaccttgacg	acaaagggaa	tattcttctt	tacatggata	348900
ttgatcgagg	gtcgcgatat	accttaggac	acgtccatat	ccaaggggtt	gagggttttgc	348960
caaaacgcct	tatagaaaag	caatcccaag	tgggccccaa	tgatctttat	tgccccgata	349020
aaatatggga	tggggctcat	aagatcaaac	aaacttatgc	aaagtatggc	tacatcaata	349080
ccaatgtaga	cgttctcttc	atccctcacg	caaccgccc	tatttatgat	gtaacttatg	349140
aggtaagtga	agggctctcct	tataaagttg	ggtaatttaa	aattactggg	aatacccata	349200
caaaatctga	cgttatttta	cacgaaacca	gtctcttccc	aggagataca	ttcaatcgct	349260
taaagctaga	agatactgag	caacgtttaa	gaaatacagg	ctacttccaa	agcgttagtg	349320
tctatacagt	tcgttctcaa	cttgatccta	tgggcaatgc	ggatcaatac	cgagatattt	349380
ttgtagaagt	caaagaaaca	acaacaggaa	acttaggctt	attcttagga	tttagttctc	349440
ttgacaatct	ttttggagga	attgaactat	ctgaaagtaa	ttttgatcta	tttggagcta	349500
gaaatatatt	ttctaaaggt	tttcgttgtc	taagaggcgg	tggagaacat	ctattcttaa	349560
aagccaactt	cggggacaaa	gtcacagact	atactttgaa	gtggaccaa	cctcattttc	349620
taaacactcc	ttggatttta	ggaattgaat	tagataaatc	aattaacaga	gcattatcta	349680
aagattatgc	tgtccaaacc	tatggcggga	acgtcagcac	aacgtatatc	ttgaacgaac	349740
acctgaaata	cggctctattt	tatcgaggaa	gtcaaacgag	tttacctgaa	aaacgtaagt	349800
tcctcctagg	gccaaatata	gacagcaata	aaggatttgt	ctctgctgca	ggtgtcaact	349860
tgaattacga	ttctgtagat	agtcctagaa	ctccaactac	agggattcgc	gggggggtga	349920
ctttttgaggt	ttctggtttg	ggaggaactt	atcattttac	aaaactctct	ttaaacagct	349980
ctatctatag	aaaacttacg	cgtaaaggta	ttttgaaaa	caaaggggaa	gctcaattta	350040
ttaaacccta	tagcaatact	acagctgaag	gagttcctgt	cagtgagcgc	ttcttcttag	350100
gtggagagac	tacagttcgg	ggatataaat	cctttattat	cgggtccaaa	tactctgcta	350160
cagaacctca	gggaggactc	tcttgcctcc	ttatttcaga	agagtttcaa	taccctctca	350220
tcagacaacc	taatattagt	gcctttgtat	tcttagactc	aggttttgct	ggtttacaag	350280
agtataagat	ttcgttaaaa	gatctacgta	gtagtgtctg	atttggtctg	cgcttcgatg	350340
taatgaataa	tgttcctggt	atgttaggat	ttggttggcc	cttccgtcca	accgagactt	350400
tgaatggaga	aaaaattgat	gtatctcagc	gattcttctt	tgcttttaggg	ggcatgttct	350460
aagatataaa	ttaaggactt	atcgaaggaa	atctttgttg	ttttcagaaa	aggcttttgg	350520
tacccttttt	ctatacccaa	gtttagtaca	ggtaattatg	aaaaaattat	tattttctac	350580
atttcttctt	gttttaggat	caacaagcgc	agctcaatgc	aaatttaggc	tatgttaatt	350640
taaagcgatg	tcttgaagaa	tccgatctag	gtaaaaagga	aactgaagaa	ttggaagcta	350700
ngaaacagca	gtttgtaaaa	aatgctgaga	aaatagaaga	agaactcact	tctatttata	350760
ataagttgca	agatgaagat	tacatggaaa	gcctatcgga	ttctgcctct	gaagagttgc	350820
gaaagaaatt	cgaagatctt	tcaggagagt	acaatgcgta	ccagtctcag	tactatcaat	350880
ctatcaatca	aagtaatgta	aaacgcattc	aaaaactcat	tcaagaagta	aaaatctctg	350940
cagaatcagt	gcggtccaaa	gaaaaactag	aagctatcct	taatgaagaa	gctgtcttag	351000
caatagcacc	tgggactgat	aaaacaaccg	aaattattgc	tattcttaac	gaatctttca	351060
aaaaacaaaa	ctagtccaag	tttaaggagt	tttctatgtc	cgaagcacca	gtctacactc	351120
ttaaacagtt	agctgagcta	ctacaagtcg	aagttcaagg	aaatatagaa	actcctattt	351180
caggtgttga	agatattagt	caggcgcaac	ctcaccatat	tgctttttta	gataatgaga	351240
aatactctag	ctttctaaaa	aacaccaaag	ctggtgctat	tattttatct	agatctcagg	351300
caatgcaaca	tgcccaccta	aagaaaaact	ttcttattac	caatgaatcc	ccttctctaa	351360
catttcaaaa	gtgcatagag	ttgtttattg	aaccgtaac	atcaggggtt	ctcgggtatt	351420
atcctactgc	agtgattcat	cctactgcac	gtattgagaa	aaatgtaacc	atagaacctt	351480
acgttgctcat	tagtcaacat	gcccatatcg	gctctgacac	atacatcgga	gctggaagtg	351540
tcattggagc	tcacagcggt	ctaggtgcta	actgtctgat	tcaccctaag	gtggtgattc	351600
gagaaagagt	cctcatggga	aaccgtgtag	ttgttcaacc	tggagctggt	ttaggatcct	351660
gtggttttgg	ttatattaca	aatgcttttg	gtcatcacia	acctttaaag	catctagggt	351720
atgtgattgt	aggtgatgat	gtagaaatcg	gagccaacac	tacgatagat	cgtgggtcgt	351780
tcaagaacac	cgtgatccat	gaaggaaacta	aaatagataa	ccaagtacaa	gtagctcatc	351840
acgtagaaat	tggaaagcat	agtattattg	ttgcccgaagc	aggcattgca	gggtctacaa	351900
aaattggtga	acatgtcatc	attggagggc	aaaccggaat	tactgggcat	atttctattg	351960
cagaccatgt	gatcatgatt	gctcaaactg	gagtcacaaa	atctatcacc	tctccaggca	352020
tttatggagg	cgctccagca	cgaccttatt	aagaaacaca	tcggttgatt	gctaaaattc	352080
ggaaccttcc	taaaactgaa	gaaagactaa	gtaagttaga	aaaacaagta	agagatctat	352140
cgactcccag	ccttgctgag	attccttcag	agatctaaaa	ttctattttat	tttattagtt	352200
ttgaaatcaa	aaaaaagacc	aaataattaa	atatataaag	aacgtactct	tctttttatc	352260
atgagaattt	tcatgatatt	tttatttttaa	atttctgggc	taactctccc	tgctccgcaat	352320
agttgcatga	ctattttcat	tccaagattg	aattcatcca	gattagaaaa	gataaaacat	352380
tctccgccag	agttttaaagc	ttttgcagtg	tgctctgtat	tggaaagtat	agacgggctt	352440
ataaaacttca	atgaagaaaa	atctacatgt	aaagcaaggc	cccgaattgt	attcgctaag	352500
ctatatctca	acgcaatagg	actcgatgaa	actgaaggta	aagtaggcac	atcattatca	352560

taaatacgtg	cttgaatatt	tccactacgc	ttgagtcctt	gaattagttt	cacatagttt	352620
aataaatcta	tatccacaat	ctcttttaaaa	attaaaagtga	aagcaactcc	atgttgcttt	352680
aaaacatccc	cgagctcctt	gcctagctca	ctcatgctct	gacaattcaa	aagagagata	352740
ttcctatagg	ttaaataata	acgtagacta	tttacaacgg	tagttcctaa	aagaagcggt	352800
aggtctagct	ttttattcac	agtaacaaca	tgctcacact	gttggtcgaa	taatccgcaa	352860
cacagtaaaa	cccctcccaa	acctatagaa	tcattttaaat	gacaaattac	ttcggtaaat	352920
tctaccaggt	cgctactaca	tccgggagaa	taaaaaaata	actgagctat	ttttttatcc	352980
atcgaagtta	acatggcaaa	caattcctta	gtttgtccca	actcttcatt	tttgaatggc	353040
aaccattgag	ttttttttta	gtagtagttt	ttagagtcgg	tcttacgatt	ctgaaattct	353100
tgagcagaag	caacaatacg	ttttgtttata	gttaaaagct	tttccctctaa	ttcttcatga	353160
tctcgagatt	tatcttctact	aggcttatga	tcaaagtttt	tgatgacacc	gtctatcgaa	353220
tccacgtaaa	actgagtggtg	tcgattaatt	ttacgagaaa	cgctccatgtg	atgtaatcct	353280
ttttgttctc	tttaaatgtc	cacgagaaaac	atattaaaaat	tttttcgatt	ttttaaaaaa	353340
acttaattat	tttttcttcg	gatagccctt	gtctttttgaa	acctaggctc	ctataatgag	353400
atcaaaaaacc	gctcccgaag	cgtctccctt	ataaaaaagt	tatggatagt	tcagcacctt	353460
ataatatagc	ttctcagggc	acagagaaat	ccacagtaga	aaggatctta	gacctttacg	353520
ggccccgctt	ctgtattaaa	tttttaaaaac	agatggttct	gattcgtgaa	ttcgaagccc	353580
gaggagaaga	agcctatcta	gaagggctag	tgggtggatt	ttaccactct	tacgctggcc	353640
aagaagctgt	agcaactgct	gcaatcgcaa	acacaggact	agatccctgg	gtgttctctt	353700
cataccgctg	ccacgcactt	gcgattcttc	tcaacattcc	ccttcaagaa	atttgtctgtg	353760
aacttttagg	gaaagaaact	ggatgcgctt	taggtcgtgg	aggatccatg	catatgtgtg	353820
ggcctaattt	ccctggagga	tttgggtattg	tcggaggaca	aattccccctc	gcagctggag	353880
ccgcattttac	catcaaatat	caagaacaaa	aaaatagagt	ttctctatgc	tttatcgag	353940
atgggtgcggt	agctcaaggt	gtattccatg	aaactctgaa	ctttgtttct	cttcaccaac	354000
tccctctaata	gcttattatt	gaaaataacg	gctggagtat	gggaacgtca	ttaaatcgtg	354060
ctgttgcaaaa	acagcccata	gcagagtctc	aaggaagttc	ctacgatata	cgtgcagtca	354120
cagtcaatgg	ttttgatcta	tttaactctc	ttttaggatt	tagagaggct	tatcgctata	354180
tggttgatac	cgaatctccg	gttttagttg	agtgtctctg	ctcccgattt	cgagggcatt	354240
ctatatcaga	tctaattta	tatagatcga	aagaagaaat	gcagtgttta	tttaaaaaag	354300
atcctattgt	cttagctaaa	gattggctaa	ttcgattaga	ggttctgact	gaagaggaat	354360
ttcaaaatat	acgccaagaa	tgcaaaaactg	ctgtttttaga	agcgttctct	aacgcaaaac	354420
tctcatcaga	tccatccgtc	accacattag	aggaaggagt	ctatgcctaa	acataaaaaca	354480
ttagaaattc	gagaagctct	ccgagaagca	attgacgaag	agatgtctcg	cgatccctaat	354540
gtctgtattc	ttggtgaaga	ggttggtgac	tacaatgggtg	cttataaaagt	caccaaaggc	354600
ttattagata	aatggggccc	taagagagtc	attgatgctc	ctattagtga	agcagccttc	354660
tctggaattg	gaataggagc	cgcattgtca	ggcctgcgcc	ctattataga	atttatgagc	354720
tggaactttt	cctttgttagc	cttagacca	atcatttctc	atgcagctaa	gatgcatttt	354780
atgactggag	ggaagttttc	cgttcctata	gtttttcgtg	gccctaattg	tgctgcagcc	354840
caggatctct	gccagcattc	tcattgcgtt	gagtcgttgt	atgctaatat	tccaggtctt	354900
aattattata	gccccttcga	acccttacga	cgctaaaggc	ttattaaaat	cagcaatcag	354960
aaataaanaa	ccccgttctt	tttttagaaa	acgagctaga	atataacttt	aaaaggggaa	355020
gtccccaccg	agaatatctt	cgttcctatt	gggaaagcac	atagagttca	agaaggaaat	355080
gaccttacaa	ttattactta	tagccgtatg	gtttccatta	caaaagaagc	gtgttctcta	355140
gccaaaaaac	gttgggggctt	gtctatagaa	attattgata	taagaacgat	caaaccctta	355200
gacatatcaa	caattttatc	atcggtacga	aaaacttcac	gctgtattgt	aattgaagag	355260
ggccactact	tcgctgggat	ttctcttgaa	attattgccc	tgattactga	gcattgtttt	355320
gattctcttg	atgtcctccc	cttaagggtg	tgccaaaaag	aaacgcctat	gccctatagt	355380
aaaatcttag	aacaggccac	tttgccctaat	gttaaccgaa	tcttagatac	cattgaaaaa	355440
gtcatgaggt	aagtttgtga	tctccttatt	gaaaatgcca	aagctttctc	caactatgga	355500
agtgggcact	atagtgaat	ggcataaaaa	aagtaatgat	caggtcagtt	ttggagacgt	355560
cattgtagag	atctctacag	acaaagctat	tttagaacat	acagcaaatg	aagatggctg	355620
gattcgtgaa	atcttacgtc	atgaaggcga	gaaaatcggt	ataggcacc	ctattgcggt	355680
actctctaca	gaagccaacg	agcccttttaa	tctagaagaa	cttcttccta	agacagaacc	355740
ttctaaccct	gaagcatctc	caaaagggtt	ttctgaagag	gtctcgctcg	caacaactcc	355800
acaagctgcc	tcagcaacat	tcacagcagt	aacttttaag	ccagagccac	ctctctctc	355860
gccttttagtc	ttcaaacacg	taggcactac	gaataatctc	tctccattag	ctagacaact	355920
agcaaaaagag	aaaaacatag	atgtctcatc	aattcaaggg	agtggtcctg	gaggacgtat	355980
agtaaaaaaaa	gatttagaga	aagctcctcc	taaaagcatt	gctggttttg	gctatcctga	356040
gtctcccgaa	gtgcctccag	gttcctatca	tgaggagaat	ctctctccga	ttcgggaagt	356100
gattgctgca	cgcctacaag	ctgctaagat	ctctattcct	cacttctatg	taaggcagca	356160
ggctgacgcc	tcacctctcc	ttaatctgct	caaagaactt	caagctcagg	gaatcaaact	356220
ctctattaac	gattgcattg	tacgtgcctg	tgctctggcg	ctcaaagagt	tcccttctat	356280
caattcagga	tttaacagtg	tcgataataa	aatcgctcgt	tttgatacta	tcgatatactc	356340
gatagctgtg	gccattccag	atggaattat	tacgcccaatt	atacgctgcg	cagaccgtaa	356400

aaatctcggc	atgatttcag	cagaaattaa	gagcttagcg	ttaaaagcaa	gaaatcaatc	356460
tcttcaagac	actgaataca	aaggagggtc	cttctgtgtc	tctaacttag	gaatgacagg	356520
aatcactgaa	tttacagcga	ttgtcaatcc	tcctcaagcg	gcgattcttg	ccgtaggaag	356580
tgttacagaa	caagctcttg	ttcttgacgg	agaaattact	ataggatcta	cctgcaatct	356640
taccctatct	gtagatcata	gagtgattga	tggttatect	gctgcgatgt	ttatgaaacg	356700
attacaaaag	atcttagaag	ctccggctgt	cctactatta	aactagcaat	ctttgaacaa	356760
aaaggactct	ttctatagct	ccttggctat	ggaaaagatc	cctgattcca	tcctgtctat	356820
ttcttaattt	ccttctccag	agcaagattt	tgtaggaaca	tgccaaatat	ctctggcata	356880
atcctgaatg	gctctgtcac	tagagaaaaa	gccattcct	gcagtattat	aaatagaaat	356940
cttagtccat	gaatctgggt	ccttaaagag	tttgttcaca	ttttcatggg	cagcgatata	357000
agactccaag	tcagccaaga	caaaaaaggg	atctccttca	tgtagtaggc	gatgtactat	357060
cggtttaaac	agatctttat	cattgctatt	gaaaaatccc	tgttctagca	aatctaaaac	357120
ctgacggatc	ttaggattct	tatcacaaat	tgtctgagga	cagtattccc	tcgcgagttg	357180
tacaatttgc	tcctccaaaa	gacaaaaaat	aaacatattc	tccttaccac	tatgtctctg	357240
cattttctata	tttgcaccgt	ccatagttcc	tatagtcaga	gctccattca	aagcaaatct	357300
catatttccct	gttccagaag	cctccattcc	agctgtagaa	atctgttctg	aaagatctgt	357360
accaggaatg	atatgctcag	ccatagaaac	tcgatagtta	ggtaaaaaaa	gaaccttaag	357420
cttatcatta	actcgagaat	cttgatttac	aacgtcagca	acgctattga	ttaacttgat	357480
aatgagtttg	gccatgacat	agccaggagc	cgccttacc	gaaaaaatta	ctgttgtagg	357540
gacgacatct	tgattagggt	tttctttcaa	gtcattataa	acatagatga	ctctaagaat	357600
attcattagt	tgctgtttat	actcatgaat	acgcttaata	tgacagtcaa	agagagaatt	357660
agggctctact	atcttcccaa	cttcattata	aattctactt	gttagatcct	gcttattttt	357720
taattttacc	cctttccaat	gatctcggaa	accactatct	tcggcaaagg	aacggatcaa	357780
tgaaagatga	gaaagatcaa	tgatataacg	atccccata	gtttcattga	gaagcttact	357840
caaacgagga	ttacagagag	caatccatcg	tcgtggagtc	acccattggg	tcacattgat	357900
aaacttctca	gggaaaaact	cataaaactc	tttaaagaga	gtatctttaa	tcagctgaga	357960
gtggaatgac	gaaactccat	ttacttttgc	agaacctact	acggcaaggt	ttgccatatt	358020
gatacgcttt	tgataccctt	cttcaacaat	ggataaagac	cggcgcttat	catcattttt	358080
aggatagcga	gagccaactt	tttctaacca	acgggaattt	atctcataaa	taatctctaa	358140
atgccgaggt	aataacttag	agaataaact	gagaggccat	ctctctaaag	cctctgggag	358200
gattgtatga	ttggtatagt	taaagatgac	tgtagtcatc	tcccaagcct	tatcccaagg	358260
taattcttcc	ctatcgacta	aaatatgcat	catcttcagca	atccctagag	cgggatgggt	358320
atcgtttaat	tgtactacga	ctttatccgc	aagggttatcc	aaacaaatat	gtgtctttgt	358380
atatctgcgg	ataatatctt	gaatggttgc	tgaaactaaa	aaatactctt	gtttgagacg	358440
caattcctgc	ccctcagtaa	tagaatcatt	aggatagagg	acgcgagaga	tgttttctat	358500
caaggcgata	tcttctatag	cctggatata	gttcccgtgg	ttaaaatagc	tgaattcaaa	358560
gcctcgcgga	gattgtgctt	gccatagcct	tagagaattt	acagtatcat	taccgtacc	358620
aggaatcgga	atatcataag	ccatcgccaa	tacctcttgg	gtatcgacaa	gatctgccac	358680
ctgtttccct	cgagaatcgg	tataatgaat	gacccttcca	taaaatcgta	cgggatagag	358740
gtactctccc	ctacagattt	cccaaggatt	tcataacgt	agccactcgt	caggagcttc	358800
ctcttgatac	ccgttgacga	tcctctgac	aaaaatacca	taatcatagc	gtataccgta	358860
gccgtaggct	ggaactgcta	atgtagccat	agaatccaag	taacaagctg	ccagtctccc	358920
caaaccacca	tttccataatc	ctgcatcgga	ttccatttct	acaagggtgg	caaagtcata	358980
atttaaagtt	tttagtgctt	tccttactaa	atctagaatt	cctaaattca	aaagattgct	359040
tgtagactt	ctccctaaaa	gaaattccat	ggaaaggtaa	taaactcttt	ttacatcatt	359100
tttatagtag	ccatttttag	ttttcagcca	ccccctggcc	aaccattcca	taacagtttt	359160
tgcaacagct	gtgaagatat	ctctaggaga	tgccgagctc	gggtgattgta	caacacttaa	359220
atacagacga	tctaaaatcg	cccgtttcat	agagtcaaca	ctgactttgt	tcttatcaaa	359280
actcgaaaaa	tcttccacaa	tgcaaccatt	tcaaatacca	tctagaacct	tccatagcgc	359340
aaatttgaaa	aaaaaaaaaag	aacttcgcct	tggtaaataa	aagagagcct	attaagagag	359400
cttaatagtt	ctgaactaga	gaaagactat	aaataaaaat	agttgataaa	ttttaataaa	359460
attaaaataa	tatctataaa	aatattattg	acaacaatta	tatagacaga	ttaaaattat	359520
ttaatttttt	actcaggaga	acaacatggc	tacagttaga	caaacacctc	agactacaca	359580
accacaacca	tcagtatctc	acaaggcaac	acatcgttat	gttctctggg	tattttttta	359640
gcctattttta	gttagtctag	gtctctctct	tgcttctctta	accaccttag	gactgggttat	359700
tgccagtggg	gtcaccttat	ccttaggaat	cggccattgt	tcttgctata	cagatagtag	359760
tgctgggtatt	gtctctgtcc	ttgctttcaa	tcataattaga	caatttaaac	aagctagaac	359820
agcggagttg	aactcaatga	aaatgatatc	tgccgctgct	gctgcaactg	tccagaagca	359880
aaaattagag	gatcggttact	cctctaaata	atcatctctt	cgctagggaa	aaattccaaa	359940
ctcttatgca	aggaatttaa	attctnnaga	aatatcttga	atagccatgt	gaatatcatg	360000
gctattttct	tcattttttt	gttcaatcaa	tcgtatggat	gagattaccg	tcgaattgatc	360060
tcttgaaaag	acatcgccca	ttctcacgta	tgatagtga	agcttctgac	gacaaaagta	360120
catggctacc	tgacgtggca	atacatattc	tcgggactga	gaacgtccta	aaatactctc	360180
ctgagagacc	ccataatatt	gagcaacatt	acgaataatc	tttaaaggag	ttaaacgaac	360240

gcttctgct	gcttctaaaa	catcttttaa	aagagttttc	acatcatctt	catatagtaa	360300
ttgggtgagag	agttttttat	acattaccct	ctttgctaaa	agattcagtg	catgcagtaa	360360
ggtcttttacg	ttggaagata	gcgcataaat	taaaaaatct	aaggccgttt	cttgaatgcg	360420
aatagataag	cgctctacct	gtctcattaa	gaaactgcgc	aatccttcct	gaaccaaagg	360480
atgtatcgga	attgcaactc	cccattcaaa	cctgctgac	aatctatctt	caacagcaac	360540
gagatccaca	ggcgcatagg	atgaagacac	tacaatcaac	ttcccttcag	aatgaagaga	360600
attaaacgta	tggaagaact	cttcttgagt	tgccgacttt	cctgaaaaaa	cctcgatata	360660
ctcaatgaat	agagcatcaa	tattgcggtg	aaaagaacgg	aatttttgca	tttctcctga	360720
acggatagca	gagactaagt	gctctgtaaa	caaaccgaa	gaaacataga	gaatcttacc	360780
tccagattca	cgaagaacac	tgatagctga	ctgcattaag	tgagtttttc	cagatccctc	360840
aggtccaaac	agataaattg	gattaaaagt	aactcctccg	ttttcatcag	gactcttagt	360900
aaattcctgt	aaaacacgaa	aaggaagatc	attttcaggg	gtaactaaaa	aattagagaa	360960
ggtcatctca	ggattcacac	ttccataatg	catggtaagg	tatgctgtct	tctcttgctg	361020
catctgcttc	tccttataaa	aaggagctgc	tttatctacc	gaagtaacgt	gaacacgaat	361080
gggcttattg	ttattattta	caagaccaga	tttaacctta	tgtcttatat	gctcctcaaa	361140
ccaagtaatt	tgaaaagaat	cttgagcttc	aagatacaaa	ttacaagcat	caaaacataa	361200
gacctttaaa	gacgcgaacc	acttgtctac	agtatttggtg	ccaatttctt	tctcttgtag	361260
caaaagaaat	tcttcccatg	ctcgcataaa	ctatgagctc	atataaatcg	cttgtttcaa	361320
taagcctgta	ttaagacaat	tgcacttttt	tttcagttat	atcgatgttt	tttattattt	361380
aaaaccactt	cattttttaag	atgttttgcta	tctaatactt	tattagtgtg	ccactgtctg	361440
acgactccta	aaatcataga	cgaaagccaa	tagatgttta	atcctgaagg	gaagttatag	361500
aacatagcgg	taaatataat	cgccatcatg	ttccccataa	cttggtgctg	tttctgctga	361560
tccgtaacag	gtcctttctt	atgcaaactc	gtgaccttct	gttgtaagaa	catcactata	361620
cctaatagaa	taggaagtaa	gtggaactca	tttccaataa	accatatcga	tgtctgccaa	361680
gaaaacaaca	catcaggagc	tgttaagtta	tcaatccacc	caggaataaa	cgaggctcct	361740
cgtaataaga	atgatgactt	taataaatca	aacatcgcaa	ttaggaaagg	aagctgtatc	361800
aataaaggta	aacaaccctg	gataggatc	actttgtttg	tcttatacaa	gcccatgatt	361860
tccatctgag	cacgcttagg	ttcgttctta	tacttttgct	gaatttgctg	aatataagga	361920
gataaaatcn	gcatacgctt	cnagatcgt	atggaccatg	cagataaagg	atagagaagc	361980
aatttcaaaa	atacagtaag	taaaataatg	gaaattcccc	aagaaccctg	aaccaatttg	362040
aagaacttca	taataataaa	taggagtgtc	gcaaaaggag	ctgtaataaa	tgcaaaaaca	362100
ccacggaaag	aaatgctatc	aagatactca	ggattttctc	ccttctcctg	agtaattgtc	362160
ttatctaata	ctttaagtgt	aggctctgcc	aagggacctg	catacactaa	aatcgatgt	362220
gtccctgcat	cttttggtgaa	aggaagcaag	gtctcatatc	caggatattt	tgatactgga	362280
tacagttgat	ttttaggaga	aatagcagac	aatcttgctg	gagccgtaga	accgaaatg	362340
tagagagatc	catagccaga	agcaatttca	gacaacggag	ttaaaataat	accgaaatg	362400
ccattcgaat	ttaaaatcca	ttgaggataa	acaccacgac	gtacagctaa	aggctctttt	362460
acttttgtaa	gcttaacttt	atctaaagac	cccttatttt	ttttgataac	cctgtattta	362520
atgggtgggg	ctgaagcatt	tgacatgatc	tccacttcag	gaactcctga	agttacccat	362580
acatcttcgg	tttctttcgt	taaagtaatt	gcagtttcaa	aaacataggg	cttttcttcc	362640
ggattctctg	gaagtgtgta	taccttctga	accgatctat	ctaagctttc	caattgaatg	362700
gaatgggggg	tataggaaaag	aactcgggat	cttaaagcca	caggagtcgc	tagctctctt	362760
cctgaaacca	catttaattgc	gtgatactct	agaggaagta	atttcttaga	atcacttaat	362820
aatcccctgc	gcaataaagg	gtagtaacct	ccaattcgagt	ttttggcttg	ttggccatca	362880
ggaagttttg	aagacagccc	agggaaaaga	gcttcaggag	atttctctga	agctaaatcc	362940
ctatcaaaaac	caatttcatt	cacaatgctt	ttattatttg	ttgaagcaaa	aggtaaattg	363000
ataccttcta	tagaaccact	ctcttcagaa	acaataatct	gcatgtaatc	attaaataaa	363060
acatagtggg	tcgcagtatc	tgacgacttt	gccgaatctt	ggtcattacc	aaaaattaca	363120
gctcgtgtaa	taggaagatc	caaagaaact	aacttttctt	ctcgagaatc	atagagacct	363180
aaaggaatat	agtcgcttcc	tgatctccaa	aagacaagcg	ctgtacccaa	gatcgtgcta	363240
tctttattgg	aaattcttcc	ttgtgcgtac	tcacctagaa	atactaaagg	ctctttattg	363300
ttacgaaact	caacaactag	tacaggtaaa	ccttcatgat	tcgtaggaag	aaaaactttt	363360
cccgtattcg	taggattgaa	agaggaaccc	tgctgacgat	ataaagccaa	gtgaatatta	363420
tcgaaaccac	acttgtgatc	tacaaagctc	caagattccc	cagaagaata	aacagactga	363480
gcagcttctc	cattatgtaa	taaaaataac	ttgtctccaa	cacgaactgc	gtagttattc	363540
ttatgttctt	ctccgtttac	atcggtgtcc	catgaagcta	cacttaaccc	tacagattct	363600
actgcagcta	gcgtctgttc	tgaaatcttt	ctttgtttct	ctgctagatt	tttgaggaa	363660
cgaaattcat	tataaccaaa	aaatatattg	catcctacaa	aagcaatccc	aattaaagaa	363720
acaaaaagca	aagtgcgttt	attcatttga	taaaactcaa	aaattaaact	taagaggtca	363780
aaatatcata	aaaccacatt	atctcccaaa	ggagaatctc	tcaatacagg	tctcttattg	363840
tgatagactg	taaaattcta	aagtctcatg	ccaaaaagat	gctgctatat	gtgtgaacgg	363900
tgcttctcag	ctttcaatga	gcaaatgata	agtaaggcca	caccaaatag	aaataaaggt	363960
atagataaaa	tttgaccaat	tgtaagtaga	caatcctctg	ctaaaacttt	cccttgatgg	364020
ctttttacat	actccgcaaa	aaaacgaatg	aaagcgacag	aaatacaggc	tatagaagtc	364080



acatatccct	tacctaataatg	caaataacgc	ttataggaaa	gaaaatataa	aattccagag	364140
acgaccaagt	aactgattcc	ctcataaagc	tgcacaggat	gcacaggaac	tccctggaca	364200
ccttgcatag	gatcagaaaa	aaccaccccc	caaggcaaaag	aagtcggtgt	tcctacaatt	364260
tcttgattcc	aaaaattacc	caaacgaata	aaaaacgctg	caattccgaa	aactgatcca	364320
cacaagtctg	taaggaagag	aaaagtcaat	tttgaaatct	tttttttata	tatccaagaa	364380
aaaatggccg	cccacaaaag	aaagccaaaag	aacgcctcca	tgactcgaca	agcctccgtg	364440
ccatatttga	atgatctctt	caggatgttg	taagtaaaaa	ctccatccat	aaaaaatcac	364500
ataggcaagt	ctagctccag	ggacaataaa	taaaatagag	tatataaaaa	agtttttctaa	364560
agccacgcgt	agctggcttt	tggaaaaact	taaatgatct	ttcaaaccat	aataggaaaag	364620
agccaaatac	cttgctgaga	gacatgctag	aaaaatccct	acagtaaaaa	agacgccata	364680
ccaagtaagt	cttagagacc	atggctcgaa	agaccagaca	atttttgagc	gatcccaata	364740
gatcacagcc	atctcagctc	gcatacttta	ataccagtta	gcaaaaaatt	catactccaa	364800
gtaaaataga	gtatttagaa	attaagtgtat	atgcactatg	gcaagaaaaca	tcaaataattt	364860
cctgatacta	tttcttggtat	ttttgtggat	atcagcagga	atgaaactct	tgctaaaagc	364920
taccgcaata	gccctagacc	ccctttcttc	tttttttacc	tactgtcttc	tatctatggt	364980
ttcttgggga	ttagcatccc	taaaacatcg	ctacttgcta	agcaaaaacta	taaggaaaca	365040
gctgagtcta	tcttctgaat	tcttttcaca	aaaaattaca	tggattgcct	atataaagca	365100
gacctttatc	tctagaaggt	ttctcatcat	ggtcattatg	attgccttct	ctttagtcct	365160
tcgtcgttat	atcagcaatc	ctcaagcctt	attcgtgatt	cgagctacag	tgggctatgc	365220
tctcattaaa	actgccatcg	cttacttctc	aaaattacag	aatgccctaa	tggaaaatcc	365280
tgaaggaaat	tagtgcgaa	tctatggaaa	tcattcatat	aggaaccgat	attattgaaa	365340
ttagccgcgt	tcgcgaggca	attgcaactc	acggcaatcg	actactcaat	agaatcttta	365400
cagaagcaga	acagaaatat	tgcttagaaa	agaccgatcc	catcccttca	tttgagggtc	365460
gctttgctgg	aaaagaagct	gtagcaaaag	ctttaggaac	tggcataggg	agcgttggtg	365520
cctggaaaaga	catcgaagtc	tttaaagtat	ctcacggacc	cgaagttctc	ctcccttcgc	365580
atgtctatgc	aaaaattgga	atttctaaag	tcattctctc	tataagccac	tgcaaaagag	365640
atgccacagc	aactgcaatc	gcattagcct	aagaatcttt	cagcatctag	tgctgctata	365700
caaccacctc	ctgcagaagt	aaccgcctga	cgatagtact	tatcctgaac	atctccagca	365760
gcaaataactc	caggacaga	agtcttggac	gttctttctc	cagtcacaat	atagcccgac	365820
tcattctaacg	tcagctgtcc	tccgagaaaa	tccgtatttg	gcttatggcc	tatagcaaaag	365880
aacacccccg	cagcttctct	agttgtaatt	tcttgagtct	gaacattctt	aatatctacg	365940
gaacggacaa	tgctatctcc	agaaattttt	acaatctcgc	tattccataa	aaatgtaatt	366000
ttttcattgt	tttgcgcccg	agcttccata	gctttagaag	cccgcagttt	atctctacga	366060
tgaactacat	atagctggct	tccataacga	gtcaggtaaa	gagcttcttc	taaagcagaa	366120
tcccctcccc	caatcacata	aagatcttta	tttttaaaaa	taggagaagc	cccacgcaa	366180
acggcacaag	cagtcactcc	tttttgccaa	aattcatcgt	ttcctgctcc	aggaattctt	366240
aaacgtttag	cagaagctcc	tgtagctatg	atacaggcat	cacaagaata	ggtttcttct	366300
tttgatttca	aaataaaaag	gcgaacagaa	aaatctacgg	aaataatatc	ttgagctagt	366360
gtcttggtcc	caaaccgcac	agcctgctcc	ttcatattat	tcataagttt	tggcccaaga	366420
atcccttcag	gaaaccctgg	aaaattctca	acttctgttg	tagtcataag	ctggccacca	366480
gagatcccg	agaaaaaccc	ctcaaataaa	agaggatgca	aaagcgctct	tgatgcataa	366540
attgccgctg	tatatccaga	tggacctgaa	ccaataataa	ttaaccggga	atgaatcatt	366600
tataatttcc	ttatctaact	ttagaaattg	agaacactgt	tcttgatcta	ctagaaaaaa	366660
gacacttaat	tctagcctat	ctaataaaca	acacttagcg	tctatgcgtc	agtttctcta	366720
tgcaaaaaaac	ttgtctttga	atagcttttg	tctagtttta	atttatacgg	atttaagact	366780
aaagtttcaa	atctcaagat	cttcatcttc	cagtaataac	acctacattt	ctgtgattaa	366840
tctttagaat	tttcttagag	ctaagaaacc	aagaccatc	ctattattta	accctcaata	366900
agtatgggtc	tacttctgaa	tgcacttggt	tcttgagcag	caaccaaaaa	gatctatcag	366960
gcttaagaac	aaagctgatg	tagcccatct	gggacgagaa	tttatggggt	gcttatgaaa	367020
aaaacgatat	gtttttctatg	cgccaaatcc	tgtttctcta	catatgacaa	ggcacattta	367080
tgataattac	cacacgtatt	ttataaaatc	tggtaatata	gaaaagttaa	aaaagaggcc	367140
ttatacatct	ctagaacgga	agtataggat	tttacgatta	attcgattat	atagaactaa	367200
tcgtctcctg	caaggaggt	cttgccctttt	ttaaggttta	tatttacact	gtcttttttg	367260
actttgtagt	tttagggaga	ataacaataa	atgccaaaac	aagctgaata	tacttgggga	367320
tctaaaaaaa	ttctggacaa	tatagaatgc	ctcacagaag	acgttgccga	atttaaagat	367380
ttgctttata	cggcacacag	aattacttcg	agcgaagaag	aatctgataa	cgaaatacag	367440
cctggcgcca	tcctaaaagg	taccgtagtt	gatattaata	aagactttgt	cgtagttgat	367500
gttgggtctga	agtctgaggg	agtgatccct	atgtcagagt	tcatagactc	ttcagaaggt	367560
ttagtgcttg	gagctgaagt	agaagtctat	ctcgaccaag	ccgaagacga	agagggcaaa	367620
gttgctcctt	cttagaaaaa	agccacacga	caacgtcaat	gggaatacat	cttagctcat	367680
tgtgaagaag	gttctattgt	taaaaggtcaa	attacacgta	aagtcaaaag	cggccttatt	367740
gtagatattg	gaatggaagc	cttctctact	ggatcacaaa	ttgacaacaa	gaaaatcaaa	367800
aatttagatg	attatgtcgg	aaaagtttgt	gaattcaaaa	ttttaaaaat	taacgttgaa	367860
cgctcgcaata	ttgttgtctc	aagaagagaa	ctcttagaag	ctgagagaa	ctctaagaaa	367920



gccgaactta	ttgaacaaat	ttctatcgga	gaataccgca	aaggagttgt	taaaaacatt	367980
actgactttg	gtgtattott	agatctcgat	ggtattgacg	gtcttctcca	cattaccgat	368040
atgacctgga	agcgcatacg	acatccttcc	gaaatggtcg	aattgaaatca	agagttggaa	368100
gtaattattd	taagcgtaga	taaagaaaaa	ggacgagttg	ctctaggtct	caaacaaaaa	368160
gagcataatc	cttgggaaga	tattgagaag	aaataccctc	ctggaaaacg	agttcttggt	368220
aaaattgtga	agcttctccc	ctacggagct	ttcattgaaa	ttgaagaggg	cattgaaggt	368280
ctaattcaca	tttctgaaat	gtcttgggtg	aaaaatattg	tagatcctag	tgaagtcgta	368340
aataaaggcg	atgaagttga	agccattggt	ctatctattc	agaaggacga	aggaaaaatt	368400
tctctaggat	taaagcaaac	agaacgtaat	ccttggggaca	atatcgaaga	aaaatatcct	368460
ataggtctcc	atgtcaatgc	tgaaatcaag	aacttaacca	attacggtgc	tttcggtgaa	368520
ttagaaccag	gaattgaggg	tctgattcat	atttctgaca	tgagttggat	taaaaaagtc	368580
tctcaccctt	cagaactatt	caaaaaagga	aattctgtag	aggctgttat	tttatcagta	368640
gacaaagaaa	gtaaaaaaat	tacttttagga	gttaagcaat	taagttctaa	tccttggaat	368700
gaaattgaag	ctatgttccc	tgctggcaca	gtaatttcag	gagttgtgac	taaaatcact	368760
gcatttgagg	cctttgttga	gctacaaaaa	gggattgaag	gattgattca	cgtttcagaa	368820
ctttctgaca	agccctttgc	aaaaattgaa	gatattatct	ccattggaga	aaatgtttcc	368880
gcaaaagtaa	ttaagctaga	tccagatcat	aaaaaagttt	ctctttctgt	aaaagaatac	368940
ttagctgaca	atgcttatga	tcaagactct	aggactgaat	tagatttcaa	ggattctcaa	369000
ggccctaaag	agagaaagaa	aaaaggaaaa	tagcatctaa	tgctggtaat	gcagaggatc	369060
gtattattta	gttctaaata	atacgtcctt	aatttagcta	tttactgatt	tccttattta	369120
caagaggagt	ataatgaata	aaaatcctgt	agctattdtt	gactacatgg	agaaagaaaa	369180
agggattcag	cgctctacta	ttataggagc	tatcgaatct	gctttaaaaa	ttgctgtctaa	369240
aaaaacctta	agagatgacg	cgaacatata	tgtaaacatt	aattctcgta	ctgggtgacat	369300
cgaagtcttt	tgtgaaaagg	aaatagtaga	aatttgtcag	aatcctagca	aagaaattcc	369360
tttagataaaa	gccagagaat	acgatccgga	ctgtcagatt	ggtcagtaca	tggatgtccc	369420
ttttgtttct	gataattttg	gaagaatagc	tgctcacgca	gcacgacaaa	ttatcgggtca	369480
aaagctaaga	catgctgaga	gagacgttat	ttatgaagaa	tatcgccatc	gcgtaaatga	369540
aactttatct	ggtgttgtca	aacgttttgc	ttaaaggttct	aatttaatta	ttgacttagg	369600
aaaagttgaa	gcaattcttc	ctacccggtt	ttatcctaaa	acagaaaaac	ataagatcgg	369660
tgataaaaatt	tacgccctac	tctatgaagt	tcaagagtct	gaaaatgggtg	gagcggaagt	369720
tatcctcagt	cgtagtcacg	cagaatttgt	taaacaatta	tttatttcaa	gaagtcocag	369780
aactagaaga	aggttctgtg	gagattgtta	agatagctcg	tgaagctggg	taccgcacga	369840
aactagctgt	aaagatcgtc	agaccctaaa	actgatcctg	ttggagcttt	tgtagggtatg	369900
cgaggttctc	gagtaaaaaa	tatcatttctg	agaattgaac	gatgagaaaa	ttgacattgt	369960
caattactcc	cccgtctcta	cagagttatt	acagaatctt	ctttatccaa	tagaaatcca	370020
aaagattgct	attttagaag	acgacaaaag	gattgcaatt	gtcggttaatg	atgcagacta	370080
cgctactggt	attggtaaac	gaggaattaa	cgctcggtta	attagccaca	ttctgacta	370140
cgagctcgaa	gtacaacgta	tgagtgaagta	caataagttg	ctagaaattc	aagcccttca	370200
attagcagaa	ttcgatagtc	cgcacttaga	tcaaccctta	gaaatggaag	ggattagtaa	370260
gctagtcata	caaaatttag	aacatgctgg	atatgacaca	attagaagag	tattattagc	370320
gagtgctaatt	gatctggcat	ctgttctctg	gatcagttta	gagcttgctt	ataagatcct	370380
tgagcaagtc	agcaaatatg	gagaaagtaa	agttgacgaa	aaacctgaaa	ttgaagatta	370440
agaatgctca	attaacgaaa	gccgcggggc	tggataagct	aaaacaaaaa	cttgcccaag	370500
caggatcttc	tgaagctaaa	tcttcttcag	aaaaaccttc	tgcgaaagaa	aagtctgtaa	370560
aagtagctct	tgccgcaact	tctaccccta	cggcaagtgc	ggaacaagct	tcaccagagt	370620
ctacttcacg	tcgcattcgt	gctaaaaaat	gttcgtcggt	ctcatcatcc	gaagaagagt	370680
cttctgtctc	tattccagtg	gatacatctg	aacctgctcc	agtcctccata	gcagatcctg	370740
agcctgagtt	agaagtagtc	gatgaggttt	gtgacgaaag	tcctgaggtt	catccagttg	370800
ctgaagttct	tcctgagcaa	cccgtattgc	ccgaaacccc	acctcaagaa	aaagaattag	370860
agcctaagcc	tgtgaagcct	gctgaaccta	aaagcgctcg	aatgattaaa	tctaagttcg	370920
gccctacagg	aaagcatatc	aatcatctcc	tagcaaaaaac	attcaaggct	cctgccaagg	370980
aagagaaaagt	cgtagctggc	tcgaaaagca	caaagcccgt	tgcttcagat	aaaacaggga	371040
aacctggaac	atctgaaggt	ggtgaacaga	ataatcgaga	aaaacaattc	aatcctgcta	371100
accgtagtcc	tgcttctggt	ccaaaaagag	atgctgggaa	gaaaaatctt	accgactttc	371160
gtgatcgctt	tgaagaaatc	gatgaaagcc	taaaggtctt	tacaggaaga	gatcggttacg	371220
gattaaatga	aggcgagaaa	gaagacagat	ggcgaaaaaa	acgtgtttat	aagcctaaaa	371280
aacactatga	cgaagcctct	atccagcgac	ctacgcatat	caaaatttcc	ttgccaatta	371340
ccgtcaaaga	tctggcaaca	gaaatgaagc	tcaaggcttc	agaagtcatt	caaaagttat	371400
tcattcatgg	aatgacctat	gtagtcaatg	atattctaga	cagcgaaact	gcagtacaat	371460
ttattggctt	agagtttgga	tgtacaattg	acatcgacta	ttctgagcaa	gataagttgt	371520
gcctaagcaa	tgacactgta	agagacgaaa	ttcaatctac	agatcccagc	aagcttgtga	371580
ttcgtctccc	tattgttgcg	tttatgggtc	acgtcgacca	cggaaaaaca	acactcattg	371640
actccttaag	gaaaagtaat	gtcgctgcaa	cagaagctgg	agcgattacc	caacacatgg	371700
gagccttctg	ctgctccacc	ccagtgggag	acataacaat	tttagatact	cctgggtcacg	371760

aaagctttctc	tgcaatgcga	gcccgtggag	ctgaagtttg	tgatattggt	gtgcttgtag	371820
tcgctggaga	cgaaggaatt	aaagnacaaa	ctttagaggc	tattgaacat	gcaaaagctg	371880
ctgatatcgc	tattgttgta	gctatcaaca	agtgtgataa	gcctaatttt	aattccgaaa	371940
ccatctatag	acaactttct	gaaatcaatc	tattgccaga	agcttgggga	ggctcgactg	372000
ttacagtaaa	tacctccgca	aaaacaggag	aagggtctttc	agaactttta	gagatgtag	372060
ctttacaagc	tgaagtcttg	gagctaaaag	ccgatccttc	agcacgtgct	cgaggacttg	372120
ttattgaatc	agaactgcac	aagggtctcg	gacctgttgc	gactgttttg	attcaaaatg	372180
gaagcttaaa	actgggcgaa	gctctcgctc	tcaatgattg	ttatggcaaa	gtgaaaacta	372240
tgcataacga	acataatgaa	ttgatgaaag	aagctggggc	atctattcct	gtgttgatca	372300
cagggtctatc	ggacattcct	aaagctggcg	atcctttctt	cgctgtgaaa	aacgagaaaa	372360
cggctagaga	cattattgaa	gctagatccg	caggacaaca	gcgttttgct	ttacagcaaa	372420
agaagcggcc	taactttgat	tctatgttac	agaataaaaa	gactcttaag	cttatgatta	372480
aagctgatgt	tcaaggttcc	atagaagctt	tggtcagttc	aatatctaag	attaaatcag	372540
aaaaagtaga	tggtgaaatt	ttaacaaaca	gtgtaggaga	aatttcagaa	tcagacattc	372600
gtttactgcc	gcctctaaag	cagttctcat	cggtttccat	acaggaatag	aaagtcattg	372660
ggaaccttta	attaagagct	taggagtcog	agttgaacta	tttaccgtca	tctatcatgc	372720
tattgatgca	attaaagaaa	ttatgacttc	tctattagat	cctattgctg	aagaaaaaga	372780
tgaaggttct	gctgagatta	aagaaatcct	taggtcttca	caagtaggat	ctattttacgg	372840
ttgcatagtt	actgaaggaa	ttatgactcg	caatcataaa	gtccgagtat	tacgtaataa	372900
agagatcctt	tggaaggta	cgttatcttc	attaaaacgt	gttaaagaag	atgtcaaaga	372960
agttcgcaaa	ggtttagagt	gtggaatttt	gttagaagga	taccagcaag	ctcaaataagg	373020
tgatgtccta	caatgtttatg	aagttatcta	tcatccacaa	aaactataac	ttgaagtact	373080
gtatgacaga	aaatagacgt	attaaacggg	taaatgcttt	attacaagaa	gccattgcaa	373140
aggtaatttt	aaaagatggt	aagcatccca	agatttctaa	tctttggatc	acggtaactc	373200
gtgtttctct	atctaaggat	ttgcactctg	cacgtgttta	tgtatctgta	atgcctcatg	373260
agaataccaa	ggaagaggct	ttagaagctt	taaaagcttc	tgctgggttt	atcgctcata	373320
gagcttcgaa	aaatgtcgtc	cttaaatatt	tcccagaact	tcatttttat	ctcgatgata	373380
ttttctcacc	tcaagattat	atagaaaacc	tgctttggca	gattcaagag	aaagaaaaga	373440
gttaataaac	tatatttttt	gggaacttga	atactattaa	agacatgact	atggatcttg	373500
cagtagaatt	aaaagagggc	attcttcttg	tagacaagcc	tcaagggaga	acttcgttta	373560
gccttatccg	cgctctaacc	aagttaatag	gcgttaaaaa	gattggctcat	gcaggaactt	373620
tagatccctt	cgctactggc	gttatggcca	tggtgattgg	ccgtaaaatt	actagacttt	373680
ctgatatttt	actttttgaa	gacaaggaat	acgaagcaat	tgcccattha	gggacaacta	373740
ccgattctta	tgattgcgac	ggcaaagttg	taggaagatc	taagaagatt	cctagtctcg	373800
aagaagtatt	atcagctgcc	gagtatttcc	aaggagagat	ccagcaactt	cctcccatgt	373860
tttccgctaa	aaaagtccaa	gggaaaaagc	tgatgaata	tgctagaaaa	ggtttatcta	373920
tagaacgtca	ccattctaca	gttcaagttc	acttgcagat	tacgaaatat	gagtaccctt	373980
tattgcattt	tgtagtctct	tgtagcaaa	gaacttatat	tcgcagcatt	gctcatgagc	374040
ttggcagcat	gttaggctgt	ggagcttatc	ttgagcagct	acgccgttta	cgaggtgcc	374100
gtttttctat	agatgaatgt	attgatggga	atctattaga	ccaccccgat	ttcgatat	374160
ctccctacct	acgagatgcc	catggaaata	gcctatagtt	taacgtcttc	gttttctgta	374220
gattctgtaa	ctgtaggttt	tttcgacgga	tgctatctag	ggcatagcaa	tcttttatct	374280
attcttactt	cctattctgg	atccagtggg	gttattacct	ttgattctca	tcctcaaacy	374340
gtactttctt	taaatcacac	gaaactcatc	aatacaaaa	aagagcgcct	ccaattattg	374400
caaacgtttc	ccatagactg	gttaggtgtc	cttacttttg	atttaaattt	tgcgaaatcaa	374460
tcggcagaag	aatttcttac	tttgttacat	cgtaacttga	aatgcaaacy	cctcatctta	374520
ggttatgatt	cttgcatagg	gaaagaacag	caaagcaata	ccgaggtctc	cgatactata	374580
ggcaagccgt	taggtataga	ggcatcatca	attcctcctt	accgtatgga	taacatagtt	374640
gtctccagca	aagcaatccg	ccagtttctg	tccgcagggg	atcttgaatg	tgctcatcgt	374700
tttttgggtc	atccctatgc	catttctgga	aaaataaccg	agggctccgg	aataggaggt	374760
tctctaggat	tcgccactat	aaatcttctt	agagaagaaa	gtttaattcc	cctaggagtt	374820
tatgcttggt	aaatacgtta	tgatagcact	acctgtcagg	gtgttatgaa	tttaggaact	374880
gcccctactt	ttggaagaga	gtcttttat	gcagaggcgc	atatcttttc	ctttgaggaa	374940
aatctatacg	gcaaagaagt	gagcattatc	ccgagaaaa	ttcttagaga	agaaaaaag	375000
tttcaatcaa	aagaaactct	aatacagca	attgaaaaag	acattttgga	tgctcaagat	375060
tggtttgcaa	agggttctct	ttaattatgaa	ggaacagcat	agtatcaccg	tcctggacga	375120
tataatcacg	tccttctata	tgtaatttcc	ctaattctcg	agcagctgca	cgaccttgac	375180
actctatcat	atcttcaaaa	gtaatcactt	cagcacgaat	aaagcccttt	tgaatatccg	375240
tatggatttc	tccagcagct	tcccaagcag	aagaccctcg	aaccactgtc	catgcacgag	375300
attcttgagg	acctgtagta	aaataagaaa	tcagtccata	agtgtcatac	gcagcacgca	375360
ctaactctatg	aagtcctgat	ttttcaagac	ctaagctcat	aagaaattct	aagcgctctt	375420
caataggtaa	ggaaacgatt	tcttcttcta	tacgaacaca	gataggaacc	actttagaat	375480
tttcttttgc	agcaacttcc	cgaacagcgg	caacataatc	attatccata	cttggtagag	375540
aactctcgtc	aacattagct	atataaaaaca	taggcttcat	ggtcaaaaac	ggatagggct	375600

ttaatgccac	aattttgttct	ggagttaatt	ctaaagtacg	tagcggcagc	cctttttctaa	375660
gtgagcaata	attgtatcaa	atagaggcaa	gagagctcct	acttcacgct	ttcctttggc	375720
tagcttttct	aatttgctat	ggatattttt	tgctgaggag	aagtcagaaa	aaatgagctc	375780
taagttgata	acttcaatat	cctcaacagg	gttgactttt	cctgaaacgt	gtgtaacgct	375840
tggatcatca	aaacaacgca	ctacatgagc	aatagcatga	gtttctcgaa	tatgagagag	375900
aaaccgattt	cccagaccg	cgccatcgga	agctccctta	actaaacctg	caatatctac	375960
aaatttcata	tccgcataga	tgatcttctg	actattgcta	atttttagcta	aggcttccag	376020
tctttcatcg	ataacaggaa	caatacccac	attaggatcg	atagtacaaa	acggatagtt	376080
acaggaggca	acttgagctc	ctgttaaagc	attgaataag	ccagactttc	ctacattagg	376140
aagccctaca	attccacatt	cagtatgact	cataagacat	ctaaaaataa	aaataatgac	376200
atgctttttc	gaatattaga	aagacaactc	ttctgtttca	aaaaagcaca	atagctagaa	376260
aaatagtacc	ttcaaaatca	agagtgtctt	gaaaatgata	aaaaaccact	ataatcgatt	376320
gaagttttcc	ctacctaata	ctttcttcat	atagaaccat	cttgaagtga	cctaaagtat	376380
tgctaaattc	aacaactttt	cgttattgtt	ctttttttct	actattcttc	tttatctcta	376440
agattcattt	ataatcttac	taagaacaaa	acgtttgggc	ttcactcttg	agaaaaacaa	376500
gagcataagg	taatttgcag	ataattccga	atatagtcct	cttaatcgaa	ccttggcaac	376560
agcatgggtg	aaaaaacaga	aaaggccacg	ccgaagcgac	ttagagatgc	tcggaaaaaa	376620
ggtcaagtag	caaaatctca	ggatttttct	tctgcggtta	cctttatcgt	ctctatgttt	376680
acggctttct	ccctatcgac	cttttttttc	aagcatttag	gtggctttct	ggtttccatg	376740
ctctcacaag	ctcccactcg	ccatgatcct	gtaattacct	tattttatct	taagaactgt	376800
cttatgctta	ttttaacagc	atcacttccc	ttactgggag	ctggtgctgt	tggtggcgct	376860
attgtagggt	ttcttatcgt	tggtcctaca	ttttctaccg	aagtttttaa	accagatata	376920
aagaagttca	accctattga	gaacatcaaa	caaaagttta	aaataaagac	tctcatagag	376980
ctaatacaat	cgatttttaa	aatttttgga	gcagccttaa	ttttatacat	aacgttaaaa	377040
agcaaagtct	ctttaattat	agaaactgca	ggagtctctc	ctataattac	tgctcaaata	377100
ttcaaagaaa	ttttttataa	agcagtaacc	tcgataggaa	ttttcttttt	gattgttgcg	377160
attcttgacc	ttgtctatca	gcgccacaat	ttcgctaaag	aattaaagat	ggagaagttt	377220
gagggttaagc	aggagttaa	agacacggaa	ggaaatcctg	agattaaagg	ccgtcgtcga	377280
caaattgctc	aagaaattgc	ctatgaagac	tcgtcatcac	aggtgaaaca	tgcaagcacc	377340
gtagtctcta	atcccaaaga	tattgtctgt	gctattggct	acatgcctga	aaaatataaa	377400
gcaccttgga	tcattgccat	gggcatcaac	ttacgagcta	aaaggatact	tgatgaagct	377460
gaaaagtagc	gaattcccat	tatgcgaaac	gtacctttag	cacatcagct	tttggatgaa	377520
gggaaggaa	taaaatttat	tccagaatct	acttacgaag	ctattggaga	aattctactc	377580
tatatcactt	cactgaatgc	gcaaaatcct	aataataaaa	ataactaacca	acctgatcat	377640
ttataatgaa	taagctactc	aatttcgtca	gcagaacact	tggtggcgat	accgccttaa	377700
acatgatcaa	taagtccagc	gacttaatcc	ttgctctttg	gatgatgggc	gttgctctaa	377760
tgatcattat	tcctttgctt	ccgcctatcg	ttgacttgat	gatcaccatc	aacttatcga	377820
tctctgtatt	cttattgatg	gtggctcttt	atattccaag	tgctttgcag	ctgtctgttt	377880
ttccctcggt	gctcctcctc	actacgatgt	tccgcttggt	aataatattt	cctcttctcg	377940
acagattctc	cttaaagcgt	atgcgggtca	tgctattcag	gcttcggaga	cttcgtgggt	378000
ggagggaact	atgtgggtcg	gttcattatc	ttcctcatta	ttacaatcat	tcagtttatc	378060
gtagtaacta	agggtgccga	gcgtgttgcc	gaagtgtctg	cccgatcccg	attggatgcg	378120
atgccaggta	aacagatggc	gattgatgcg	gacttacgag	ctggatgat	tgatgccaca	378180
caagctcgtg	ataaaagggc	tcaaatccaa	aaggaaagtg	aactctacgg	agccatggac	378240
ggtgccatga	agttcatcaa	aggagacgtt	atcgctggta	tcgttatctc	tttgattaac	378300
attgttggcg	gtttgacgat	tgggttggtt	atgcacggca	tggaacctcg	tcaagcagct	378360
cacgtctaca	ctcttctctc	cattggagat	ggtttagtct	ctcaaattcc	ttctcttttg	378420
attgcttgga	cagcgggtat	tgtcacgact	cgtgtatcga	gtgacaaaaa	tacgaacttg	378480
ggtaaagaga	tttctactca	gctcgttaaa	gaaccacgag	cactactcct	tgcaagtgct	378540
gcaactttag	gggttggttt	cttcaagggc	ttccctctat	ggctcttctc	catttttagca	378600
ttaattttct	ttgccttagg	gattctccta	ctgactaaga	aatcagcggc	aggaaaaaaa	378660
ggtggtggct	caggagcttc	aacaaccgta	ggggctgctg	gtgatggcgc	tgctactggt	378720
ggggataatc	ccgatgacta	ttctctaact	cttcccgtaa	ttctagaact	tggaaaagat	378780
ctctctaagc	ttatccaaca	caagacaaaa	tcaggacaaa	gctttgttga	tgatatgatt	378840
cctaaaaatgc	ggcaagctct	ctatcaggat	atcggaatcc	gataccctgg	cattcatggt	378900
cgcacagatt	ccccttcttt	agaaggatac	gattatata	ttctgcttaa	tgaagtccct	378960
tatgtgctag	gaaaaattcc	tccgcaccat	gtgttaacca	atgaggtgga	ggacaatctc	379020
agccgttata	atctaccttt	cattacctat	aagaatgctg	cgggtcttcc	ttcagcttgg	379080
gttagtgaag	atgcaaaagc	tattctagag	aaggcagcaa	ttaaatattg	gacgccgctc	379140
gaagtgatca	ttctccatct	ttcgtacttt	ttccataaaa	gctctcaaga	gtttttggga	379200
attcaagagg	tacgttctat	gatcgaattt	atggaacgtt	cattcccggg	cttagtgaag	379260
gaagtcacaa	ggcttattcc	attgcaaaa	cttacggaaa	tctttaagag	attggttcaa	379320
gagcaaatct	caattaaaga	cctacgtaca	attctagaat	ctctgagcga	gtgggcgcaa	379380
actgagaaag	atacagtttt	gcttacagaa	tatgtacggt	cttcttttaa	gcttttatatc	379440

agcttcaagt	tctctcaagg	acaatcagca	atttctgttt	atctcttaga	tccagaaatt	379500
gaagagatga	ttcgtggagc	aattaaacag	acatcggcag	gttcttacct	tgctctagat	379560
cctgattctg	tgaaccta	tttaaaatct	atgaggaata	cgatcacgcc	aacacctgca	379620
ggaggccaac	caccagtatt	attgacagca	attgatgtaa	gaagatatgt	acgaaaatta	379680
atagaaacag	aattccctga	cattgctgtg	atttcttatt	aagaaatcct	accagaaatc	379740
cgcattccagc	cttttaggaag	aattcagatt	ttctaattga	tacgttgctg	ctcataggag	379800
gcataatggca	gcatacaggag	gcacagggtg	tttaggaggc	actcagggtg	tcaaccttgc	379860
agctgtagaa	gctgcagctg	caaaagcaga	tgacgcagaa	gttgtagcca	gccaagaagg	379920
ttctgagatg	aacatgattc	aacaatctca	ggacctgaca	aatcccgag	cagcaacacg	379980
cacgaaaaaa	aagggaagaga	agtttcaaac	tctagaatct	cggaaaaaag	gagaagctgg	380040
aaaggctgag	aaaaaatctg	aatctacaga	agagaagcct	gacacagatc	ttgctgataa	380100
gtatgcttct	gggaattctg	aaatctctgg	tcaagaactt	cgcggcctgc	gtgatgcaat	380160
aggagacgat	gcttctccag	aagacattct	tgctcttgta	caagagaaaa	ttaaagaccc	380220
agctctgcaa	tccacagctt	tggactacct	ggttcaaacg	actccacctt	cccaaggtaa	380280
attaaaagaa	gcgcttatcc	aagcaaggaa	tactcatagc	gagcaattcg	gacgaactgc	380340
tattggtgcg	aaaaacatct	tatttgcctc	tcaagaatat	gcagaccaac	tgaatgtttc	380400
tccttcagg	ttcgctcttt	gtacttagaa	gtgactggag	acacacatac	ctgtgatcag	380460
ctactttcta	tgcttcaaga	ccgctatacc	taccaagata	tggtctattgt	cagctccttt	380520
ctaataaag	gaatggcaac	agaattaaaa	aggcagggtc	cctacgtacc	cagtgcgcaa	380580
ctacaagtgc	tcatacagaga	aactcgtaac	ctgcaagcag	ttcttacctc	gtacgattac	380640
tttgaaagtc	gcgttcctat	tttactcgat	agcttaaaag	ctgagggaat	ccaaactcct	380700
tctgatctaa	actttgtgaa	gatagctgag	tcctaccata	aaatcattaa	cgataagttc	380760
ccaacagcat	ctaaagtaga	acgagaagtc	cgcaatctca	taggagacga	tggtgattct	380820
gtgaccggtg	tcttgaactt	attcttttct	gctttacgtc	aaacgtcgtc	acgccttttc	380880
tcttcagcag	acaaacgtca	gcaattagga	gctatgattg	ctaatacttt	agatgctgta	380940
aatataaaca	atgaagatta	tcccaaagca	tcagacttcc	ctaaacccta	tccttggtca	381000
tgattaaaaa	aggattgcca	tgcaaaacca	atagcagcaa	ttactagaat	ccttagcacc	381060
cctattaaat	acgacacttg	ctccagataa	aaataactct	tgtttaatacc	gtttcagcga	381120
tacctatgct	cctgtgcaaa	tagaagaaga	tggaaattcc	ggagatcttg	cagtatcgac	381180
actactaggt	actcttctctg	aaaacgtatt	tcgcgagcgt	attttcaaaag	ctgctctctc	381240
tgtaaattggc	tcgtttccaat	ccagcatcaa	gggaattcta	ggctacggtg	aggtcactca	381300
acagctctat	ctttcagata	tcctgagtat	gaactacctg	aatggagaaa	agttattcga	381360
gtatctcaag	ctcttttctt	tgcatgctaa	gattttggatg	gaatccctaa	gaacagggaa	381420
tcttctctgac	cttcattgttt	tgggaattcta	ctacgtcgcg	tgaatgtttt	aaaatacaca	381480
aaacactcac	cctcagcaca	tgcttggaaa	cttataggaa	cctctcctaa	acacgggatt	381540
tatctccac	tattttcaat	acacacaaaa	aataagctgtg	gaatcggtga	atttttagat	381600
ctcattcctc	tgatctcttg	gtgccaaaaa	cagggtctca	gcgttattca	gcttctccct	381660
ttaaatagata	ctgggtgaaga	tacgagtccc	tataacagca	tctcttccgt	agccctgcaat	381720
cccctattcc	tttccctatc	ctctcttcca	aatatcgata	ccatccctga	agttgccaag	381780
aaacttcaag	atattgcata	gttatgctcg	actccatcag	tcagctatac	tcaagttaaa	381840
gaaaaaaaat	gggcattctt	aagagagtac	taccaaataat	gttgcaagtc	ttccctcgaa	381900
ggaaactcaa	atttttctga	gtttctagaa	agcgagcgct	attggcttta	tccttatggg	381960
acctttctgtg	caatcaaaca	tcatatgcac	ggagaacctg	tttaataactg	gccgaagtcg	382020
ctcacagatc	aggagaattt	tccggactta	actaaaaaat	tccatgatga	agtcctcttt	382080
ttttcctatc	tacagtttct	ctgttaccaa	cagctctgctg	aagtgaagac	ctatgcagat	382140
caacaccacg	tcctgcttaa	aggagacctc	cctattctta	ttagcaagga	tagctgtgat	382200
gtttgggtatt	tcggagacta	cttttcttca	tcaaggctctg	taggagctcc	tcctgacctc	382260
tacaattctg	aaggacaaaa	ctggcatctg	cctatttata	atttttcaca	acttgccaaa	382320
gacgactaca	tttggtggaa	agagcgctctg	cgatatgctc	aaaacttcta	ttccgtctat	382380
cgcttagatc	atattatagg	atttttccgt	ttgtggattt	gggattcttc	aggaagagga	382440
aggttcattc	cagacaatcc	taaagactat	ataaagcagg	gcacggagat	cctttctact	382500
atgctcggag	cctcttctat	gttacctatc	ggagaagatt	tagggattat	accccaagac	382560
gtcaaaacga	cattaacaca	cttaggaatc	tggtgaaccc	ggattccacg	atgggaacgc	382620
aactgggaaa	gcgacagtgc	cttcattccc	ctaaaagatt	ataatccact	ttctgtgacc	382680
actctctcta	cccacgactc	tgatacgttt	gcccattggt	ggctcaattc	acctaaggaa	382740
gctaagcaat	ttgttaaatt	tctacatctt	ccttttcaaa	aaacctgac	tacagaaact	382800
caaatagaca	tcttaaaact	ttctcatgaa	tcagcatcta	tctttcatat	caacctcttt	382860
aacgattatc	tcgcccctctg	ccctgattta	gtatcaaaaa	atctacaaaag	agaacgcatt	382920
aatacacctg	ggacaatttc	taaaaagaat	tggtcgtatc	gagttcggcc	ttccttagaa	382980
gaactcgcta	ttcataaaaa	atttaattggt	tacattgaga	agatcccttac	aggactgtaa	383040
ggatagcaat	aaaacattta	agtcttttta	tagtaagaac	cttataataa	tttcctggaa	383100
cgaccgtctt	tcttaaaaga	attccttcat	tatcaacaac	agacaatcac	attttctaag	383160
aaaacctctt	ccccatatat	tcgaaaagct	ctagtataga	ttccttttca	tagagttgct	383220
ttattgagcg	gatgttagag	aattcatagg	aagaatatgt	caagaaagtg	cccacttaca	383280

ggaaagagac	ctcgccgtgg	ttatagctat	acacttcgag	gtattgctaa	aaagaaaaaa	383340
ggaattgggt	tgaaagtga	agggaagact	aaaagaagat	ttttccctaa	tatgttgacc	383400
aagcgtctat	ggtctacaga	agaaaaccgt	tttcttaagc	ttaaaatttc	tgctagcgct	383460
cttcgtcaca	tgataagct	cggattagag	aaagttctcg	aaagagctaa	aagtaaaaaat	383520
ttttaattta	acttaagtat	agggaaatat	ttatgtcttt	cttaaggcgt	catattttctc	383580
tttttcgttc	acaaaaacaa	cttattgatg	tttttgctcc	cgtaagtcc	aacctcgagt	383640
tagctgagat	tcatcgctcg	gttattgaag	atcaaggccc	tgcccttctt	tttcataatg	383700
tcatcggtac	gtcattccca	gtcctgacca	atctctttgg	aacaaaacat	cgtgtagacc	383760
aacttttttc	tcaagctcct	gataacctca	tcgctcgagt	tgccacacct	attttcttcta	383820
caccaaagct	ttcttctcta	tggaaatctc	gggatctatt	aaaaagaata	agctcttttag	383880
ggctcaaaaa	agctcgattc	cgctcgcttc	cttttggttc	tatgtcctca	gttaacttag	383940
atcaccttcc	cttactcaca	agctggcctg	aagatgggtg	agcctttctc	acacttcctc	384000
ttgtctatac	ggaatcgccg	actcttacta	cacccaatct	tgggatgtat	cgcggtgcaac	384060
ggttcaatca	aaacaccatg	ggcctccatt	ttcaaattcca	gaaggcgga	gggatgcac	384120
tgtatgaagc	agagcaaaaa	aagcaaaaac	ttcctggttc	ggtatttttg	tctggaaaacc	384180
cctttttaac	cttttctgcg	attgcccccc	tacctgagaa	tgtctcgga	cttctctttg	384240
ctaccttctc	ccaaggagcg	aagctccttt	ataaaaaaac	aaacgaccat	ccccaccctc	384300
tactctacga	tgcggaattc	atcctggctg	gagaatctcc	ggccgggaaa	cgctgctctg	384360
aaggtccttt	tggcgatcat	ttcgatact	acagtctcca	acatgacttc	cctgaattcc	384420
actgtcataa	aatctatcac	agaaaagatg	caatctatcc	tgctacagta	gtcggcaaac	384480
cctaccaaga	agatttttat	atagggaaca	aactccaaga	atacctctcc	cctttatttc	384540
cgttagttat	gcctgggtgtg	cgtagactta	aaagttacgg	agaatcaggg	tttcatgcac	384600
tgactgcggc	tgctgttaaa	gaacgctatt	ggagagaatc	tctaaccaca	gctctagaa	384660
ttcttgagaa	gggccaactt	tccctaacga	aattccta	ggtcacagac	caagagggtgc	384720
ctctcgacag	gttctcgtg	gttctagaaa	ccattttaga	gcgctctacag	ccagaccgag	384780
atcttattat	tttctcagaa	actgcaaacg	atacgttaga	ctatacagga	ccaagcttaa	384840
ataagggctc	caaggggaatc	ttcatgggaa	taggaaaagc	catccgagac	cttccccatg	384900
gatatcaggg	aggaaaaaatc	catggagttc	aagacatcgc	tcccttttgt	cggtggttgc	384960
tagtggttga	aacatccctc	gaggaccgat	gtattaaatc	tctccttcac	catccagatc	385020
taaaatcatg	gcctctgatt	atccttgccg	ataatctgag	agaaaccatt	caaagtgaaa	385080
aagattttct	ctggaggacc	ttcacacgat	gtgccccagc	aatgatctt	cacgcgctcc	385140
acagcctttt	tgctactcac	cgctccta	acaactttcc	cttcggtatc	gatgccctga	385200
tgaagccttc	ctatcctaaa	gaagtagagg	tcgaccatc	tacaaaacaa	aaggtttccg	385260
aacgatggca	cgcatatttc	cccaataaag	aaacttttta	tatttaataa	gaatcttatt	385320
ctattaaacg	tttaattaaa	ttagttattt	ttatttttaa	aaatatataa	aaacaaaaaa	385380
gctattttta	gagtaaaaaa	tgaataaaaag	acaaaaagat	aaattaaaaa	tctgtgttat	385440
tattagcacg	ttgatttttag	taggaatttt	tgcaagagct	cctcgtggtg	acacttttaa	385500
gactttttta	aagtctgaag	aagctatcat	ctactcaaat	caatgcaatg	aggacatcg	385560
taaaattcta	tgcatgcta	tagaacacgc	tgatgaagag	atcttcctac	gtattttataa	385620
cctctcagaa	cccaagatcc	aacagagttt	aaactcgacaa	gctcaagcaa	aaaacaaagt	385680
tacgatctac	tatcaaaaat	ttaaaattcc	ccaaatctta	aagcaagcca	gcaatgtaac	385740
tttagtgcag	caacctccag	cagggcgtaa	actgatgcac	caaaaagctc	tttccataga	385800
taagaaagat	gcttggttag	gatctgcgaa	ctacaccaat	ctttctctac	gtttagataa	385860
taatctcatt	ctaggaatgc	atagctcgga	gctctgtgat	ctcattatca	caaatacctc	385920
tggagacttt	tctataaagg	atcaaacagg	aaagtatttt	gttcttcttc	aagatcgtaa	385980
aattgcaata	caagctgtac	tcgaaaaaat	ccagacagct	cagaaaacca	tccaagttgc	386040
tatgtttgct	ctgaccact	cggagattat	tcaagcctta	catcaagcaa	aacaacagg	386100
aatccatgta	gatattatca	ttgatagaag	tcatagcaaa	cttactttta	agcaattacg	386160
acaattaaat	atcaataaag	actttgtttc	tataaaatcc	gcaccctgta	ctcttcacca	386220
taagtttgca	gttatagata	ataaaaactct	acttgcagga	tctataaatt	ggtctaaagg	386280
aagattctcc	ttaaatgatg	aaagcttgat	catactggaa	aacctgacca	aacaacaaaa	386340
tcagaaactt	cgaatgattt	ggaaaagatct	agctaagcat	tcagaacatc	ctacagtaga	386400
cgatgaagaa	aaagaaatta	tagaaaaaag	tcttccagta	gaagagcaag	aagcagcgtg	386460
atgatctaaa	atagtcacag	aagaaggcct	agctcgtgat	tcaagtatgt	ctaggcctct	386520
tcactctttt	gataaaaaag	agtggaggca	gtttctaaag	ctcctttatt	tctagcaatt	386580
acccaagctt	ctgtcgtcgc	tgcaattgcc	tgagaagcgg	cagcccttaa	agagatgcc	386640
ttttttttct	ttgtaacttt	aatagatcgc	ttctgtttgt	ttttttcgtc	tttttcttga	386700
tcttcttttt	tcttactatc	gcaatatagt	tttttaaaat	ctaaatgcac	atgacgcaac	386760
tgagaaagca	agaccttggc	ttgcttttgt	ccgagtagct	tataacgatg	cctctgtttc	386820
ttctcctctt	gttcgcgatc	tccaatagct	agcaaggcaa	gccgaatcgc	ttcattcgta	386880
gcaatttcc	cagaaatttt	ttctactaaa	ggagagtttt	gacgggaatc	tttagctatg	386940
ctttgtgcac	atagcgcacc	ataaggatca	aaacgaatta	tagcatcac	atcaaacgga	387000
cttaaaaccc	taaatatccg	tagataattt	ttttcccttc	ttttcttgac	gggaagcttt	387060
ctggcccgaa	gatcctcttc	tttgatctcc	gctaaaaacca	ccactatttc	ccccccacc	387120

atcgtcatga	actgaagcag	cttcaggcctt	tccttgaacc	gatagacgtg	aagatcctga	387180
aaacggctgg	ggagaacgga	gaacaattgg	cggctcaaca	gcaacatttc	gatactgata	387240
aatcaaagga	tctggaggac	ctccaggacc	tttatgagct	tcgagcttct	ctttatagtc	387300
atcagtagca	cgaggtagag	gagcgagtaa	agacactcca	cgttgcgcaa	ggaaatgata	387360
tgaggaaactc	acagcatcac	ttcctaaagc	ccctcccgtg	ccactttcct	tagggaaaac	387420
actctccaca	gcaatagggg	gaaagttttg	actgctattc	tctggatttt	tgaatgccgt	387480
agattcttta	acaacggcct	caggttccct	cctggaaacg	atgctatctt	taggaaaacg	387540
atacatactt	tctggatgag	gcaaactttt	aacctcagca	ctcttcacag	taccttcccg	387600
aagaggagaa	agttcgtat	ggttcgtact	cttctctatt	cctggagatt	tatgctttga	387660
tttatctccc	gatctctggg	tgggtaaagt	tcctgaaaac	ttgggaggag	gaaatactgt	387720
agaaggacca	gaccaaacag	aattactcaa	tacctcttga	ggcgctgccc	ctgtaagaag	387780
cccagccata	gcacgtgcaa	gcatcatctg	atcctcactc	aactgctctc	gactttcttg	387840
tttctctgct	tccttttccg	ccctttctaa	agtattagaa	tttggaattc	ctggttgatt	387900
cgcttctgga	gaatcagang	aagatacctt	tacttttccct	tctactgctc	tgggagatgt	387960
catggctgta	ctganctctt	cctgtcctaa	atcaganaga	tctatcatgc	cttcgttgcc	388020
tgttgccatt	gcccgtgcga	ctaagtatga	ggtctcaaca	ttgggatcga	gaagagagct	388080
gaccatctcc	cctctaaac	gagccactgt	ccaagcattt	accttctcct	cactcatagg	388140
ctctatggcc	ttttggaaaag	atccaaacga	agccacggaa	ctagattctg	aagagcttaa	388200
acttaaaactc	ctggcacctg	aaaatgctga	agatttcaaa	gcctctaaag	aaagctgaga	388260
aatatcagag	gaactccctc	ccatacccg	agcatctaag	aaaaatccct	gcatttcagg	388320
tgaaatacgg	tttcccttct	ttagagcaac	atccatctct	gtcggcaata	aggatgttcc	388380
ctcaccacta	tcggaagcac	gctttgctga	cactctcgaa	gcccagagatc	cgaatcctga	388440
catgaatcct	tgcacactag	cgcgcattht	agaaaatgta	cctttcaatt	tggattttgg	388500
agaggttgat	gatcgatctt	gagctttacg	atacttagcc	ttatttatct	gagattctgt	388560
tgcatacatt	cctgtagatc	ctgaacgcac	taagctttcc	tgcttcgcag	cagaggaggc	388620
ctgcttggtt	tcagaaaata	tagattcttt	tagcggagac	gggccttctg	cctgctctcc	388680
ttgcagagca	ggattccact	ttcctggatc	cgaagaaggc	tgaacccctc	cgccacctga	388740
aactgccata	atgattctct	gaatttataa	aataaaactt	ataactactt	ataattttaa	388800
aacaaaaaat	aattaattta	aaaaaaagaa	cttacaacaa	aatttttaaa	atctaaaaaa	388860
caaaaaaaa	cgcaagggtga	aaacaccttg	cgtaaaaaaa	cttatgggag	gacagagaac	388920
agcgagtaga	tgcaacaaag	tgcatcgctg	tcgagctaga	gggatcactc	ggatccgact	388980
gtctaggtat	taagattttg	gagatcttaa	taccgagaca	gttcctaact	ctaaattaat	389040
taccagggt	tcctgtcggt	ccatcacggg	atagtcctcg	tctgcgattt	ttttttaatt	389100
taaccccgcc	taaagacgga	tagagtactt	actaaaatgg	tccttgctcag	taaaaacaaa	389160
cccattctca	taattgaaaa	tcaaaacttt	atcgggtgtcc	ttcttctgag	aatctaagag	389220
agagcgaact	aactgatcgt	attcttgagc	acgggtgtta	agagttttct	gttccttagc	389280
aataagaaat	ttcgacgatt	tttagctttt	atccgcgcag	gcttcttcaa	cacttccgtt	389340
gatttctttt	gaatctcctg	agccaaagcc	ctatccgttc	tgtcttctt	aggcttcccc	389400
ataaaaaata	caaaaacaaa	aaaatcaact	taataaacta	attttaatta	aaaaacttat	389460
taagaataaa	ctaattttta	tctaaaaata	aaatattata	ttaataattg	tttaaaagca	389520
gtttagataa	acataaaaaa	tcaagctaag	aatcctatgc	tttgctatat	acaagtctgc	389580
aaaacctttt	gaaatcgata	atcataatc	aaagcgtaaa	ccatgtctgt	ccacataaca	389640
ccgcgcaaat	gctttatttt	gtgtatttta	tccatgttca	cccttccaac	gctcttccct	389700
aaagcacatc	tgatcctttt	ttccccttat	attgttcttt	gtttctattg	tttctcaaaa	389760
gataagggac	tggtactcgc	tctaggctgt	ggtgtcttaa	gtgatcttgc	cttaggaagc	389820
cgcggtgtat	ttctactgct	ctaccctcta	actgctctga	tcaccataaa	ggcacacctc	389880
atthtttcaa	aagagagcaa	agccgccttg	gtcattgtga	atatgatttt	ctatggagtc	389940
tttttactcc	taaccattcc	tatgtgcgcc	ttgttcggac	atgaagtcgg	ttgggtcaata	390000
gatgtgctaa	tgatacctct	aaaatgttct	ttcttagata	atctcatctt	cacttctgta	390060
atctatatac	ttccttgccg	aataaactca	ggaatccata	aaatgatata	tttttttagg	390120
agattgggtat	gttactgaga	gggattcctg	cagctgaaaa	aatccttcag	agactcaaaag	390180
aggaaatctc	acaaagtcct	acctctccgg	ggcttgctgt	ggctcctgatt	ggcaatgacc	390240
ccgcatctga	ggtgtacgtt	ggcatgaaag	tcaaaaaagc	tacagaaatc	ggaattatct	390300
ccaaagcgca	caagttaccc	tctgactcta	ccctctcctc	agtccttaag	ctcatagaac	390360
gattgaatca	agatcctagc	atccacggca	tcctcgtgca	acttcccttg	cccaaacact	390420
tggacagcga	agtgattctc	caagcgatct	ccccagacaa	agatgtggag	gggcttcacc	390480
ctgtgaacat	gggaaaagttg	ctccttgga	atthttgatg	acttctaccc	tgcactcctg	390540
caggaattat	tgaactcctg	aactattatg	aaattcctct	tcgaggccgc	catgccgcta	390600
ttgtagggag	aagcaacatc	gtggggaaac	ccttagcggc	cctcatgatg	caaaagcatc	390660
ctcaaactaa	ctgtacagtc	acagttcttc	atagccagtc	ggaaaacctc	ccagaaatct	390720
taaagacagc	tgatatcatt	attgctgctc	taggagcacc	gctthttata	aaggaaacta	390780
tggtagcccc	acatgctgtg	atcgtagatg	taggaacaac	aagagtcctc	gcagacaatg	390840
cgaaaggcta	tactcttctt	ggagatgtag	atthttaata	cgttggtgaca	aaatgcgcag	390900
aatcactcca	gttcctggag	gcgttggtcc	catgactgtc	gctatgctca	tgagcaatac	390960

atggcgatgt	taccaaatt	tttcttagtt	cttttatgtc	ttggactctg	ttcatgctct	391020
caaaaaacga	caacaatcga	aggagagcag	atgacaatct	tctatcgcat	tgttctggga	391080
acctctttat	ccgcaaaaga	aaaagcatct	ttatcccaac	aaattgatag	atgctttcat	391140
aagatcgact	cgatttataa	caactggaat	ccctattctg	aactctcgat	aatcaaccga	391200
gctccagcag	atgtcccat	aactttatct	gtagaacttt	ccgagtttct	agatcaggta	391260
gatacacttt	acaaactttc	agaaggacgt	tttgacccta	ctgtaggacc	tttaaaaacc	391320
ctatggcttc	tacatctcaa	aagtcaaacc	ctcccccta	aagacgtttg	ggaacaacat	391380
tataaagaca	tgggctggca	acacttgag	tttcagtcaa	acacaaaac	tctaatacaa	391440
aagaatcctc	atgttcaaat	cgacctctgt	gggtgtgtca	aaggttatgc	cgtagattgt	391500
ctaaatgaaa	tttgcaatac	cttttgctcg	aacaactatg	tagagtggg	aggagagatc	391560
aaaacgtcag	ggcatcatcc	ctcggaaga	ccttggcgta	tttttctga	agcagcaggt	391620
acgatcttag	atatcgatga	tatggcaatt	gcaacaagt	gaaatcatat	tcaaaaatgg	391680
tgtgttgaag	gaaaaattta	cacccatatt	cttgatactc	gtacagggaa	acccttagag	391740
ctaagctcct	atcctatcca	aagtgtttca	gtagtccatc	cgactgcgca	tacgccgag	391800
ctattgccac	agtcctcatg	acttttgatt	ctaaaataga	agcaaaacag	tgggctgaag	391860
aacaccatat	cctaaccctat	atcaatgatg	gcgcctcttc	atagcagcgg	caacttcacg	391920
ttccttttct	ctttctatga	tcgtacgacg	cttatcataa	gcttttttcc	cacgacaaca	391980
acccaaacgt	accttaacat	agccgcgact	cagaaacatt	cccagaggaa	tcaaagtcac	392040
gcccttttga	gcaatcttac	cctctaactt	acgaagtcca	tatctatgaa	gaaggagttt	392100
acgtttacga	cgctcctcat	ggttatagat	atttccaaac	cgatagggag	caatactcgc	392160
gtttaataac	cacccctcac	ctttagaaac	aatgacataa	gcatacccca	ggtttcccc	392220
atgatcgcg	aacgacttaa	tctcagtccc	agtcaaaacg	atgcctgctt	ctaaagtctc	392280
tataactccc	tagttacgca	gagccttgcg	attagaacaa	atttcttttt	gtgccataag	392340
atcctcccc	ataattgggg	acaaaaacca	gtataacaaa	aagcaatttt	tcttcttaa	392400
gacaatgatt	agaatcctct	ttccttgatt	tccagggag	atttctcaa	tctaaagcct	392460
tttttattag	taaaatatct	agaagaccag	aaaatcactt	tgtagtaata	tcccgatcgt	392520
acctctaccg	tctctcctag	agaggcgtag	cccttcatat	aaagttagac	tcagggtata	392580
ggaaaatatg	aaattcggtg	tatcccgaac	tgagctagga	aaccttatca	aaaaaattca	392640
aagtgtcgtc	cctcaaaaca	cacctattcc	agtactcacc	catgttttga	ttgaaactta	392700
taatgatgaa	ttagttttca	ctgctacgga	tctgacagtg	agcacacgtt	gcgtcaccaa	392760
agctaaagtc	tatgagaaag	gcgctatttc	cattcccccc	aagagatttt	ttcaattagt	392820
aaaagaatta	acagaggcaa	atttagaaat	ttcctcttca	gcaggggaaa	tggcacaaat	392880
cacctcgga	tcttcatatt	tcgcctactc	agcatggaaa	aagaagactt	ccccatgctc	392940
cctgatatac	aaaatgcttt	gcgtttttcc	ttgcctgcag	agcagctaaa	aacctatgcta	393000
cagagaactt	cattcgctgt	atctagagaa	gaaagccgct	atgttcttac	tggagtcctg	393060
cttgctatcg	ccaatggcgt	ggctaccatc	gtagggactg	acggaaagcg	tttagcaaaa	393120
atagatgctg	aagttaactt	agataaaagt	ttttctgggg	aatatattat	tcctatcaaa	393180
gcagtagaag	aaattataaa	gatgtgctcc	gatgaagggt	aagctacgat	cttcttggtat	393240
caagataaga	tgcgggtga	atgtgacaat	actctctga	tcacaaaact	tcttctgga	393300
gaatttccca	atttctcccc	cgctcatatc	acagaaagca	acgtaaaact	cgatctgcat	393360
cgcaagaac	taattactct	gctcaaaaca	gtggctttat	ttacaaatga	gtcctctcac	393420
tccgtgaagt	tttctttctt	acccggagag	ctcactctaa	cagccaactg	tactaagggtg	393480
ggtgaaggaa	aggtaagcat	ggctgtaaat	tattctggcg	aactcctaga	aattgccttt	393540
aatccctttt	tctttttaga	tatcctgaag	catagtaagg	atgaattagt	cagcttaggg	393600
atctcggatt	cctataatcc	tggaaatcatt	accgattctg	cctcaggatt	atttgcctac	393660
atgcctatga	ggctacatga	tgattaataa	actccctaa	gagaatcctt	taggtcacta	393720
ccctgccgat	gtttatgaaa	atctgctctc	tgaagctaaa	aaattttcgt	aaccacagt	393780
atttagaaat	ctcactgggt	cctaaaactca	attatgccca	aggaaaaaca	aacctcctag	393840
aagcgcttta	tgttttgtcc	ttgggaagggt	ctttctgcac	gcaacatctc	acagatacca	393900
tcaccttcgg	atcttcccat	ttcttcttag	aaacacagtt	tgagaaagac	caccttcccc	393960
aagctctctc	catctataca	gacaagcaag	gaaaaaaaat	ctgctataac	caacttcccta	394020
taaaaacctt	atcgagcgtg	atagggaaag	tacctattgt	gcttttctct	tcaaaagacc	394080
gccttctaatt	ttcaggagct	cctgcggatc	gtcgcttttt	cctaaatctg	cttttatctc	394140
aatgcgatac	ccactatacc	ctctgcttat	cgctactaca	tcgcgctctt	tcagagagaa	394200
atgctctctt	aaaaagcaag	caaacctcaa	ccgtggcctc	tgggatgaac	agttgggtcaa	394260
acacggcacc	tacctatcca	tccaacgggt	tctctgtagt	cagaaaacttt	cagattttatc	394320
caaagaactt	tggcttaaca	acctaaaaga	acaattggcc	ttaaaattta	aaagttcctt	394380
aattaaaaat	tctgatattt	ctgaaactgc	tgttgccgaa	gaatttcata	aacagctctc	394440
tatatcactt	cctagagatc	tcgaatgggg	aagcacttcc	gttggccctc	atcgcaaga	394500
ctttctactc	actatgaacc	aaatgcctgt	gtctcaattc	tctagtgaag	ggcagaaaca	394560
cagtcttttg	gcaatcttaa	ggcttgctga	gtgcctatat	ctaaagcaat	ctcatcacgt	394620
ctccccctta	gtctgtctag	atgatatcca	tgttggtatta	gataatgaac	gttcggtca	394680
actccttgac	cctgccccaa	ctctgggtca	gactctgatt	acttccacc	atatgcatgg	394740
ggaacttcca	aaaacaagcc	ttgttttaag	tatcgagaac	gctcaagttt	ctgagcaaat	394800



tatctaaaac	aataacatca	tttttctttt	gcgttaaaaag	taagcgaatt	agttattttt	394860
ataaataagt	tttaataaac	atattctttt	ttaataaaaa	acttatttaa	aataattata	394920
tcggtgacac	atgaagaaat	ttttattaac	tatactcttt	ttagctgtgg	gtaatccttt	394980
attctcggaa	acctcggtaa	tccaaaccct	tccatctgga	attgggggat	taaaggaaac	395040
ctcaaaacaa	aaagaatccg	tggctctgct	gcatgcgttt	ttaagatctt	atacatcttt	395100
aaaacctatt	gctcgcgttc	tagaaaaaga	acattacgat	gtctttattt	ggaattatga	395160
gacgcgcaag	tttactctag	aaaagcatgc	tgaacatctc	aatcgcttgc	tgaaaaaaat	395220
agctgaactt	aagcctggag	tccctataaa	cttcgtaact	cattctattg	gaggagtcac	395280
tgttcgtgct	cttgctgaaa	aaaatagctg	aacttaagcc	tggagtccct	ataaaactcg	395340
taactcattc	tatttgaggga	gtcattgttc	gtgtagcact	cgctcacctt	gattgccccg	395400
aagaagccaa	aaaaggaaaa	gctattctca	tggtctctcc	gaacgcaggg	tctacactag	395460
ctagacgcta	ccgctgtgtg	aaattcgtac	agttcgtatt	tggaggaaaa	ttaggacgac	395520
agcttcttac	ctactgcccc	acaaagatgt	taaatgtcgg	gaaactccct	tcgtcttttag	395580
acgttctcat	tcttagtggg	aacagacata	gcaaattcct	tcctttccgc	ctgccctatg	395640
aaaacgatgg	taagggtatgc	actatagaga	caaagctaga	tactccacat	aaagcttacg	395700
tgatccacac	gagtcatacc	tacatcatta	ctaactcgaa	gtcgctctat	cttatgaaag	395760
agttttttaa	agaaggaaat	acaaccctga	taatcgagca	cgttcccga	gcagcttttag	395820
aacaaactgt	tatgggaagac	aaacaaaaga	actcaagact	taagccttac	cctaaccaag	395880
acatctacgt	tatacactgc	tttggttctc	gtccttacaa	cctttacgga	tttccaaaaa	395940
aatggagcct	taaccaaaaa	aacgaaataa	atcctgaaaa	gttagaaaaa	taaagaagat	396000
gatcaataaa	aaagtgaacg	gaaccaaaat	cctttccaca	atcttcatat	tcaaacgtct	396060
tcttgtgact	atctcccaca	aacatagaag	gatataacct	ccatccaaaa	caggaatagg	396120
aagcaaattc	aagacagcca	aattcatact	aattagaccg	atccaaaaaga	gcacttcaga	396180
aaaccctacc	gaccatcctg	tatgtaaaac	ctgcacaata	cccacaggtc	ctgaaagcca	396240
ttgtggactc	agatgtccag	taactaaagc	tttcaagggt	atcaaacttt	ccttagtaat	396300
atttgataac	ataaccacag	gtgaaggatt	atacctcacc	ttaagatctt	tcaaagaaat	396360
ccctaaagat	ggtttttgct	tctcagcatc	aagacgctcc	aaatagtatc	tttgtttatc	396420
cttgttctta	atcttcttag	ctacttccaa	ctgtttatcc	aaactctccg	aagaataaac	396480
atcaatccaa	ggacgaggct	gaacagggtc	aagaagacga	taaggacccg	cgacttctac	396540
tgggtgagac	tctcctaaat	ggttcaaaaat	ttgtaacaga	tcttcggaat	gataagaggc	396600
gataaaccgc	ttatcagcat	ctcgagaatt	caaccttcca	agttcttgcg	gactcatctg	396660
ctgaacaata	atagagaccc	gatgggtctg	aacaagacgt	aaaatatcta	cacttccaga	396720
aacaggagtg	ccatcaatag	ctagaatgct	atccccaagc	tgtagcctct	cttgagggtg	396780
tggcaaagga	gactctggat	ctatagcagt	aagttcacct	tctatgtatc	cataactatt	396840
gattacataa	ggcaatgtat	ataacgaaga	ccacttgccct	ttaagtccag	cctcatactg	396900
cgtatctata	agctcattac	gaaggtaggg	agtgtaatgt	aaaacggaag	ccaataccct	396960
aggttgacga	gaaaagaaga	ttttgtcatt	ccgtgctact	ttcacaaaaa	cataagactc	397020
attgagtatc	tgagatatct	gagccattga	gaaaagaagt	gtgccatcca	tccaaacgaa	397080
acgatcattc	ggacgtagct	ctgaattctc	cataggagag	ttcttcgtta	ggggcacctg	397140
gttgccatac	aaaagataac	tcgctccaga	acagggaacc	ccgaattttg	tgggatcaaa	397200
ctcaacatca	ctatcgaaact	ctttgctagg	aactgtcaaa	tagccaggac	gtttgatttc	397260
tagattgaga	tgccctctca	ataaagaggt	tgtagcatg	tccttatctc	ccacataagg	397320
cttaccatta	cacgtaagaa	tctcgtctcc	agggagcaat	ccttctgcct	gtaaaacagg	397380
atggacccaa	cctaccactt	tagaacagtc	gctataattt	ttacttcttc	ccccattcat	397440
gtaaagaatg	ctgaaagcca	agacagctaa	taaaatattg	gcaagaggac	cagcaacaag	397500
aaccagaatg	cgtttccaag	gagacttact	aaaaaatccc	tgaggaatat	catagacaga	397560
gtctatcttc	cccttctccc	ctttttcttt	ggtacgttcc	atacctctga	tacgaacata	397620
gcctccaaaa	ggaatgcac	caatgcgata	ttctatgccg	cctatacgtc	ttttaaataa	397680
agcaggacca	aagcctatgc	taaaactctc	tacagccatt	cctacagctt	ttgctactac	397740
cagatgacca	agttcatgaa	ttaacactaa	aatccctaaa	gctagggctg	ctagaataaa	397800
atagattatt	gtcatatacc	tactcgatta	tatttcttga	gcaagagctc	tagcctcacc	397860
atctacttct	aaaatatctt	ctaaagagtg	gcaggcataa	accttatgac	attccataag	397920
agtcgttaat	ttgcgtaaaa	tgtcacacca	agaaatctct	tcgcaaaagga	acctccgcac	397980
taataacttca	ttggctgcat	taaaaaagct	tccagaagac	ccctgtttct	ctaataacctg	398040
ttgtgctaaa	cggatactag	gaaatcgctc	ctcatctacc	ggaaaaaaat	ctaaagtttg	398100
tttcttcgaa	aaatccatag	catccctagg	catgcaaaaa	gcgtctggag	ctgttaaagc	398160
gtattgtatt	gggaagagca	tatcaggcgg	attcatgata	gaaatcacac	tcccatctaa	398220
aaactctacc	ataccatgga	ttaagctctg	aggatgaatt	acagccagga	tttcaacatt	398280
ttctaaacca	aacagccaat	acgcctcgat	aatttcgagt	cccttattga	ccaatgtgga	398340
tgagtccaca	gtcacttttg	aacctcatatt	ccatatagga	tgggtcaaaa	catcttgttt	398400
tgttacacaa	gaaagctctt	ctaaagactt	gttgagcaga	ggccctccag	aagctgtaag	398460
aatcagtttc	ttgattccct	caatcgctct	gccttctaaa	cattgatata	aagcattatg	398520
ctcgttatca	ataggaagaa	cttttatacc	attttctttt	gcagtcttag	aaaccaattc	398580
gccagcacaa	actaaaattt	ctttgtttgc	taaagctagt	gcttttctct	ttttcatcga	398640



ctctagaatc	gcgggtagcg	cctcgattcc	tgaagaagca	gcaacgacag	tagtgactgt	398700
atccatgata	caaagttggg	ttaaaccctc	ctggcctagg	aaaaattgca	tatgggggaa	398760
tcgctgacag	gcctcgttat	aaacctcttc	gttatagacc	gctgcggtca	acggagcaaa	398820
ctcctgnagt	tgctgaaaaa	taaccttaga	ttattttccat	aagaagccat	agaaataatt	398880
ttaaattctg	aaggatagcg	ccgcacaatc	tctaattgtt	gacggccaat	actacctgtt	398940
gacccaagaa	cggctaaatg	tttcaagcat	gctaccttta	actaggtgaa	aaagagaatc	399000
catactccgc	aagtcgagga	attgtcaatt	ctctattgat	actatttcta	actaaagtgg	399060
actaaactct	aaaatttcat	tctttttaa	cactgcta	attgagaact	tttctcactt	399120
atTTTTTcaa	aattttttaga	aaaatagcct	cgaaaatagc	ttataaattt	aaccacgatg	399180
tacatcatcg	tcaagaacac	tacagagatt	cccgaagtcg	ataaccccaa	atcataagca	399240
ctaagaattg	ctctcgaaga	tgcaggagct	aaaaatgctg	tancaatact	aaaaactaac	399300
gaccaagcca	taagactcct	tatcgatttt	gcaataacct	tagcaataag	cgatggaatg	399360
atcagaaaag	caagtgccat	taatacacct	acagccttaa	aagctcctac	aagacatgca	399420
gaaagttgaa	aaataatcaa	ataatcaacc	aaccgaatag	gaattcctaa	agaagaggca	399480
aatacagaat	cgaaagaaga	acaaactaag	ctacggaacg	caaaaaatag	aattacagca	399540
ttagccaaaa	tcacaatagt	gacagggaaa	atatcctctt	tcgttaaaga	atctgcgttt	399600
cctaacacaa	gctccgttcc	tatatgagca	ttctttgtca	taaagactaa	caaaacaagg	399660
ctcagagaga	ataataaaga	aaagactaga	gcggtgctgc	tctcttctga	aactttaaaa	399720
gtattacgaa	taaagtaa	aagaaaccct	gtcagcatag	ctgttgccat	tgctgcaaga	399780
gtcaaggtag	ccaaagagag	ggtcgtagt	tgatgcgtaa	acaaacaaac	acagaccaa	399840
ccaaaaagga	cagtatgaga	gacagcattc	gcatacatag	ccatctttcg	caagactaaa	399900
aaagttcctg	caaaagcacc	tgaacaggaa	atagcaagga	atactataat	ctgaatatca	399960
tcaatataga	gagaaccgct	gaaaagactt	ccagaaaaaca	gtctcgaaaa	aaatactgaa	400020
aaaaattgga	aaaaagatac	tccataataa	ggagaaggtc	ccaaagccat	tagacttctt	400080
tttttttatt	tgggataa	tgctgatgag	gatcataaca	aggatcattg	agaatctctg	400140
tcaaggtag	atccaatctt	tcagtaagaa	catgctctat	ttcctcagcc	aactcatgaa	400200
cactttcctt	gctaaaatct	aaagaattca	caagatacga	ttcccataat	ctgtgagcac	400260
gaactaatct	taaggcctca	cttcttctct	ttttgtgtag	tcgataataa	tcttgttctt	400320
ttttaacata	accccgccat	tctaaaatct	gaactctcca	tctagggaaa	ggcttaggcc	400380
caaaatactc	ctgatactta	taactacaga	caaaatctcg	aactactaat	ttctctaacc	400440
gattatgaga	aatagccaa	aacaccttta	aaaggtgttc	ttgatccttt	gaaaacgaaa	400500
agtgtctcct	acgggcaaaa	cgaatgaccc	acccagattt	tggagaaaaa	agcaaacata	400560
gaccggccaa	taatccagca	caaatgacaa	ccaaaggtcc	cgtaggcaag	gttacaggca	400620
ccgctgttg	ccctataata	gcacgacatg	tgaatgctac	agagatatag	cttcctaaag	400680
ctccgcta	ccctccaaag	aatgcagaaa	ggataagaat	tgtacttaga	cgatcgga	400740
gctgacgagc	acctaagaa	ggagccacaa	acatagcaga	aattaaaaca	atccctacgc	400800
ttcgaactcc	acttacgatc	accaacgata	taaaaattag	actgagtgt	tcataaagaa	400860
cagtctttaa	gccacaagta	acagcaaaa	ctttatcaaa	agtagtcaca	acaatttgtc	400920
gataccacca	ccataaagca	aataacgaag	cacaaaagac	gatcgagcc	aacgtagctt	400980
caagaaaaacc	taaagtggct	gcttgcccat	atagataggc	gttaatgcga	ttgtatagcg	401040
tagggctact	ttccttgaca	taactggcta	aaatcactcc	gatagcaaag	aataccacaa	401100
gaacaaaaca	aagggcgag	tctttatgta	atttacatac	tttccctaag	aaaacaatga	401160
tcccataac	caaataccga	agcagcacac	ccaaacaaca	caatccaaaa	aatagaagct	401220
tgcaatgaga	aaacatattg	cgccatcaaa	gctccaacta	gaagtccctg	atacgacgcg	401280
tgagataaac	tttcgcttaa	aagaggctgc	ttgctaatac	agagaattgt	ccccacaaa	401340
gctgtggtca	tacaaatcaa	agtgcagct	aaaaaactag	ataagaaaat	cgtatcagaa	401400
aaaacacaa	tgagcataat	cagcacgatc	caaattgttt	tcctcgagag	agcttcaggg	401460
tttgttccaa	aagttcaatt	tcacaaccat	acgtttggaa	aatagtgtct	ccattcagac	401520
attcatcagt	agggccacaa	caaatacaac	gcttattcaa	taaaaccaca	tgatcaaata	401580
gttgacgcac	atgactcaag	tcatgatgaa	caacgacgat	agtctttccc	tgatctcgca	401640
gctcttgcaa	aacccttaca	gatgttttaa	acgaagccat	atcaatcgct	gaaaacaact	401700
catccataag	atatagatct	gcttttttga	tcaaagcacg	tgctaaaaat	gctcttttgt	401760
gctgtcctcc	tgagagctgt	cctattttgtc	tatctgtac	ggattccaaa	ccaactcttt	401820
ctaaaatag	aaaggcctcc	cttcgatcat	ccgaagaaat	tctccccac	atctctttat	401880
agctgtaaca	ccccataagg	gctaaatcta	agacagtc	tggaataatcc	caatccacgc	401940
tagctctctg	aggcatatag	gctatgcgct	gacgcacctt	cttaaatttt	tgattaaaaa	402000
aataaacagt	ccccgaagag	ggtttgatca	ggcctaagga	agcctttaag	agagtgtctt	402060
taccagctcc	attaggacct	aaaatagcag	ttaatgaccc	ctttcccaag	gaaaaggata	402120
tgtgataaag	aacggctgca	tgctcatagt	ttacacaaag	gttgtgtaca	gacccaaaag	402180
tctcatcttt	gacattcaag	agccacccct	cctaattctt	ctgtgataag	gcagacatta	402240
tgtttaaagg	tgctaaaata	attgtcgtcc	acattatcac	tatacaatgg	tttttgagct	402300
agacgaacta	aatgactttt	cttcagagaa	gaaaacaatt	ttttcaacgc	atcttggttc	402360
agagtatcct	cagggaatac	cacactgaca	tcatgctcat	taatataatc	tacaaccgcc	402420
ataatatcac	gaacactgat	ttgagcttct	ggagatagac	cctcaggaga	aatacaacga	402480

gacctccatg	ctccggaagc	cactttcttca	ggagtagcta	aatagcgacg	tgtaaagtaa	402540
ctgaacgcat	tatgacctga	gacaagatac	cgtaaatfff	caggaattgt	gctcaagcat	402600
tgtttcgccc	aagaatctaa	aatagacatt	tcacaaacaa	gttcctcact	atftgcttta	402660
aattcagcag	accattcagg	gaacttttca	atgagaactt	ctgtaatttc	tatgacagct	402720
tccttccaaa	tagaaagatc	catccagata	tgaggatcgc	aaataccgtc	ttcttctaga	402780
ggaacaaagg	ccccacgcgc	tatcaaccgc	tcccctaact	tgacactatt	gggattatft	402840
tctaaatgct	tccgcaaact	taatgtatgc	tcaagaccca	ggccgttaca	aaaaattacg	402900
gcacttccag	caatcttgtc	cttatccctt	ttaaccatct	catacgcatg	agggctctaag	402960
gatcctttga	tcaaaacagc	ggtagcaagc	ctattcccca	cgactctttc	aacacaaatca	403020
tgaatcatgc	gattcatgga	tagtatacaa	ggacgtgaat	ttgcattctg	aaaccagaa	403080
ttggtacatc	caaaagttat	accacatgcc	acgaaacaga	aaatccaacg	catcacttta	403140
aatatatatc	ccattttcgc	atccatctct	ctagaagcat	tttttaagat	ccattaaaaa	403200
ccacttaacg	aaccaccaa	catcaaagct	ataacccgat	ctaaaagatt	tattattttac	403260
atftttcgtat	cccagaaact	aatgaaaaag	caaagtacca	gaaaaacaag	ttctattcaa	403320
aatatatttt	atccagcaag	aaatacaact	aatagaaatg	aaagaaatat	ctttgttcag	403380
gatagtttta	aaaaaattag	aaaaccggtt	tgftttataa	gaaaaacaaa	tgttatagaa	403440
aaaaatcttct	ttacttttacg	atfttttatgt	tttgaatttt	gttaagaaac	aaaaagatcc	403500
tgagaggaaa	aatattgcaa	aaaggagaa	ttgcaatata	atfttatgttc	gctgattgat	403560
taaaacagcg	ctttaatttt	atfttctctaa	acattaaatt	gaaagtatgc	cacattcttt	403620
cttgtaaaat	atgtaagcat	caattataaa	aggtgggttt	catggccgta	gaacaatcac	403680
atataaaaaga	agaaatagaa	aaactgatcg	gaaaagctat	taaaagagtc	tgcggaacaa	403740
aagaaaacga	tttatgtcgc	tatcttccag	gccctagcgg	cgtttatatg	catcattttca	403800
ctctaaaaaa	gatgaaaagc	gctgctcccg	aacaactttt	aaaaatgtta	aaaaacttta	403860
ttttagaatc	ggaaacccca	cgcacaatta	atcctaagcc	tagagctcct	agaggctcta	403920
aaaaacgctc	tgactttatt	aactttacta	aaacagatat	tgaacgcgtt	ttagaactgg	403980
caagacaagt	tggagacaaa	gacctcctcg	ctcgccttag	ccctaaaaaa	ccgttaactt	404040
ctttaaaaag	ggagttaatt	cgttcgattc	gcaacggtat	cgtgagcgta	gagctatgga	404100
atgcctacgt	cgaagctgtg	aaggctgtaa	gctctcccaa	ccttgaagtt	acctctcctt	404160
tcgtttaatt	aaaaataaaa	ttttacaggc	gacttagcaa	taaagtcgcc	taagaactct	404220
taatccctta	ggagtatccc	tttctctttg	tcaatagaga	gaaaagatgg	tatatataaa	404280
ggtcttttca	aatggaaaac	attcaagtta	gtccacaacg	aaataaaaaa	ctatcagaat	404340
agaaaataaa	agtatttcag	agggtaaata	tgacaaaaac	cgaagaaaaa	ccttttggaa	404400
aattgcgctc	tttcttgtgg	ccgatacata	ctcacgagct	aaagaaagtt	ctgccaatgt	404460
tcctaattgtt	cttctgtatt	acattttaact	atacgggtgtt	acgcgataca	aaagacactc	404520
ttattgtggg	agctcctggg	tctggtgcag	aggcaatacc	tttcatcaag	ttttggcttg	404580
ttgtccctcg	tgctattatc	tttatgctta	tttatgcaaa	gctaagtaat	atftttaagta	404640
agcaggcctt	atftttatgca	gtgggaacgc	ccttttttaat	tttctttggc	ctgttcccga	404700
ctgtaattta	tccgctacgc	gatgttttac	atcctacaga	atftgctgac	cgftttacag	404760
ccatcttacc	tccaggattg	ctaggactcg	ttgccatctt	aagaaactgg	acatttgctg	404820
caattttatgt	acttgctgaa	ctatggggaa	gcgtcatgct	atctctaatg	ttctggggat	404880
ttgctaataga	aattacaaaa	atccacgaag	caaagcgttt	ctacgctctt	ttcgggtatcg	404940
gagctaataat	ttcttttacta	gcttctgggtc	gtgcaattgt	ttgggcttca	aagttgagag	405000
cttccggtttc	tgaagggtga	gatccttggg	gaattttctt	acgtcttttg	atggctatga	405060
ctattgtatc	tggacttggt	cttatggcca	gttactgggtg	gatcaataag	aacgtattga	405120
ccgatccctcg	cttctataat	ccagaagaaa	tgcaaaaggg	gaaaaaagg	gctaaaccta	405180
aaatgaatat	gaaagatagc	ttcctctatc	ttgctagatc	tccttatatt	cttttattag	405240
ctctctttggt	tattgcctat	ggatatttga	ttactttaat	cgaagtgact	tggaaaagtc	405300
agctgaaact	gcaatatcct	aatatgaatg	actatagtga	gttcatgggg	aacttctcct	405360
tctggactgg	cgtagtatcc	gtacttatca	tgctattttgt	tggtggtaac	gtcattcgta	405420
aattttggatg	gttaactgga	gccctagtca	ctcctgtcat	ggttctctcta	acagggtatcg	405480
ttttcttctgc	tcttggtatc	tttagaaaacc	aagcttctgg	gctggctcgt	atgttcggta	405540
caactcctct	catgctagct	gtgggtgtcg	gagctataca	gaatattctt	tcgaaatcca	405600
caaaaatacgc	tctctttgac	tcaactaaaag	aaatggccta	tatccctctt	gaccaagagc	405660
aaaaagtcaa	aggtaaggct	gctattgatg	tagttgcccgc	ccgcttcgga	aaatcaggag	405720
gagctttaat	ccaacaagg	ttgctcggtta	tattggagag	atgaccctt	405780	
atcttgacgt	gattcttctt	ttcatctattg	ctattttggtt	ggtttctgca	actaagttaa	405840
acaaaactatt	cttagcgcag	tctgctctta	aagaacaaga	agtggtctcaa	gaagattcag	405900
ctcctgcttc	ttcatagagt	tgcttctctt	actcttggtg	atccctacct	gcttttttagt	405960
ggggtaggga	tttttttttat	taactcccat	ttcacgaatt	cgtacgcttt	tttcaatcaa	406020
aaaagggttat	aataaccgtg	agacattctg	gttggtactat	gaagtgtagt	cctttaacac	406080
tagttcccca	tatatftttta	aaaaatgact	gcgaatgtca	tagatcttgt	tctttaaaaa	406140
ttaggacaat	tgcccgaactc	atftcttgggc	ttgttctagc	tcttggttagc	gcacttctctt	406200
ttgttttctt	tgctgcgccg	attagctatg	ctattggagg	aacttttagct	ttagccgcta	406260
tcgtaatctt	gattataacg	ctagtcgtag	cactgctagc	taaatcaaag	gttctgcca	406320

tccccaacga	acttcagaag	attattttaca	atcgctatcc	taaagaagtc	ttttattttcg	406380
tgaaaacaca	ctccctgact	gttaacgaat	taaaaaatatt	tattaattgc	tggaagagcg	406440
gtacagacct	gcctccgaat	ttacataaaa	aagcagaggc	tttcgggatc	gatattctaa	406500
aatctataga	tttaaccctg	tttcagagat	tcgaagagat	tcttcttcaa	aactgcccgt	406560
tatactggct	ctcccattht	atagacaaaa	ctgaatctgt	tgctggggaa	atcggattaa	406620
ataaaacaca	aaaagtttat	ggtttacttg	ggcccttagc	gtttcataaa	ggatatacaa	406680
ctattttcca	ctcttatata	cgccctctac	taacattaat	ctcagaatca	cagtataagt	406740
tcctatatag	taaagcgtct	aagaatcaat	gggattctcc	ttctgtgaaa	aaaacctgcg	406800
aagaaatatt	caagggaactc	ccccacaata	tgattttccg	gaaggatgtt	caagggaatct	406860
cacaattctt	atttcttttc	ttttctcatg	gtatcacttg	ggaacaggct	cagatgatct	406920
aacttataaa	tcctgataat	tggaataatgt	tgtgtcagtt	tgataaagca	ggaggccact	406980
gttccatggc	aacatttgga	ggctttttga	atactgaaac	aaatatgttc	gatccagtat	407040
cctctaacta	tgaacctaca	gtgaacttca	tgacgtggaa	agaattgaag	gttttactag	407100
agaaagtaaa	agaaagtcct	atgcacccag	cgagtgtctt	tgttcagaag	atatgcgtaa	407160
atacaacgca	ccatcaaaa	ctgttaaaac	gatggcaatt	tgttcgtaat	acgagttcac	407220
aatggacatc	aagctttacct	cagtatgctt	tccacgcccc	aacctacaaa	ctagagaaaa	407280
agaatagaaa	gcagctctccc	tatacgatct	tccttataag	gggagtctga	tcatttgcaa	407340
tacctacaag	caaattgctg	ttgaaagact	ttttataatt	gagattttaga	aatataaaaa	407400
aatctttaat	ttttataaaa	agaatacgtt	attcccaatc	gggaaaagaa	caaaaagggg	407460
ctcgcctttt	ttttaaaaaa	agcataacaa	gctctctcgt	tattcttctt	ctagaagcta	407520
tcttcaatga	aaacttttca	tcaataatac	aaaacaattt	caataaaaaat	tttaaaaaata	407580
aaaacatttc	tattaatagg	attttttgtta	aatttacgat	ataatacgca	aattgtgag	407640
cctaggaaat	gtatgagtaa	tataacctcg	ccagttattc	aaaataatcg	ctcttghtaat	407700
tattattttg	aattaaagaa	ttcaacctct	attcatattg	ttatcagtg	catcttactc	407760
tgcggaactt	gatagctttc	ttgtgtgtag	cagctcctgt	ttcttatatt	ctaagtggcg	407820
cattgttagg	attaggatta	ttaatagcct	tgattgggtg	gatttttagga	ataaaaaaaa	407880
tcacgcctat	gatttcatca	aaagaacaag	tattccccca	agaactcgt	aatagaatca	407940
ggcgcgacta	tcctaaatth	gtctctgatt	ttgtttcaga	agctaaacca	aatctttaaag	408000
atctcataag	ttttattgat	cttctaaatc	aattgcactc	tgaagttgga	tcactacaaa	408060
attacaacgt	atctgaagaa	ctacaacaga	aaatagatac	gttcgagggg	atcgcagctc	408120
taaaaaatct	agtcctgact	gcttctctta	aaagacttga	aagcgtctgt	tcttcccgtc	408180
ccctcttccc	ctctttacca	aaaatctttac	aaaagggtatt	tccatttttc	tggttagggag	408240
agttttatttc	tgacggcagc	aagggtgttag	agctccatcg	agtttaagaaa	attggaggca	408300
gcctcgaaga	agaccttagt	gattatataa	aaccagagat	gcttctctacc	tattgggttga	408360
ttccttttaga	tttttagacca	acaaattcct	ctattctaaa	tctacacaca	ttagtttttag	408420
ctagagtctt	aactcgtgat	gtttttcaac	atcttaagta	tgcagcatta	aatggcgagt	408480
ggaacctgaa	tcatagtgat	ctaaatacta	tgaacacaga	gctctttgct	aaatatcatg	408540
cggcgatatca	atcctataaa	catctatctc	aacctctctc	tcaagaggat	gaattctata	408600
acctgctctt	gtgtattttt	aagcatagg	actcgtggaa	gcagatgtcc	ttataaaaaa	408660
cagtcctcgg	tgatttatgg	gaaaacctct	gttgcttgac	tttagaccat	acaggacgac	408720
cccaagacat	ggaatttgcc	tctctaattg	gtactctcta	cacacaaggc	ctaattcata	408780
aagaaagcga	acattttctt	cttcattgac	actccttagt	ttagatcagt	ttaaaacgat	408840
ccgtcgtcag	tcaaccaata	tagcgatgtt	ccttgagaat	ttagcaactc	ataattccac	408900
ctttagaagc	ttaccaccta	taacagttca	tccactcaag	agaagcgtct	tctcccaacc	408960
tgaagaagac	gagtcctccc	tgctgatagg	ttagagattt	ctatttttga	ataagaaaaa	409020
ttctactccc	tctcgtagcc	ccttttcgaga	ctaaaaagct	agttacctgg	tttagtcttt	409080
aaagaagata	ctcgtcttcc	tatgaattct	agctcctgtt	acaaaattga	cgtcataaac	409140
cctagctctg	gcattttccat	gctctagagc	tattctgtga	agacctgtc	ttataacact	409200
ctctaattgc	ttagaaactg	aactcaaatg	ccttaacaag	aatttaccta	gttctttctt	409260
tggtctcatca	gaagcagaaa	atgcttgaac	agcttctttt	agatcctgaa	tcacatacag	409320
gcctagggtt	acatcaaaat	cgatagaaga	ttcgtcaaga	agattttggg	atgacaaagc	409380
tcctacaaga	gcacaaagct	gaagggttga	tgcggtactg	ttatctacaa	aacacagcca	409440
atcccaagca	tctctaggaa	gttgagtgat	cagctgtagc	tgatcaaaa	aatagccatg	409500
caagctcaac	aatagcaatt	ccttactgat	tgctcttttt	gtaagtcctc	ctgcttcggt	409560
cttttagagt	cctcgtgccg	tataggtagt	gtagatacgc	tctacaattg	ctttgacttc	409620
atcagtatcc	cattttctct	gaagagcctt	gttttttaat	aaaagaacgt	cctctttcgt	409680
taattgttga	agaatatgat	gcgtctcttt	acaaaaaatt	gtagccttag	ctgtactgta	409740
tcccaaaggc	cctagccaat	agtacccata	acattctcta	gggacaccta	ggctcttaca	409800
aacttggtga	tctcttgctg	atataaaatt	ctgaagccaa	tataacgggc	aggtttggct	409860
taaaagatct	tcaaatattg	gccaaattatt	ctttttctaaa	tcacctgcga	gcctgctaatt	409920
acaaaaactc	tctactttac	ttcgcaattc	agaaggcaat	tgtttgattt	tctcttcagg	409980
agatatgtta	cacaacaggg	cagtagaaaa	ttgtctaaac	tcggctaagt	ttacctgctg	410040
ttctcttaca	aatgcagaga	ttgaaaggcc	ataagcttca	tctatcacgt	gagtaaatct	410100
atcaggaatg	attcttggtg	ttgggtggaag	cttcttctct	ccaaaaatca	aagctaaaat	410160

tactaaagaa	agaatgacaa	aggcaataaa	agctaaaaca	ctcccaacaa	tataagaaac	410220
gggaggagcc	aaacagccta	aagctgctaa	tgcacctata	caaaagaggc	tggcaatggc	410280
tattcttaca	atagtccttg	aactcaaagg	aaaggtagaa	tgacactcgc	aatgattttt	410340
aaataaagca	tgtggaacga	tcgtcatgct	catagccaac	tccttagata	tagatctatt	410400
gaaggcagta	tagattatgt	gtaaataaaa	atctctaat	caagaatttc	ctgtaataaa	410460
aaatcccatg	aaaaatagct	ctctcttacc	cttcagatta	ggcaaaacttt	ttacaatccc	410520
cgaaaaaaat	gcagatcgaa	cacttaagga	tttcaaaaat	ttctgccaag	ctgacctagg	410580
atTTTTTTT	cactccctat	ctaaatggta	tttaggataa	ttcaagaagg	tatttttcgaa	410640
ccttttgattt	agatctaagg	aacctaggta	ctgtctaaac	ctttgaaagt	gtttttcaaa	410700
tacattacaa	agatcttttg	caaccccggt	ttttgttggg	ttgcttaaca	aactgcattt	410760
ctatcagttc	ttcccagggt	aatagagaaa	cctcaggaag	gtaaaattgc	tcttttgctt	410820
cgtataatgc	ccaggacgaa	tgtaacagcc	caaccagacg	tgataactgg	aatccctcgc	410880
cttgagaatc	aaaatcacaa	agccaatccc	atccggactc	attcatatat	tgaaataatt	410940
gcacttgctt	tcaagagagc	ttgtgagaaa	aaataagggt	aaggagggaa	tcaaactgtt	411000
cgtaatcagc	gtttaactct	gcttcatcta	cctcttcttt	atcagcataa	tatcttgtaa	411060
aaagggtttg	tctgatttga	acgagttccg	aagaactcca	cgtgtttttc	ttgagaccat	411120
cttctaaaaag	agcaaaactct	ccaaagctaa	ttttctttta	caatagaaga	gatcgacgtt	411180
caaaaagaga	gggagcggtt	tcgtacagtc	ctaaaggacc	acaccaatag	tatccatagg	411240
ttcctggagt	gacatccgat	accatgggat	ataccagacg	tcccaaccaa	tgcaatgggc	411300
aatgctgtag	aagaattttct	tcaaaattag	ggagcttact	tggtgttaca	tctttgaact	411360
tctcaatgcc	aaactgtaag	agtttttctt	gtaaatatac	tggtgctttg	tcgaaaacat	411420
tcgtcttatt	aagaatagag	atcaagtgat	gtatctcata	aatggaaacc	tcctgatctc	411480
taataaaaatc	aacaacaata	cttgagataat	gttcttggat	gagttccatg	attttcttag	411540
ggatcagcaa	ctccttaggt	tcttgtctca	tcttataaat	cataaacata	gcagaagcaa	411600
aaagaataag	agaaactaga	acaagagcag	ttcctaactc	tatggataaa	agagattgac	411660
tgcataccaa	agctacaata	gcgagtacag	cagcaacaac	agaaacgata	atcaggctaa	411720
gcgctggctg	gcacaccgaa	aattgggtag	cctgactata	gttgacttgg	gtattcctat	411780
acacaggctg	tatattaacc	atagaagctc	cattgtgact	tgagtatcag	cgtgttatat	411840
tatttttcta	atcatttttag	aattcatgga	attattttac	ttctataaat	ttctttcaca	411900
tagactccag	agcttgaaaa	aatcgattgc	gaagacctga	actcctactc	aaatagactc	411960
cctgactttc	cagttcttca	ctacattgaa	gagcactatc	tcggacataa	gaacactcat	412020
tcctctctta	tactcttgga	tcgagtcgat	ttactatct	caaaccctaa	tgctttcatg	412080
aatttttatta	tgcttgtcta	aatgactgaa	aaaatgacct	gcaaggactt	tagatgaaca	412140
tatgtaaatg	gtaaatattt	ttttatctct	tttagaatcg	gtttcccttt	ctatagaatc	412200
ctgagtggga	atcagtttca	tactaacgga	gagcacttct	tctcacttag	ttttttctac	412260
tgctagccac	tctggaaactc	tacctcaaat	cagattcgac	tttaaaccct	tgtgggtttct	412320
acatctcacc	tattatactt	tcatctatcc	aaagctaaag	atgaccgcat	gatcattttg	412380
ctaataaaga	gatgcagttc	gcaaaagtat	ttgagaagct	ggtctttgtc	tgaaggaggc	412440
ttctcaatgc	agctttatga	aaccaggaat	aaactacag	tacattttga	412500	
aagaatataa	gatagagaac	attcgcaatt	tttcaatcat	agcgcatatt	gatcacggga	412560
agtctacaat	tgctgatcgc	cttttagaaa	gtacgagcac	agtagaagaa	cgggagatgc	412620
gtgagcagct	cttagattcc	atggatcttg	aaagagagcg	tggcattaca	attaaagctc	412680
atcctgtcac	catgacgtat	ctatatgaag	gagaggtgta	tcaactgaac	ctgattgata	412740
cccctgggtca	cgtggacttt	tcgtatgaag	tctctcgatc	tctatctgca	tgtgagggag	412800
ccttacttat	tgtagatgcc	gcccaggggg	tgagggcaca	aagtcttgct	aatgtctacc	412860
tggcccttga	aagagattta	gagatcattc	ctgtattaaa	caagattgat	ctacctgccg	412920
ctgatcccg	gagaattgct	caacagattg	aagattatat	aggcctagac	actacgaaca	412980
ttattgcctg	ttctgcaaaa	acaggtcagg	ggatccctgc	aatcctgaaa	gcaattatcg	413040
atcttgttcc	tcctccaaaa	gcacctgcag	aaacagagct	ttaaagcttta	gtctttgatt	413100
ctcattatga	cccttacgtt	ggcattatgg	tctacgtacg	cattatttagc	ggggaattaa	413160
aaaaaggaga	ccgcattact	tttatggcgg	ctaaaggctc	ctcgtttgaa	gtcttaggta	413220
taggggacct	tctccctaaa	gcaacattta	tagaagggtc	cttacgccct	ggtcagggtg	413280
gttttttttat	tgccaatctc	aaaaaagtga	aggatgtgaa	gatcggcgat	acagtcacga	413340
aaacaaaaca	tctctgcaaaa	actccttttg	aaggcttcaa	agagatcaat	ccggtagttt	413400
ttgctggaat	ttactctata	gattcttctg	attttgatac	tttgaaagat	gctttaggaa	413460
gactacagct	caatgattct	gctttaacta	tagaacaaga	aagcagtcac	tctttaggct	413520
ttgggttttcg	ttgtggcttc	ttaggacttc	ttcatcttga	gattatcttt	gaaagaatca	413580
ttcgagaatt	tgacttagat	attattgcaa	cggctccaag	tgtcatctat	aaagtcgtct	413640
taaaaaacgg	gaaagttcta	gatattgata	accctcagg	atatccggat	cctgcgatca	413700
tcgagcatgt	ggaagagcct	tgggttcgat	tgaatattat	cacccctcaa	gaatatctga	413760
gcaacattat	gaacctctgt	ttagataaac	gtgggatctg	cgtaaaaaca	gaaatgctag	413820
atcagcaccg	tctagtctct	gcttacgaac	tcccttttaa	tcgagattgtc	tcggatttca	413880
atgacaagct	gaagtcagta	actaaagggt	atggactcct	tgactaccgt	cttggggatt	413940
accgtaaggg	atcgatcatc	aaattagagg	ttcttattaa	cgaggagccc	atagatgctt	414000

tttcttggtt	agtccataga	gataaagcag	aatctcgtgg	aagaagtatc	tgcgaaaagc	414060
ttgtggacgt	gattccacaa	caactcttca	agattcccat	ccaagctgcc	attaacaaaa	414120
aagtcattgc	cagagaaaacg	attcgtgctg	tttctaagaa	cgtgaccgca	aagtgttatg	414180
gcggagatat	tactaggaaa	cgcaagctgt	gggaaaagca	aaagaaagga	aaaaaacgta	414240
tgaaggaatt	tggaaaagtt	tccattccca	atacagcttt	cattgaagtt	ctaaaattag	414300
attaacattg	agcgttaaaa	tcagcacact	gcttacaatt	gaaaattcgg	tagtggtgaa	414360
ctaaatctcg	agctacctag	ggtcttctcg	agatttttta	tttttacttc	actctttctg	414420
tagttttcgt	gtgcacccaa	tcggtatgat	agaactctcc	tcgagggcga	tcgttacgct	414480
cgtaggtatg	agctccaaaa	taatctcgca	gtccttgagc	taacgacatt	gaagagcttg	414540
ctgtacgata	gccatcataa	aacgtgattg	ctgctgctaa	acaggggaata	ggtagccctg	414600
caccaattgc	agtcactact	gttctacgcc	atccccatctc	cgcattggcgt	aatgctccac	414660
ggaaatatct	ttggaagatg	agcgaggtat	tctctggggt	ggcagcaaat	cctttatgta	414720
taacatctaa	aaatgcactt	tgaataatgc	atcccccgcg	ccacatcaaa	gcaatttctc	414780
ctaggtctaa	tccccaat	tattcttttg	aagcttctcc	taaaagcatg	aatccctgag	414840
catagctgat	gatcttgga	gcgtataaag	catgaaagac	atcttgatg	aataccgagg	414900
gatcatgggg	catttcaaat	attaaggggg	ttcttgata	attacgggca	gcttgctcgc	414960
gtatctcttt	ccaagaagaa	aggaaacgag	caagaacagc	tcctatgatt	aaggaaaggg	415020
gaactccaga	atttaaagca	tcgattgcgg	tccactttcc	tgtacctttt	tggccacaga	415080
catctaaaat	cgtatcaata	acagggattc	cttccggatc	tttcaatgct	aggacttcag	415140
aagcaatacg	aattagatag	ctttccaact	ctagagtatt	ccactctttc	aaaattgtag	415200
caacggcagt	tgcggagagc	tttaggaaat	ctcttaagat	accgtaagtt	cgcataatcaa	415260
ctggatatacg	ccgtattcta	taccattgtg	aacagccttt	acatagtggc	ctgcaccgcc	415320
agttcctacc	caagaacagc	agggacggcc	ctgtactttt	gctgctattg	attgaaaaat	415380
aggagccact	aatggccacg	cctcaggatt	tcctccaggc	ataattgatg	ggccgtgacg	415440
tgcaccttct	tctcctccag	aaatccccac	gcctaagaag	agaatccctt	tttcttgcaa	415500
ctctttacat	cgtcgttcgg	aatcttttaa	atagctattc	cccccatcga	taatcacatc	415560
gccgggttct	agaaaaggca	gtaacgcgat	aatgctctga	tccacaggtt	tccttgcctg	415620
aatcatcaac	atgatctttc	gtggtctctc	caatgaattc	acaaagtctt	ctaaagattc	415680
aaaccctaca	agctctcggt	ggttagggta	ttctttcaag	aagtcctcgg	ttttctctgg	415740
ggtcgcatga	tagacagaga	cagaaaaacc	atgatctatc	atgtttaaga	caagattttt	415800
ccccatgaca	gctaagccaa	taagaccaat	attcgtttgc	aaagctacct	agcctcctta	415860
aactaattta	aatatagaac	aagctttcgt	tttttacctt	gagccaacaa	cacatagtga	415920
ccataacaga	tgtcttggtc	ttcacaaaca	ctatgctcat	tagcgatggg	cacattatta	415980
atatataccc	ctttttgttc	aattagcctt	cgaatttccc	cttttagattt	acatagtccc	416040
aaaacaagaa	ataggtctaa	ccaacgtttc	cctaacacct	cggattttatc	caatgaggcc	416100
cccatccctc	ctgcaaacaa	ttcatgaaaa	tctttttccg	ataaggatga	aagattccct	416160
ggatgcatgc	tacgagttac	agaaagagcc	tcttcaagcc	ctagatctcc	atgaatgaca	416220
cttaagatat	cctgggctac	aaattccttc	actgcaactg	gatccgtctg	tacacgccta	416280
tcaatatctt	gaatttcttc	attgctcaat	aaagttaacg	tacgagcaat	tttagggatg	416340
gtatcatcgg	gcaaacggag	taagtattgg	tacagctcaa	aaggagaggt	taaatctgaa	416400
tcgagccata	cagttcccga	ctctgttttc	cctatttttt	tcccctgagc	attcggtaat	416460
aaaggatagg	taaggccgta	ggcctgaccc	aaccctttac	ggcgaataaa	atcgattcct	416520
gaagtaatat	tccccactg	atcgctacca	ccgcactgca	agatcggtgc	ataattttta	416580
aataagtgat	aaaaatcata	ggattgcagg	attaaatagc	taaactcggg	atagctaatt	416640
ccttcatcag	aatgcaccg	ctgctttatt	gtatctttca	ctagcatttg	gcctaaacga	416700
aagtgttttc	ctatatccct	taagaaatca	atcagggaga	tctcctgcaa	ccagtctgca	416760
ttattttaca	gagtcacccc	gggaagatag	cgctggagac	acgccgtgat	cttttgactg	416820
ttatcaaaaa	cttcacttgt	ctgaagtaac	gatctctcgc	tctgtttccc	tgagggatct	416880
ccaaccatac	ctgtggctcc	cccgaactaa	gctatggggg	taatccccag	agcagcgagt	416940
ctcttcaaga	aacaaatccc	aatccaatga	ccaatatgta	gagcaggtgc	ggtaggatca	417000
aatcctaatt	aagcggcgat	aggtccctct	acggattcca	aacctgcggg	aaaattctct	417060
aaaatatttc	gctcttgtaa	agattgtaac	caggattgca	tgagtgatcg	tacataatta	417120
agaattgcca	agctctatct	tatcgatcct	aaagcttata	tgcaaggcac	cacctatcta	417180
acaataaaga	aaagattgta	cgctgagagt	aatccttttg	ctgagatacc	ataacttcta	417240
tcttctctaa	agattaggtc	gctatgtcta	catctccaat	tgggggttccg	tcgatgctaa	417300
acgccgcaac	tagtctaaat	gccacaacta	gcaaggcacc	ccttccctacc	tctaccctag	417360
ccgaacgtat	taaagaatgg	ctgccccgca	ttcttctctt	gattgttagga	gcaatcttca	417420
caattgctgg	ctgcattggt	atggcggtga	ctaaacaaat	tctttacgga	ttactctgtg	417480
tcgtaggagg	gcttctccta	gctctaggac	tgctcttaaa	acctgagaac	tgtatttatc	417540
gaaatgcaga	gagtcctgcg	gaagcttaag	caatgcttta	gagtgaattt	gagagacgcg	417600
agactcactt	accccaagga	ccttaccgat	ttctctaagg	acaagttctt	catagatgta	417660
cagggccatg	accttgcggt	ccttttctct	aagttcctga	atcgatttgg	ctaaacataa	417720
agaaaattct	tgtttatcta	caacatcgta	ccctgtctcg	gcacgttcat	cggggattct	417780
ctcttcaaga	gccattccgg	ctccttcac	actttgtgaa	ggccactctt	cattcagaga	417840

cacgattaat	gcaggacggg	cagatacaaa	ccatcccga	agctcttggt	gcgaaatatt	417900
gagatactca	cacagttcaa	gatccgtggg	ttccttgcc	aaagactggc	gaagagaatc	417960
catagctcct	gacaatttat	tcgctttttg	atggacacta	cgaggaaccc	agtcttgctt	418020
acgcagatca	tcaataatgg	cagccttaat	cagaaatacc	gcataacctt	caaaacgacg	418080
acttctctca	ggattataac	gttccaccgc	acggacgaga	ccttcaacac	ccgaagcata	418140
caaatccctg	gtctttacat	gggaaggcat	ccttgaaatc	aaacgatgaa	ccacactttt	418200
tactaaaggc	aaatagaact	caattaagct	atcgcgatac	tctatttcct	gagtctccca	418260
gtagaagttc	caaacctcta	tgatgttttg	agtttgctgt	gttttcacaa	attttttttt	418320
atctagttat	ttattagatt	aattcaaaaa	aaatttttaa	acaatattta	caccaacaaa	418380
aaaaatacga	aagtaatagt	gcttacagaa	gattaaatta	aattaaggaa	ctaaaacctc	418440
atctgaaacg	atccctaaga	aggaaatagg	gattttctta	ggaagctcat	catgagataa	418500
aaccaaaaga	tcagggaat	gtgggtcgag	catttttttc	atctcaaate	gtgtttcaca	418560
gctcgtaact	atgggtcgaa	aatcttttaa	taccgaccgt	tctaaaagac	tgtctactcg	418620
acggatcaca	ttctcttgca	ttacaggatt	agactttgag	tatgagctgt	ttatcaattc	418680
ttcaacatga	aaatctatgg	taattacctc	aagggtttgt	ttctgatccc	agagacttct	418740
cccaatccaa	tatccgagag	actttcgcac	tttttcgcga	aggatctcca	agctgtctcc	418800
agaatttttg	tataccgcaa	cggtctctag	aatctttggg	naaagcttaa	gcgataccct	418860
ttctctaaca	aggaggcgag	aaagaactac	aagagagctt	aaagagattt	tcttaggaac	418920
gatgtcttca	acagcgatgc	caaacactct	ctctgattcc	tcaaggtact	tttgaactac	418980
ctcggcattg	agagcctcat	gagcgatgtt	tctaaggaaa	ggaagcacag	cctctggagt	419040
catttcatct	aagtatacat	tctggccaaa	tactcggagc	caaggacgct	cttcaatcag	419100
tagagaagta	agcacaggca	atctaactcc	taaatcttca	aatacttctt	cggatgctgc	419160
acgatatact	tgtatagaact	gtgattcttg	ttccttaggg	caggcccccct	caacataaga	419220
gaacgcacgt	tctatacaag	aatcttctga	tgcaggctct	tcttttcgat	acgccaaacca	419280
taaaagactc	gcgagcaaaa	cgatagggaa	ttttggagaa	ctgggaatgc	agcacaaga	419340
aaagatcaat	aacgacacca	ccctgaaatg	ctgacgcaac	tgtttgtagt	attcgaacag	419400
gtaattttaa	aggctctctt	ccttatcgat	tttactaata	agagtggctg	cagcacacga	419460
agtaagtaaa	gcagggtactt	gactcactaa	agcatctcct	aaaactgtaa	accacatctg	419520
ctcaagagca	taaccggaag	tataataaag	acaagttaca	gaaactacgt	tcacgagtaa	419580
aaggatacaa	ctaataattg	catccccctt	aacaaaacga	aagaccccct	ccatggcaga	419640
gaagaaatcc	ccttcttcta	taagggcatt	tttttgtttt	ttgacagcct	tataagaagc	419700
tcttccagaa	acaagatcag	aatctaaagc	catctgtttt	gctggaagag	cctctaagaa	419760
aaaccgcgaa	cggacctctg	cgattctttc	cgaacccttt	gaaaccatca	aaaagttcac	419820
aaagaaaaga	aggaggcacg	caaacgttgc	tgcccataga	cttcctaaag	agaagaaact	419880
gcctaaagaa	acaatcagag	aagaggcggt	tcctgaagag	acaatccatc	gtgttgatgc	419940
aagattcaat	cccaaccgca	ataggcaaa	atataagaaa	aatggaggaa	aaacttcgct	420000
gaattgcttg	aatttaaggt	aaagacccaa	cagaccgtta	gtaaagacaa	tgcaaaacta	420060
atacacaatc	aaaaatcaag	aaggatctga	ggaagaggtta	aaaagattag	tactaggatg	420120
ctaagaggga	caaagatcat	tccccctaca	ccatctttct	tcccagacac	aaaaacagcc	420180
tcctagagaa	tccctgcctt	ttctcatact	tccctcttcc	atatactctg	aagtaaaact	420240
ctaaagagac	gttatgaagc	atctttgatc	ttgtcgacta	tttccttcta	tgctaacggt	420300
gatctctttt	actcgaaaat	tttattttac	ggagtatagc	gcagcttggt	tagcgcggtt	420360
gctttgggag	caatagggtcg	gggttcgaa	tccctctact	ccgaacttca	ttttaatcta	420420
tccgacaata	cgtagaagga	aaactccatg	gccaagctag	tcattacctc	tgatgatgaa	420480
caacaagagt	tcgagttaga	agacaatagt	gagatcgcag	agccttggtg	atccatgggc	420540
attccctttg	ctgtgtacaga	aggtgtctgt	ggaacttggt	tgatagaggt	cttagaagga	420600
cgtgagaatc	tttctgagtt	tacggaacca	gaatacgatt	ttctaggaga	acccgaagac	420660
tctaacgaac	gtcttgcttg	tcagtgcgcg	atcaaagggtg	gctgtgtcaa	agttactttc	420720
taatcttaga	aaataaaaa	tttatattaa	tacaacttct	attctgacga	actcttttct	420780
aagtagttat	gcgactcttt	gcattcagga	aaggcttgat	ttactcgcga	gcctttcccc	420840
tatctttctt	gttttcaaaa	aaaatttaac	taataaaact	tattattttt	tatattttact	420900
tagaaaagatg	acaaattaaa	aaatattttt	aaatgcagaa	atgtttttta	ttattttaat	420960
atcaataaaa	gagatataat	ttaaaggaac	tcaggtgaat	tccttaatta	tggctacaat	421020
ctcaccata	tctttaactg	tagatcatcc	cctagtagac	actaaaaaaa	aatcctgcag	421080
caactttgat	aagattcagt	ctcgaattct	attgattact	gcaatctttg	ctgtcttagt	421140
tactataggg	accctactta	ttggtttgct	tttaaataat	cctgttatct	atttcctcac	421200
aggaattttca	tttattgctg	ttgttcttag	caactttatc	ctttataaac	gagcaaccac	421260
cctcttaaaa	ccgcgtgctt	gtggcaaaaa	caaagaaata	aaacaaaaaa	gggtctccac	421320
caacctacag	tattcttcta	tctctatcgc	aatcaatcgt	tctaaagaaa	actgggaaca	421380
ccaacccaag	gacctacaga	atctccccgc	accctctgca	ttactcacag	ataaccctta	421440
cgagatatgg	aaagctaaac	attcactggt	ttccctagta	tccctcctac	cgggaggcaa	421500
tcccataaaca	tctcttaaat	tcaagctttc	gaaaattttac	gaaagactct	gttaattgaa	421560
gaaacctcgc	aaaatgcgcc	tatatcctcc	ctacgtagat	accactccct	ccccaaaatc	421620
cttgctcaat	gaggcaattc	aggaaaccag	ggtagaaata	aatacagaac	tccctgcggg	421680

agattcagga	gaacgtttat	actggcaacc	cgatttccga	ggccgcgtct	tcctcccaca	421740
aataccaaca	actcctgaag	ccatctacca	atactactat	gcactctatg	tcacttatat	421800
ccagactgcg	atcaatacga	acacccaaat	tatccaaatc	cctttataca	gcttgaggga	421860
gcattctctat	tctagagaat	tgcccccgca	atcaagaatg	caacaatctt	tggctatgat	421920
tacagcagta	aaatacatgg	ccgagctgca	cccagaatat	ccgctaacta	ttgcttgtgt	421980
tgaagatcc	ttagcccaac	tacctcaaga	aagtattgag	gatctctctt	aggatctcta	422040
tctcactcaa	aacggctatc	ctaaaaatcaa	gggtacagta	gattcgcgaa	cgaaaaaaca	422100
aactcttggt	acgcatcttt	tcagtttggt	tatctcgaga	tgatgaggga	caaaaaggct	422160
cctaaagcct	ccaagatctt	tccatgacgc	aattcaagaa	aaatcaaaat	agcccccaa	422220
taatagaaaa	aacactctca	cgacttatac	aaatcaaaata	cgtaatat	tacgcacgaa	422280
ttcttaggta	ctcttggttt	aataaaaagat	attgcaacac	ttctcttcta	agttaaatta	422340
aaaactcatg	tttttataaa	aaaatattac	acaaaagaaa	atatagaatt	ttattctcta	422400
ataaaaaatta	aattaaggta	taatatctgc	gcaaatttta	attaaaggat	attaaataa	422460
atgggatatc	ttccagtatc	tgctacggag	gttctttttg	aaagtccagc	cgctccctta	422520
atcaatagcg	caaacacaca	aaatcagaaa	ctcatagaac	tcaaggggaa	gcagcaagct	422580
gagtcttctc	cacggacaat	cacttctgtc	atattggaag	ttctcctagt	gatcggtatgc	422640
tgccatcatag	ttcttagttt	attggcaatc	cgccctgctc	tgcaattcac	tctagaaact	422700
ggacatccag	ctgccattgc	agtccttgct	gtctcaggaa	caattctatt	ggtggctggt	422760
atcatcttgt	tttgcttttct	agcagctgtg	ccattcgcgtg	ctaagaaaac	ttataaatat	422820
gttaagacgg	ttgatgacta	tgcttcttgg	cattctctatc	agcaaacacc	gaccctaggc	422880
actatctttt	caggtatcgt	ctatgcagaa	tcccaggcgc	aattatagct	ctcctaaccct	422940
tacaaacttt	cttattgaga	cctctacaaac	tcaccaggtt	tgtgattgac	ctcctttttg	423000
tttaagatag	agattatgaa	gacccaaaaa	gcggaatttc	ttataagtct	gactgtaccg	423060
acttatagac	aaaagataag	ccactgcctg	tgtcttcaaa	ttaaaactca	ttaaattggt	423120
attaaatgaa	aataatttcac	aaatagttaa	tttctacact	gttgtaaaac	atcgttctcc	423180
ctaccccccc	cttttattga	cctctgaaga	tgatatatgg	gccttcgaaa	gtaaacctga	423240
tgtcctccgt	tacccatgcc	catgaaatac	acatgtcttc	acccccatt	agaatctcaa	423300
gtagtattgt	cgatctaaga	agtccttgaa	tcccatggct	ggggtagaat	cggtccccc	423360
aaaaccacaa	acgccaccct	tttgaaccaa	gtggagaaaa	aactctgtgt	ggcaccact	423420
tagagtctct	ttatgaacta	aacaataagg	tgcgcctcta	cgcttcaact	cattaaaatt	423480
aatgaaatta	aaaagaattt	ataaaaaatct	ttattatcaa	agaaaaagat	tttttgnaa	423540
aaacaacaaa	ttaagatata	atcttttctc	ttaaatagat	attttatgac	taaaaccact	423600
tcaatcccag	atgtacacga	gaatcaatca	catttgtctg	tagatgagag	attgatctca	423660
gaatcacccg	tgcttactaa	gaaagaagtg	attgctaaaa	taataaaact	cacagctctt	423720
attcttgctt	tagccatagc	tgtagggact	gcagttgttg	ctggagtctt	tggatgcct	423780
ctcatggcta	tagccactgg	tgtctctctc	cttgcagcag	togtactctc	ttgtcttctt	423840
ttaagaagaa	gagagccatc	caaacccgac	tgagagctcc	ttggggcccca	aaaacatgtc	423900
cccaaggata	ttgcagctca	agtgcacccc	tcagtccctc	tggattacca	aaagctgctg	423960
agaaatgaat	ggaccctagt	caatactctc	tcagaaatca	atatatcctg	gactctccaa	424020
gatcctaata	aaagatacta	tgtctgggaa	catcaaggag	ccccaattac	cttagtagcc	424080
actacaggag	acatcgctaa	accacgcctg	aaaacctcag	gaagagtcac	gattgttaac	424140
gcagcgaatt	cgaacatgca	atctgggtgga	gccggaacca	atgctgctct	ctcagcagcc	424200
acacacccta	cttgttgga	caatacagaga	acatctgggg	gaaaaataaa	cactggcaaa	424260
ggattatctg	tgggtgaatg	ccgctcagca	ccctggatca	atagagactg	gacgaataaa	424320
tgatacgaac	ccaggagaag	cacatttctt	agcacactct	cttggctcta	aatatgaagg	424380
agaattgaaa	gcacatcctg	agaaattaaag	caatgttatt	aagaaagcct	atttgaactg	424440
ttttgatgaa	gctctcaata	accaagccac	tgtgggtccaa	gtgcctctga	tctcttctc	424500
tataactca	cctggaggaa	agctggaact	agaaccctga	aaccaaacaa	agcctaatag	424560
cagtgcata	aagctttacc	acatccgtac	gtagtgggta	aatgatataa	agaaaggctc	424620
tatggaagct	cttcgctcct	ttgctgcgca	gcacccctca	actcccatgg	actataatcc	424680
ttacagacca	caaacagcta	cttatgggtcc	cttttaacta	aaaagatcta	tttcaatagg	424740
atgcattaat	aaactaattt	tgttttataa	aaaaatctaa	taaaaataca	aattagtaat	424800
ataatagtgt	aaaattgtat	tattaataaa	atattatgac	agattctaat	cccctaccct	424860
cttatacaga	gccagctctc	tacagaactc	ctgcgaaaca	ttcctatccg	attagactcc	424920
ctctcaaccg	tacagataga	atcgagaaaa	tactgaaaat	tgtcacccctc	acactagccc	424980
tagcgtgcgc	tttgggcttt	agcattgctg	ctggcatttt	ggctatgcct	attttttctg	425040
ccgtagtgtg	cataacatta	gcaattgctg	cggtctcact	ttactccctt	ttaaagaaac	425100
ctaaattata	cgagattctt	cctcaaatcg	aaccggaatc	tgagcaaagt	tctctgtctc	425160
cctctcccca	gcctcctgag	caacaggacc	tccctttgca	gatcgatcca	cttcccgatc	425220
ccgaatcact	ccccgaagtc	tctcttgctg	atctaacacc	acccccagaa	gaacttaccg	425280
ctatcacggg	cactcctggc	tatgaggctc	ttcttgaaca	aaactgggat	cttcttccga	425340
gcttagccgc	tgtagacca	tcgtttacta	cagaaacacc	tcagcagccc	tgtttttatt	425400
ggaagcttaa	agactcgaag	cttatcttta	tatctacctc	aggagatatt	gcagttccaa	425460
gaatcaaaac	tcaaggcagg	gtgatgattg	ttaacgcagc	aaacgagaa	atctcccag	425520



aaggaggggg	aacgaataaa	gctctatccc	tggctacaag	tctacagtgt	tggaaacgcat	425580
ctaggctccc	tagagcgac	tctcgttctg	gatcccaact	acagccagga	gaatgccgct	425640
cagcaaaatg	ggaaaatagt	gatcacacct	caaacgacca	tgtcccaggc	aaagcacact	425700
tcttagcaca	actgcttggt	ccggaagctg	ctaagtgtaa	caacgatcct	aagcaagcat	425760
ttgaagtaag	caagaaagcg	tttcataacc	tggtccaaga	agctgaaatc	ataggcggtg	425820
atgtgattca	actccccctc	attggatgta	atctatttgc	tccatcaaga	cttctaaacc	425880
tcgggaaaac	aagagcagaa	tggatcgagg	ctataaaatt	ggcactcatc	acatctcttc	425940
aagatttttg	atgggaacaa	gacaaccagg	aagagcaaaa	aattatcatc	cttacagaca	426000
aggaccagcc	tcccatcatt	cgcgcccggt	tcgatctaac	gactccctag	tctatgtcgg	426060
aaagcgtcg	tgcttccaat	cgaacagctt	tctaaaaaca	cagccaattt	atcctgatca	426120
caagcacccc	ctagattcct	ggctctaagc	cgcattccaat	acttttttaa	gtgaaaatgt	426180
tgtctatttta	ttatttttaa	taaacaactt	ctattttaaa	tataaataac	ttcacataaa	426240
aaagaatctt	ttttaaactt	tttggttttt	atttaaaaag	ttttatgtcc	accacagaac	426300
ccaatttgac	taacgtaaat	ctaaccatgc	tgatcagcag	cgaagcatg	cccacgcaac	426360
tcgcatctca	taagctcaaa	ggtctggacc	ttgtcgcttt	tattctaatt	ataggaattg	426420
ctgtaagttc	tggaaaccgct	gctataattt	taggcattcc	tctattattt	attcttaccg	426480
ctctagcagt	cttggctttt	agtattcttc	tctattttct	cttaagagaa	cctaaaagtc	426540
ctataagcgt	aacgcatcag	ccgacgccc	tcataaaaga	tacagacctt	cctcctgtcc	426600
cgcccttagc	actcacccca	gtgcctacgg	aagctgtcct	agaagagccc	ccgcttcctt	426660
cccctagaac	ccatcaaaca	ctgttacaag	aaaattggga	ccgtatacct	gatctacagg	426720
ctaacacaga	tatgcctttc	atcgctgctg	acaattcaac	cggttatgct	tggcatttga	426780
aaaactcaaa	cgtgactttg	atctctacgt	tagggcccat	tgaaaagcct	cgctataaaa	426840
ctcaaggcat	cgtcatgatt	gtgaatgcag	ccaccccaaa	catggcaaac	aacgtaaaag	426900
gaacaagtct	cgcacttgcg	aaagcaacta	gtgtacgctg	ttgggaaaat	tcgaaaaaat	426960
ctccggatcc	tctccgttca	aaacagcccc	tacaattagg	agaatgccgc	tcagcaaaat	427020
gggaaaatct	aaacggaacc	acgaatgcag	gtaaagcagg	actaccgcaa	ttcttaggac	427080
aacttctagg	gccgaaagct	tctgactata	actacaatcc	taatgatgcg	tttacctttt	427140
gtaggcaagc	ctaccttaac	tgtttgaatg	aggccaagcg	ccgtaaaaca	accgtagttc	427200
agctccccct	gctttcctcc	catttccctg	gctctccaaa	agacgaagag	actactatgc	427260
tacgtctgca	atggattgat	gggtgtgaagt	tagccttgat	agatgctctg	cagacatttg	427320
gatcagaagc	agaaaatcaa	aatcaaccgt	gggttatcat	tttgacaact	cttgctagac	427380
atccccctcat	cacaccctaa	tctctcccc	tggttaaagca	aaagagagta	gatgcctttt	427440
tgtgaaaagg	aaatcctttc	ttaaaaaatg	gtaagacttc	tctcttttaa	acatccaaaa	427500
catagaagat	tttttaaaaa	atcttttcta	actttctaaa	ccacgctata	ctttctcaag	427560
caaatagaaa	cgcctctgct	ctccataaga	caaagctttt	gcgaaataaa	gaaaattcta	427620
actaaaagac	gatgcccgtg	tcctcagccc	ccctaccacc	aagccaccgc	ccttcccttg	427680
gaaatctagg	cctcatggaa	ccaaattcca	aagctctaaa	agcaaaagcat	caagataaaa	427740
cgacgaagac	gattaaactt	ttagttaaaa	tccttggtgc	cattctagta	atagaagttt	427800
taggaataat	tgcagctttc	tttattcctg	ggactcctcc	catctgcttg	attatcctag	427860
gaggccttat	tcttacaaca	gtactctgtg	tgcttcttct	tgttataaag	cttgcccttg	427920
taaacaaaac	cgaaggaaca	actgctgaac	agcagataaa	acgtaaaactc	tcttctaaaa	427980
gtatttctta	gacaaacagc	gggtgttttt	actcattata	aataaaaatat	tttattccct	428040
aggtcataga	aaatatgaga	gtgtctcctc	ctatttttagt	aggagattaa	tttgtaaaac	428100
actaattaca	ttgcatttaa	aatagaaaac	tataaaatta	tagggcttgt	catagaaaaa	428160
taggaaatca	cattgtcttc	ccagtagtca	caggaacatc	aagtgcactc	ccagtggaac	428220
aaacaaagct	tgggaatttc	ctagaaaagt	tatcgggatc	aggacgatgc	ataaaaaattg	428280
cctttgcggc	ttcaactgct	ttactcctcc	tcaatacctt	tgtttctgga	atcgttgcta	428340
tagccatgat	ctttgtagca	acatctgtcg	gagcctactt	tacagttata	gggcccttat	428400
tcttgctctc	cctaactcct	ctggctatca	tgtaaatctc	gatgtataaa	atcacgcac	428460
catcacaaaa	tacaccgatt	tcaaattaga	aaaaagcggt	cccaaagtac	gagccccaag	428520
cactcctctt	gggaactcct	tctctttgtc	aaacttcggg	attcgttcta	cgaacacaaa	428580
aacagattcg	agttccttac	gaatcgctct	ctaaagcaaa	atctttatcc	ccttgataag	428640
tatgaaataa	ttattttta	tcacaataat	ctctccatat	actctcttga	tggcctgaaa	428700
cactcggcca	tccaaggtcg	tcgtttctct	ctgaaaattc	ctcttattga	ggtgaagttc	428760
tgtaaaattg	ataaatgtag	gcattccttag	agaagcttta	tcagcttcaa	caaaattctc	428820
tcggctttta	taattgataa	aactctgaaa	tttttgagat	ttttatgaca	ctcattacc	428880
ctgccatcaa	ttcctcgcg	cgcaaaaccc	atacagtaag	aataggcaac	ttatacatag	428940
gcagtgacca	ctcaataaaa	acccaatcaa	tgacaacgac	attaaccaca	gacattgaca	429000
gtacagtaga	gcaaactctac	gctctagcgg	aacataaatt	tgatattgtc	agagtgcactg	429060
tacagggaat	caagggaagca	caagcctgtg	aaaaaattaa	agaacgtctg	attgctctag	429120
ggttaaatat	ccctttgggt	gcagatatcc	acttttccc	tcaagcagct	atgttagttg	429180
ctgattttgc	tgacaagggt	cgcataatc	caggcaacta	catagataag	aggaacatgt	429240
tcaaggggac	gaagatctat	acagaggcaa	gctatgccc	aagtctcctg	cgtcttgaag	429300
aaaagtttgc	tccttttagta	gagaaatgta	agcgactagg	caaggctatg	cgcattggag	429360



tgaaccacgg	gtcactttcc	gaaagaatca	tgcaaaaata	tggcgacact	atcgaaggaa	429420
tggtagcctc	agcaattgaa	tatatcgctg	tatgtgaaaa	gctgaattat	agagatgttg	429480
tcttctcaat	gaaatctagc	aatccgaaga	tcatggtaac	tgcataccgc	caacttgcta	429540
aagacttaga	tgctagaggc	tggctctatc	cccttcacct	tggagttact	gaagctggaa	429600
tgggctgga	cgggatcata	aaatccgcag	taggaatcgg	aactcttctt	gccgaaggac	429660
tcggggatac	catacgctgc	tctctcacag	ggtgtcccac	tacagaaatt	cctgtctgtg	429720
atagcttgct	acgccatacg	aaaatctact	tagaccttcc	agaaaagaaa	aatccctttt	429780
ccctacaaca	ctccgaaaac	tttgtttctg	ctgcagagaa	gcctgcgaaa	acaacacttt	429840
ggggagacgt	ctacggagtc	tttttaaaac	tctatctcca	ccatcttacc	gactttactc	429900
ctgaagaact	cttagaacac	ttgggggtaa	atcccgtaac	aaaagaaaaa	gcattcacaa	429960
ctcctgaagg	ggtcgtcggt	ccccctgagt	taaaagatgc	tcctattaca	gatgtacttc	430020
gagaacactt	tttagttttc	caccaccatc	aagtgccttg	cctatatgaa	cacaatgagg	430080
agatttggga	tagccctgct	gttcatcaag	ctccatttgt	gcattttcat	gcttcagacc	430140
ccttcattca	tacctcccga	gatttctttg	aaaaacaagg	acaccaagga	aaaccgacca	430200
agctagtatt	ttcaagggac	tttgacaata	aagaagaagc	tgctatttcc	atagcaacag	430260
agtttggagc	tctgcttctt	gatggccttg	gagaagctgt	ggttcttgac	ttaccgaacc	430320
ttcccctaca	ggacgtgcta	aaaattgcct	ttggcactct	acaaaatgca	ggggtgcgcc	430380
ttgtaaaaaa	agagtacatc	tcctgtccta	tgtgtggtcg	gaccctcttt	gatcttgaag	430440
aagtcaccac	acgtatccgc	aagagaacgc	agcacctacc	aggacttaag	atcgctatca	430500
tgggttgtat	tgtgaatggc	cctggagaaa	tggcagatgc	agattttgga	tttgtaggtt	430560
ccaaaacagg	gatgatcgat	ctttatgtaa	aacatacttg	tgtaaaagct	cacataccca	430620
tggaagatgc	tgaagaagaa	ttaattcgac	ttttacaaga	acatggggta	tggaaagacc	430680
ctgaagaaac	taagttgaca	gtatgactct	atccttccac	actcaccttc	tgaactattg	430740
gactttcgaa	gaattcgatg	gtttgcctat	acgccacgga	gtcttttcaa	aacaaaagga	430800
tgccgagggc	acggtcttcg	cagccaagaa	tcctgagatt	gcttcagctc	tccaatctcc	430860
gaagtattgc	gaccttcatc	aacgccacgg	cacttccgta	cgttgtgtta	cacctacatc	430920
ccccacctac	caacctgcag	acggactgtg	cacgcagtct	ccgctcctct	ctctccatat	430980
ccgccattcc	gattgccaa	cagctatctt	ttatgatcga	gaacaccacg	caatcgcaaa	431040
tgtacacagc	ggatggcgag	gattgcttgg	caatatctat	gctgtcaccg	taggtactat	431100
gaaaaaatta	tttcatacaa	aaccacaaga	tctcttcgta	gctatcggcc	cttccatcgg	431160
tccagattat	gctatctatc	ccgattacgc	tacgttattt	cctcgtagct	ttcttccctt	431220
tatgaatccc	aaaaaccatt	ttgacctgcg	tgcgattgct	cgcaagcaac	ttacgaattt	431280
aggaatctct	aaagaccgca	tttttatctc	agacctctgt	acctacacgg	aacacgacgc	431340
tttcttttct	tcaagggtacc	ttgctcacca	tcccgatccc	aatctcacag	gccaacattc	431400
aaaaaataga	aataatgtaa	ccgccgtcct	tctcctaccc	agagattaaa	aagatccagc	431460
caagcttctt	ttcctttccc	ctaaggacct	tagcttctag	aagaacatgc	ttcgttccaa	431520
cccactcaga	cttcttgatg	cttcttgatg	aaaaacaaca	tgtaaactac	aatttttagg	431580
aaaaaattta	gcttaaagac	tttctatgaa	attaggcgca	tcaactaatc	ataaagttca	431640
cgaaccagtg	aagccaaaaa	aagccaaact	cgctgagatt	gaagctanca	aaacccaagc	431700
tacagaaggc	acactcagaa	gtaaaagtct	tgctcttcaa	attgcgcgtg	ctgttcttta	431760
catacttttc	gctgcactaa	tgtagtagcgc	tggaatcacg	ttcgttacct	tcgaagcttt	431820
aggcttccct	ctaatacagg	cgtatagcat	tgctgggtatt	atcacactcg	tgggattagc	431880
catcgggctc	gtgcttctca	tcttgagctt	gttgccctaaa	gaagacgagg	aagcagatgc	431940
actttctaga	aacgctcttc	ttccattaac	catcattgta	atcgagcaac	aacctcacc	432000
tcttaaacct	gagatccctt	attcttattt	aactaaacta	gccctattaa	catcattgtt	432060
ccttacctta	cgacgctctt	cctcccaaag	aaaaactcac	taaagaaatc	aaaattacag	432120
aagctacgaa	ttgtgaaatt	caccatctaa	agaagggtcc	ttaatttaag	gttggtcacag	432180
ctaaagctcc	taatctcaca	gaaattagag	atcacggggc	tcgcgtacct	tcgctattcc	432240
tcctttccac	agaaacttcg	cattggaaa	gggataagga	agtctcggct	cccctaaagc	432300
aactgcaaga	tctcttagga	gaggaacagt	gggaagctat	gaaaactaaa	atgaactcta	432360
gaaaaaaagc	aggtcaatgg	gcaattttca	attctccaac	tcctgggtgc	agttcaactt	432420
tagtttttag	atggactcct	tgggggttatt	acgacaagga	tgtacaagat	atcttagaaa	432480
gaaaagatcc	gatgagctct	tcgctttctg	aaaaagactc	aaaggagttc	ttgaaaaatc	432540
tgtttgtaga	tctcttagaa	aatggcctta	catcagtaca	tattcacgca	gaagaagctt	432600
tcactcctct	tgatcatacc	gggaaacctc	actttaaaag	agacaatgtg	tacttaccog	432660
gaaagtgtgt	aggcgccttg	aatgaggctg	cggtacaagc	caatgtaagt	gcggatactc	432720
aatttacatt	gttccttact	caagatgagt	gcaatccttt	tcatgataag	aaaagagggt	432780
aaaaaatctg	aaaaggctct	aaaagagcct	ttatgagaat	cagagaaatt	acaagtcgag	432840
taatgaggca	ggattctcta	ggccttcttt	cactttgact	aaaaacccaa	cagcctcttt	432900
cccattcaata	agacgatgat	catagcttaa	acgacataac	atcatatctg	atctataaat	432960
ttcattatca	agaacaacgg	ggcgcttttc	tatcttatgc	atccccaaaa	tccccacttg	433020
cgggggattg	ataatgggag	tcgaaagtag	cgatccatat	acgcctccat	tggttaattgt	433080
gaaacctcct	ccctcaagct	ccgctattgc	aagtaggcct	tcacgagccc	gaagggaag	433140
atctgcgagt	ttctgctcaa	tctccccggt	agaaagttaa	tcgcaatcgc	gtatcacagg	433200

aaccacaagt	cctcgatcga	tacctacagc	aatagaaatg	tcataatagt	gacggtaaca	433260
atctcctcgc	catcaatata	ggcggttact	cgtggatatg	ccttcaaagc	ctctaagaca	433320
gctttcacaa	agaaagacat	aaatcctaac	ttcaccccat	atcgagatag	aaactcttct	433380
tgtttttcc	ttcgcaaatg	aaaaagaggt	gtcatataga	cctcattgaa	tgctcgtgagc	433440
atcgcgagact	catgtaaagc	agacaaaaga	cgccgcgaaa	ttgtcttacg	aatcgagggtc	433500
atgcggttctc	gagttttctcc	tcgatctcct	gcagaaagac	cctgggatcc	ttgggtccatc	433560
tgatcacgaa	gaggaataaa	cgtttttattc	tctggaggag	actgacgcac	cccagactga	433620
ggaaagcaaa	tgatctcagc	ttctatagtc	tcttttagact	gagaatctcc	aagctcttcc	433680
ccttcacctg	cgggctctat	ttttccctact	accccccta	caggaacaac	atcgcttct	433740
gaaacctccc	agaaaattct	tcccgatact	ggggcataaa	tgagctgatt	taccttatca	433800
ctttcaattt	ctagtaagcc	ctggttttct	tgaatcagag	cacctctgt	aactaacaag	433860
gaagctacgg	tcacctcgct	aatcgactct	gcaatattag	gaatgcgtac	ttctgtagtc	433920
ataattttacc	ttaaagaaaa	gaggggttcc	atacacgtga	ccagctcttg	acgactgact	433980
tcgctgatcc	agaagctgtg	gaactactcc	gaggacgtcc	tatatatagc	agtttctcag	434040
gaagaatgtc	ttgcaacgcc	ataaacatat	agtcataggc	ccccatattc	ttggattctt	434100
ctttagtagcc	aacaaaatgt	ttcaaatgag	aatacttctc	gataaggctc	actaaatcct	434160
caagagctaa	aggatacaag	ctctctatac	gcaagcaaga	aaagtcctta	cgccgatctt	434220
gaggaagcat	ttctgcataa	tcataataga	tctttcccga	acacaatacc	aaaatagaag	434280
catcataatt	aggatcggca	tcttcgagaa	tagcacggaa	tccccaggt	tctgtgaact	434340
cctcgatact	acttacacat	tgtaggatct	tcagcagcaa	cttaggagta	aagatcacca	434400
aaggcaaaaga	aagatctctc	ttagcatgct	ctctgagaat	ccgaaaatat	tgacacaggag	434460
tggaaggcaa	gaccacttga	aaattccagt	tcgcggctaa	ttgcaaataa	cgttctctac	434520
gagatgaaga	atgctcgggt	ccttgccct	cataccatg	gggaagaagc	agaacaatgt	434580
cagagtgtaa	atccccattc	tgaattcccg	aagagatata	ctgatcgaaa	atgatttgtg	434640
caccattagc	aaaatcccca	aactgcgctt	cccataacac	taaagtcttt	aatgcctggt	434700
gagcatagcc	atactcaaac	cctaaaattg	catattcgga	aagaggagaa	ttatacattt	434760
ctacagagcc	ctgctctgca	gaaagatggt	acaatggaga	gtaggatctt	ccagtcacag	434820
tatcactcca	taccaaattgt	cgttggtgta	atgtcccgcg	aatagaatct	tgacctgaga	434880
gtctcaggtt	gtacccttcg	attaatagcg	aagcaaaggc	taattcttcg	gccatcgccc	434940
aatcataacc	aacccccact	tctgcccattt	tcattctttt	ttctaaaaga	gtcttaattt	435000
taggatgggg	atgaaaaattg	tcaggggaaac	caaaaagacg	cgagctcata	tgaaaaagag	435060
tctcgcgac	caaagaaaca	tcacaatcat	gcaaaaataag	ctcgcctgta	tttaagcgat	435120
cgcagtgatg	acattctttt	ttaggaaagg	gttctggatc	cgtccctttc	aatacttgaa	435180
actcacgatt	cagactctct	tgaatctctt	tttcaataga	tgccaaagtt	tcttcagaaa	435240
tatctgcaaa	ctgcccttcc	aacagatatt	gcctaaacag	ctcgcgaata	ctcttctttc	435300
tcttaattctg	atcatagagt	aagggagctg	ttactgaggg	atcgctcactt	tcattatgtc	435360
catacttgcg	ataacagcag	agatctatga	tcacatcaca	actaaatctc	tcacgaactt	435420
gcagagcgta	ctctatagct	tctatacagg	caacgcgtc	ctcgtatttc	actcgaaata	435480
caggaatccc	tagcatttta	gcaatatccg	tacaataagg	ggtggacctt	gactcccgtg	435540
gcactgcggt	aaaccttatg	taattattca	caacaatgtg	aagcgtaccc	tcagtagaat	435600
accctggaac	acgactcagc	tgagaggttt	cataaaccac	tccctgacca	gaaaatgctg	435660
catctccatg	aactaaaatt	gctaagctgc	tttgctcttt	acctgcgtga	ccttggtggt	435720
gcaaggcagc	cacgaccccc	tcgacaatag	gatctacaga	ttcgagatga	ctagcggttg	435780
gcaacatcac	aaaggtagtt	tccctatctt	tctgatggga	ctttagcaca	tacctttat	435840
ggtactttac	atcccccaaca	ctctctaaac	cagtgctgc	aggatcgctc	tcaaatccca	435900
taaagacata	acggttaaggc	tttcccaaaa	cattcggtta	tacattcaaa	cgacctcgat	435960
gggccattcc	taaaacgtag	ttagaaattc	ctaattgccga	tccataatga	acaagatgct	436020
ccaacatggg	gaccaagggtc	tctccgccct	ctaaagaaaa	acgtttctga	cctgtaaatt	436080
ttatctgtaa	gaactettca	aaaaacgttg	ctttacataa	gtctttatag	gagcgaaggga	436140
gctgctctgc	aaagcgctcc	acttgctcgt	tctccataag	attccaaaca	aactcctgca	436200
actcaggagt	acatgttagg	gtttctaaag	taagacttcc	gcaatagcat	ttttttaaag	436260
cttcgatcag	ctctcgtacc	gaaacctgag	ctttaggaag	tagaccgcga	gaaggcacct	436320
gctcatccag	atcaatctta	gcgatctttt	cctgaatgaa	tcgagaatct	gtagttgggg	436380
caagcggtga	aatttgactt	tgcaaatatc	cataataacg	ataaatcgta	catagaaact	436440
gagatttttg	tcttggaagc	atagcaatag	tttctattcc	agaaatctta	gtactagctt	436500
ctgatggaga	tgctgcttga	ccgagctgat	accttcaaaa	aaaatacttc	caagaaggat	436560
ccaaagtctc	gtgattcata	aatctctgat	acatagactc	gatccaatcc	atatccgaag	436620
aatatacttg	ccccacaaac	tcggaatcca	taaaataatt	aaactcaata	aatacgatct	436680
aatgtctgct	ttcatagcaa	atTTTTtatt	ttcaaaaaaa	aaaaattttt	tttttttctt	436740
gcagttgaaa	aaacaaaaaa	atgctatgca	cctgctctcg	aatacaggat	gggaacctt	436800
ggatgaaaag	cgaacgtctt	aaaaaattag	aatcagaact	tcatgacctt	acgcaatgga	436860
tgagttggg	tttagtgcca	aaaaaagaaa	tttagcaggca	ccaagaagaa	atccgaatct	436920
tagaacataa	aattttacgaa	gaaaaagaac	gtctacaact	cctcaaagaa	aacggagaga	436980
ttgaagagta	cgtcacacca	cgacgcagtc	ccgcaaagac	tgtctaccct	gatggtccta	437040

gtatgtctga	tattgaat	gtggaaccca	cagaaacaga	aattgatatc	gacccaggcg	437100
aaaccgtaga	actggaactc	accgatgaag	gacgtgaaga	tggggcagta	gaagtcgact	437160
attcccacga	agacgatgaa	gaccctttca	gcatcgcaa	tcgctggaga	cgcggtggta	437220
tcattgatcc	cgatgcta	gaatggtaag	gctcccctag	ctctttatat	tcataattccc	437280
ttctgcacaa	aaaaatgtcg	ctattgcagt	ttttatacaa	tcccctacaa	aagtgaatct	437340
gtatcgctct	attgtaatgc	tgtaatccaa	gaggggctaa	gaaagctagc	ccccatccaa	437400
gagacgcatt	tcatagagac	tgtgtttttt	ggagggggaa	caccttcatt	agtttctcct	437460
cttgatctta	agcgcattct	caaagagcta	gccccccatg	cccgggaaat	tacttttagag	437520
gccaaccccg	aaaatctcac	cgtaagctat	ctacgtcaac	tacaagagac	tccaataaat	437580
agaattagcg	ttggcgtaca	aaccttcgac	gactctatcc	tacagctcct	cggaagaacg	437640
cattcttcat	ctgcggaat	cacagcactg	caagaatgcc	agaatcacgg	attctctaat	437700
ctttctatag	acctaattcta	cggactgccc	acacagtctt	tggagatatt	cctaagcgac	437760
ctacatcaag	ctctgactct	ccctatcact	cacatttctc	tatacaacct	cactatagat	437820
ccccacacct	ccttctataa	acaccgcaaa	attctagctc	ccacaattgc	ccaagaagaa	437880
attctagctg	agatgagcct	ccttgctgaa	aatctcttac	tctcccaagg	gttccaacgc	437940
tatgaacttg	cttcatatgc	caagccagat	taccccgcaa	agcacaacct	ctattactgg	438000
acagatcgcc	ctttcttagg	cttaggagtt	tcagcttcgc	aataccttca	cggagagcgg	438060
tcaaaaaatt	atagtcatat	ttctcactat	ctacgtgctg	tacgtaagaa	tctccctacc	438120
caagagacct	cagaaattct	ccccaaaaaa	gaacgaatca	aagaagcctt	agccctgcga	438180
ctccgactcc	ttgaaggagc	agacctcgcg	gagttcccct	ccacacttat	ctccatgctt	438240
acgcaagatg	taaaattaca	aaacctattc	agtggtgcag	gacaatgtct	tgccttaaat	438300
agacagggcc	gtctcttcca	cgatacaata	gcggaagaga	ttatgggata	ttccttctaa	438360
tcctgcgga	aggctaaaac	ctagactctg	cccttcggac	tcctgatgct	ccgggaaaca	438420
tcagagaact	cttaaaggta	aagcttcttt	ctcggtcttt	cttttttttg	ccgtgctctt	438480
atgttaaaaa	taccaagatg	tctccaaaga	tacattagcg	acgacgacgc	ctagaatggc	438540
gtaatacggg	cttcacaaag	aaccatagat	ttacgaacaa	gacgaaagca	cataagatga	438600
agtttaaatg	ttggccaaca	gctaatacat	caccactgct	ccaattttct	tcagcacttt	438660
tattatgtag	atcataaaca	gcagtgttat	ttggacgtac	taagatacgt	ggaacttgta	438720
ttgcaatctg	gttaagcacc	ataatggata	ccggcaataa	aagtcctcca	tgtacagttt	438780
gtaaaaagcc	tatgataaag	cctgcacgat	cgcgataaga	agctcgtact	gttctctacag	438840
gcaggccact	tcctataact	cgttgctgca	caaattgttg	tacacgatgt	ctaagacctc	438900
gccccatcca	gcgagtgcac	tctacaaaga	caatactccc	tgaaattgta	gacgcagaaa	438960
taaaaattgc	tcgtaagatt	tcctgaggca	tcctatagtt	acgcaggacg	ttgccacaat	439020
caaaaacaag	aacaaggatg	cttggtaaat	atagagattg	tgctacgatt	cgtgcagtac	439080
ggaatctctc	tctagactga	ggataatttg	taaagagtaa	gaaaaaatac	cggaccgcaa	439140
acgtcgtgtg	catcaaaatt	aaagagtaac	agatctgcaa	gtctaagccc	tcataagacg	439200
aggctaggat	ccattcctgc	gcaagtccctg	aaactctaga	aattgcataa	agcgcagaaa	439260
gagctacatc	aggacaccgt	tggggatagg	gattgatttc	catatctgat	gaaggcgatc	439320
cttgattcaa	ccattctaca	agcctactca	tagaactagg	atccgtagaa	tcaatgacaa	439380
cagctagatc	tctttcactg	tgtggtaact	gtgatctttc	ggcatcttga	gaaagacctc	439440
ccctatcttc	tacatctcca	cccctattcg	caaccaagca	ttgctctcca	aaacgcaccg	439500
cccaagtaaa	agaaggacaa	cggatagaag	gcagaaaaac	accctcaaga	cccgaagaat	439560
acggcagtat	cgtgggtgtc	tccgcccctag	ttccccgaca	atccagagaa	ctaaagaagt	439620
ctccagaaac	acggtaatta	tggaccctaa	agtcctcttg	aataaagacc	gtcggggaaa	439680
tcctacaaac	aacaatacgt	ggactatgcc	tagattgcgt	taacgcctgt	tgtatataag	439740
gcgatgcac	cccatagaaa	atcactagaa	actcacgatt	ctgattttca	ggagcagaga	439800
aaaactgttc	ccaaaccgtc	aaaagggcct	gacataaagg	atgatcgaga	gtaggaagag	439860
tacgacaagg	actgatgggc	caaggagaca	tgccgcttcc	atcgttatag	agaagacgaa	439920
cggcctctcc	ccgtacttca	ctaataataca	gcaattcctg	tacagcttct	tgatgcgttt	439980
gccaacttcc	atttacatag	agagtacgta	cctcagaatc	tgggggctca	ggatcctcat	440040
caccgccaca	aaggcaaacc	aactcataca	catccgaagc	cacagaagca	gatgaagaac	440100
ttctagggcc	tcctgcaatg	aagaccgaga	tatcttcagc	cgaagatgca	actggttgata	440160
cgtctagaga	aggaggagat	attgtaattc	tcgggatttg	gatatcggcg	ggaataggat	440220
ttggggatag	aggttccgtt	tcttcgagta	gtgttggttg	tgaagatcga	gattctgtgg	440280
gtgctgtcat	caacgctcta	aacttatttg	gcaaagatta	taaaataagt	attgataaca	440340
cgcaatagag	gattacgatt	attttaaaaa	gacgcaaacc	tatgattatg	cgctatttag	440400
aatcatgcaa	cctttaattt	ttgcttatga	tcacaagaaa	aatatccccg	aagagcttac	440460
atgctaagaa	actcctgaca	atgataccgg	ggataaaaaca	agctaagaaa	aaattaattc	440520
gggatgtgga	aaagaaatat	tgttgggact	ttggttatac	tttgcttcac	agaacctaatg	440580
tcctcagtag	ttctccatga	ttgcacttgg	cgtgtgagaa	caagttcact	cggggccgaa	440640
aggtcagagg	caacacaaag	ctccgcatag	gaaggtaaaag	tatctagaag	agactcaaaa	440700
gtatagacgt	tacgataagg	agtttctata	catactgaag	tagataacctc	tttggagggtc	440760
gctgcctttt	ttatcgactt	tacacgttcc	ttaggacttt	gcggggaggta	tccccaaaac	440820
gtaaagctct	gggaaggcaa	gcctgaaagc	atgagcgcta	acgttatcga	acagggacct	440880

gaaaaagcct	gcacaggaat	ccccaagca	cgtgcacgac	gcactaaact	cgctccagga	440940
tctgcaatac	aggggaagacc	cgcatacagag	atcagtccccc	aattctcccc	gtgtttttacg	441000
ataggctcta	gataaaaaatc	ccaagcctta	gggaggcgcg	catgttttact	aagaatagca	441060
agaggaaatt	tatgaacttc	gggaatttttc	cataaactta	gaaatgccct	acccccacga	441120
tcactttteta	caatcagccc	atctagtcta	tgaactaatt	ctcctataac	ggagggggaga	441180
gtctctacag	cacgggtacc	gagagtattg	ggaagaagat	ataaagtcac	aggttaacca	441240
ttctaatac	taaagtttcc	acagctacta	taggatcttg	gacattattt	ttaattaagg	441300
tttctgcata	aaataaagaa	tttaaggcctt	gggtgtagtct	ctcctttcca	taaaggacga	441360
acattcgggtg	tttatttttct	ttcgatccct	cttcaatact	acgtaaacca	tagagacatt	441420
gggtacgaag	gaaagtaata	atccccaagg	gatcttcacc	atcctcgagt	agaaaatgca	441480
actgctgggtg	accttctacc	ggatccctct	tcaatagaga	gtctcgaaat	ttccataggg	441540
aagcctttttc	tttttttgaca	acgagctctt	taatatcaga	gtgatccaag	gacgttttct	441600
tgccaacaga	gcacagtagc	ttatcgaatt	cactgagaat	atcaggaaga	gaggttgaag	441660
caagtgcacg	caaaaaacaaa	gatgccaatg	attgagagca	agaaatcccc	acacgctcag	441720
ctctttgcaa	caggaggcgt	atgatccctt	tctgacgac	tgccgggccac	tcaccaata	441780
aactcaaaga	aagagccgat	ggcaaggcctt	ttgacagttc	tcgaaagcat	tcttgttttg	441840
tggtgaagat	caaaatcgta	aggtgaggtt	gaggattccg	agcatagcgg	cttagaaatt	441900
ccttagttgc	tagaggggaat	ttctctgcat	gaataatccc	caaagtttca	tgctcttgaa	441960
agagtgcata	cgtctcggtc	caagacatga	gggttgctgg	catgagtcct	tgaccaccga	442020
gctctttgaa	gctctcagag	actaataatt	caatcagcgc	atcttttatcg	tcttccaaag	442080
cactccctat	aagagctata	gcgggcactt	tctctgcata	cgctctggga	aagtcataca	442140
aactcgtaaa	ggatttttgc	ataggtagag	tcataaaagt	agtatcctga	acctactata	442200
cgtattttcc	taccaactgt	acagcatgaa	gcctgaagat	ctcgtctctat	aaagcttttt	442260
aaccttaaaa	agaaaaacgg	gaaggaaaacc	caatgtttcc	ctttcccgtt	aacatgagca	442320
ataatgcgaa	aatcacaaat	tatcgagaca	tcattttgat	cagttggtga	cgccagccat	442380
nagctgtacg	aacacggctt	ttagagccat	gctttctcgt	agctgttgaa	gaacagacac	442440
gtttacaact	agatgtatgc	ttatggtttt	ngtggcatgc	taaagcacag	gctgcagctt	442500
tcttaggaga	acctttagcc	actgtagttt	ttctagctac	aggcttctta	gcaacagctt	442560
tgccaaccgc	tctcttagct	gtagtcttct	ttgctactgt	cttttttact	acacgtttag	442620
cagcaacttt	cttaactgca	ggcttcttag	caacagctct	acgaaactgtt	ctcttagctg	442680
tagtcttctt	tctactgtc	tttttagcag	ccgtcttacg	aactgcaggt	ttttttacag	442740
cggttttgcg	aacagtagct	tttttaaccg	tacgttttagc	cgcaactttt	ttagcaggct	442800
tccgtacagc	tcttgaagct	gtctttttac	cgctttgctt	tttttgcgct	ccaatcatct	442860
ttattcccct	aattagacag	gtaattactt	acctgatcta	tcggcaggga	cgattgaaaa	442920
ctttaataaa	aaaaatgact	tttatttttaa	aaaaactaaa	ataaaagtca	ttactaaaac	442980
ataaataaat	agaaagcaac	tacttagaaa	gactattttc	taagtaataa	agaatagAAC	443040
gaacaccaaa	acctgaagca	tattttggat	aacggtcttc	ttctttttca	tgatagcag	443100
tacctgcaat	atcaagatgt	gccaagcta	ccgaagattc	ttccaaaaat	ctctgcaaga	443160
ataatgctgc	tgtaatagcc	cctgcacggt	tactgcctag	attttttcata	tcagcaatat	443220
cagaatgcaa	tgtttttatca	tacttcttaa	ctagaggaag	tctccataac	ggctcggagg	443280
tttcggctga	cgctctaaa	agatcttcag	ctaaaacatc	gttattggaa	aagaaacctg	443340
caacctcttc	tcttagagag	actaccatag	ctcctgttag	agttgcaaaa	tctataatac	443400
gtgtcgggtt	acaatatattt	aaagcatatg	taatcgcac	agcaggata	agacgtccct	443460
cagcatcggt	actacaaatc	tcaacagaaa	gccccgacat	tcctacatag	acatctccca	443520
ttttatagga	ggcgccatcg	atagcattct	ctgtaagcag	gaatgatccc	cgtgacattt	443580
ataggaagct	ctaaaantgc	taacgccgag	agaatccccg	ggactgtagc	cccacctgcc	443640
atgtcttctt	tcataagtaag	catggatttt	ccaggcttga	gggtctaaacc	tccagagtca	443700
aaagtgaccc	ctttccctat	caagacggtg	tgatcttttag	acttaggacg	tccttgataa	443760
cggacaacga	taaagtgtgg	atccacacaa	gaacccttgg	aaacagccaa	taggagtcct	443820
attttctctt	tggcgatggc	atcttttccc	aagaccttag	tatcaatact	agggaaactct	443880
tttcccagat	tcagagcaac	ctctgccaat	ttcttagggg	taatttcac	agcattcctg	443940
ttcacaagat	ctcgagttag	atatacgctt	tcgaaaatgg	cggcttcttt	cctaaagata	444000
gcatccgcca	ttttgggaac	gataccgata	accgtgactt	tagaaagagg	agtttcaaga	444060
ttacgatcta	ccttattata	acgtgggtag	tcatagttta	atgacaaaat	tcctgaggac	444120
aaacccacta	agaattcttc	ggcagaaagc	cgcaattcag	aaattgtagg	taagatgata	444180
ttgactgtgg	aacactttgc	tttacgtaag	acacgagtta	gtgtcgcata	ggtttggaag	444240
acaacatcag	aggtgagctc	ttcatttttc	cctaagccta	agaggacaat	gcgtttttcc	444300
ttagcttttag	gactactata	aaggagttca	atctccccgg	tttttccttg	aaagttttct	444360
aaagcgggga	gatacgaggg	ttcaaactcg	gcttcaaaaag	aagctgcatt	ttttgcatcc	444420
ttaaaatgcc	aaaagggcag	gactatagca	tctgccttaa	cacgattacg	cccagaggct	444480
tgagcatgaa	ataaaaccac	aaactctcct	ttaagtacta	ggaattaaaa	aggaacatct	444540
tcacagacat	actgctgttc	ttgaccataa	ccagcataca	tatctttatc	tttaatagct	444600
tctgcgtcca	gtgcttcacc	ttcaaaccct	acggatacag	attcatatcc	cacttgctga	444660
tgattgtctt	ctaaagatgg	agaacggctg	ccttcattgc	gaccgaaagg	actgaatttc	444720

aaagaatcta	cactaatcac	taaagaagaa	ttgcggtgaa	accatctttg	ctcatgtaac	444780
tctctacaga	gatatcgcca	gcaacaatga	ctcctgagcc	tttcttcaag	taaggaagca	444840
tcttatcata	gcgattgtgc	caaataattgc	atttgcacca	aacagtttca	tctttcattc	444900
caactcgagt	cttactctcc	agtctcagag	tgatcacacg	ttttcctttg	gaagtcatcc	444960
gctcttcagg	atctgcccc	aggtaaccag	caaaatgcc	aaacatcata	agatagcctt	445020
tagatttcta	ttttaatact	tctttaatta	atacatctta	agaacttctc	aaaacagatt	445080
caggacaaaa	acgagaagtc	aataaagtca	tttcttctct	aagaagagct	ttatcaatct	445140
tttaaattag	aaaaaagatg	tagtacttat	atgcttaatt	aagcacgaat	acctgtagga	445200
ggaggttgca	ttccaccacc	gccttgaggc	atttgtggca	ttgtatctac	agaaggttct	445260
ctaccagcac	aaatatcagc	acacacggta	cgccacttaa	caacagtttc	aataaacaat	445320
tgagcaaagt	cttttagtaa	attcgtttca	gcatatttca	tatccaaaac	gcagtgcata	445380
agaatgagct	gttccttagt	agcaacacct	actccacctc	cagccatctg	accgccaagc	445440
atagatcctt	ctaataattt	ctcatataag	gccaaatttc	tctgagtatt	atcagggagt	445500
ccatctaaca	gaggagcgta	gacataaaga	cgatcagaat	gttcttcata	agtaagggtga	445560
agagagaact	caccatcaac	aaataaaatg	cacgtgttat	tctgatcaaa	agctacatcc	445620
ggcagtttta	attcttttagc	aaaatttttt	agattttcct	cagcattttg	cctgggacat	445680
gagggaatct	ccttgtaata	gattgtgtgt	gtttcaagtt	accataagag	tgattttgta	445740
gtaaacgatt	tcagaggcct	aaaatcaaaa	actcccttgt	atttctggcg	ccgttatgat	445800
atctgatcga	cgatggaaaa	agtttcttct	tatccctcag	ttcctttacc	tcttggggct	445860
tctaaaattt	ccccaaaccg	ctatcgattt	gctttatatg	cttcacaagc	taccgaagtc	445920
atccttgctt	taacagacga	aaattcagaa	gtcatagaag	tccctcttta	ccccgataca	445980
caccgcacgg	gtgcgatttg	gcatatagag	atcgagggtg	tttctgatca	atcgtcttat	446040
gcatttcgtg	ttcatggggc	taaaaagcat	ggaatgcaat	actcttttaa	agaatatctt	446100
gcagatccct	atgcgaagaa	tattcattcc	ccacagagtt	ttgggttcgcg	aaagaaacag	446160
ggggattatg	cattttgtta	tttaaaggaa	gaaccatttc	cctgggatgg	tgatcagcct	446220
ctgcatttgc	cgaaagaaga	gatgatcatc	tatgagatgc	atgtacgttc	cttcacgcaa	446280
tcttcttcat	ctagggttca	tgctccggga	accttcttag	gaatcattga	aaagatcgac	446340
catctgcata	agctgggaat	caacgctgtt	gaactcttac	ctatctttga	gttcgatgag	446400
actgcgcatc	cttttagaaa	ttcgaaattc	ccttatctgt	gcaattattg	gggttatgct	446460
cccctaaatt	tcttttctcc	ttgccgacgt	tatgcttatg	cctctgatcc	ttgcgctcca	446520
agtagagagt	ttaaaacttt	agtaaagacc	ttgcatcaag	aaggatttga	ggtcattctt	446580
gatgttgttt	ttaatcatat	gggcttgcaa	gggacgacct	gctctttgcc	ttggatagac	446640
actccgagct	attatatatt	agatgcacaa	ggtcacttta	caaattattc	aggctgtgga	446700
aacactctca	atacaaaccg	cgccccacg	acccaatgga	ttctcgacat	cttacggtat	446760
tgggtagaag	aaatgcatgt	cgatgggttc	cgatttgatc	ttgcttctgt	cttttctcgt	446820
ggctcttcgg	gatctccctt	acaattcgct	cctgttttag	aggcgatttc	ttttgtacct	446880
ttacttgca	gcacaaagat	tatagctgag	ccttgggatg	ctggcggttt	gtatcagggtg	446940
ggctatttcc	ccacactgtc	tccaagatgg	agtgaatgga	acgggtccgta	tcgtgataac	447000
gtgaaagcat	ttcttaatgg	ggatcaaaat	ctcataggaa	cctttgcttc	tagaatttca	447060
ggatctcaag	acatctatcc	tcacggctcg	cctacaaatt	cgattaacta	tgatcagttgc	447120
catgatgggt	ttacgttatg	tgacactgtg	acttataacc	acaaacataa	tgaggctaac	447180
ggagaggata	atcgtgacgg	cacagatgcg	aactacagct	acaatttcgg	aacggaagg	447240
aaaacagaag	accctggcat	tcttgaagtt	cgtgaaagac	agttacgaaa	tttttctcct	447300
actttgatgg	tctcgcaagg	cattccgatg	attcaatcag	gagatgagta	tgcccatacc	447360
gcggaaggca	atacaaccg	ttgggctttg	gattcgaatg	cgaattactt	cctttgggat	447420
cagcttaccg	caaagcctac	actgatgcac	tttctctgtg	atctcattgc	gtttcgaaaa	447480
aaatataaaa	cacttttttaa	tcgaggcttt	ccttccaata	aggaaatcag	ttgggtagat	447540
gctatgggaa	atcccatgac	atggcgccct	ggaaatttct	tagcatttaa	aataaaatcg	447600
ccaaaagcgc	atgtatatgt	tgctttttcac	gtgggagctc	aagaccaact	tgcgacctta	447660
cctaaagcct	ccagcaactt	tcttctcttat	caaatagttg	ccgagagtca	gcaagggttt	447720
gtccctcaaa	atgtagcaac	gccgacagtg	tcgctacagc	cccataccac	gctaattgcy	447780
atcagccatg	cgaaagaggt	tacctgatct	ctccgtccag	ttcttcattc	caggattcta	447840
taactacaaa	atccacatcc	ttgtagaact	tctcaagaat	ctgacgtgca	ttgaatcctt	447900
ctatagcaag	acgatctacg	ttggactgca	agagcccttg	tgcatctata	attaatcctt	447960
gagggtctatc	cacaactaaa	cgagctgtcc	agtctatagc	ctcttctaca	ccatagaact	448020
gcttgggtcac	accaaactct	gcataccctt	ccttcttcagc	tttaacatgc	caaaagtttt	448080
gaggattttct	tgcaaggagc	ttttcgtata	gagcggttct	ttctagaatg	atgcaagcag	448140
atagagcttc	tttatctagc	tcttcaaggt	actttataga	aagtacagat	ttcagataat	448200
cttcgatttg	aacttcgtta	gaaaccatga	tgcaattggt	gtctttacga	tgaacgtata	448260
gggaacctgt	atactgaatc	ccgttaaaaa	aaagagaagc	agtgtcatct	acaggctcga	448320
tctttaaaca	ctggagtcgc	ggataaaaatt	ctccccaacg	gatcccttcg	tatagagcgt	448380
ggaccacgca	acgctggcct	tgaatcgctg	tgtctaataa	gacattatct	ccataaatgc	448440
gataaggacc	tttggcttct	atgagagctg	tggtgctttc	attagataaa	aggacacgaa	448500
ttttaggttc	aacgcacagta	tcttgcttca	caaaagtatc	ggataccttt	acttctgaga	448560

atcctgagat	actcactctg	aagaaaagac	ctaaaagtac	gtttttcaat	agtttctactg	448620
tccttctcct	aaactcaata	agttcttttg	atgtcttttt	aaatgggtcgt	aagcaagttg	448680
tgttaccatt	ctgcctctgg	gagtcctttt	gataaaacct	tttaaaatta	aaaacggttc	448740
ataaacatct	tcaagagttt	tgatatcttc	tcccacagct	accgataagg	ttttaattcc	448800
aacggggacca	ccttggtagt	agtcgatgat	tgtagtgaga	agtttgatat	caatttcatt	448860
caatccccc	tcacttatta	atagcatagc	caaagctttt	tctgctacgt	ccccattgat	448920
acagtttctc	tctcggatct	gagcaaaaatc	tctgacccaa	cgtagaagat	gatttgccag	448980
tcgtggcgtc	cctcgggatc	tcttagcaat	ttctagtaat	gcggagctgt	cagcttcgat	449040
tccgagtaaa	tgtgaggagc	ggactaaaat	ctctttttaga	tcttgatccg	agtaatagga	449100
aagtctcgca	ctaaaagcaa	agcgtgttct	taaagggttcg	cttagcattc	ctgatcgagt	449160
cgttgctccc	actaaagtga	aaggagcaag	atcgacacgg	accgagcgag	ctccgggtcc	449220
tgaatctata	gtaatatcga	ctttgaaatc	ttccattgca	gaatacaggt	attcctcagc	449280
aactttcccc	atacgatgga	tctcatcgat	gaaaaacacg	tccccttctt	gcaaacatagt	449340
taaaagtcct	aacaggtccg	agggtttgat	taactgaggc	cctgatgcca	agaccagccc	449400
tttcccccac	gtgtaggcaa	cgatgtgagc	aagtggaggt	ttccctaagc	ctgggggtcc	449460
aaaaaacaag	caatgtcctg	gaacttctcc	tcgttgcaat	gctgcgcaaa	gaaatagatc	449520
taggcgttct	tttaaatgat	gctgtccata	aaattcttct	aacccttttag	gtcttaacga	449580
aacatcaaat	tttttatcct	gatgcaagac	agctacttga	tgcgtcatgt	acgaaccttc	449640
tctatcgctt	tttcttttagg	tggattttat	atttttttga	aactctcatc	gataacgccg	449700
atcgggttata	ctcggcatag	tacacgagat	actatataga	agtacactat	ggacctcttc	449760
tttctatcaa	ggagagcagg	gccaaagtac	gagcactaga	acctctccat	cattttcatt	449820
ttatgattta	aacttctctg	ggtgatctag	atttcttttg	tcttaaaaca	gataaattaa	449880
agatggcgaa	ctatttttaa	aaacattttc	cactgagaag	ttggtagtaa	aaattctcta	449940
gcttatcaat	aaggagatgt	taatcttttt	atgaatccaa	gaagttctta	tcaaggtcct	450000
cgcgatgaatg	cattcaagag	aaccaagatt	cttctactat	aagagtaaag	agcagacctt	450060
cctgaagttc	tccctaaaaa	taagggtttgc	ctttttccct	taggattatc	taacattacc	450120
tctagggttc	gtgataaaaat	tgtagccttt	gggataggct	tttcttgttt	atacaactgg	450180
tcttttcaag	agataatcaa	agtctatctt	atacttagaa	aagttccccc	caaaaaccag	450240
taaattgaaa	aacagaatat	cattaagaaa	gcaatttcaa	actgttaagg	tttctaattg	450300
agcataaaa	agataaagt	gatacgagag	atggccctaa	atgccgatat	gatccatccc	450360
tttgtaaatg	gccaaagtga	cgtaaatgag	gagacaggcg	aaaaacttat	aagttacggc	450420
ctatcgagtt	atgggttacga	cctccgccta	tctcgagaat	tcaaagtgtt	caccaatgtc	450480
tataactctg	ttgttgatcc	aaaatgcttt	actgaggata	tcttcatctc	tattactgat	450540
gacgtctgta	ttgttcctcc	aaattctttt	gctctagctc	gtagcgttga	gtatttccga	450600
attcctagaa	atgtcttaac	aatgtgtata	ggaaagtcta	catatgcacg	ctgtggaatt	450660
atcgtaaatg	tcacaccttt	tgagcctgaa	tgggaagggc	atgtgactat	agaaatttct	450720
aacactacgc	cattgcccagc	gaaaattttac	gctaattgaag	ggattgccca	ggctttattc	450780
tttgagtcta	tcacgacctg	cgaggtttct	tatgcagaca	gaaaaggaaa	gtatcaaaaag	450840
caacaaggca	tcaccgtacc	ttgtgtctaa	agtttcagta	agaaaaaaaa	actgggggtt	450900
tagattacta	gaagaagtga	tgatcaaadc	ctgggtgggtg	atcttttagca	tcttaattgg	450960
aggctttggt	tatgatcggtg	ctatccagga	gttacgtaca	gaagagctac	gcttacaaaag	451020
caaggtctct	tctttatgcc	aagacattct	ttctgctcaa	gaaaagcagc	gtcaactcca	451080
attacatctg	caacactggc	aagactccgc	tgctatagaa	gctgctttaa	tccagcgctt	451140
gggtctcatt	cctaaaggct	ataagaaact	ctgtgtctcc	ccaaagcaac	aatcagcaaa	451200
taaggactga	aaagagacca	tgattcctac	catgttaagt	ttcttcatta	tctgttttac	451260
tttatgctcg	ggattcattt	cgttatctca	aattgctttg	ttttctttgc	ctacgagttt	451320
gatctcgcac	tataagcgct	ctaaatctaa	gaaacagcag	cgagtagcta	cccttcttct	451380
acatccccac	cacctgctca	tcaccttaat	tttttgat	atcggaactga	atattgctat	451440
tcaaaaactgt	tttgccattc	tatttgagga	tgcagcttcg	tgggtggtta	ctgtaggtct	451500
tccttttagca	attactttga	tcttaggtga	gattctccct	aaagcagtag	ctcttctctt	451560
taatacacag	attgctagtt	ccgtagcccc	tcttattctt	tgtgttacta	aaatcttcaa	451620
acccttactc	cactggggta	tcgtaggaat	taattatgtg	gtccaatgga	ttttatcgaa	451680
gcaacagatt	gatatcatcc	aaccccaaga	gctgaaggaa	gtattgcaaa	gttgtaaggga	451740
tttcggcgta	gtcaatcaag	aagaaaagcg	tttactctat	ggttatcttt	ctcttagtga	451800
ttgtagtgtt	aaagagcgta	tgcagccacg	ccaggatatt	ttattttatg	atatccaaac	451860
cccttttagag	aacctctatc	ttttattttc	taaacagcat	tgtctcacgag	ttcctatatg	451920
taacgataac	ctccaaaacc	ttctgggcat	ttgcacagcg	cgtctctctc	ttttacatga	451980
caagccactg	caatcttcgg	atgatctcct	ccccttgctg	aaaaaacctg	attatatgcc	452040
agaaaaccatc	tctgcaaaaa	tggcttttatg	tcagatggca	gctgaagacg	aaaccctagg	452100
gatgatcatt	gatgaatagc	gatctattga	aggattgatc	actcaagaag	acctctttga	452160
aattgttgct	ggagaaattg	tagaccagag	agataataaa	atactctata	ccacctcagg	452220
agctgatggt	attattgcct	caggaacttt	agaactccgt	gagtttagtg	agatcttcga	452280
tatcaacctta	ccgacgaaca	ataatattgc	gactatagga	ggctgggttaa	tagagcaaat	452340
cggaacgatt	ccgacaacag	gaatgaaact	ctcttggaat	aacttgcttt	tccaggtatt	452400

agacgctgct	ccgaatcgca	ttcgccgtgt	gtatataagg	aaattgtatg	actaattctg	452460
ctctcttttg	gataggagtc	aacattatct	gtattgtctt	acaaggattc	tattcgatga	452520
tggaaatggc	ctgcggtgca	tttaaccgtg	tacgattgca	atactatctg	actaaagatc	452580
ataagaaagc	tcgctacatt	aatttctctga	ttcgccgccc	ctatcgttta	tttggaaacgg	452640
tgatgttagg	agtgaatata	gctctacaag	tcgggtctga	gtcctcaaga	aattgctatc	452700
gagcttttagg	aatcactcca	gattacgctc	ctttcactca	aattttttata	gttgtgattt	452760
ttgcagaact	tctacctcta	acaatatcac	ggaagattcc	tgaaaaatta	gcactttggg	452820
gagcaccgat	tctctattat	tcccactata	ttttctatcc	tctgattcag	ctcataggaa	452880
gtctcactga	gggtctttac	tatcttctaa	atattaggaa	agaaaaattg	aactctacat	452940
taagtagaga	cgagttccaa	aaagcttttag	agactcacca	tgaagaacaa	gatttcaata	453000
caattgctac	aaatattttc	tctttaagtg	cgacttgtgc	agatcaggta	tgccaacctt	453060
tagaacaggt	taccatgctt	ccttcttctg	caaagtgtta	agatttttgc	cggactataa	453120
aaaatacaga	tatcaacttt	attcctgtct	atcacaaggc	ccgaaaaaac	gttattggga	453180
ttgcccattcc	taaagacttt	gtcaataaag	ctcttgatga	acccctaata	aataatctac	453240
actcgcccttg	gtttatcact	gcaaaatcaa	aacttattcg	tatcctcaaa	gagtttcgag	453300
acaaccgttc	gagtgttgct	gttgtcctca	atgcttctgg	tgaacctata	ggtattctta	453360
gtttaaatgc	aattttcaaa	atcttattca	acactacaaa	cattgctcat	ttaaaaccca	453420
agaccattctc	tgttattgaa	agaacgtttc	ctggcaactc	tcgcataaaa	gatctgcaaa	453480
aagaactcga	tattcaattt	ccgcaatata	ctgtagaac	cctagcccaa	ttgggtattgc	453540
aactgctaga	cagtcctgca	gaagtaggaa	cttctgtaat	tatcaacaac	ttgcttttag	453600
aagttaaaga	gatgtcttta	tctgggataa	aaaccgtatc	gattaaaaac	ttactctcat	453660
agattctgca	ataagagtca	ggagtgttct	ttcagcttag	aaacatgttc	tcttttaaga	453720
cttaggaatt	tttcaaacgt	tctacgactt	tttctataat	tccaacggct	ctttcaacat	453780
cttcttgcaa	gagaagatgg	ctaaaagaaa	acctgagtgt	tgccagggtc	aactctcat	453840
caacacccat	gctgacaaga	gattttaaag	gtgcggtagc	acctgaagag	catgcggatc	453900
cataaccaca	agccactcct	tctatatcta	aggcgatttg	caatacctca	ccttccaacg	453960
gagggaaagc	aattgctgag	acgttggttg	cccggtggtg	atccgcacaa	tgaatatgga	454020
catcaggaat	gcgtgctttg	attgcctttt	caaaaccatt	tctatgggta	agaatttcct	454080
gagagatacg	ctcttgatga	agatctaggt	atttgaaaat	ataaagcaga	gaggcgattc	454140
cccaaagatt	ttctgtgcct	gcgcgcagcc	ctccttgctg	acctcctccc	cacagctgag	454200
gatgtagttt	gactcctgga	gagaccagaa	gagctccgat	tccagagagt	gcattgaaat	454260
tatgtccact	gaatgtctgc	atagtgcac	cagagggaag	aactatcctc	tccttaccta	454320
catttgccagt	cgcattccaca	ataaattgca	attgtcggtc	ttgcgcgaag	tgggctatag	454380
cagctatata	agctttggca	ccagtctcac	tattgaccca	acctaaagatg	attgctgaag	454440
ttttaggagt	cacagctctt	tcaatctgct	ctatagtaag	aacacatctc	ccttcttcgg	454500
gattttaaata	agaaacggaa	agcgagggaat	gttttaaagg	ctctaagatg	gcgggggtgtt	454560
cgctacctga	ggtgataaca	tgactgtctt	tagggagggt	tgctattgct	aaatttaaac	454620
tctcagtagc	ccctgaggta	tagaggacac	ggccctgaaa	cgaaaggacc	ttttgcatcc	454680
agtgtgaagc	ttctagaacc	agttgacgag	atttttttacc	taattgatgg	acgctcgaag	454740
gattcgcgta	cgtcccttct	ataaggaagg	ttttttggag	aaattccaaa	agtcctcctc	454800
ctgggggtgt	catcgcatgt	ttatccaaat	agatcatgga	atactatcct	tagcaaagga	454860
actattgtat	tcggactaat	acgacagtag	cgttgtcatc	gcctccacga	gtattggcta	454920
gagaaattaa	tgcatctccc	cgttcttcta	gggtggcggtg	ctggttcaag	atatcacgaa	454980
tatcgatata	tggaacctatg	tttgtcaatc	catccgaaca	gaggcagtag	aaatcttctc	455040
tttcacaagg	aagattccga	atgtcaggca	tgacataggg	acgacttccc	aaaacattag	455100
tcagaatatg	gcgataagaa	tacaccttat	ctgattgttt	aggaagccca	taacgatttt	455160
ttaattgatt	ttctaaagaa	tggctcttcgg	taaggcggtg	cagttctccc	tcacgaatac	455220
gataaattcg	actatctccc	acatgaaata	gccattccct	atccttccgg	aattggatga	455280
agctaagagt	ggttcccata	ccctggagat	gctcttccat	ttggccgtgt	tcatagacca	455340
caccattgac	ctctaaaagg	atctttttta	aagtctcctt	atactggtca	tcctcatacc	455400
ccatcaattt	tgactgttgc	tcatcaatca	gctccataag	gctagtact	gcctcttgag	455460
aagcaatgtc	tccaccaaga	cgccccccaa	caccgtcagc	aatagcaacc	acttgagaca	455520
tgagggtttac	ctgccaaaaa	tcttcatttc	tagcgcgcac	cctaccaata	tcactcagac	455580
caaaataatc	aaaatccaca	aagtgtcctt	aaagagatcc	tggaacacaa	atagagtccg	455640
cccctataga	cattctctaa	tttcatatca	ttattataaa	gaattgaatt	ttcctgacga	455700
aatcataatt	tatcgctaaa	ttaatggctg	catgatcggt	aattacaaaag	aaaaatttga	455760
taataatacg	ccctagagct	aggctggaaa	ggtcaattaa	cctaaggatg	aataatgaaa	455820
aaagcattct	ctttactatt	atcttggtta	gtattgttag	ctcttagtgg	ttgcgtccct	455880
cctcaataag	ggttcaacta	cgcaccatga	gttttaatac	caaactcatg	gtgttcctta	455940
gaagttcact	aagaaccttt	tcatcatagt	ttttatgatg	ataaagtaaa	aattgctata	456000
aatcgaagaa	ctgcctatgc	aaatagaaaa	tagtagtatt	ctttttgcag	aggtagtcat	456060
gaagtgggtt	attttttctg	tgatctcagc	tccagttgta	ttcctcccag	ggtgcacatt	456120
gattcctaaa	gaaaaagtta	ccaaagttcc	ctcacaactt	tggtcagaat	ccctttctca	456180
accttgagtt	tctaaactaa	aactgagacg	gtctctttgc	ttgtttttat	ttttttcttt	456240



gatataagct	aatgagagtt	ttaaattggaa	aattctctcaa	ttgcgaaagt	attgatctta	456300
aaagtaaaaa	ctttcccagg	gctagaatct	tttgcaaaat	aagcaattta	aggacagtga	456360
ctatgcgaaa	aatgttggtg	ttattggcat	ctttaggact	tctatcccca	accctatcca	456420
gctgcactca	cttaggctct	tcaggaagtt	atcatcctaa	gctatacact	tcagggagca	456480
aaactaaagg	tgtgattgcg	atgcttctctg	tatttcatcg	cccaggaaag	agtcttgaac	456540
ctttaccttg	gaacctccaa	ggagaattta	ctgaagagat	cagcaaaaagg	ttttatgctt	456600
cggaaaagggt	cttcctgatc	aagcacaatg	cttcacctca	gacagtctct	cagttctatg	456660
ctccgattgc	gaatcgtcta	cccgaacaa	ttattgagca	atttcttctc	gcagaattca	456720
ttgttgctac	agaactgtta	gaacaaaaga	cagggaaga	agcaggtgtc	gattctgtta	456780
cagcgtctgt	acgtgttcgc	gtttttgata	tccgtcatat	taaaatagct	ctcatttatc	456840
aagagattat	cgaatgcagc	cagcctttta	ctaccctagt	caatgattat	catcgctatg	456900
gctggaactc	aaaacatttt	gattcaacgc	ccatgggctt	aatgcatagc	cgtcttttcc	456960
gcgaagtgtg	tgccagagtt	gagggctatg	tttgtgctaa	ctactcgtag	tctaaggaaa	457020
tgtccaagtt	tattcttctc	ttgtcccttg	gcgtcgctgc	tctagcttcc	aaaaacttct	457080
ttatctggcc	agcacctctc	gggaaaacac	ctttaaantc	cgccaagttt	tatttggttg	457140
tgtcttctct	gttttttctt	cccttgtagc	tcttagcgtg	agctcacaaa	ctgcggaatt	457200
actttccacc	atgacaggaa	ttagccttgc	ctttgcatct	ctgttctacc	tgcnttttct	457260
ccccaggat	atcacacgtg	ctatactttt	ctctggagaa	agancggtta	aaacttcatg	457320
gcgtgctcta	ggatctgcca	tcagaatgtg	gatcatcatc	atcccagtaa	cacaactgat	457380
tgggattatg	atgagtaaat	ttataacttt	ggttcttctc	acgcaagaga	ttcacacaca	457440
agaagtcact	caagaagttc	agaactctct	gcctataaca	ggacactaca	ttagcatgat	457500
tctaaattta	ggcgtcctca	ctccatttgg	agaagaggta	tttttttagag	gaattctaca	457560
gacattcttg	aaaaacaaaa	tgacgcgcct	agctgcggta	ctatgctctt	ctattatttt	457620
ctctttcatt	cacattgaac	actctttagg	aagttgggtc	ttttgtcccc	gtgctctttg	457680
tttttccctt	atctgcaggg	tttctatatg	aaaaagatcg	gcacattctt	tctcccattg	457740
cactgcacgg	gttggttaac	ctcacctcat	tgctattttt	gggaataaag	taaaaagagt	457800
aagttggaga	acattctttt	agcaaaaaga	aactctcctt	agggctgcta	ccttccagtc	457860
ctgaccgat	tcgcagggtc	cttctcttaa	aaggccccc	acttaccctt	ctttgatagc	457920
atatattctg	ttttttcaaa	agcaccatat	gcttaaaaat	agaccaaaac	ttcaactatg	457980
tagattcatt	tttctctcgg	tgcttagcaa	gctcccaaag	gcgatcggcc	tcttcaatcg	458040
agaccggctt	gtaatcttca	gcgaatatat	aaggagcacg	gcgacgcaat	ttttccatag	458100
cctcattggc	aacgtcttctg	gaagcaagta	cgccctctcg	ttctaacaga	aaacataaaa	458160
ttagaactaa	agttaagaca	tccccgggtt	cggaaaccaac	ctcttgtagc	gtcttacctt	458220
gtaagacggc	ctcgtgaaat	tccgtgacact	ctccaagaat	atgctctacc	atagagacta	458280
gggattgctg	aagtgaccaa	ggacaacgtc	cttcaactac	catggcacgg	acagtcccta	458340
tcaatttaga	aaaagcgtga	tctcgcctct	atactcctat	tgattctcta	gacctgacat	458400
ccccgaggta	gattagcaaa	gcattctttaa	tctttttgtg	tcctgaagaa	aaagctaagt	458460
gatctatatc	actcaaaaaga	tgcaattccc	cgaactgagg	cagagaagtg	gctttaaaaa	458520
ttataggaca	caaatgaacc	ttatgattag	taaagcctat	ccgctgttct	ttaagggtac	458580
ctaagaattc	caaagggtct	tctaagaaa	gtccatctt	cttagtaaat	ccttctatat	458640
cttgaagacc	ttcctctggt	tcaacttcaa	tataaggaaa	ttcatataag	cctgccatca	458700
tttctttagg	acgtctcttc	tcgacaacca	aagagccatc	gtacaataca	atcgctacca	458760
aacgatgcaa	aaagatgacc	ttttttctgg	catgacgtac	cggcaatacg	aactgtttgt	458820
tctccctcca	agctccacat	gcttgacgga	caggacaacg	atgacattga	ggaacttttt	458880
tacagataca	agctcccaac	tctatcagag	cctcagctat	aacctcgga	ctcttatgag	458940
gaagaagcgc	ttgagcaatc	ctagaaaccc	aagtacgagt	tgattctaa	tctatagaag	459000
tttctatcaa	aaatatccgg	ctaagaacac	gcaagacatt	gccatccaca	gcagcagcac	459060
gcctcttaaa	agcaaaaggct	agaatagcat	gaaccgtata	aggaccaact	ccacgaattt	459120
gagcttaagga	aatggcatca	tcagggatct	ttccatgaaa	ctcctccata	accatgcgag	459180
ctccctctaa	aatgtggcgc	gctcgagaat	aataacccaa	tccctcccat	aacttaatga	459240
catcttcttc	ttttgctgca	gctaaagact	ctatggtagg	aaatctctcc	atccactgat	459300
taaaataatc	tataacaact	tcagctcgcg	tttgtgtgag	cataacttcg	gaaaccaca	459360
cactataggg	agtcgggtta	tctctccaag	gaagagatcg	tttatttttt	tcaaaccatt	459420
tttttaaatgc	ctctacagga	aaattctttg	ccttttccaga	aaaagctatc	tttgtcatac	459480
aaaatctctt	aaaattttat	gcaattatca	aatgataaaa	gggctgcttt	acaatatatt	459540
atggaaaatt	tttctctggct	tgccacacaa	gtctcaagat	tatcttcttt	tcttagatct	459600
caactgccta	atcatagcaa	gcaagaaatc	ttggcgtcta	ttcgccaaca	tcgatgtcga	459660
gtgaacgggt	tcatagaaag	atttgaatcc	tacaaggtag	aacctggcga	ccgtgtttcc	459720
ctatctctga	tccctcctaac	aaaacaacaa	cctagcatcc	tctgggagga	tgactatagc	459780
attatctacg	aaaaacctcc	ccatcttact	actgaacaaa	tgccacacat	gacacgggtt	459840
tttactgtgc	ataggttaga	caaaggcacc	tctgggtgtc	ttctcatggg	aaagtctaaa	459900
caagcggcta	ctgagctcat	gaaattgttc	aagcaaaaga	aaatccataa	acaatacata	459960
gctttcgttt	ttggtcatcc	taaaaaaaaa	tttggaaccg	taaaatctta	tacggccccc	460020
gtataccgga	ggtgtggagc	tgtgattttt	ggagccgcag	gcccatacaca	gggagaaccc	460080



atcaaattccg	cttacaaatg	ggattgctgg	gtcatcctat	tgtcggagat	gtcgactacg	460140
gacctaaaga	acagcctccc	cagatcttcc	gccctctcct	ccatgctcac	tccttagaat	460200
ttatctcccc	attcacaaat	cttcccctaa	aaatttgtgc	gtcatcaacc	gaagatccta	460260
gagaatgtgc	tcggcactta	cttcaagaaa	aacccttaga	actttacaat	tagagattca	460320
taaaactgta	attggagtcg	tttacctgc	ttcaaaacat	aacctcctct	tcttcatctt	460380
ctaaatcccc	cctttctacc	cttccggggt	gcgacctagg	agaaatcaca	cttaaaggta	460440
aaactacagg	aaaacgccct	ctagaagaca	caggggaacg	ctctctagca	cctaataaag	460500
aaggttgaga	cgtaaccaca	ggatctgggt	gaggttgccg	atgtgccgtg	actccagaag	460560
gtgtgggtac	agggggcggt	tgtaaaattta	gtcccgcgt	atgcatcaat	gaagttgaca	460620
tctgtagtag	gcacttatct	ctttcttgaa	cattgttagc	atcgcttaac	aaacttgttt	460680
tcgtaagaga	attctcaaaa	catcgtgcag	ctaattctaa	atagcgtgac	gaggaagatt	460740
ctccccctcg	cttcccttcc	agatcgacac	gcctgcccac	cccccgagcc	aaaatagcat	460800
tgacttctgg	attacctaaa	atgttgccac	gttggggatc	tcctgtgggt	gggacaaaat	460860
aacattgata	gtgagataaa	accaaagcaa	ctaacgccat	cagattttct	ttggtgatcc	460920
aaatcggagt	gcttctctca	ttggtagcta	caaagaaaat	agacattaat	agattcatgc	460980
aggatgcaga	caactggatt	cccattgtct	cttcttaagg	gagaagacct		461040
taagtgtagg	gaaagacata	catatcctct	ctaggttaaa	agggctacaa	acctgtgctc	461100
cttgctctcc	ccatgaagaa	agaaccatca	ctttgctttc	acactcgaat	tcctgttctc	461160
gaagagaaga	cttagcaatc	cctgaggcaa	ttgctgtact	ccaaaaagga	tcctgtaata	461220
aaccatccac	acaactcgcc	gcctccgccc	acagatccat	gctttgagac	ttcaagatct	461280
cacaaaagtc	catagaacac	cggtcacatg	cagccatgac	ctccgcgatt	ggaggaaatc	461340
cctcgagtgc	atgtcctgat	aataagctca	tggtatcaat	gccaagctca	cttaacgcaa	461400
ttaaaagaac	agccttgcca	tatttctgtt	ctaaagcttc	gagttcttat	aaagggattg	461460
cgggttcttg	ggatccctct	cctatcccg	aacaattttt	ccatacacca	cagaaaaaac	461520
ggccaaatcc	tcacaaaccg	cactgtccgt	ctggacagcc	acaggtagga	caaccgcagt	461580
tgcttggca	ggtctctcca	caataattat	aacaaaattc	gctagttttc	tttgctccag	461640
gacttggtac	tgctgcataa	atgatctgtg	ccaacgatgc	agctgtccct	aaaggatttg	461700
ctgctgcaga	tcctgttgcc	gataacaaat	tcaacagtac	cgaagcggcc	tgctcctgct	461760
gagttccacc	acttctctct	tgagacgtag	tcatctgggt	caccaagcta	aggagttgct	461820
gtaattgctc	tgaactcacg	gacgatccgc	cacttctctg	tgtcttgtct	aagataagtt	461880
gcaaaagctg	ttgctgcata	cttgactgg	aagaggaggc	tcccgaaagt	cctgctgaag	461940
ttgatggttg	tcctactgat	gggtgtccca	catttaataa	attagtaagc	aacgcttgca	462000
cttgatcagg	tgaaagtcct	aatgcagagg	ctccggatgc	ggtagtagtt	gtcgtgtgag	462060
aggaggcagc	tcctccgggt	tgaagaaaac	cttgaactgc	agatgagact	gcttgtgggt	462120
ttgtggaaga	aggcgctatc	gtaacaacct	gtggattctg	tggtgagggg	aatttcccta	462180
aaggattcgt	caaacaacct	cctaagtaat	cagtgaacc	caaactacga	taagttcgga	462240
tcgtaaatcc	ttttgaaaat	tttttttagca	gtacgcggga	gtgagaagtt	tggatattct	462300
ataaaatatg	taaagaaaaa	aatttaaaga	atttacgttt	ctattttacat	tggaggcagg	462360
atctcccctg	ttgaggcacc	aaaaggtttt	cttaagataa	gaaagatttg	ttacttctct	462420
tcctaataagc	ttcaaaagta	taaggcggat	tcatgtctaa	gattgatcta	acaggaaagg	462480
tagcatttgt	tgccggcatt	ggtgatgacc	aaggatatgg	ctgggggtatt	gctaaacttc	462540
ttgcagaagc	aggagctacg	attattgtag	gaacatgggt	accgattttac	aaaattttct	462600
ctcagtcttg	ggaattagga	aaattcaatg	aatctagaaa	attatcgaat	ggcactctct	462660
tagagattgc	taagatctat	cccatggacg	caagttttga	tagccctgaa	gatgttctct	462720
aagatattgc	tgaaaataaa	cgttacaagg	gcattacggg	attcacgata	tcagaagtcg	462780
cagaacaggt	aaaaaaagat	tttggtcata	ttgacattct	tgccactcgc	ctggcaaata	462840
gtcctgaaat	ttctaagtct	ctattagaaa	catcaagaaa	aggttactta	cgggctctca	462900
gtgcctctag	ttattctttt	gttagccttc	tctctcactt	tggaaagtac	atgaaccgtg	462960
gtggatcgac	aatatcgctc	acctatttgg	cttctatgcg	cgctgttctc	ggatacggag	463020
ggggcatgag	ttcggcaaaa	gcagcttttg	aaagtgcac	caaaactctt	gcttgggaag	463080
cgggacgcgc	ttggggcata	cgtgtcaata	ccatctctgc	aggaccttta	gcaagccgag	463140
ctggaaaagc	aattggtttt	attgaaagaa	tggtagacta	ttaccaagag	tgggcgccta	463200
ttcccgaggc	tatgaatgcc	gagcaggtgg	gtgccgttgc	agctttctta	gcacacctc	463260
tagcttcagc	aattactggt	gagaccttat	acgtagatca	cggagccaat	gtgatggga	463320
ttggtcctga	gatgttccct	aaagactctc	aaggtcgtca	taatagcgga	caccagcttc	463380
ccaagcttaa	agaatgccat	tcttatctgc	tgggggagct	agaaagtccg	catgaacgtg	463440
catctcttca	ggtgcggaac	tcatcacaat	tttaaaatct	cctctctcaa	taagatcgag	463500
atcattagca	tcatctcctg	aagccatgac	aaagggtttc	tttccatcat	aaagtatatt	463560
gacaacacga	tctaaggctt	tgcttttaga	gacgctttta	tctgttaaaa	acaagatggc	463620
atagcgaaag	tcaaagggcc	agcgcattaa	cgtcatcgtc	gcgactgaag	tcagtgtctc	463680
ttggcgttcc	agctcctttt	gaattctgat	gacctcatct	cgcagtccaa	agacttttgc	463740
tgcagcaaaa	ctaggaaaag	catagtcgct	ttttaaagag	cgcgtttcaa	atggatctct	463800
tctttcctta	gcattaggaa	agtacctagg	atttaccat	tcgtgtaaat	cttgagctat	463860
aggagtcggt	gaaaagcgat	agtagtgatc	cccgtaaagga	gtccttgatt	ccacggaaaa	463920

aagagccggtt	gccccctcca	tacaatcttg	taaaatacat	aataaatctg	agggtaaact	463980
tttagaatag	agaagatttg	atgatgttga	agaccataca	gaagcgccgt	tttggcatcc	464040
taataaatat	ggagcatcaa	aatcagaaaa	caagcgtgca	gcatatttat	aataccttcc	464100
cgtcaagaaa	aacaacttcc	aaccagcttg	gtgcagcgca	tagagccgct	catacacctt	464160
tttatctaaa	tgatgagatt	gatgggtaat	tgtaccgtca	atatcagtca	ctagtaactt	464220
ttccatagca	tcaccatagt	tttattaagc	gctgccaaag	aattttctcag	gcaacttgaa	464280
aaaattcttt	gcatccaccg	acagactgct	gtcgttttgt	ctatgaaaga	caagagcttg	464340
ggctctgtgg	aacgagcaca	ccctagaagg	gtataaagga	gtctgtgaat	tacccaaatc	464400
atctagggga	gctctctaga	cggtaacttg	aggaatatac	atgattacgg	tttaatctgt	464460
acttggaagt	cattgtacta	taattttatat	agcatcgact	aaaactatac	ttcattatta	464520
cttgtagtga	gttggtataca	aatcgggcta	ccactataat	tttatagaga	tgatcgcggg	464580
tcttacacat	gttttttaat	cttttttctt	tagtttttaa	gctttctgat	gagcttgctc	464640
ttgcagaaac	gatccaagag	cccatttctg	tacatgaaat	gttcccagga	agcatgaaat	464700
tagaaatgtt	taaaatgcta	ggatctttga	ttctactttt	aacaattttt	ggctttggag	464760
tttgggcggt	taaaaagttt	gtgagatcaa	gaagtcacgg	ttttggaggc	tcgtctcaaa	464820
tcaaaaatcct	agaacgacgt	tccttaacgc	cgaaaacttc	tatttacctc	attcgagtgt	464880
tgaataaaaac	tcttgtgatt	gcagaaacac	cagaaaaaat	tacgctactg	acagagtttc	464940
ctcccgacac	tgatatcaat	catctacttc	aagaaaaata	taagcagtct	tcttcctctg	465000
caacctctga	tttcctcagt	aaagcaatac	aaaagataca	aaaaaaacaa	cagacgaatc	465060
aagattagat	ctagtattat	cagccagcaa	tgatgcaggc	tctaggaaca	acttgaggta	465120
tttcctaaat	gacgacatgg	acattaaatc	aaaataatct	cacaaaaattt	cttaaaagtt	465180
cggatgaaga	acctttctta	gaaagagaaa	gcggtcttac	ttacattaac	attcaagcta	465240
atggcaatga	actcccttta	ttttttgtaa	tccgcagtga	gggagaaata	ctgcagttga	465300
tttgttacct	tccttaccac	ttgcatgaat	ctcataaggc	atcaacagct	cgtttactcc	465360
atctcttaaa	tagggacatt	gatattcccg	gctttggcat	ggatgaagaa	cagggattga	465420
tattttatcg	gcttgtgttg	ccctgcctaa	acggagaaat	tcatgacaca	ctattacgga	465480
tatatatcga	tacaataaag	ctagtctgtg	atagtttttc	tcatgctatt	gggttgatct	465540
cttctgggaa	tatgaatttg	gatgaactaa	gacgtcaggc	tcttcaagag	caacaagaaa	465600
aacgtaatga	gtagtcaaac	tatggatgtt	cttattttct	atgatacggg	gaccacagga	465660
acacaaatag	aaagagatcg	cattatagaa	attgctgcct	acaatagtgt	cacagatgag	465720
tcctttctta	cttatgtgaa	tccggaaatt	cccattcctg	atgaggcatc	caaaattcat	465780
ggaatcacta	cggatgcggt	actttctgct	cccaaatttc	ctgaagccta	cgagggattt	465840
aggaaatttt	gcgagagagga	cagcatctta	tgggctcata	ataatgacgg	ttttgatttc	465900
cccctactcg	gtgaaggaaatg	tcgcagacat	tccttagagc	ctctgacaaa	ccgtacaata	465960
gactctctaa	aatgggcaca	aaaatatcgc	cccgatctac	caaaacataa	tttacaatac	466020
ctaagacaag	tttacggttt	tgctgaaaat	caagcacacc	gagctctaga	tgacgtagtg	466080
atattgcaca	aggatatttac	ttctttaatc	ggtgattttac	cgccccagca	agtcctcgac	466140
ttgctgcaac	agagctatca	cccgaagtc	ttcaaaatgc	cttttgcaa	atacaaaggg	466200
cagcctcttg	tggatattec	taagtcttac	ttcgaatggc	tggaaaacca	aggagctttg	466260
gataagcctg	aaaataaaga	catcaaagcc	gctatagctc	tattacatca	accgacatga	466320
tactgactgc	tgcctttttct	ccttgccgga	atgatatttt	cctttttcgt	tctttcttaa	466380
aagaccccca	attcaggcct	cttcttaacc	aggtaacaat	tgcggatatt	gaaactttga	466440
ataccctagc	tctgcagcga	cggctctccc	taatgaaaat	gtcagcagcg	ctcttccctc	466500
tagttttctga	ttattataat	cttatggacg	taggaaatac	cttaggatac	aacagcgggc	466560
ctatcgtcct	ctccttagat	cctgaatgtt	ctctagatac	cttggaact	cctggagaga	466620
tgacaaccgc	tcattgctctc	tgtaaaacttt	actatcccaa	ggcaaaactc	attcccatgc	466680
cttatgacaa	aattctatcc	gcgatactgc	aagggaaagt	cgatggaggc	gctctgattc	466740
atgaagagcg	cttcagctac	gatctccaat	tgacattgcg	ggcagacttt	ggagagctat	466800
ggcgccgtaa	gaccatcttt	ccccttcctt	taggatgttt	agccattgcg	aaatatgttc	466860
ctatggctac	agtggatgct	ctaacagcag	cattaagaaa	gtcttttaatt	tgctccctga	466920
aagatcctat	aactgcggga	gcaaaagcag	tagaatactc	taaaaataaa	aacgtgaccg	466980
tgattcatag	attcatagga	acctatatca	acaaagaaac	ctttcaacta	tctaaaactg	467040
ggaaaaaagc	tttacatatg	ctctggaagg	ccaatgaatg	ctgtcaatac	acctaaaaaa	467100
atcctttgca	ttgttgacga	ctatagagaa	atttctcctc	taattgaaca	acttgatttt	467160
acacagatca	acgagcatct	ctatagttat	cgttgtactg	actaccatct	agatctctat	467220
attgtccatg	tttggggaag	tacagccggt	ttaaatgctc	ttcaaagcta	ttgccaagca	467280
tatacagatt	acgatctgtg	gatcaatcca	ggttttgtgg	gggcatgttc	tcccagatt	467340
cctttaggtc	aatgttacac	tattgagaaa	attgcaaacc	tcactacgga	tacacctcct	467400
gttctctctg	aagatccccc	ttatctcttt	gacgctctac	cggattctct	acctaaaagc	467460
tctctgggta	cctctccagt	attgtaccat	tatgggtttc	aataagacgt	ttaaacttct	467520
agatatggaa	aggctatgct	aatagcctca	caagcagcag	aacatcacat	cccctgttct	467580
tttctcaaga	tcacttctga	ttatactgtt	ccaggagact	gtcccttcag	cagattggag	467640
gaggatcac	aaaagctaac	tcagacactt	gtagagttgt	tggcctgagc	tcattggagag	467700
agcgatccca	cctaagttgt	tattgccatg	tccgtaggat	ttgcgactaa	tttgtgatca	467760

ggaacaaaga	ccctgttata	ttcttttagtc	cctgagagct	cccacatttt	taaaaattca	467820
ggacacgtct	gtaagagttc	ttctttttag	ccttcggcaa	ttttttgacc	attttctatg	467880
tagagcacgc	gatctacatg	ttcaagagtg	gtcagcttat	gggcaataat	gatttgtgtg	467940
cactgtcctt	taagctctcc	aatgatattc	ttaatgtaat	tttactaat	ggcatctaga	468000
gctgacgttg	cctcatctaa	aattaagatg	gaggcgtttt	tcaacagagc	acgtgctatt	468060
gccaaacgtt	gctgctgtcc	tcctgagaga	ttcttcccag	attcttcgag	cacgctatgg	468120
actcctttag	ggagctttaa	aataaaactca	tcagcgtagg	cacgttttag	agcttctaaa	468180
acagcctcct	cctccatata	cttaccacag	gtaaggttat	tccatacagt	atcatagaat	468240
aagaaaggat	tctgtaatac	acaggcgatg	tgatttcctta	aggacccttt	gttatattcc	468300
gtaataggaa	gagagtcgat	aagaatcttt	ccttgggaga	cttcgtagag	cctaggaagt	468360
aatttaacaa	gtgttggttt	tccagatcct	gtaggctcta	caatgcctag	agcttcgcct	468420
ttatgtaagg	taaagcttag	atttttgagg	atgtgcttat	cttcttgata	gccgaaggaa	468480
acattctcga	atgtgattgt	attagaaagt	ccaaggaact	cgatttctct	ttctttttga	468540
ctatgaagat	cggggtgatt	caagacttca	taaaatctct	ccgcagcagc	acatcccctc	468600
atgatggagg	tatnttcac	cccgaacttc	ttaatagggt	cgtagattag	gtagacaaa	468660
ccacaaaata	cgataagttc	ttcggggaga	atagcaaatt	tataaattcc	gataacgacg	468720
acaaaaggca	aaaataaaga	agctatggta	tgcaggagggt	gtcgtggaag	caaaccgtaa	468780
gcagcacttt	tctcctctaa	agcagaaatc	ttattgttat	gtcacaata	ttttgtgaag	468840
gcaaattttt	ctgtacgaaa	gacttttact	gtcataaccc	cagcaagaaa	atcataaaga	468900
acggaggaaa	atgaatcctg	actcttttga	atacgttttg	ctaaattttt	gatctttcta	468960
gcgatcacga	caatgggaag	gataaagata	ggaaaggcaa	cacaaataag	aattgaaaac	469020
ttccatgaaa	tcgacagaca	gactcccaat	gtcaatatga	aggtaattgg	ggcttgaatg	469080
tagttaatca	ttaaagagtt	tactgctaag	gcaatgcttg	cagaatctgt	catgacacga	469140
ttactttaat	taccgatata	atgatcatgg	aagaagggtca	tggggagttg	ttgtagggcc	469200
ttaaagtagt	cctgacgtaa	gtctcggctt	acccgatatag	caacgacttg	cccaaggaaa	469260
cgttggaaaa	ataaggtgac	tgctttaaaa	atagcaacgc	agattaagaa	gattgccagt	469320
cctcgaaagc	ggctcacatc	gatgtagtta	cggacaaact	tagagagctt	gctcgtcaga	469380
gaggctgtgc	ttttcccatg	ttcggcgatg	tatgtcgtgg	catcagagac	tgtaagtgtc	469440
tctgaatcct	tactaattgc	ctgccaattc	tctaaaatat	ctttctgact	tagttctgaa	469500
acctttacaa	gtttttccaga	ttccttacgt	ccaaaaagta	aaaaggcgtc	ggggcctgtt	469560
ttagcaatca	tccctaaaga	aaaaatctcc	atctgagatg	aaaaggtaag	tcctaaaatt	469620
gcgagtagag	aacagcctaa	tataacgaga	tgatttttctt	gcctcaggac	cgctttcaga	469680
agtagtttca	taaagaccta	tagagcgaaa	tttttcgtac	cgttttctcca	acagctcttc	469740
tatagctaga	tcttttaate	gtaaccactc	ttggatgata	aactctcgaa	cattgctata	469800
taccaatgca	ggatcgtggt	gagctcccc	aatgggctct	ttgataacag	tatcgataat	469860
gccaaattgt	tttaagtttt	ctccatgcat	tttcaacatg	gaagctgctt	cgctattttt	469920
cttaggatct	ttccaaagaa	tggaggcgca	tccttctggg	gaaattacag	aataatagga	469980
atgctctaac	atagctacag	aatcacctac	agccatgccc	aaagctccac	ctgaacatcc	470040
ctcaccgata	acgacaataa	tcacgggagt	ggcaagtctt	gagagctcaa	aaagattttt	470100
ggcaatttcc	catccttgct	ctctctcttc	agcagtcaat	ccaggatatg	ctcctggggg	470160
atcgacaaga	aagaccacag	gcaagccaaa	cttttcagcg	agttttctta	agcgaagggc	470220
ttttctgaaa	ccctcgggac	ataacatacc	gaagtctcta	tgaaggcgtg	acgctgtatc	470280
gcaccccttt	tcttgcccaa	taaggacaaa	acgctgaccc	tggattttta	caaagccacc	470340
aacaactgcg	ggatcatctc	ggaaggtgcy	atctccacaa	agctcgacaa	actcctcaca	470400
catcccttca	atatagttga	cagtacgggg	acgcgaaggg	tggcgacata	tttgtacacg	470460
ctcccaagga	gtcaaattccg	aatagatctt	ttcttttaat	ttatctaaac	gcttttccaa	470520
tttctgaate	tctgaagaag	ataagagaga	atttttctta	tttttttctt	taaattcggc	470580
tatagccttt	tcataattcaa	ctacttgttt	ttcgtgtgga	agaagttcca	ttagaatgtg	470640
ctctcctcgt	ataaaaagaa	tcatttttaat	acaaacaatt	cttaaacaca	attacagacc	470700
caaaattaat	tcattcttcgt	aaagaatctt	cctttctcag	aggctacttt	tttttcaaaa	470760
attaacatga	cgccctcttc	tttgtaagga	atattaatca	aaaagtctgc	attccaaaat	470820
ttttctttgc	cttgcaaagc	aaaaatttcc	atatagggac	ttgcagaaac	aatgttgatt	470880
gcgtcatttt	ccccaaagaa	cataatgtcg	tttcggggac	ctttataaga	atctagggaa	470940
caggagcgca	agcgagggcc	gtcaacaacc	tgacaattct	tccccttaca	gaaaatagaa	471000
aacgtcatgg	cagaggtggc	ctcagccaac	gcagcgtgca	cgcgatattg	cttctcgcaa	471060
atagtgatct	tacagcggat	cggcagatgt	acataggaat	ctcgaaggta	ggaaaatccc	471120
gtattttctg	gatgaggctt	tcctgtagag	gtgagaaaag	aaatctctgt	agtttggtga	471180
ganttttggc	acacgaactc	tttagcgatt	ccacaacatc	caaaataata	acaatcacta	471240
atgtctccag	agcaaggtcc	ataagcgata	acaccgacat	cccctgagga	atacgctccc	471300
aagctacttt	gacatcctga	agcggctaca	aaagcggatg	agaacgcgt	tctttgcatc	471360
cagaacccta	gtgcaggatc	ctcaagactg	tattctgggt	gaatttgcat	tcctaattgg	471420
aagagaaacg	attggctaag	agttgtcttt	tcttttagga	gtcgagagtt	ctcctggctc	471480
cagagagagg	gaaagacgct	cccttggtga	tcaaagagtg	cctggtgaaa	atgactcatt	471540
ttagagacgt	atgectgact	ctcttcataa	aactctgcga	tctgtaacag	gagtaggcca	471600

aattccgcat	gttctgcagg	ataaggtaat	cctttccaag	gaaatcccc	acaagaaaac	471660
agttctacag	cacctgaagg	gtactgctgt	acatttaaaa	agcttaagcc	taaatcctcg	471720
ccttcttcta	aggccatcaa	aagatagacg	gcccagacaa	tatcatgaat	ttttagtaaa	471780
ggatggtagc	ggaaaatcct	gagtacagac	tgccttaatg	tcttatcttg	gcacgcatag	471840
ataaactgtt	ttacttgtga	atcaaagttc	gaattctggg	acacttctat	acaatgttgt	471900
aacctggatt	gcagcccat	tatcacgcac	aatttgatca	gaaaagcatt	gcaccaaacg	471960
ataataataa	caaaaattag	agtcaagccc	ggtaaaaaac	cggctctgact	ctaacaactg	472020
agacaaaaga	gactacaaga	attaagaatg	cttattcgga	gtttctatca	agcgcttcat	472080
tcttttccct	ggagtaaaact	ttacagcgcg	tctagcagga	atatgaatgg	ggactgctgc	472140
attcctagga	ttacgtccta	cctttggttt	tctttctact	acttgcaaca	caccaaatac	472200
tctaaactca	agcctgtcac	ctttaaccaa	ggcgtcggtc	attttatcta	gaaaattctg	472260
aatcacggta	cgtacgtgat	taggatgaat	tttgtgatct	tgtgagatcg	tgctgattag	472320
tttcttcttt	gtcatggtag	ccatattaga	caatgcctcc	tattaaagtg	ccctaaagta	472380
gctcgttgag	taaccgtaaa	taataaaactt	ttgaagtcta	agctcatcat	atctattcat	472440
cctttggatt	caagacattt	tttaaaaaat	gcgcaatcac	tataaaccat	atcgattaat	472500
gcgaataaact	atatttctag	aacctagaaa	aatcattccc	acatcttgag	aaaaacttcc	472560
cctaaattgc	tagcgtgcat	ctaacacgtg	acttctttaa	tctaacttgg	taaagtgcgtg	472620
gtcctttgct	cctcgtagct	cagcaggata	gagcggttgc	ctcctaagca	gcaggccatg	472680
cgttcgaatc	gcacgagga	cgattttttg	cctttgactc	ctaaagtact	aatttgcttg	472740
tatctgtggt	ttacgtatct	tagcgatatt	ctggttttgg	ttctgaaaac	taggtccaga	472800
aagaaaatta	tgaactccct	cggcgatgcc	tttcgctaca	tgcatacgat	agcgagcatc	472860
ttgcagggcc	gcacgttcac	gactattgga	taaaaacccg	gtttccacca	aaactgcagg	472920
catagaagta	tctctaatac	caacaaagtt	cgcagttttc	aaacctcgag	acttcaaaat	472980
gccatttttt	tccatagcag	ctaaaatggt	ttttcccagt	acttctgaca	tgcgattcct	473040
agtcggagat	ccgaccttac	cattataaaa	atatactctg	gtgccaaagg	ctgctgcgtt	473100
tgaagaatga	ttacagtggg	tgctgataaa	gacatcccc	tgcccacggg	tcgacaaagc	473160
aacgcgtttc	cctaagtcaa	cgtatacatc	agaagatcgg	gttagctgag	gtttataacc	473220
catccgcttt	aagtaacttt	gaaccgtcaa	agcaagagac	agggtcaggg	acttctcttc	473280
ataatgaagt	tccttacttg	ccgtgccttg	atcctttccc	ccgtgtccag	gatctataaa	473340
tataacctca	ctgcgtcgta	cacgctgagg	aggattcggt	gtttgagcaa	aaatcgggtg	473400
acttcctaac	acacataaag	caaaaaacga	cagttgctta	gacataggaa	gcgagtacct	473460
cacaaacagt	ctgcttatca	tcgaacgcaa	ctggttggtg	tttaaatatt	tggtaaagct	473520
catgcccttt	tcccgcattt	aacactatat	ctctatctga	ggcaatagac	agagcatatg	473580
taattgcttg	ttttctgtcg	atttcgatga	aatagttttt	tgaataaaac	ccatcacaaa	473640
tttcattcac	aatatcttca	ggaggctcgc	tcctagggtt	atctgaagtt	acaacagcaa	473700
aaccataacg	ctctaccacc	tgggccatca	acttcggttt	actgcgatct	ctatctccac	473760
cgcaacccaa	aacaacaatc	agtcttcccc	cctcaggaag	taactcatgc	aatcctgtta	473820
agacattgtc	taaagcatcg	gggggtgtgtg	cataatcaat	atatacaggg	cagggaccca	473880
taagtacagg	atccaaacga	cctggaggag	gttgacacaa	gcctatcttt	tctagcaaat	473940
cttcaagatc	gcaacgcaaa	cttgcagtga	ctgtagagat	cgcagcaagt	aggttataga	474000
cgttgtaact	tccaataaat	gaggaagagc	acgcaatttt	ttgggtcccc	tacaccaagg	474060
tatactttgt	tcccagaggaa	gaaagttgga	tatcgggtggc	tcggtagtca	gcagcactct	474120
ctataccata	agtgatgacc	ggtgcctttg	cactctcaat	acactgagaa	gcgtagggag	474180
agtctgtgtt	gataacaacc	attcccgaag	ggggcacgag	agagaaaagc	ttggctttcg	474240
ccgcaacata	ggtttcaa	gtgccatgaa	aatcgagatg	atctaaggta	atattagtca	474300
gaactgctgt	atcaaaattg	gtataggcta	ctcttccaga	ggcaagtcct	atagaagaga	474360
cttcataaac	aacagcgtct	ctattttgac	gtaccatagt	ggctaaatac	ttctgtaaaa	474420
gagcgggtgt	aggtgtagta	aacctatctt	taatcacccc	ctctcctaag	atatgctcta	474480
tggttcttaa	aagccctgaa	gggttttgat	agctatccaa	taaagcttta	atcaaacatg	474540
taactgtagt	tttcccattg	gttccagtca	ccccaatggg	atggagctta	cttgaagggg	474600
attcgtaata	ctttgcagaa	agctcagcct	ctaattcttc	gagattagga	gtgatgatct	474660
gaacaacgga	aagaaacgga	ttgtatagtg	aagaagcaat	ggcaattgct	ccattagcta	474720
aagcatcgac	agcaaaatca	tttccgtcgt	agcgtgtgcc	cttatgggct	ataaaaaatg	474780
cgccaacact	cacacaacgg	gaatcacgtg	tcaagttgcg	cacttcaaga	gggcgaactt	474840
tcccgtagat	tttagcttga	accccatgga	gtaactcttt	taaatccatt	tacgctccag	474900
ggactattga	aaaacaactt	ttttcataaa	aagccctcta	ggggcatgct	ctcactctga	474960
tttttaaaaa	atgcttaaaa	gatttcttta	ctcgtaggtc	gacaaaaaat	tcaatcaaga	475020
tagtatataa	gcaatcacaa	aaaactgtcc	ataaagttct	tactcttctc	tgaatatata	475080
aatttcgctc	tcctgtttct	acgaacagaa	gcctccttta	tcccaaatct	aaatccccaa	475140
acacacagcc	ttacctcccc	cttcataaaa	cttcaataga	ccgtctcatc	aagactttgg	475200
tctcttattt	aggggaagaa	agctaaaagt	atttctatag	tttaggacct	accctagcca	475260
taacataaac	tactcataga	ggataaagag	gagaacgggc	tctctgatag	agagtctttg	475320
ctcaacggta	aaagtctata	gcaagatgga	aatagagatc	ctcacctcgt	tcccccttgt	475380
ttcggagaac	gattccattc	ttcatagaga	cgctttaatg	cagcagcttc	ttcgtcgcaa	475440

tttcttagct	tcttgtctgg	aagaatccct	aaatagagga	gtgtgcggtc	agcaacccta	475500
gaaaaaatgg	gtgccgcaca	acgccccccc	atataatttt	tcgtgccgtc	ggctcgcaaa	475560
ccatattcag	gatcatctat	ggagacgagc	atcactaaag	gtgggaaatt	tcctctcgag	475620
ctctctacgg	gagtaaaacc	tataaaagaa	gcaatatgac	ggcgtttatc	atattttcca	475680
tgaatcatct	tttctgtagt	tcctgttttc	ccagcactag	agtgatgctt	aggagaggct	475740
cgaaatcccc	aacctccggg	taacgttgta	aaacgcattg	cacgaacaac	ttctctagta	475800
atttcttctg	aaaagagtcg	tgtcttctct	ttagtaggaa	gatgatattc	ctctcctgaa	475860
gcagagacga	tctttttttac	taaagtgggc	cggacggcat	aacctccgtt	tgcaaggata	475920
gcgtaggctt	gaaccatttg	tatccctggt	gccaaaatat	tatatcccat	agccaaagaa	475980
tatggagtag	ataaggacca	ttccagggaa	ccattaatat	ggaaacgatg	gggagaaggc	476040
accaaaccag	aggcctcact	gggaagctcg	atccctgttt	ttcttccaaa	ttccagagct	476100
agcaacttct	gttggtacca	ggccactcct	aaagattgta	tgatgcggtc	agccagctga	476160
gctacataga	cattcgaaga	tttctggata	gccatgtaca	tattcaattg	agagtttcta	476220
gaaatatcct	taagcggaga	tccttttcgt	ccagggaaga	gtgtcctggg	cacatcgata	476280
ggttcttcag	gatcaaaaat	ctttttctgc	gattttaagc	tagcctcttc	gttagcttgt	476340
aaagcaatcg	ccacagtcaa	aggtttcatg	atcgaccggg	gttcaaaaac	ctcgtcaca	476400
aaagatacct	tcgtatgttc	gatgcgctct	ttgttattga	agtattcctt	ataatttgtg	476460
ggatcgaaaa	cggatatttg	agccagtgcg	agaatctctc	ctgtttggga	gttcattaga	476520
atgagcctac	ccccctgggc	tttagcttct	agcacgcccc	gttcgagttc	ttcctctgca	476580
atgggtctgga	tcacaggatt	gatcgtaagg	tagatatcag	agccatcttt	aggcagtttg	476640
ataacacgat	tcgtatctaa	acggttcaaa	ggagaacgca	acagctttct	ctctccaacg	476700
tccccttcca	gaatatgatt	aaagtacgcc	tccatcccgc	ctgtgggaaa	ggcttttctt	476760
gtttttctcat	ccttaatttc	tcttaaggta	tggagaactt	gtccaaggag	cttcccaaaa	476820
ggatacgagc	gttggtagtc	cgtaataaaa	aatagggcgt	ttgttggtaa	gcgatgcttt	476880
gttgcatatc	ctttccacca	aagggatagc	cggctatgga	cagaaacatc	taataaagga	476940
tacagctttac	aataccgaga	tttcttatct	aactttaggg	agaggctcgt	gtaggctctg	477000
ccctcaataa	attggagaat	cccttggtatg	atctcatcac	gatgacattc	gggaatagct	477060
aaaggatctg	cacaaagggtg	aaattttgtg	atatcgacag	cgaaaggctg	ctgaagggtc	477120
ttgtctccct	tacgtactgt	cgtgttagca	aaaaagggtg	cccttcgaaa	aggatcacgg	477180
acacaaaatt	cgtgttgccc	gagagcttct	gcgccccagt	gggtctcctt	acaaatttgc	477240
nttttataat	aacgcaatac	tagaagagca	taaagagcaa	acactcctag	aacaattaga	477300
gtcgaacgtt	tacggtagct	cataggataa	aagactgata	ctttcttctg	agggatattc	477360
caaataattga	tattcgggaa	gagctgctat	ttccatcaaa	tgatcagggtc	tttctatttt	477420
atcaatttaa	aaacgtaaa	aaatattttg	ctgctcaagc	tgacgcaagc	gtacagataa	477480
acaaggaatt	tcgaggcgta	atttcgtcag	cgagttctgc	ttattaatat	agaaataaaa	477540
gagacttcca	caaaagcata	gacagcagca	taaacgtaaa	aaacgacttt	tgttcattgg	477600
gaagcttttt	caaaacaccg	tagttttgct	gatctcgatc	taggatttct	tcgtacttct	477660
tggttaggtag	gttggtatcac	tttctttgtg	attaccttcc	ccaggccaga	agcttccgcc	477720
tctttaaaaa	accacttcac	aggacgatcc	tcagagctac	aaaaagaaat	aatgacaagc	477780
cgtcccttag	gagccagcca	agatatagca	gatgttagta	aacttttcaa	ttgtctatcc	477840
tctccattca	cataaacacg	tagagcttga	aaaatcaagg	tgagtggatg	tatttttcta	477900
tgaaaacgat	agtgagggaa	aacgccaaaga	agagcttctt	ttacatcctg	gatcgaaaga	477960
atttttttat	gcttacgaaa	atggacaaca	gcttttagctg	cagatttcca	ttgtgggtcc	478020
tctccatatt	cacgaaaaat	tctccctagt	tcttcttctt	ttagggagtt	caggacatcg	478080
ctagcggaaa	gctcttgctg	ttgatccata	cgcataatcca	actcttcttt	ttcccttga	478140
aagctaaacc	ctcgggatag	agtatccagc	tgcatagaag	agactcctaa	atctgcaaga	478200
actccgtcat	aaagacgtgg	agtgggttgg	ttcgcaagat	cttcaaaaaga	ggcgtgggaa	478260
aaggagactc	tatcttgaaa	gggtctccaaa	cgtttttctg	caattgccaa	agcctgaaga	478320
tctccttcgg	agccatcata	acaagttaga	gagggatcacg	cctcaagaaa	agcatacgca	478380
tgctctccag	ctcctaagggt	gacatctcga	aaagtctgtg	gaggacgttg	agcaaataaa	478440
gctaaacatt	cttcaactaa	tacgggaata	tgcgcacgtt	cggacataag	aatttcctaa	478500
gctcttggtc	tcaaataagg	acaaagatac	aggattccat	agaaagaaga	aagccttccc	478560
ttatctttaa	ttctcgctag	ttcgccactc	taaatttttt	gataggggtg	agcttttttc	478620
ttaagtgcct	tcgataagga	gaaaagggtc	aggcttctga	tcaagactat	tgactttttc	478680
ctagaccgca	ctatcatcta	gagatagaga	cggtttttta	aggcctcgcc	atggtagaaa	478740
tttttaatta	tagcacgtct	atatatgagc	aacatgcttc	caataatagg	atagtcagcg	478800
actttcgcaa	agaaatccag	atggaaggca	tctccattcg	tgatgttgcc	aagcatgcgc	478860
aaatttttga	tatgaacccc	aagccttcgg	ctttgacgtc	tcttttacag	acaaatcaaa	478920
agtcgcactg	ggcatgtttt	ttccctccaa	ataattttta	caaacagcgt	ttttccacac	478980
cctacctggc	accttcttta	ggatctccag	accaacaaga	tgaagacata	gaaaaaatct	479040
cctcattttt	aaaagtcttc	actcgaggga	agttttccta	tcgcagtcaa	attactccct	479100
ttttgtctta	caaagataaa	gaagaagagg	aagacgaaga	tcctgaagaa	gacgatgacg	479160
atcctagagt	acaacaaggg	aaagtgtctt	taaaagctct	agatcttgga	gtcaagtcta	479220
caaatgtgat	gatagactat	gtgatctctc	gtatctttca	atttgttcaa	ggataatgta	479280

tggttgataa	tgaatggaaa	gcaatcttag	gctggggaga	tgatgagtta	gaagaactca	479340
gaatctcagg	atattctttt	ctacgccaa	ggcattatct	aaaagcgatt	cttttttttg	479400
aagctctagt	gatcttagat	cctttaagta	tctatgatca	tcaaactctt	ggaggtcttt	479460
atctccaaat	tggtgaaaat	agtcaggcgc	ttgctgtttt	agatcaggca	ctccgcgatgc	479520
aaggagatca	tctgcctaca	ctcttaaata	aaacaaaagc	tctcttctgt	ttgggacgaa	479580
ttgaagaagc	tactgccatt	gccacctacc	tttcatcctg	tcccatacca	gcaattgcta	479640
atgatgctga	agctctattg	atgagttata	gtaaagcaac	caaaaaaaat	gctgcgttag	479700
ttcgtttaatt	ttttctccta	tagaaaacgt	atttcgtgat	tgaagaactc	cggatttctt	479760
tagttctttt	tccattttta	ttacaaaatt	tcataattat	tttttcttga	atttgtgggt	479820
ccttattgcc	taacgaaacc	aacgatccaa	tttgcccttaa	aacctagtaa	tcggtagagt	479880
tattttatcg	gcagagcgta	ccgcgtttac	ctgcggagga	aggggtgtata	ggatccattc	479940
ctaacaggaa	cttcacccag	ggaatgcagg	atccaatctg	aacgcgaaga	gtcattgcac	480000
tcagtgcatt	gaatagtcaa	gatgcaatga	gatttttctg	ccatcactca	tgggatgggt	480060
cgattgtatt	tggaagagct	ttataaataa	agagagcggc	atgttaacct	gtaacgagtg	480120
cactacttgg	gaacagtttt	taaattatgt	taagacacgt	tgctcgaaaa	cggcttttga	480180
aaattggatt	tctcctattc	aagttcttga	agaaaactca	gagaaaattc	gcttagaagt	480240
ccccaaattt	tttgtacaaa	attatcttct	tgataactac	aaaagagacc	tctgttcttt	480300
tgccccctta	gattgttcatt	gagagcctgc	tttagaattt	gtagttgcag	aacacaagaa	480360
accttcagcc	cccggtggctt	ctcaaaaaaga	atcaaacgaa	ggaatttctg	aggtctttga	480420
agaaactaaa	gattttgaa	ttaaagctgaa	tctctcctat	cgctttgata	atttcattga	480480
aggtccctca	aatcaatttg	tgaagtctgc	agctgttaggt	attgctggga	aacctggccg	480540
ctcctacaac	cctttattca	tccatggggg	tgtggggatta	ggcaaaacgc	atttacttca	480600
tgccgtaggt	cactacgtaa	gagaacatca	taaaaatcta	cgcatccatt	gcatcactac	480660
agaagcgttt	atcaacgatc	ttgtctacca	tctcaaatcc	aagtctgttg	ataaaatgaa	480720
aaatttttat	cggtccctag	atttacttct	tgttgatgat	attcaatttt	tacagaatcg	480780
ccaaaatttt	gaagaagagt	tttgcaatac	ccttgagact	ttgatcaacc	tgagtaagca	480840
aattgtaatt	accagtgata	aacctccaag	tcagctcaaa	ctttccgagc	gtatcattgc	480900
tagaatggaa	tggggactgg	ttgtctacgt	cggcatccct	gatttagaaa	ctcgggttgc	480960
gattttacag	cacaaggcgg	agcaaaaagg	attgtctcatt	cctaatagaa	tggcatttta	481020
tattgcggt	cacatctatg	gcaatgtccg	tcaattggaa	ggagctatca	acaagctgac	481080
tgccatttgt	cgctcttttcg	gcaagtctct	tacagaaact	acagtcagag	aaactctaaa	481140
agagctcttc	cggttctcaa	caaaaacaaa	aatttctgta	gaaacgatct	taaaaagtgt	481200
tgctacagta	ttccaagtta	agctgaatga	tcttaaggga	aactcacgct	ctaaagatct	481260
tggtgttagct	cggcaaatgt	ctatgtattt	agcaaaaact	cttattacag	attcttttagt	481320
tgcaatagga	gctgcttttg	gtaaaactca	ttcgacagta	ctttatgcct	gtaaaaactat	481380
agaacataaa	ttacaaaatg	acgaaactct	taagcgtcaa	gtaaatctct	gtaaaaatca	481440
tattgttgg	taatttaggg	ggtgtcccat	gttccgtaga	acaggaaaag	gtccttttga	481500
agatgtgcaa	acactttacg	aagaagaaac	ttcttcacct	tccagctact	cgccatattc	481560
aagatccgag	cgcccagaga	cccttccaag	tctttttgac	aacctaaag	cttcggaagc	481620
tcgccccttg	aatcacatt	taactgaaga	attctctctt	cctcaatggt	cctcaactcc	481680
aagaacagaa	tctctactcc	ctcttgaaaga	acctgaaact	accttaggag	aaggcgtcac	481740
ctttaaagga	gaacttgctt	ttgaacgtct	cctacgtatt	gacggaactt	ttgaaggcat	481800
tttagtctca	aaaggaaaaa	ttattatcgg	tcctaaagga	gtggtaaagg	cagatattca	481860
gctacaagaa	gccattattg	aaggggttgt	agaaggaaat	atcacagtat	ctggaaaagt	481920
cgaactccgt	ggaggcgcaa	tcattaaagg	agacatccaa	gcgaacacgt	tgtgtgttga	481980
tgagggcgta	cgtattcttg	gttaccttgc	aattgcagga	attactgatc	attctgagag	482040
agaaagagac	ttatagatac	tagagggtgat	gcactccctc	caacgatagt	ttgcatccat	482100
ttttgtgata	aaggataggc	cgacaaaaag	cagataacct	ccccttttagg	aagtttttct	482160
atttgtcttt	tcttaggaag	ccacggccac	aagggaatgc	gtaaaagctt	ttctagttta	482220
gcaacttcta	ctacgatttt	cctagaaaatt	gtcgatgtta	tataggcaat	acaactcggg	482280
gtctcatcca	gtgaagctag	ctcaaaggcg	atactcttag	aaaaaaactg	cagagcgggt	482340
cgcttacctt	cacaagcacg	agcatatacc	gagagggccg	tttgcgaaag	aagggtacaag	482400
ctgaaagctt	gaagttgtga	agaggggtgaa	cactggctac	atagacgtgt	ttcggaagaa	482460
ccaagataac	gaaaaacaatg	tagacaacgc	ccttctctat	cttctacgag	aagtttttcc	482520
aagcagttgg	aacaaaagta	ggctcctgga	gcttgacagc	cataacataa	ctttggaaac	482580
agcaacgaaa	aaagttaccat	ctatttttga	atcatgaaaa	tttttattcc	taaaaattta	482640
agcagtttgc	tacgtttttg	aacgtgtaga	agcttcaact	tttctctcaa	tcacaatgct	482700
caaaaaattc	ataaattctc	tttggaact	atgtcaacaa	gacaagtatc	agcgttttac	482760
tccattgtgc	gatgcgatag	atacattttg	ttacgaacct	attgaaaccc	cttccaagcc	482820
tcctttcatc	cgcgattctg	tagatgttaa	gcgttggatg	atgcttgttg	ttatcgcttt	482880
gtttcccgcg	acctttgttg	cgatctggaa	ttcaggactt	caatctatcg	tttatagctc	482940
aggcaatcct	gtgctgatgg	agcaattctt	acatatttct	ggatttggtg	gttattttatc	483000
ctttgtttac	aaagagatcc	atatagttcc	tatcctttgg	gaaggactta	agatctttat	483060
tcctctactt	acgattagct	atgttgtcgg	gggtacttgt	gaggtcctat	ttgctgtagt	483120

tctgtgggcat	aaaatcgcag	aaggactgct	agtaaccgga	atcctctatc	cccttactct	483180
ccctccgaca	attccttact	ggatggcagc	cttagggatc	gcctttggta	ttgttgctcag	483240
taaagagctc	ttcggaggca	cagggatgaa	catcctcaat	cctgtcttat	caggaagggc	483300
attccttattt	tttacgtttc	cagcaaagat	gagtgggtgac	gtttgggtag	gaagcaaccc	483360
cggagtgatt	aaagatagcc	tcatgaagat	gaactcctcg	acaggaaaag	tactcattga	483420
tggatttttca	cagtctacct	gcctacaaac	tctaaattcg	acacctccct	ctgtaaagcg	483480
tctgcatgtc	gatgcgattg	ctgcaaatat	gcttcacatt	cctcacgtcc	ctactcaaga	483540
tgtcattcac	tcacaatttt	ctctttggac	agagacgcac	cctggttggg	ttttagataa	483600
tctcactctt	acacaacttc	aaacgtttgt	tacagctcct	gttgctgagg	gaggattggg	483660
gctgcttccc	acacagttcg	attctgccta	tgtattacc	gatgtgatct	atgggattgg	483720
gaagtcttca	gctgggaatc	tcttttgggg	aaacattata	ggttctctgg	gggagacctc	483780
cactttcgcc	tgtctgttgg	gtgcaatatt	ccttattgtt	acaggcattg	cctcttggag	483840
aaccatggca	gcctttggga	taggagcctt	tctcacaggc	tggctcttta	agtttatcag	483900
cgtactcatc	gtgggacaaa	acggagcttg	ggcacctgct	cgattcttca	ttcccgccta	483960
tcggcagctt	ttcctcggag	gacttgcttt	tggtttagtc	tttatggcta	cggatcccg	484020
atcatcgccg	actatgaaat	tagggaaatg	gattttacgga	ttctttatag	gatttatgac	484080
tattgtgatt	cgtcttatca	atcctgcgta	tcttgaggga	gtgatgttag	cgatccttct	484140
gggcaatgta	tttgcccttc	ttatcgacta	ttttgctgtt	agaaagtata	gaaaaagggg	484200
agtctagaat	atgtctaaag	gctcttcaaa	acataccgtc	cgcataaacc	aaacctggta	484260
catcgtttcc	tttatcctgg	gcctcagctt	at ttgcaggga	gtgctgttat	ccacaatcta	484320
ctatgtgctc	tccccaatac	aggaacaagc	tgtacttttc	gatcgcaata	agcaaatgct	484380
tttagctgct	catatttttag	at ttttaaagg	aagatttcaa	attcaggaaa	aaaaagagt	484440
ggtgcctgcg	actttcgata	aaaaaacaca	acttcttgaa	gttgctacaa	aaaaagcttc	484500
tgaggttttc	tatcctgaat	tagagctgta	tgcgagcgc	tttgtccgtc	ctctacttac	484560
agatgcccaa	ggcaaggat	tttcttttga	agaaaaaaat	ctgaatccca	ttgaattttt	484620
tgagaaatat	caagaaagcc	ctccgtgtca	gcaatccccc	ctcccccttt	atgtcatttt	484680
agagaatacc	tctcgcacag	aaaatatgtc	aggagccgac	gttgcgaaag	acctttctac	484740
agttcaagct	ttgatcttcc	ctatatcagg	attcggcctt	tggggcccca	tccatggcta	484800
tctaggagt	aaaaacgacg	gtgacactgt	attgggaacc	gcattggtacc	aacaaggaga	484860
aactccaggt	ttaggagcaa	atattacaaa	tcccgaatgg	caagagcaat	tctatgggaa	484920
gaaaatcttc	ctacaagatt	cttctggaac	tacaaatttt	gcaacaacag	acctagggct	484980
tagggtagtt	aaaggttccg	tgcgtactac	tttgggagat	tctccaaaag	ctctttctgc	485040
tattgatggg	atttctggag	ccaccttaac	atgcaacggt	gtcactgaag	cttatgtaca	485100
atctctggct	tgtatcgctc	agctccttat	aaatttttct	aat ttaaccc	atgaaaagaa	485160
aacaggcgaa	tgacaagtaa	aaagtcctat	aaaagctatt	tctttgatcc	tctatggagc	485220
aacaacccaa	ttctcattgc	gattttgggg	at ttgctcgg	ctctggcagt	gacaacaaca	485280
gtacaaacgg	caattactat	gggaattgct	gtcagcattg	ttacaggatg	ctcgtctttc	485340
tttgtttcc	tattacgtaa	gttcaactcct	gacagtgtga	gaatgattac	tcagctaatt	485400
atcattagct	tgtttgtgat	tgttatcgac	cagtttttaa	aagctttttt	ctttgatatt	485460
tccaaaacac	at tttctgtt	tgtgggtctt	atcatcacca	attgcatnnt	gatgggaagg	485520
tctgaaagtc	tagctaggca	tgtgactcct	attccagcgt	tcttagatgg	gtttgcctct	485580
ggcttaggat	acggctgggt	cttacttgct	attggagtca	tcagagaact	ctttgggttt	485640
ggaactcctt	atgggggttt	gcatcatccc	tcaatttggt	atgcttccga	aaccaccccc	485700
gatggatacc	aaaatttaag	tcttatgggt	ctagcacctg	cggctttttt	cctacttggt	485760
attatgattt	ggcttggttaa	cattcgagac	tctaaagaga	aaaangtagt	ttatgtgggt	485820
aggtgcgtat	acttggtcta	atgtctttgg	tattcttcta	caagcagcct	ttattcagaa	485880
tatecttctt	gcgaatttct	tggggatgtg	tagttacett	gcttgctcta	ctagggtttc	485940
tacagccaat	ggcttgggga	tgtccgtagc	ccttggtctc	actgtaacag	ggagcatcaa	486000
ctgggttggc	catgctttca	tcacgggccc	ttaaagctcta	acttggtatc	ctccatcttt	486060
agcttctgta	aacctaggtt	ttctggagct	gattattttc	atcgtgggtga	ttgcggcatt	486120
cacgcaaata	ttagagcttc	ttttagaaaa	ggtctccagg	aatctatatc	tctccttagg	486180
gatcttccct	cccttgattg	ctgtgaactg	cgcgatcccta	gggggtgtgc	tcttcggaat	486240
cacacgtagt	tatcctttta	ttcctatgat	gatcttctct	ttaggagcgg	gatgtgggtg	486300
gtggctcgct	attgttattt	tagccactat	caaagaaaaa	ctcgcctact	ctgatattcc	486360
caaaaacctc	cagggaatgg	ggatctcctt	cattacaaca	ggcctcattg	ctatggcttt	486420
tatgagctta	acaggtattg	atatttctaa	accttcagca	aagattcaaa	gagctcctct	486480
agagactgaa	gttggtgaaa	acacgaccaa	tccactaaaa	gaatcttcgt	ccaaacacca	486540
gccaagtatt	tctaaagcac	gaacgcagcg	tcgctctctc	taggaacttt	cctagagtcg	486600
agtttctagt	gaacttttgt	acacagagat	gcttctaaac	aatttcaatt	cgagatatgg	486660
aaggcggctt	tttgcaagct	gtggcgattt	tacttgcgat	acaataaaca	acgatcgctc	486720
gtaaaaacaca	aatagcaaga	gctataccta	tatatagagc	gcagagtctc	agttgagaac	486780
cttcacaaga	aaacaaagtc	acggcgaaag	ctacagctaa	cgaagtgagg	agaatatgcaa	486840
gcactttcgc	aaaaatccga	taagataaag	aattctccga	atggagaagg	acactagaat	486900
accgttttag	gaaggtcaga	gtatcgggat	tttgtcgaga	acgggggaacg	tacttaggta	486960



atgtagtcat	gatttttcaa	tcaataaaaat	gtccaactca	gcttttcatgc	gctaccttag	487020
ttttttctaa	ggcattggaa	atctttataac	gccaaacacgc	acaaaactaac	atagataagg	487080
taatgcaact	cgcagcaatc	cagatcgaga	gctgtagagg	tgccgatccc	gttaaaaaata	487140
ggccacaggc	taccaaagaa	atcgctatca	atgaaaggac	catgatggct	atagtaagct	487200
tcttcacacg	agataccccc	gaagataatg	cggacaattc	ttcagaagat	agttgcacat	487260
gatctttag	gacatgaggg	gctaccggac	tagctggatc	catagaataa	ttctgatgta	487320
tttttttaaac	cttagacata	aatttttaaat	gttttttagcct	taaaaaaata	cctcttatct	487380
tctgaaaaaa	atgagtatat	ctaataaaaa	atttactctt	catccatcaa	agaaagatta	487440
gaaggatccc	agtcctgggc	tagtcggact	acagccaacc	atccctcacc	ttctggagct	487500
tcgttaaatct	tctgaggatt	atccactaaa	tcaaggctga	tatcgataac	ctctcctgat	487560
acaggactta	acacctctta	tagcagattt	agaagattcc	agaatgacta	aaacctcacc	487620
ttctttacat	agactcccta	ctgaaggtaa	atccacatgg	agaatggctc	ctaaattttt	487680
ctgcattttt	tctgttaacc	cgaggcgac	caccctctca	tggaacgggca	aaatccaaac	487740
atgataatca	gaataccaca	tcaccttacg	acccctgtt	ctataaagcg	ttccatatag	487800
gacctaataa	gttcttcatc	tagctgactt	ttagctaaaa	atagtttatc	cagcttagca	487860
ggacgatcat	acagtaaagt	agagaggcat	tgataataac	agggcccttc	gttaggactc	487920
atgaatacag	aagaatagtc	tcctaccttc	atagagaaaa	tcctatcaaa	ctcttggggc	487980
agctccttgt	ctcctcgga	aaaagtcttc	aatgagcgat	ctaagctcca	agagaaagac	488040
ccctcgagat	gccttcccaa	tctgtggttt	tccactacct	tccaaagacg	tcgttgccat	488100
aggctagcgc	cttcttctcc	tgataaccgt	gtacgcaacg	cagattctag	acgctccatg	488160
tcaacaagat	gaccatgaga	agtaagtaac	tgtgaggcca	aatctctctt	taaaacctca	488220
cgataaggaa	gcacttcttc	tttttcaaaa	gaactattaa	caataatagt	ataataggtc	488280
tctgcatect	ggctatataa	atctaaaacc	tcgttttcaa	gcaacacttt	ggctaattgc	488340
tgaccgtcgg	atattcctgg	tagagcacta	ttcttcctgt	cgataaagag	aacttcttgg	488400
ctctgtcttag	gaacttgctg	tagcgattgc	agaattctct	cagggcgggc	ccttaagatt	488460
tccttgctgtg	tgaaaagaga	aatttttatct	cgcagcgcag	gcttaagatg	ttggaagtct	488520
ttatacgact	gacacgtctc	aacgtcagga	aactgctgga	gaatctctctg	gaagtgtca	488580
gaattttgtt	gccagtgcag	cacttcaacc	ataggtacag	tagctgctaa	gtcttgcaaa	488640
gcgactctct	tatagtctat	agaaaaccgt	ctgcctacta	accgaggctc	tttagctttt	488700
atggctcgcta	taggaaggat	ctcattagga	acatccaaac	tatccgattt	aggtaaactc	488760
actaacttta	aatagacttc	gaaagctttt	aactcttgtt	ttgtttttaa	gctatactcc	488820
ttagggagtc	taaagaactc	tacttgatg	gaactttttc	cttgaacgaa	aaatgtagt	488880
agaggttgga	agtcaaaaga	aacgcctccc	tgcaatagga	gaagagctct	tttgacacac	488940
aatatgtctc	gtacatatct	gaaaaattcg	gactcagaga	tctctaaaaa	ctgaaaatac	489000
gagtttacaa	attcttcaaa	tcctaaggaa	aattccttat	tcttactgat	cttagtatag	489060
gcatnttcgc	cttatcataa	aagtcgtcac	gagctttctt	gttttgaggg	cctgggaagt	489120
acttttttct	gctcgtcaat	aaagcggatc	aagagctcaa	cagcagcaga	aaggtaggca	489180
tcocccaaacc	agtcttgaat	cgtctggtag	ccaaataacc	gcaagtcttt	cccgcgagat	489240
aaggcttcat	ctgggggaag	agcaaacatt	tgctgcggta	ctccaacatt	tgctgaagca	489300
cataatgagg	gaaccttctc	tcttctaaaa	agagcttggc	tctagcaaga	aatccttctt	489360
ttgatattgg	gttctcgatt	tgttgaaaaga	ccttcaggat	ctctaaaagc	tggggagctg	489420
aagattttcca	aacttcttca	gaggaaataa	aaggagcgtc	aaaacgacga	tacggctggt	489480
aagctttctc	cttactaaaa	attttctctc	ccggatggta	cactttttaa	aagagttttt	489540
ctcccaccct	tgctgtaga	aaataatcag	taagtagccc	ctcattgata	aaattccaag	489600
ctctaggggt	ccctgtaaat	ggatacgctt	cgtgagcaaa	gaacttcttc	atagccatga	489660
aatctttctc	tacataccgc	ttccctgaag	cggtagtaaa	aacagtccga	cgtgagggtg	489720
actctgcaga	accttttcta	gagaatcgct	cccaaccac	tccaatacca	gaaacacaaa	489780
ctcacgcaat	gacaatgccg	ataaattttt	tttgatgctt	atagaagaac	gataacaagg	489840
tccaccctct	acccaaacaa	taaaagcgta	gtgtaaacga	tagcagagaa	aaaaaccagg	489900
caggatccct	gcagagcctg	cagaagagat	cctgttggta	gattcgacac	cagggacgct	489960
aggctggcat	ataggtcagc	tgcaaagtgc	ccaaagtgtg	gtgtacggaa	tggaataacc	490020
aagagaaaaat	gtcgccatga	cttacaggaa	tcgacaatcc	gatatcttta	ttgaagactt	490080
tgtagctttt	tgacgcgact	tctggagatt	cgataactac	aatactttcg	taatcaaagg	490140
catcactttt	ctttccaaaa	ttataacttc	cgatcacaaa	aatttcatca	tcgataatca	490200
tacacttctt	gtgcaactgc	gtttcccaaa	tagcaaaactc	ataaatagaa	acccgctcat	490260
aagggttttag	cttttcgcaa	aacctttttt	tccaaagagg	ataccgtttc	ccatagagca	490320
aggcgaaaata	gttaatacgg	ttcccccaag	cataggggtcc	tgtaattgca	ggacttaatt	490380
catgacagcc	gttcgtaatt	aaactcagat	gaacaccgtg	attatgagaa	acgtcgacaa	490440
gagcatttaa	aagctcgtcc	ttagggatga	aatacatgtg	agcaagcttc	acagaagatc	490500
tagctccctg	gataagtttc	aaatattctt	gagtcacagga	ttgggttgct	tatcgtgggg	490560
accacctaata	actatcctga	tcttggaaga	gtcgacaaga	acaagatctt	catgtttgtc	490620
aaatccagga	aatactgtct	cctcggcttg	ttctaaagtc	agtggaggac	aggcgccctgc	490680
aaactgttca	ggattatcaa	tgaaccacat	atgatgtgca	tagtagtccc	acatagcaaa	490740
ttgcttatga	tattcttctc	tgagctgcaa	accgaatgct	gtagaacgca	acatgatatc	490800



ctgatcacga	aatgctaggg	gccgacgcac	tccactgaca	aataaacgtg	ggttatccac	490860
tttctcagga	acctcatccc	ctggagtgc	cataaactct	tcaaaattgg	taccacctaa	490920
aatacaatat	ttcccatcga	tgatagaaag	tttgatatgc	atttcaatga	cattaggagc	490980
gaggatgctt	gttgaggggtg	ggcaccctgt	aaaaacgtag	aaaaaccggt	tgggatgacg	491040
ttctttgaga	gctttgagta	attttttggtc	ttcagcatcg	gtaaacgtgg	gttgataat	491100
gatattagct	acagagctct	ggaaccagat	ccatacagagc	ctcgaggtga	tcttaccatc	491160
tctttaagcg	ttcggcctcc	tgatcatgcag	ggacacagtt	ctacataaaa	atttgcattga	491220
tctatgcaat	ccaatatctg	ttgaaaggcc	tctacactat	tgtcataaac	aagaactcca	491280
accttctcct	tgtctgaagc	tacgattgtc	tttgctgaaa	cagaattagg	aaccagcaaa	491340
ataaaaaata	ttccaagagc	tgccaagcga	aaacgcaacc	gactcatcat	aaccctccac	491400
cacaaaacaa	tttaataaac	gcctctttga	cttgctgacg	cgctcctgc	agcacttcat	491460
cagcagcttc	caaacctaaa	gggaaaaacg	cgtgaatctg	gatttgttca	ataatttctt	491520
caagaacctc	gggtttttaa	aatctctggt	aaaactcaga	agaacttccc	gataagaata	491580
aggatccttg	atgtaaaaaat	ccctgttgca	ccttgcggtg	ggcagcgccc	cctgcttctt	491640
gtccccaann	aagaacgtca	tacttcgaag	ttttggccat	acaaaaattt	cctgaatctc	491700
tggaagaaga	gttttcgtct	tctggagcta	acattccctg	gatccgaaat	actttctcta	491760
gaaccttcgc	tacaaaagag	tttacagtat	ggtagttctc	aagtaccgaa	gaagaatagg	491820
aaggatgtgt	cgcagacata	agaacagaaa	aagcataatc	tcccttatgg	aagacaaatc	491880
ccccctccgt	aggccgcact	gcggcgctcca	atcctagatc	cgcatagttg	gaaagtaaaa	491940
atttttctgg	acgcataaaag	tgaccgtacg	tcagagaaca	aggattctcc	cactcataaa	492000
ggtgtaaaat	gagctcccca	tcttgacagag	attctaataa	atctctgtcc	ttagccatgt	492060
gggaggccgc	tgaagatttt	cctgaatcta	cgatacgaac	tttcataata	caaacataaa	492120
actaattaag	actgtttcaa	aagaagctga	actattgtat	catatacaaa	aggtttgtgc	492180
ataactttcc	cttaaaactca	gaggaatttt	accaaatttg	ctggtttaga	gcgaagagtt	492240
gcatcattat	tttaaatttc	gtatatgctt	aaggaaagtt	ctacccctgt	cttttagggt	492300
tttatgtttg	agaagttcac	taatagagca	aaacaagtca	ttaaactggc	gaaaaaggag	492360
gctcagcggt	taaatcataa	ctacctgggt	actgagcaca	tcctgcttgg	tcttctcaaa	492420
cttggtcaag	gggtagctgt	taatgtatta	cgcaacctcg	gtatagattt	tgatacggca	492480
cggcaagagg	tggaacgcct	gattgggtat	ggtccagaaa	ttcaagtcta	cggagatgct	492540
gcccttacag	gaagagtaaa	aaaatctttt	gaatcagcaa	atgaagaggc	cagcctttta	492600
gagcacaatt	atgtcgggac	ggagcattta	ctcttaggga	tcctacatca	atcagatagt	492660
gtcgctcttc	aggtattaga	aaacttacat	atcgatccaa	gagaggttcg	taaggaaatt	492720
cttaagaagt	tagagacctt	caatctacaa	cttctctcct	cgctcgctgc	ttcttctca	492780
tcctctcgaa	gcaacccttc	atcttcaaaa	tctcttttag	gtcaaagctt	aggttctgac	492840
aaaaacgaaa	agctttctgc	tctgaaagca	tatgggtatg	atttaacgga	gatgggtccga	492900
gagtctaagc	tcgatcctgt	cattgggtcg	tcttcagaag	tcgaacgggt	gattttgatt	492960
ctttgccgaa	gaagaaaaaa	caatcctgta	cttattggag	aagctggagt	tggttaagact	493020
gcaattgttg	agggctctggc	tcaaaaaaat	attctgaatg	aggttcctga	tgcttacgg	493080
aaaaagcgac	aggtattact	agatctagca	ttaatgattg	ctggaacaaa	atatcgaggg	493140
caatttgagg	aacggatcaa	agctgtcatg	gatgaagttc	gcaagcatgg	aaacatcttg	493200
ctcttcattg	acgagctcca	cacgattgta	ggagcaggag	cagctgaagg	tgctatcgat	493260
gcttcaaaaca	ttttaaaacc	tgcgtttagcg	cgaggtgaaa	ttcagtgtat	tgaggaact	493320
acgatagatg	agtatcgcaa	gcacatagaa	aaagacgcag	ctttagaacg	tcgtttccaa	493380
aaaatcgtgg	ttcaccctcc	tagtgtagat	gagactattg	agattttacg	tggcctcaag	493440
aaaaagtatg	aagaacatca	caatgtcttc	attactgaag	aagctttaaa	agcagctgcg	493500
actctttctg	atcaatatgt	tcattggcag	ttctctcctg	ataaagcaat	agatctttta	493560
gatgaagctg	gggctcggtg	ccgtgtgaat	acaatgggtc	agcctacaga	tttaatgaag	493620
ctagaggctg	aaatcgaaaa	tacaaaattg	gccaaaagagc	aggccattgg	aactcaagaa	493680
tacgaaaaag	ctgcagggtt	acgtgatgaa	gagaaaaaac	ttcgcgaaacg	tctgcaaagt	493740
atgaaacagg	aatgggaaaa	tcataaagaa	gagcaccaag	ttcctgtaga	tgaagaagca	493800
gtcgctcagg	tagtttctct	acaaacagga	attccctcag	caaggctcac	agaagctgaa	493860
agtgagaagc	ttctgaagtt	agaagacacg	ttaagaagaa	aagtcattgg	tcaaaatgat	493920
gccgttacca	gcatttgccg	tgccatccga	cgttctcgaa	cagggatcaa	agatcctaac	493980
cgacctacgg	gctccttctt	attccttggtg	cctaccggtg	tagggaaaaag	cctgctcgcc	494040
caacaaattg	ctatagagat	gttcggtggt	gaagacgctc	tgattcaggt	agacatgtca	494100
gagtagatgg	agaaatttgc	tgctaccaag	atgatgggat	cacctccagg	atatgtaggt	494160
catgaagaag	ggggccacct	tacggaacag	gtacgtcgcc	gtccttactg	cgttgttctc	494220
tttgatgaga	tagaaaaggc	acaccagac	attatggacc	tgatgttgca	aatttttagag	494280
caaggacgtc	ttactgattc	ttttggtcgc	aaagtggatt	tcggtcatgc	cattattatc	494340
atgacctcca	atttggggagc	tgatctcatt	cgtaaaagcg	gagaaattgg	ttttggcttg	494400
aagtcccata	tggaactataa	ggtcatccaa	gagaaaaatcg	aacatgctat	gaagaaacac	494460
ttaaagcctg	agttcattaa	ccgtttggat	gaaagctgtga	ttttccgtcc	cctcgagaaa	494520
gaatctctat	cggagatcat	ccatttagag	atcaacaaac	tggaactcgag	actgaaaaac	494580
taccaaatgg	ctttgaacat	cccagactct	gtgatttctc	tcctagtaac	gaaggggcat	494640

tctccagaaa	tgggagcacg	tcctctacgc	cgtgtcattg	agcagtacct	tgaagatcct	494700
ctagcggagc	tcttgcttaa	agagtcctgc	cgtcaagaag	ctcgcaagct	acgagcaacc	494760
ttgggtgaaa	atcgcggttg	ctttgaaagg	gaagaagagg	agcaggaagc	tgctctccct	494820
agccctcact	tggaaatcata	ggaacgtcga	taactccact	accaaggcag	gtatctccct	494880
gataaaacgc	tattgtttgt	cctggagtta	ccgccttgac	gggttggtgaa	aatcgcacct	494940
tgacctcgtc	acctgagcta	taatctatcg	tgcaagcttc	atcaggagaa	cggtagcgga	495000
ctttagcgct	acagtgcacat	ccggatttag	gaggggtaaa	ccaattgagc	tctctagctg	495060
ttaattcccg	taggtagagc	tggggatggt	cttccccct	cacaatataa	atgctatttt	495120
cctctatat	ttttcccaca	acataacnng	gtttctcgga	tcctccaaga	tcaagtcctc	495180
gccgctgccc	tatagtataa	tagtgacttc	cctgatgttg	ccctacaatt	tccttggtat	495240
cccaatcgat	aacgttgccct	gttttatttg	gaagaaactt	ctctaggaac	tctttaaaag	495300
ggcgcttccc	tataaagcaa	atgcctgtac	tatctttttt	ttctgctgtg	ggaagagctg	495360
cttgagctgc	aatcgcacga	acttcagctc	tattcatttc	cccaagagga	aagagcacat	495420
tgtgaagagc	acttttagga	gttcctgata	aaaaatagct	ctgatctttt	tgaggatcgc	495480
aacctctaag	gagttgggtt	tcttgagctc	cggatatttaa	tcggcagtag	tgccctgtag	495540
cgaggtaatc	tccgccaaagt	tcctggactt	ctttttgtag	aaggctcaaat	ttgatttctc	495600
gggtacaaa	aatgtcgggg	ttaggagtgt	agcctaaaga	gtattccttg	aggaaacgag	495660
cgaacactct	ttctctatat	tctttagcaa	aagatacggg	gtaataaggg	atatacgagct	495720
gaagacatac	cctctcgaca	tcttcataat	ctttagtaga	cgagcaaagg	ccgccttcgc	495780
tatectcttc	ccaattcttc	atgaagaggc	caataacctt	ataattggta	aattttttga	495840
ataaataggc	aacgacagaa	gaatccacgc	ctcctgacat	tgctacaatt	acagtttggt	495900
gcataatttc	tcttacttgt	ctcctcatag	gaagggttaag	gttttaaaaa	tttgaataac	495960
taagaggcat	gactcgctta	ctaattgact	aaaaatacca	tttttcttaa	attattttct	496020
caaataatag	agttctcttt	gtgtctagta	ctttaaacgg	ggattttccc	tcattccctt	496080
cgggaagagc	tgctgattta	ttcattacga	ataaggagat	cgtagctttg	ggggagaaag	496140
gcaatgtttt	tctcaccac	tccattccta	tgcatattgc	tgcgattacg	atcttagtga	496200
ttgtagctct	tgctggaatc	gctattatct	gtttgggttg	ctatagccaa	agcattctgt	496260
tgattgccgt	tggcattggt	cttactatct	tgactcttct	ctgcctacaa	gccttggtag	496320
gatttattaa	attcatcccg	cagctccctc	agcagctcca	tacgacagta	caatttatca	496380
gggagaagat	tcgacctgaa	tcctctctac	agcttgtaac	caatgcacag	agaaaaacca	496440
ctcaagatac	gctaaagtta	tacgaagaac	tctgcgacct	ctcacaaaaa	gagttcaaac	496500
tgcaatcaac	tctttatcaa	aaacgttttg	agctttctca	caagaatgaa	aagacaaatc	496560
aaaactagtt	agcaacgatt	cgaggaaaca	acatggcaac	ttccgtagcc	ccatcaccag	496620
tccccgagag	agccctctc	tctcatgcta	cagaagttct	caatcttcct	aatgcttata	496680
ttacgcagcc	tcattccgatt	ccagcggctc	cttgggagac	ctttcgctcc	aaactttcca	496740
caaagcatac	gctctgtttt	gccttaacac	tactgttaac	cttaggggga	acgatctcag	496800
caggttacgc	aggatatact	ggaaactgga	tcattctgtg	catcggtctg	ggaattatcg	496860
tactcacact	gattcttget	cttcttctag	caatccctct	taaaaataag	cagacaggaa	496920
caaaactgat	tgatgagata	tctcaagaca	tttctctct	aggatcagga	tttgctcaga	496980
gatacgggtt	gatgttctct	acaattaaaa	gcgtgcactt	tccagagctg	acaacacaaa	497040
atcaagaaaa	aacaagaatt	ttaaataaaa	ttgaagcgaa	aaaggaatcg	atccaaaatc	497100
ttgagcttaa	aattactgag	tgccaaaaca	agtttagcaca	gaaacagccg	aaacggaaat	497160
catctcagaa	atcattttatg	cgtagtatta	agcacctctc	caagaaccct	gtaattttgt	497220
tcgattgctg	attagaaaaa	ttctagtctc	ttcatcccc	taaatctagg	gaaatcttct	497280
tgaaagtccc	tcctgagtag	gaaaattatt	agatagtaat	ttaaaaatta	cgtatattcc	497340
atttcaatct	ctagtaacgt	tggagaatct	tacagaacat	gttcaaactg	ctcttccaca	497400
tcgctgcatt	tgcgggacac	gtactctcga	ctcctatttt	tattgttcaa	gatgcttggt	497460
gaattgatga	agaagcatgt	aaaaatcctc	ctccacgtcc	tttctctgct	caggtacaat	497520
acctaaggtt	gaacgatgct	aaatttaaaa	agctgcctca	tcaaactata	ggctatcgct	497580
aatacgatgg	aacgtttctc	tgcacacttc	cgattacaga	gcattctggg	ctactgtttt	497640
ctactggcta	tataggtgct	gatattcaat	ggaaaagctc	acttccctatt	tcggagacag	497700
atcctaattg	acttgggttg	gcgactttcc	aagatacttc	tttttataac	tatgttctcc	497760
tctcttttag	agcttatata	ctctccntta	aaaaattggc	agtgggtctat	cattctttct	497820
gggcttgtgg	atcctaaaaa	tattgagatg	ggttatggac	tctatcaagg	agttctttct	497880
ggaaaatacc	aggccactga	gaagctttct	gctatttttg	gcgtcattaa	tgaaacaggc	497940
ctccatcaag	agaaggcttg	gccttttagta	ggtgttagtt	acaaggctac	cgaccaacta	498000
actctcaatt	gcacttatcc	tgtgaatttt	tctattgatt	accgctcgac	atctgtctgt	498060
aacttagggc	ttgcttaccg	ccttacaaga	ttccgaaaaa	aactttacaa	aaatcaccta	498120
atctcttctc	gcggcatctt	tgaatatcaa	ggacgtgaaa	tcgaagctaa	cgtgaagctc	498180
accccttggc	cgggaagttt	tattaaggga	ttttacgggt	gggtctattgg	gaatgatatc	498240
tcgatagctg	atgatcacaa	caataataaa	acgtcccata	ctttttaaac	ctccgcattt	498300
ttcgggtggt	ccgctgtaat	gaacttctaa	tttccagttt	ccagaaagat	ttttttacag	498360
gcccatacaa	aaacttcagg	agattttgtc	tacttgtgtc	tctcattttc	ctgccttttc	498420
aggaatttgc	attgtctaaa	aaccactatc	ctcttagaat	ttttacataa	tttttcataa	498480

aatattctct	ttcaaacgga	tatgggattc	aaaaatatct	gcaaacaagg	ctctcagcta	498540
tacctgaatg	gcatttttcc	ggaacgaata	ctagctcgaa	aattaaaaaa	ctgtgcgaag	498600
agctatccca	gaactgctct	taccatagaa	gtactggat	cctcgggtct	aggagctctt	498660
aaggttatcc	tgatcccttg	cgcttctaca	tatgctgcct	tgaccctacc	cctacgggct	498720
ctctttaacg	ctataaaaaa	aaaaagctgc	caacatcttg	cttcgtatgc	tatggcttgg	498780
ctcctccaca	ttcttacgat	tgtgtgtgatt	atcgggtctgg	tcttttagtct	ggtctttatc	498840
ccccctccag	ttgtctttat	ctccttgggg	cttctcatgt	ctgtaactac	tagcgttacc	498900
ctcttccaag	tgcataaaaa	tcttttcccc	ccgtatgagc	ctccaccctc	acgacctcac	498960
acgccccctc	catttgctga	tgagtatgtc	cctctcataa	gcgagtctta	tttcgactaa	499020
aagttccaaa	taaaaataac	ttaaagtttt	agttaaaaat	ctgttaagat	tttaacaaat	499080
aaacttttatt	taataaaaaa	gttaagactc	agaagaaaag	agaactaact	aaatcctatt	499140
aaatcttata	atagtatgaa	atatatccta	tgaatgaaaa	ttcatggggc	taatgataat	499200
tacagtaagt	tgatagtatg	agccaacccc	ctataaaccc	tttaggtcaa	cctcaagttc	499260
ctgcagcagc	atccccatca	gggcagccaa	gcgtggtaaa	acgtttaaaa	acgtcatcca	499320
cagggttatt	caaaagattt	attactgttc	ctgataaata	tcctaaaatg	cgctatgtct	499380
atgacacagg	cattattgcc	cttgcgggcaa	ttgcgatcct	ttcgattctc	ctgactgctt	499440
caggaaacag	ccttatgctt	tatgctctcg	ctccggcact	tgccctggga	gctttgggag	499500
ttactctact	tatttctgat	attctggaca	gtccgaagcc	aagaaaatcg	gtgaggcaat	499560
cactgctatc	gtcgttccta	tcattgtatt	agcgattgct	gcgggtctta	ttgcaggggc	499620
tttcggttgc	tctagtggga	cgatgttagt	ctttgccaac	cctatgtttg	tcatgggatt	499680
gattacggtg	gggctatact	tcattgtcctt	gaataagctc	accttagatt	atttccttag	499740
ggaacacctc	ttgaggatgg	aaaagaaaaa	ccaagagacc	gcggacctat	tctagtgaat	499800
ccatccgcgc	acgatgcaaa	aaaaatcgca	gtggaaaaaga	aaaaagatct	ttctgcatct	499860
gcccgcattg	aggaacacga	agcttcacaa	cgccaagatg	ccgctcatcg	taggatcggt	499920
cgggaggctc	aaggatcttt	cttctattcg	tcacgaaatc	ctgagcatag	acgctccttc	499980
ggcagcctct	cacgttttaa	aacaaaaccc	tcagatgcgg	cttctacacg	acccgcatct	500040
ataagtctc	catttaagga	cgattttcag	ccttatcact	tcaaagattt	aagaagcagt	500100
tcattcggta	gtggagcgag	cagtgcgttt	acaccataa	tgcttgcaag	ttcccgtctt	500160
cctaatttct	ccacggggac	ggttctacac	cctgagccgg	tctaccctaa	gggaggaaaa	500220
gaacctcaa	ttcctcgagt	ttcttcatct	tcccgcggtt	cccctcgatg	tcgccaagat	500280
aaacagcagc	aacagcaaaa	tcaagatgaa	gaacagaaac	agcaatctaa	gaagaaaagc	500340
gggaaatcga	atcaatctct	taaaactccg	cctccagacg	gaaaaagcac	ggctaacctc	500400
agcccccca	atccattctc	tgacggttat	gacgaaagag	aaaaacggaa	acacagaaag	500460
aacaaataag	gatccgtggt	ttagataacc	atcttctcta	ctctctcctt	ctaaaattca	500520
agaaggctca	aaagcaaaac	cgcttgatca	ccttctcccc	tacccttaag	catttccctt	500580
atgttttaag	ggactcttaa	atatagaaaa	ataccttaaa	tgcttctctc	ccaagattga	500640
aacttctata	actgagagtc	ttctccagag	catttacttg	atttatttaa	ctgtattctc	500700
tattggtgca	ccatgctcct	aaagccacat	gctatgggag	tatttttgat	aaaaagcttt	500760
tccccaaaga	cacatgaaat	attctttacc	ttggctactt	acctcttcgg	ctttagtttt	500820
ctccctacat	ccactaatgg	ctgctaacac	ggatctctca	tcattccgata	actatgaaaa	500880
tggtagtagt	ggtagcgcag	cattcactgc	caaggaaact	tcggatgctt	caggaaactac	500940
ctacactctc	actagcgatg	tttctattac	gaatgtatct	gcaattactc	ctgcagataa	501000
aagctgtttt	acaaacacag	gaggagcatt	gagttttggt	ggagctgatc	actcattggt	501060
tctgcaaacc	atagcgctta	cgcatgatgg	tgctgcaatt	aacaatacca	acacagctct	501120
ttctttctca	ggattctcgt	cactcttaat	cgactcagct	ccagcaacag	gaacttcggg	501180
cggcaagggt	gctatttgtg	tgacaaatac	agagggagggt	atctgcgactt	ttactgaaca	501240
tgccagtgtc	acctccaaa	aaaatacttc	agaaaaagat	ggagctgcag	tttctgccta	501300
cagcatcgat	cttgctaaga	ctacgacagc	agctctctta	gatcaaaaata	ctagcacaaa	501360
aaatggcggg	gccctctgta	gtacagcaaa	cactacagtc	caaggaaact	caggaaacggt	501420
gaccttctcc	tcaaatactg	ctacagataa	aggtgggggg	atctactcaa	aagaaaagga	501480
tagcacgcta	gatgccaaata	caggagtcgt	taccttcaaa	tctaatactg	caaagacggg	501540
gggtgcttgg	agctctgatg	acaatcttgc	tcttaccggc	aacactcaag	tactttttca	501600
ggaaaaataa	acaaccggct	cagcagcaca	ggcaaaatac	ccggaagggtt	gtggtggggc	501660
aatctgttgt	tatcttgcta	cagcaacaga	caaaactgga	ttagccattt	ctcagaattca	501720
agaaatgagc	ttcactagta	atacaacaac	tgccaatggg	ggagcgatct	acgctactaa	501780
atgtactctg	gatggaaaca	caactcttac	cttcgatcag	aatactgcga	cagcaggatg	501840
tgccggagct	atctatacag	aaactgaaga	tttttctctt	aagggaagta	cgggaaccgt	501900
gaccttcagc	acaaatacag	caaagacagg	cggcgcctta	tattctaaag	aaaacagctc	501960
gctgactgga	aataccaacc	tgctcttttc	agggaaacaaa	gctacggggc	cgagtaattc	502020
ttcagcaaat	caaggagggtt	gcgggtggggc	aatcctatcg	tttcttgagt	cagcatctgt	502080
aagtactaaa	aaaggactct	ggattgaaga	taacgaaaaa	gtgagtctct	ctggtaatac	502140
tccaacagta	agtggcgggtg	cgatctatgc	gaccaagtgt	gctctgcatg	gaaacacgac	502200
tgctaccttt	gatggcaata	ctgccgaaac	tgaggaggga	gcgatctata	cagaaaccga	502260
agatttttact	cttacgggga	gtacggggaac	cgtgaccttc	agcacaaata	cagcaaagac	502320

agcaggggct	ctacatacta	aaggaaatac	ttcctttacc	aaaaataagg	ctcttgtatt	502380
ttctggaaat	tcagcaacag	caacagcaac	aacaactaca	gatcaagaag	gttgtgggtg	502440
agcgatcctc	tgtaatatct	cagagtctga	catagctaca	aaaagcttaa	ctcttactga	502500
aaatgagagt	ttaagtttca	ttaacaatac	ggcaaaaaga	agtgggtggtg	gtattttatgc	502560
tcctaagtgt	gtaatctcag	gcagtgaatc	cataaacttt	gatggcaata	ctgctgaaac	502620
ttcggggagga	gcgattttatt	cgaaaaacct	ttcgattaca	gctaacgggtc	ctgtctcctt	502680
taccaataat	tctggaggga	agggaggcgc	catttatata	gccgatagcg	gagaactttc	502740
cttagaggct	attgatgggg	atattacttt	ctcaggggaac	cgagcgactg	agggaaacttc	502800
aaactcccaac	tcgatccatt	taggtgcagg	ggctaagatc	actaagcttg	cagcagctcc	502860
tggtcatacg	atattttttt	atgatacctat	tacgatggaa	gctcctgcat	ctggagggaac	502920
aatagaggag	ttagtcatca	atcctgttgt	caaagctatt	gttcctcctc	cccaacccaaa	502980
aaatgggtcct	atagcttcag	tgctgttagt	ccctgtagca	cctgcaaacc	caaacacggg	503040
aactatagta	ttttcttctg	gaaaactccc	cagtcaagat	gcctcgattc	ctgcaaatac	503100
taccaccata	ctgaaccaga	agatcaactt	agcaggagga	aatgtcgttt	taaaagaagg	503160
agccacccta	caagtatatt	ccttcacaca	gcagcctgat	tctacagtat	tcatggatgc	503220
aggaacgacc	ttagagacca	cgacaactaa	caatacagat	ggcagcatcg	atctaaagaa	503280
tctctctgta	aatctggatg	cttttagatgg	caagcgtatg	ataacgattg	ccgtaaacag	503340
cacaagtggg	ggattaaaaa	tctcagggga	tctgaaattc	cataacaatg	aaggaagtgt	503400
ctatgacaat	cctgggttga	aagcaaaactt	aaatcttcct	ttcttagatc	tttcttctac	503460
ttcaggaact	gtaaatttag	acgacttcaa	tccgattcct	tctagcatgg	ctgctccgga	503520
ttatgggtat	caagggagtt	ggactctggt	tcctaaagta	ggagctggag	ggaaagtgc	503580
tttgggtcgcg	gaatggcaag	cgttaggata	cactcctaaa	ccagagcttc	gtgcgacttt	503640
agttcctaata	agccttttga	atgcttatgt	aaacatccat	tctatacagc	aggagatcgc	503700
cactgcatag	tcggagcgtc	cctcacatcc	agggatttgg	attggaggta	ttggcaacgc	503760
cttccatcaa	gacaagcaaa	aggaaaatgc	aggattccgt	ttgatttcca	gaggttatat	503820
tggttggtggc	agcatgacca	cccctcaaga	atataccttt	gctgttgcac	tcagccaact	503880
ctttggcaaa	tctaaggatt	acgtagtctc	ggatattaaa	tctcaagtct	atgcaggatc	503940
tctctgtgct	cagagctctt	atgtcattcc	cctgcatagc	tcattacgtc	gccacgtcct	504000
ctctaagggtc	cttccagagc	tcccaggaga	aactccccct	gttctccatg	gtcaagtttc	504060
ctatggaaga	aaccaccata	atatgacgac	aaagcttgcg	aacaacacac	aagggaatac	504120
agactgggac	agccatagtt	cgctgttgaa	gtcgggtggt	ctcttctctg	agatctaaac	504180
tacagatacc	ttaccagcta	ctctccctat	gtgaaactcc	aagttgtgag	tgtaaataca	504240
aaaggattcc	aagagggttg	tgctgatcca	gctatctttg	acgctagcca	tctggtcaac	504300
gtgtctatcc	ctatgggact	caccttcaaa	cacgaatcag	caaagcccc	cagtgccttg	504360
cttcttactt	taggttacgc	tgtagatgct	taccgggatc	accctcactg	cctgacctcc	504420
ttaacaaatg	gcacctcggtg	gtctacgttt	gctacaaact	tatcacgaca	agctttcttt	504480
gctgaggctt	ctggacatct	gaagtacttt	catggtcttg	actgcttcgc	ttctggaagt	504540
tgtgaactgc	gcagctcctc	aagaagctat	aatgcaaat	gtggaactcg	ttattctttc	504600
taagattctc	cgagaatctt	agaaaaacat	actttttata	aagatgaata	cgttattgag	504660
atcgactgtg	atcgctatcag	agggggaggg	catccccctc	tcatacaaga	gattcttagg	504720
atccgtatga	agagaagtaa	aagatccgcc	atccttgggg	ttctgattct	ccgcatcaat	504780
caattccttg	cgtttccctt	gatttctttt	tttctttaca	gtatttgcta	atttaatttc	504840
cttgtttcaa	aaaagtgcct	acaaatgaag	tcctctgtct	cttggttggt	cttttcttca	504900
atcccgtctc	tttcatcgct	ctctatagtc	gcggcagagg	tgaccttaga	tagcagcaat	504960
aatagctatg	atggatctaa	cggaactacc	ttcacgggtc	tttccactac	ggacgctgct	505020
gcaggaacta	cctattcctt	actttccgac	gtatcctttc	aaaatgcagg	ggcttttagga	505080
attcccttag	cctcaggatg	cttccatgaa	gcgggcggcg	atcttacttt	ccaaggaaat	505140
caacatgcac	tgaagtttgc	atttatcaat	gcgggctcta	gcgctggaac	tgtagccagt	505200
acctcagcag	cagataagaa	tcttctcttt	aatgattttt	ctagactctc	tattatctct	505260
tgtccctctc	ttcttctctc	tcctactgga	caatgtgctt	taaaatctgt	ggggaatcta	505320
tctctaactg	gcaattccca	aatttatatt	actcagaact	tctcgtcaga	taacggcggt	505380
gttatcaata	cgaaaaactt	cttattatca	gggacatctc	agtttgcgag	cttttcgaga	505440
aaccaagcct	tcacagggaa	gcaaggcggt	gtagttttacg	ctacaggaac	tataactatc	505500
gagaacagcc	ctgggatagt	ttccttctct	caaaacctag	cgaaaggatc	tggcgggtgct	505560
ctgtacagca	ctgacaactg	ttcgattaca	gataactttc	aagtgatctt	tgacggcaat	505620
agtgcctggg	aagcgcgtca	agctcagggc	ggggctattt	gttgactact	gacagataaa	505680
acagtgactc	ttactgggaa	caaaaaacct	tctttcacaa	ataatacagc	attgacatat	505740
ggcggagcca	tctctggact	caaggctcag	atttccgctg	gaggtcctac	tctatttcaa	505800
agtaatatct	caggaagtag	cgccgggtcag	ggaggaggag	gagcgatcaa	tatagcatct	505860
gctgggggaa	tcgctctctc	tgctacttct	ggagatatta	ccttcaataa	caaccaagtc	505920
accaacggaa	gcacaagtac	aagaaacgca	ataaatatca	ttgataccgc	taaagtcaca	505980
tcgatacag	ctgtacggg	gcaatctatc	tatttctatg	atcccatcac	aaatccagga	506040
accgcagctt	attccgacac	attgaactta	aacttagcag	atgcgaacag	tgagatcgag	506100
tatgggggtg	cgattgtctt	ttctggagaa	aagctttccc	ctacagaaaa	agcaatcgct	506160

gcaaacgtca	cctctactat	ccgacaacct	gcagtattag	cgcggggaga	tcttgtactt	506220
cgtgatggag	tcaccgtaac	tttcaaggat	ctgactcaaa	gtccaggatc	ccgcacttta	506280
atggatgggg	ggactacact	tagtgctaaa	gaggcaaata	tttcgcttaa	tggcttagca	506340
gtaaatctct	cctctttaga	tggaaaccaac	aaggcagctt	taaaaacaga	agctgcagat	506400
aaaaatatca	gcctatcggg	aacgattgcg	cttattgaca	cggaagggtc	attctatgag	506460
aatcataact	taaaaagtgc	tagtacctat	cctcttcttg	aacttaccac	cgcaggagcc	506520
aacggaacga	ttactctggg	agctctttct	accctgactc	ttcaagaacc	tgaaaccac	506580
tacgggtatc	aaggaaactg	gcagttgtct	tgggcaaata	caacatcctc	aaaaatagga	506640
agcatcaact	ggaccctgac	aggatacatt	cctagtcctg	agagaaaaag	taatctccct	506700
ctaaatagct	tatggggaaa	ctttatagat	atacgctcga	tcaatcagct	tatagaaacc	506760
aagtccagtg	gggagccttt	tgagcgtgag	tatggctttc	aggaattgcg	aatttcttct	506820
atagagattc	tatgccacc	cgccatgggt	tccgccatat	cagcgggggg	tatgcactag	506880
ggatcacagc	aacaactcct	gccgaggatc	agcttacttt	tgccttctgc	cagctctttg	506940
ctagagatcg	caatcatatt	acaggtaaga	accacggaga	tacttacggt	gcctctttgt	507000
atttccacca	tacagaaggg	ctcttcgaca	tcgccaattt	cctctgggga	aaagcaacc	507060
gagctccctg	ggtgctctct	gagatctccc	agatcattcc	tttatcggtc	gatgctaaat	507120
tcagttatct	ccatacagac	aaccacatga	agacatatta	taccgataac	tctatcatca	507180
agggttcttg	gagaaacgat	gccttctgtg	cagatcttgg	agctagcctg	ccttttgtta	507240
tttccgttcc	gtatcttctg	aaagaagtcg	aaccttttgt	caaagtacag	tatatctatg	507300
cgcatacagc	agacttctac	gagcgttatg	ctgaaggacg	cgctttcaat	aaaagcgagc	507360
ttatcaacgt	agagattcct	ataggcgctca	ccttcgaaaag	agactcaaaa	tcagaaaagg	507420
gaacttacga	tcttactctt	atgtatatac	tcgatgctta	ccgacgcaat	cctaaatgtc	507480
aaacttccct	aatagctagc	gatgctaac	ggatggccta	tggtagcaac	ctcgcacgac	507540
aaggtttttc	tgttcgtgct	gcgaaccatt	tccaagtgaa	ccccacatg	gaaatcttcg	507600
gtcaattcgc	ttttgaagta	cgaagtctct	cacgaaatta	taatacaaac	ctaggctcta	507660
agttttgttt	ctagattatc	gaaaacgtgt	taattaattg	aaccaagca	tctttctatg	507720
aaaataccct	tgcacaaact	cctgatctct	tcgactcttg	tactcccat	tctattgagc	507780
attgcaactt	acggagcaga	tgcttcttta	tcccctacag	atagctttga	tggagcgggc	507840
ggctctacat	ttactccaaa	atctacagca	gatgccaatg	gaacgaacta	tgtcttatca	507900
ggaaatgtct	atataaacga	tgctgggaaa	ggcacagcat	taacaggctg	ctgctttaca	507960
gaaactacgg	gtgatctgac	atttactgga	aagggtatact	cattttcatt	caacacggta	508020
gatgcggggt	cgaatgcagg	agctgcggga	agcacaactg	ctgataaagc	cctaaccattc	508080
acaggatttt	ctaaccctttc	cttcattgca	gctcctggaa	ctacagttgc	ttcaggaaaa	508140
agtactttta	gttctgcagg	agccttaaat	cttaccgata	atggaacgat	tctcttttagc	508200
caaaacgtct	ccaatgaagc	taataacaat	ggcggagcga	tcaccgcaaa	aactctttct	508260
atttctggga	atacctcttc	tataaccctc	actagtaata	gcgcaaaaaa	attaggtgga	508320
gcgatctata	gctctgcggc	tgcaagtatt	tcaggaaaca	ccggccagtt	agtctttatg	508380
aataataaag	gagaaactgg	gggtggggct	ctgggctttg	aagccagctc	ctcgattact	508440
caaaatagct	cccttttctt	ctctggaac	actgcaacag	atgctgcagg	caagggcggg	508500
gccattttat	ctgaaaaaac	aggagagact	cctactctta	ctatctctgg	aaataaaagt	508560
ctgaccttcg	ccgagaactc	ttcagtaact	caaggcggag	caatctgtgc	ccatgggtcta	508620
gatctttccg	ctgctggccc	taccctatct	tcaaataata	gatgcgggaa	cacagctgca	508680
ggcaagggcg	gcgctattgc	aattgccgac	tctggatctt	taagtctctc	tgcaaatcaa	508740
ggagacatca	cgttccttgg	caatactcta	acctcaacct	ccgcgccaac	atcgacacgg	508800
aatgctatct	acctgggatc	gtcagcaaaa	attacgaact	taagggcagc	ccaagggcaa	508860
tctatctatt	tctatgatcc	gattgcatct	aacaccacag	gagcttcaga	cgttctgacc	508920
atcaaccaac	cggatagcaa	ctcgccttta	gattattcag	gaacgattgt	attttctggg	508980
gaaaagctct	ctgcagatga	agcgaaagct	gctgataact	tcacatctat	attaaagcaa	509040
ccattggctc	tagcctctgg	aaccttagca	ctcaaaggaa	atgtcgagtt	agatgtcaat	509100
ggtttcacac	agactgaagg	ctctacactc	ctcatgcaac	caggaacaaa	gctcaaagca	509160
gatactgaag	ctatcagtct	taccaaactt	gtcgttgatc	tttctgcctt	agaggggaaat	509220
aagagtgtgt	ccattgaaac	agcaggagcc	aacaaaacta	taactctaac	ctctcctctt	509280
gttttccaag	atagtagcgg	caatttttat	gaaagccata	cgataaaacca	agccttcacg	509340
cagccttttg	tggtattcac	tgctgctact	gctgttagcg	atattttatat	cgatgcgctt	509400
ctcacttctc	cagtacaaac	tccagaacct	cttactgggt	atcagggaca	ttgggaagcc	509460
actggggcag	acacatcaac	tgcaaaatca	ggaactatga	cttgggtaac	tacgggctac	509520
aaccctaate	ctgagcgtag	agcttccgta	gttcccgatt	cattatgggc	atcctttact	509580
gacattcgca	ctctacagca	gatcatgaca	tctcaagcga	atagtatcta	tcagcaacga	509640
ggactctggg	catcaggaac	tgcgaaatttc	ttccataagg	ataaatcagg	aactaaccac	509700
gcattccgac	ataaaagcta	cggctatatt	gttggaggaa	gtgctgaaga	tttttctgaa	509760
aatatcttca	gtgtagcttt	ctgccagctc	ttcggtaaag	ataaagacct	gtttatagtt	509820
gaaaataacct	ctcataacta	tttagcgtcg	ctatacctgc	aacatcgagc	attcctagga	509880
ggacttccca	tgccctcatt	tggaagtatc	accagcatgc	tgaaagatat	tcctctcatt	509940
ttgaatgccc	agctaagcta	cagctacact	aaaaatgata	tggatactcg	ctatacttcc	510000

tatcctgaag	ctcaaggctc	ttggaccaat	aactctgggg	ctctagagct	cggaggatct	510060
ctggctctat	atctccctaa	agaagcaccg	ttcttccagg	gatatttccc	cttcttaaag	510120
ttccaggcag	tctacagccg	ccaacaaaac	tttaaagaga	gtggcgctga	agcccggtgct	510180
tttgatgatg	gagacctagt	gaactgctct	atccctgtcg	gcattcggtt	agaaaaaatc	510240
tccgaagatg	aaaaaaataa	tttcgagatt	tctctagcct	acattgggtga	tgtgtatcgt	510300
aaaaatcccc	gttcgcgtac	ttctctaattg	gtcagtgagg	cctcttggac	ttcgctatgt	510360
aaaaacctcg	cacgacaagc	cttcttagca	agtgtggaa	gccatctgac	tctctcccct	510420
catgtagaac	tctctgggga	agctgcttat	gagcttcgtg	gctcagcaca	catctacaat	510480
gtagattgtg	ggctaagata	ctcattctag	ttctactttt	cctccctaaa	cttttaggga	510540
ggaattctta	taaaaaccct	gtagattctt	aacttactag	tctctccttt	cctcttgctt	510600
tctttaattt	attgcagtat	gtggtgaaat	aatttggtta	accacctata	gcccctctaca	510660
tgaatcctc	tcttcattgg	tttttaattc	cgtcatcttt	agcacttccc	ttgtcactaa	510720
atctctctgc	gtttgctgct	gttggtgaaa	tcaatctagg	acctaccaat	agcttctctg	510780
gaccaggaac	ctacactcct	ccagcccaaa	caacaaatgc	agatggaaact	atctataatc	510840
taacagggga	tgtctcaatc	accaatgcag	gatctccgac	agctctaacc	gcttctgct	510900
ttaaagaaac	tactgggaat	ctttctttcc	aaggccacgg	ctaccaattt	ctcctacaaa	510960
atatcgatgc	gggagcgaac	tgtaccttta	ccaatacagc	tgcaaataag	cttctctcct	511020
tttcaggatt	ctcctatttg	tcactaatac	aaaccacgaa	tgctaccaca	ggaacaggag	511080
ccatcaagtc	cacaggagct	tgttctatct	agtcgaacta	tagttgctac	tttggccaaa	511140
acttttctaa	tgacaatgga	ggcgccctcc	aaggcagctc	tatcagctca	tcgctaaaacc	511200
ccaacctaac	gtttgccaaa	aacaaagcaa	cgcaaaaagg	gggtgccctc	tattccacgg	511260
gagggattac	aattaacaat	acgttaaact	cagcatcatt	ttctgaaaat	accgcggcga	511320
acaatggcgg	agccatttac	acggaagcta	gcagttttat	tagcagcaac	aaagcaatta	511380
gctttataaa	caatagtgtg	accgcaacct	cagctacagg	gggagccatt	tactgtagta	511440
gtacatcagc	ccccaaacca	gtcttaactc	tatcagacaa	cggggaactg	aactttatag	511500
gaaatacagc	aattactagt	gggtggggcga	tttatactga	caatctagtt	ctttctctctg	511560
gaggacctac	gcttttttaa	aacaactctg	ctatagatac	tcagctccc	ttaggaggag	511620
caattgcat	tgctgactct	ggatctttga	gtctttcggc	tcttggtgga	gacatcactt	511680
ttgaaggaaa	cacagtagtc	aaaggagctt	cttcgagtc	gaccactacc	agaaattcta	511740
ttaacatcgg	aaacaccaat	gctaagattg	tacagctgcg	agcctctcaa	ggcaatacta	511800
tctacttcta	tgatcctata	acaactagca	tcactgcagc	tctctcagat	gctctaaact	511860
taaatggctc	tgaccttgca	gggaatcctg	catatcaagg	aaccatcgta	ttttctggag	511920
agaagctctc	ggaagcagaa	gctgcagaag	ctgataatct	caaactctaca	attcagcaac	511980
ctctaactct	tgcgggaggg	caactctctc	ttaaatcagg	agtcactcta	gttgccaagt	512040
ccttttcgca	atctccgggc	tctaccctcc	tcattggatgc	agggaccaca	ttagaaaccg	512100
ctgatggatc	actatcaata	atctgttctc	aatgtagatt	ccttaaaaga	gaccaagaag	512160
ntacgctaaa	agcaacacaa	gcaagtcaga	cagtcacttt	atctggatcg	ctctctcttg	512220
tagatccttc	tggaaatgtc	tacgaagatg	tctcttgga	taaccctcaa	gtcttttctt	512280
gtctcactct	tactgctgac	gaccccgcca	atattcacat	cacagactta	gctgtgctac	512340
ccctagaaaa	aaatcctatc	cattggggat	accaagggaa	ttgggcatta	tcttgccaag	512400
aggataactgc	gactaaatcc	aaagcagcga	ctcttacctg	gacaaaaaca	ggatacaatc	512460
cgaatcctga	gcgtcggtga	accttagttg	ctaacacact	atggggatcc	ttgtgtgatg	512520
tgcgctccat	acaacagctt	gtagccacta	aagtacgcca	atctcaagaa	actcgcgcca	512580
tctggtgtga	agggatctcg	aacttcttcc	ataaagatag	cacgaagata	aataaagggt	512640
ttcgccacat	aagtgcagggt	tatgtttag	gagcgactac	aacattagct	tctgataatc	512700
ttatcactgc	agccttctgc	caattattcg	ggaaagatag	agatcacttt	ataaataaaa	512760
atagagcttc	tgccatgca	gcttctctcc	atctccagca	tctagcgacc	ttgtcttctc	512820
caagcttggt	acgctacctt	cctggatctg	aaagttagca	gcctgtcctc	tttgatgctc	512880
agatcagcta	tatctatagt	aaaaatacta	tgaaaaccta	ttacacccaa	gcaccaaagg	512940
gagagagctc	gtggtataat	gacggttgcg	ctctggaact	tgcgagctcc	ctaccacaca	513000
ctgctttaag	ccatgagggt	ctcttccacg	cgtattttcc	tttcatcaaa	gtagaagctt	513060
cgtacataca	ccaagatagc	ttcaaagaac	gtaatactac	cttggtacga	tctttcgata	513120
gcggtgattt	aattaacgct	tctgtgccta	ttggaattac	cttcgagaga	ttctcgagaa	513180
acgagcggtc	gtcttacgaa	gctactgtca	tctacgttgc	cgatgtctat	cgtaagaatc	513240
ctgactgcac	gacagctctc	ctaataca	atacctcgtg	gaaaactaca	ggaacgaatc	513300
tctcaagaca	agctgggtatc	ggaagagcag	ggatctttta	tgccctctct	ccaaatcttg	513360
aggtcacaag	taacctatct	atggaaattc	gtggatcttc	acgcagctac	aatgcagatc	513420
ttggagggtaa	gttccagttc	taaaagcggt	cctgatccct	tagaaattct	aagagatcct	513480
gagtgtatct	agggacttct	caaagacaat	gcgccttggt	tagacgagga	gaagtcaaaa	513540
gatcagagga	atctaagaac	tagaaaaaat	cccagattac	aagagggtcga	agattcaaa	513600
aagtcgctag	atcacaagaa	agaatgggca	gagtacgtga	tctcacgaac	tccgcccgtc	513660
ttagaatcca	aagacttttt	agtatactaa	gactgtctat	gatccaatag	ccaaagactc	513720
ttgaatatct	aaatgttttc	tatgatccga	aaactcttag	agtcgataaa	aactccggat	513780
tctttatccc	cagatctctt	tagcaatctc	tttcacaaag	gcgatcttct	tccactgttc	513840

ttcttcagtc	attctatggt	ctccctcaca	agaagcaaac	ccacattgcg	ggctcaaaga	513900
aagtctctct	aagggaaatgt	agctcgcagc	ttcataaata	cgagaaacca	cagcatctcg	513960
atctttcaata	caagaatggt	tgctggagat	caatcccaag	cagacgtgtt	tctctccaga	514020
gacgtaagct	aaaggctcag	cacctcctga	atacttatca	tcaagagccc	aataatagtg	514080
ataactatcc	acatcggtct	tagcaaataa	aggctcctct	atagaatcat	aagctcgtct	514140
agagaaaaac	tcggcctgat	aatcaccacg	acagacatgc	agacttacaa	aaagatcctc	514200
gggtctatcc	ttcatcacta	aattatggat	ccataaaaac	tggtctaaaa	tttctgcaa	514260
cctgtcatga	gaatcaacac	cataccaaga	aggcgctcgt	atatccaaga	ggcgacacca	514320
agcacaatcg	tccaactgca	aattacgaca	acctgcagca	taaagatctt	ggatgacttg	514380
gcgataataa	aagacaatat	catcaattag	ctcttgattc	gtaggataaa	acttccgagt	514440
atttttcaga	ttaggagcaa	aatcatctc	atggaaaaat	tgtagtggag	aaggaaatcgt	514500
ttgttttgct	tttgcatctc	ccttctcaaa	agttttgaca	aactcgaaat	gttctataaa	514560
cggatgtttt	gatacggaga	ttttatcttt	aagatacact	ccaatttcag	ggtcattaga	514620
gtccctgcga	cgatccacgc	catggaatcc	ccacataaag	tcgaaatccc	aactatacct	514680
acggaattcc	ccatcagtaa	aaaagataag	acctgctttt	gtttgctttt	ttatgagatt	514740
acgaatagca	gcactcttga	caactcgcac	ctgctcatag	acaattcttc	cttcttcaaa	514800
atcagagcgt	gctcgtgtaa	gactttcagg	acgtaagaaa	cttcccacaa	catcaaaatg	514860
acattgctca	ggttgttgga	atgggctcat	cattttccatc	cttagagatg	atcctaataa	514920
aatacatttc	cactcatgga	tctctcttct	cgatggttga	ataaattaaa	gacaagaaaa	514980
cagctagatc	aaaacataaa	gtacgattgt	aaaagttact	gcctgagggg	aatctcacaa	515040
atcttaggat	gggtgtaaca	acaccccttc	ccttaaaaaa	gaaagagacg	taccgtctct	515100
gcaactctaa	tctttgcagc	tattctctat	aagaagcata	acaaaaacca	cttaaaattt	515160
aggatctaaa	aatagtgaat	tatcttattc	aataagaatt	aaagaaacgt	atttttaaga	515220
acgggtttct	attaaaaaat	ttccttaatt	ttaaaacgtg	tttgtaacaa	gaaaggcaga	515280
gtacgtgacc	tcacgaactc	tgccctcttg	cctttttaat	ccccgatctc	tcctgggtca	515340
aaaacaaggt	gagtcgtggt	taagaaaatc	ctaaatgcga	tctctctcag	aatttctgag	515400
acatgagaga	cgctcctaga	attggaactt	acccccaaga	tctacattat	aaatccgtga	515460
ggatccacga	acttcaaaga	caaactggcc	gagcacttca	aacataggag	agaaggcgta	515520
gtgactgcct	gcacgcactt	gcaaggcctg	tcgtgctaag	ttattggcat	aagtttccca	515580
agaggctccg	ctgattacaa	gtgctgtagt	gcatttggga	tcattgcgga	taagatcagg	515640
aacataggat	aaagtcagat	cataagaaaa	gtcattacaa	tcagagaact	tctcaaactt	515700
cacctctata	ggcaaaagata	aattgaagag	gttgctgtca	tcaaaagatc	ttccttctgt	515760
acctttctcc	gagaagctgt	cctgacgtat	ataggtcaga	ttcagtttga	tgtatggagc	515820
ataggtatca	aaacaatgca	ggtattcagg	ataagaatga	gaagaagctc	ccaacatcat	515880
gttaaaagca	ttattcccc	aagaaccttt	cacctcagga	tacgcagtat	actttgtctt	515940
cagatcatta	ctgacgtggc	tataagcgag	ctgcccttct	aaaacgaggg	gtttatgact	516000
ccaagagcca	ggaagtttat	ctaagagaca	acctatgaac	ccactacatt	ctgtaatgtg	516060
ttggatatag	aaggctcctg	cataggtatc	agtatgattt	ttagcgacta	agaaatcttt	516120
atcgctacca	aagagttggc	aaaaggcaaa	gctaattaag	ttttcagaac	aagtttgctc	516180
tgacctccg	atagcatatc	caccagattt	atgacgggat	ttgcgttttt	cccccttctt	516240
atctttatct	aagaaattgg	cgactcccgc	agcccagaag	cctcgatctg	aacaaagagt	516300
caaagcactt	ctctctatga	caccttgaat	cgcttggatg	tctgaaaaag	atccccaaag	516360
gctattagga	actaaaggtc	cttgacgctc	aggattcgga	aggtagcccc	tattgggtcca	516420
agctaattgtc	gctgtcttag	tctttggagt	gcttgccgta	tcatcaaccc	aagtcattcc	516480
ccaagtacct	tgatacccat	agtgcgtagg	agttgctact	gtaggaaccg	ctggaacatc	516540
tgtagttgtt	gcagtaccga	gagcagagag	gtgcacaaat	gaaaagtctt	gagtttttcc	516600
taagtcgtga	ttttcataag	cattcccttg	gttatccaaa	agaagaatcg	gaccactaag	516660
ggctacattt	ttacttgctg	cagaagcagc	aattacaact	ttcttaccct	cgcctaaaga	516720
gtctacagga	atggaaagac	ctgttaaagt	gacctcctct	gtacttgctt	ttaacgttgt	516780
gccccgatcc	ataataacag	aggaacccgc	ggctctgagta	aagcctttcg	tatcgagagt	516840
gacaccacgt	ttaagtacta	aatttcctgc	agttagagtt	acaggctgct	tcagcgtaga	516900
agtgaggttg	tctgcaactt	ttgcttcate	ttcagagagc	ttttcaccag	aaaaaacaat	516960
cgaccacta	taatctgtac	tattacctgc	atcagcttta	ttgagattta	aagtatctgt	517020
agaatccgca	gccgtattag	cagtaatcgg	atcgtagaaa	aagatgctat	gcccagatat	517080
tgacggtaaa	ttcgtgatct	ttgcagtaga	tcctatgtca	atagaatttc	ttttcgtagt	517140
ttgtggtgta	gttgcaacaa	tggcattccc	attgaaggta	atgtcccctg	cttctgctga	517200
aagactacac	tctccagctg	ccagtataga	aatggctcca	ccattacctg	cagtgggtacc	517260
ttggactata	ttgttagaaa	aggagatacc	ccccccccc	cccggagacc	agtgtaaagt	517320
tcttagcata	aatggctccg	ccattagcta	cagcttggtt	tcctgagaaa	gttacactct	517380
gattcccaga	tatggtaaca	tcggcatctc	cagaaagagc	tcctccattt	cctgcggtcg	517440
ctgtcacact	attttcagaa	aatacaagag	acgtattccc	tgtaattgta	cagtttctct	517500
tgctatttat	agctccacct	gcagcttcag	caatattggt	cgagaagagg	gtaggagccg	517560
tattatttgt	aatattcaca	gtaccagtag	cacaaaatagc	ccacctttt	ttccctgttg	517620
cgctcgattt	attcccttca	aaagaaatcg	atcccggtgct	gtttttcaaa	gaaagattct	517680



tggtagaaat	gtccgccatt	ttcctcacag	taatcttgtt	taaataaaat	agttccattg	517740
ttatcaaatg	taagatcccc	tccacattta	actgcacctt	ttcctgaggg	ggttgtgatt	517800
accgatgatg	gggccgctaa	gaaagtaaga	ctcgaaaatc	ctgttagcga	cagattttta	517860
tcagttgtaa	cagaaagtnt	gcgccttcag	cactagactt	natattttaa	aaagaaagtg	517920
agtaccctt	accggc aaaag	cttaaagatt	ccgtagtgtc	agaaaaacaa	cccttcgtta	517980
aagctgccga	atccccaaag	ttttgcagag	ttatatctcc	tgtagagta	tagtctattc	518040
cagtagtcgt	attttttagga	gtataggtgc	ctgtgttagt	acttccgtca	aagctatcag	518100
aggggcctat	attttccagca	gttgcagcaa	aaacagtggg	acaactagta	aaacatgccca	518160
atgtcgaaga	gagcactaac	caggaaaatt	gcgatttcat	aaaccactt	tattattaaa	518220
ttcttacttg	cgatcatataa	aatagaaaac	tcagagagtc	aagataaaaa	ttcttgacag	518280
ctgttttgtc	atctttaact	tgatttactt	attttgtttc	tattattgatg	cgaatagtgc	518340
tctaaaaaac	aaaagcatta	ccatgaagac	ttcgattcct	tgggttttag	tttccctccgt	518400
gtagcttttc	tcatgtccacc	tacagtccct	agctaaccag	gaacttttat	cacctgatga	518460
tagctttta	ggaaatatcg	attcaggaac	gtttactcca	aaaacttcag	ccacaacata	518520
ttctctaaca	ggagatgtct	tcttttacga	gcctggaaaa	ggcactccct	tatctgacag	518580
ttgttttaag	caaaccacgg	acaatcttac	cttcttgggg	aacggtcata	gcttaacggt	518640
tggctttata	gatgctggca	ctcatgcagg	tgctgctgca	tctacaacag	caaataagaa	518700
tcttaccttc	tcagggtttt	ccttactgag	ttttgattcc	tctcctagca	caacgggttac	518760
tacaggtcag	ggaacgcttt	cctcagcagg	aggcgtaaat	ttagaaaaata	ttcgtaaaact	518820
tgtagttgct	gggaattttt	ctactgcaga	tggtggagct	atcaaaggag	cgtctttcct	518880
tttaactggc	acttctggag	atgctctttt	tagtaacaac	tcttcatcaa	caaaggagg	518940
agcaattgct	actacagcag	gcgctcgcct	agcaataaac	acaggtnatg	ttagattcct	519000
atctaacata	gcgtctacgt	caggaggcgc	tatcgatgat	gaaggcacgt	cgatactatc	519060
gaacaacaaa	tttctatatt	ttgaaggga	tgtagcga	actactggcg	gtgcgatctg	519120
caacaccaag	gcgagtggat	ctcctgaact	gataatctct	aacaataaga	ctctgatctt	519180
tgcttcaaac	gtagcagaaa	caagcgggtg	cgccatccat	gctaaaaagc	tagccctttc	519240
ctctggaggc	tttacagagt	ttctacgaaa	taatgtctca	tcagcaactc	ctaagggggg	519300
tgctatcagc	atcgatgcct	caggagagct	cagtctttct	gcagagacag	gaaacattac	519360
ctttgtaaga	aataccctta	caacaaccgg	aagtaccgat	actcctaaac	gtaatgcat	519420
caacatagga	agtaacggga	aattcacgga	attacgggct	gctaaaaatc	atacaatttt	519480
cttctatgat	cccatactt	cagaaggaa	ctcatcagac	gtattgaaga	taaataacgg	519540
ctctgcggga	gctctcaatc	catatcaagg	aacgattcta	ttttctggag	aaaccctaac	519600
agcagatgaa	cttaaagttg	ctgacaattt	aaaatcttca	ttcacgcagc	cagtctccct	519660
atccggagga	aagttattgc	tacaaaagg	agtcacttta	gagagcacga	gcttctctca	519720
agaggccggt	tctctcctcg	gcatggattc	aggaacgaca	ttatcaacta	cagctgggag	519780
tattacaatc	acgaacctag	gaatcaatgt	tgactcctta	ggtcttaagc	agcccgtcag	519840
cctaacagca	aaaggtgctt	caaataaagt	gatcgtatct	gggaagctca	acctgattga	519900
tattgaagg	aacatttatg	aaagtcatat	gttcagccat	gaccagctct	ttctcttatt	519960
aaaaatcacg	gttgatgctg	atggtgatac	taacgttgac	atcagcagcc	ttatccctgt	520020
tctgtctgag	gatcctaatt	cagaatacgg	attccaagga	caatggaatg	ttaattggac	520080
tacggataca	gctacaaata	caaaagaggc	cacggcaact	tggaccaaaa	caggatttgt	520140
tcccagcccc	gaaagaaaat	ctgcgttagt	atgcaatacc	ctatggggag	tctttactga	520200
cattcgctct	ctgcaacagc	ttgtagagat	cggcgcaact	ggtatggaac	acaaacaagg	520260
tttctggggt	tccctccatga	cgaacttcct	gcataagact	ggagatgaaa	atcgcaaagg	520320
cttccgtcat	acctctggag	gctacgtcat	cgggtggaagt	gctcacactc	ctaaagacga	520380
cctattttacc	tttgcgttct	gccatctctt	tgctagagac	aaagattggt	ttatcgctca	520440
caacaactct	agaacctacg	gtggaacttt	attcttcaag	cactctcata	ccctacaacc	520500
ccaaaactat	ttgagatttag	gaagagcaaa	gttttctgaa	tcagctatag	aaaaattccc	520560
tagggaaatt	cccctagcct	tggatgtcca	agtttctgtc	agccattcag	acaaccgtat	520620
ggaaacgcac	tatacctcat	tgccagaatc	cgaaggttct	tggagcaacg	agtgtatagc	520680
tggtgggtatc	ggcctagacc	ttccttttgt	tctttccaac	ccacatcctc	ttttcaagac	520740
cttcattcca	cagatgaaag	tcgaaatggt	ttatgtatca	caaaaatagct	tcttcgaaag	520800
ctctagtgat	ggccgtggtt	ttagtattgg	aaggctgctt	aacctctcga	ttcctgtggg	520860
tgcgaaatc	gtgcaggggg	atatcggaga	ttctacacc	tatgatctct	caggattcct	520920
tgtttccgat	gtctatcgta	acaatcccca	atctacagcg	actcttgtga	tgagcccaga	520980
ctcttgga	attcgcgggtg	gcaatctttc	aagacaggca	tttttactga	ggggtagcaa	521040
caactacgtc	tacaactcca	attgtgagct	cttcggacat	tacgctatgg	aactccgtgg	521100
atcttcaagg	aactacaatg	tagatgttgg	taccaaactc	cgattctaga	ttgctaaaac	521160
tccctagttc	ttctagggag	ttttctcata	cttttagggg	aatattttgct	atagggaatg	521220
ctttccttgc	aaactgtaaa	aaataacatt	tgctccctct	caaaaaagat	ttctttta	521280
aatttctagt	tataatttta	ttttaaaaac	agttaaataa	ttaatagaca	ataatctatt	521340
cttattgact	tctttttttc	ttgttttatta	aagtgcttc	aaccttattg	atttaacgag	521400
gaaaccatga	ccatacttcg	aaattttctt	acctgctcgg	ctttattcct	cgctctccct	521460
gcagcagcac	aagttgtata	tcttcatgaa	agtgatgggt	ataacgggtg	tatcaataat	521520



aaaagcttag	aacctaaaat	tacctgttat	ccagaaggaa	cttcttacat	ctttctagat	521580
gacgtgagga	tttccaacgt	taagcatgat	caagaagatg	ctgggggtttt	tataaatcga	521640
tctgggaatc	tttttttcat	gggcaaccgt	tgcaacttca	cttttcacaa	ccttatgacc	521700
gaggggtttt	gogctgccat	ttcgaaccgc	gttggagaca	ccactctcac	tctctctaat	521760
ttttcttact	tagcgttcac	ctcagcacct	ctactacctc	aaggacaagg	agcgatttat	521820
agtcttgggt	ccgtgatgat	cgaaaatagt	gaggaagtga	ctttctgtgg	gaactactct	521880
tcgtggagtg	gagctgcat	ttatactccc	taccttttag	gttctaaggc	gagtcgtcct	521940
tcagtaaate	tcagcgggaa	ccgctacctg	gtgttttagag	acaatgtgag	ccaaggttat	522000
ggcggcgcca	tatctaccca	caatctcaca	ctcacgactc	gaggaccttc	gtgttttgaa	522060
aataatcatg	cttatcatga	cgtgaatagt	aatggaggag	ccattgccat	tgctcctgga	522120
ggatcgatct	ctatatccgt	gaaaagcggg	gatctcatct	tcaaaggaaa	tacagcatca	522180
caagacggaa	atacaataca	caactccatc	catctgcaat	ctggagcaca	gtttaagaac	522240
ctacgtgctg	tttcagaatc	cggagtttat	ttctatgatc	ctataagcca	tagcgagtcg	522300
cataaaatta	cagatcttgt	aatcaatgct	cctgaaggaa	aggaaactta	tgaaggaaaca	522360
ataagcttct	caggactatg	cctggatgat	catgaagtgt	gtgcggaaaa	tcttacttcc	522420
acaatcctac	aagatgtcac	attagcagga	ggaactctct	ctctatcgga	tgggggttacc	522480
ttgcaactgc	attcttttaa	gcaggaagca	agctctacgc	ttactatgtc	tccaggaacc	522540
actctgctct	gctcaggaga	tgctcgggtt	cagaatctgc	acatcctgat	tgaagatacc	522600
gacaactttg	ttcctgtaag	gattcgcgcc	gaggacaagg	atgctcttgt	ctcattagaa	522660
aaacttaaa	ttgcctttga	ggcttatttg	tccgtctatg	actttcctca	atttaaggaa	522720
gccttttacga	ttcctcttct	tgaacttcta	gggccttctt	ttgacagtct	tctcctaggg	522780
gagaccactt	tggagagaa	ccaagtcaca	acagagaatg	acgccgttcg	aggttcttgg	522840
tccttaagct	gggaagagta	cccccttct	ctggataaag	acagaaggat	cacaccaact	522900
aagaaaactg	ttttcctcac	ttggaatcct	gagatcactt	ctacgccata	atctctaagt	522960
ctacactata	attaaggga	tcccccttaa	gaagattttg	ggacctatct	gtattcagag	523020
ataggtccct	ctatgcacac	atgttcacga	gtctcgggcg	tagcgccatt	ttctacttta	523080
caggttctct	aaaacatctt	cgtttgggag	aatttcttga	gatttttcaa	aaatagaatc	523140
gccattttct	atcaagtatt	cttctaagaa	agcaatgtaa	gaaatgggaa	aatgcccttt	523200
aaaatatcct	gtaatcttaa	agctgtcaaa	attaagagat	taaaactgtg	tcttattgta	523260
cttggttttt	tacagccttt	cccttatttg	taggataatc	tggtttcacc	tctacgtgca	523320
aatgaaaacg	tctattcgta	agttcttaat	ttctaccaca	ctggcgccat	gttttgcttc	523380
aacagcgttt	actgtagaag	ttatcatgcc	ttccgagaa	tttgatggat	cgagtgggaa	523440
gatttttctt	tacacaacac	tttctgatcc	tagagggaca	ctctgtattt	tttcagggga	523500
tctctacatt	gcgaatcttg	ataatgccat	atccagaacc	tcttccagtt	gcttttagcaa	523560
tagggcgggg	gactacaaa	tcttaggaaa	aggtgggggt	ttctccttct	taaatatccg	523620
ttcttcagct	gacggagccg	cgattagtag	tgtaatcacc	caaaatcctg	aactatgtcc	523680
cttgagtttt	tcaggattta	gtcagatgat	cttcgataac	tgtgaatctt	tgacttcaga	523740
tacctcagcg	agtaatgtca	tacctcacgc	atcggcgatt	tacgtacaa	cgccccgtct	523800
ctttacaaac	aatgactcca	tactattcca	atacaaccgt	tctgcaggat	ttggagctgc	523860
cattcgaggc	acaagcatca	caatagaaaa	tacgaaaaag	agccttctct	ttaatggtaa	523920
tggatccatc	tctaattggag	gggccttcac	gggatctgca	gcgatcaacc	tcatcaacaa	523980
tagcgctcct	gtgattttct	caacgaatgc	tacagggatc	tatgggtggg	ctatttacct	524040
taccggagga	tctatgctca	cctctgggaa	cctctcagga	gtcttggtcg	ttaataatag	524100
ctcgcgctca	ggaggcgcta	tctatgctaa	cggaaatgtc	acattttcta	ataacagcga	524160
cctgactttc	caaaacaata	cagcatctct	acaaaactcc	ttacctgcac	ctacacctcc	524220
acctacacca	ccagcagtc	ctcctttgtt	aggatatgga	ggcgccatct	tctgtactcc	524280
tccagctacc	ccccaccaa	caggtgttag	cctgactata	tctggagaaa	acagcggttac	524340
attcctagaa	aacattgcct	ccgaacaagg	aggagccctc	tatggcaaaa	agatctctat	524400
agattctaat	aaatctacaa	tatttcttgg	aaatacagct	ggaaaaggag	gcgctattgc	524460
tattcccga	tctggggagc	tctctctatc	cgcaaatcaa	ggtgatatcc	tctttaacaa	524520
gaacctcagc	atcactagtg	ggacacctac	tcgcaatagt	attcacttcg	gaaaagatgc	524580
caagtttgcc	actctaggac	tacgcaaggc	tataccctat	acttctatga	tccgattaca	524640
tctgatgatt	tatctctgca	tccgcagccg	ctactgtggt	cgtcaatccc	aaagccagtg	524700
cagatgggtc	actattgtct	tttcaggaga	aacctcact	gctaccgaag	gctaccgaag	524760
cagcaacccc	tgcaaatgct	acatctacat	taaacccaaa	gctagaactt	gaaggcggtg	524820
ctctcgcttt	aagaaacggt	gctaccttaa	atgttcataa	cttcacgcaa	gatgaaaagt	524880
ccgtcgctcat	catggatgca	gggaccacat	tagcaactac	aaatggagct	aataatactg	524940
acggtgctat	caccttaaac	aagcttgtaa	tcaatctgga	ttctttggat	ggcactaaag	525000
cggctgtcgt	taatgtgcag	agtaccaatg	gagctctcac	tatatccgga	actttaggac	525060
ttgtgaaaaa	ctctcaagat	tgctgtgaca	accacgggat	gtttaataaa	gatttacagc	525120
aagttccgat	tttagaactc	aaagcgactt	caaatactgt	aaccactacg	gacttcagtc	525180
tccgcacaaa	cggctatcag	caatctccct	atgggtatca	aggaacttgg	gagtttacca	525240
tagacacgac	aaccatacag	gtcacaggaa	attggaaaaa	aaccggttat	cttctctatc	525300
cggagcgtct	tgctccccct	attcctaata	gcctatgggc	aaacgtcata	gatttacgag	525360

ctgtaagtca	agcgctcagca	gctgatggcg	aagatgtccc	tgggaagcaa	ctgagcatca	525420
caggaattac	aaattttcttc	catgcgaatc	ataccggtga	tgcacgcagc	taccgccata	525480
tgggtggagg	ctacctcatc	aatacctaca	cacgcatcac	tccagatgct	gcgttaagtc	525540
taggttttgg	acagctgttt	acaaaatcta	aggattacct	cgtaggtcac	ggtcattcta	525600
acgtttatct	cgctacagta	tactctaaca	tcaccaagtc	tctgtttgga	tcacgagat	525660
tcttctcagg	aggcacttct	cgagttacct	atagccgtag	caatgagaaa	gtaaagactt	525720
catatacaaa	attgcctaaa	gggcgctgct	cttggagtaa	caattgctgg	ttaggagaac	525780
tcgaaggga	ccttcccatc	actctctctt	ctcgcatctt	aaacctcaag	cagatcattc	525840
cctttgtaaa	agctgaagtt	gcttacgcga	ctcatggggg	catccaagaa	aatacccttg	525900
aggggaggat	ttttggacac	ggctcatctac	tcaacgttgc	agttcccgtg	ggcgtccgct	525960
ttggtaaaaa	ttctcataat	cgaccagatt	tttacctat	aatcgtagcc	tatgctcctg	526020
atgtctatcg	tcacaatcct	gattgcgata	cgacattacc	tattaatgga	gctacgtgga	526080
cctctatagg	gaataatcta	accagaagta	ctttgctagt	acaagcatcc	agccatactt	526140
cagtaaatga	tgttctagag	atcttcgggc	actgtggatg	tgatattcgc	agaacctccc	526200
gtcaatatata	tctagatata	ggaagcaaat	tacgatttta	aaccttattt	aacgacaggg	526260
ttgaggcatg	cctctttctt	tcaaatcttc	atctttttgt	ctacttgctt	gtttatgtag	526320
tgcaagttgc	gcgtttgctg	agactagact	cggagggaac	tttgttcctc	caattacgaa	526380
tcagggtgaa	gagatcttac	tcacttcaga	ttttgtttgt	tcaaacttct	tgggggagag	526440
tttttcaagt	tcctttatca	atagttccag	caatctctcc	ttattagggg	agggcctttc	526500
cttaacgttt	acctcttctg	aagctcctac	aaatagtaac	tatgcgctac	tttctgccgc	526560
agagactctg	accttcaaga	atctttcttc	tataaacttt	acagggaacc	aatcgacagg	526620
acttggcggc	ctcatctacg	gaaaagatat	tgttttccaa	tctatcaaag	atttgatctt	526680
cactacgaac	cgtgttgctt	attctccagc	cttgttaact	acgtcggcaa	ctcccgaat	526740
cactacagta	actacaggag	cctctgctct	ccaacctaca	gactcactca	ctgtcgaaaa	526800
catatcccaa	tcgatcaagt	tttttgggaa	ccttgccaac	ttcggctctg	caattagcag	526860
ttctcccacg	gcagtcgtta	aattcatcaa	taacaccgct	accatgagct	tctcccataa	526920
ctttacttct	tcaggaggcg	gcgtgattta	tggagggaagc	tctctccttt	ttgaaaacaa	526980
ttctggatgc	atcatcttca	ccgccaaact	ctgtgtgaac	agcttaaaaag	gcgtcacccc	527040
ttcatcagga	acctatgctt	taggaagtgg	cggagcattt	gcacccctac	gggaactttc	527100
gaattaaaaa	acaatcaggg	gaagtgcacc	ttctctata	atggtaacac	aaatgagcg	527160
ggtgcgatct	acgcgaaac	ctgcaacatc	gtagggaacc	aggggtgcctt	gctcctagat	527220
agcaacactg	cagcgagaaa	tggcggagcc	atctgtgcta	aagtgtctca	tattcaagga	527280
cgcggtccta	ttgaattctc	tagaaaccgc	gcggagaagg	gtggagctat	tttcataggc	527340
ccctctgttg	gagaccctgc	gaagcaaaca	tcgacactta	cgattttggc	ttccgaaggt	527400
aatattgctg	tccaaggaaa	catgctcaat	acaaaacctg	gaatccgcaa	tgccatcact	527460
gtagaagcag	ggggagagat	tgtgtctcta	tctgcacaag	gaggctcacg	tcttgtatct	527520
tatgatccca	ttacacatag	cctcccaacc	acaagtccgt	ctaataaaga	cattacaatc	527580
aacgctaatt	gcgcttcagg	atctgtagtc	tttacaagta	agggactctc	ctctacagaa	527640
ctcctgttgc	ctgccaaac	gacaactata	cttctaggaa	cagtcaagat	cgctagtggg	527700
gaactgaaga	ttactgacaa	tgcggttgct	aatgttcttg	gcttcgctac	tcagggtctc	527760
ggtcagctta	ccctgggctc	tggaggaacc	ttagggtctg	caacaccac	gggagcacct	527820
gccgctgtag	actttacgat	tggaaagtta	gcattcgatc	ctttttcctt	cctaaaaaga	527880
gattttgttt	cagcatcagt	aaatgcaggc	acaaaaaacg	tcactttaac	aggagctctg	527940
gttcttgatg	aacatgacgt	tacagatctt	tatgatattg	tgtcattaca	atctccagta	528000
gcaattccta	tcgctgtttt	caaaggagca	accgttacta	agacaggatt	tctgtatggg	528060
gagattgcga	ctccaagcca	ctacggctac	caaggaaaag	ggctctacac	atggctccgt	528120
ccctgtttaa	ctccagctcc	tgatggagga	tttctgggag	gtccctctcc	tagcgcaaat	528180
actctctatg	ctgtatggaa	ttcagacact	ctcgtgcgtt	ctacctatat	cttagatccc	528240
gagcgttacg	gagaaattgt	cagcaacagc	ttatggattt	ccttcttagg	aaatcaggca	528300
ttctctgata	ttctccaaga	tgttcttttg	atagatcatc	ccgggttgct	cataaccgcg	528360
aaagcttttag	gagcctatgt	cgaacacaca	ccaagacaag	gacatgaggg	cttttcagggt	528420
cgctatggag	gctaccaagt	gcgctatcta	tgaactacac	ggaccacact	acgttaggac	528480
tttctttcgg	gcagctttat	ggaaaaacta	acgccaaccc	ctacgattca	cggtgctcag	528540
aacaaatgta	tttactctcg	ttctttggct	aattccctat	ctgactcaa	aagagcgagg	528600
ccttaatttc	ctggaaagca	gcttatgggt	attccaaaaa	tcacctaaat	accacctacc	528660
tcagacctga	caaagctcca	aaatctcaag	ggcaatggca	taacaatagt	tactatgttc	528720
ttattttctg	agaacatcct	ttcctaaact	ggtgtcttct	tacaagacct	ctggctcaag	528780
cttgggatct	ttcagggttt	atttccgcag	aattccctag	tgggtggcaa	agtaagttca	528840
cagaaactgg	agatctgcaa	cgtagcttta	gtagaggtaa	agggtacaat	gtttccctac	528900
cgataggatg	ttctttctca	tggttcacac	catttaagaa	ggctccttct	acactgacca	528960
tcaaacttgc	ctacaagcct	gatattctat	gtgtcaaccc	tcacaatatt	gtgactgtcg	529020
tctcaaacca	agagagcact	tcgatctcag	gagcaaatct	acgccgccac	gggttgtttg	529080
tacaaatcca	tgatgtagta	gatctcacgc	aggacactca	ggcctttcta	aactatacct	529140
ttgacgggaa	aaatggattt	acaaaccacc	gagtgtctac	aggactaaaa	tccacatttt	529200

aaaactctaa	gctctgctta	gagttttctg	tagccccggt	cgtcttagaa	tcctctatcc	529260
atcatcgaag	aacttagcaa	tgaaggccaa	gattctcact	ctatgagaac	gccccccct	529320
ctctcaagtc	tatttgaaaa	gaaagaatat	cttttgaaac	tatagtctgt	tttggaagaa	529380
agagaatacg	atctgctttg	catccctagg	gaaagcatct	ttcatcaatg	cgattacttc	529440
acgttgcaat	ggcttcactt	gtttatgcat	acgttaacaa	ggattatgaa	tccttgaaag	529500
actcgctctc	ctctcgattc	tcgtgtagaa	ttcactccct	aggttttatc	tttagagctc	529560
gcagcagatg	aaacttttagg	attcagttcc	tcactcccat	catcagaaat	caaagggtct	529620
ttaccagaaa	tgggcaacac	gtcactgggg	cataagaact	ctatttggct	cgctaactta	529680
tcgaatgctg	cacagttcac	aatgagtgtg	tgctcttgag	aggtagcgac	gatactacta	529740
tcttctatga	ctatgccctg	agaacttggt	tacggtatca	tgtctaaatt	tgaacgtaa	529800
gatactaaag	catctgttac	tgaagcctct	agagcttctc	tctcataagc	aaaaagatcc	529860
ggattgcgga	atctccacac	agactgtttt	atcacggcgt	ctagagcaaa	ggctagattt	529920
ttctctgtgg	agactgtgtt	gcagaggagt	gtccttaact	gctcttcagt	taaagaccct	529980
tgcattgttt	gttcttgttt	ctctctgac	tcctcccgct	aggcaatatg	actggagacc	530040
caagggagat	gctcatcacc	gaaagcgacc	actttacatc	ctgaagcata	ggcatcagca	530100
gcttcttttt	cacagaaaac	aaaaattctt	tcggatgcca	actgcaaatt	ccgaatatcg	530160
gggtgccctt	caggaagctc	tgagatcacc	accgtcatag	atctcccttc	atcggcattc	530220
aatagcagac	gttggtgaac	tgtagtctcc	ccggagagat	cacaacgcac	tacattcaga	530280
tagctatagc	cttcatcgct	aagctcttca	ataagctgag	agactgcttc	aggaggcagg	530340
ccgaggatat	taggttcaga	atgattacaa	acgacaacta	cgtctttctc	cttctcatca	530400
taggacacta	aaagtaaaaa	gcgagccac	gactctacgg	aagtatcggt	agcaaaaattt	530460
agagatacct	cacgaagctc	tttcttactt	atgttcttag	catccacaaa	tgctgaaaat	530520
aacaaaaatt	tcagctcttc	atgggtgaga	ctgcaagat	aggaaatggc	gtgagaccct	530580
tgagataaag	gagcatggag	tcgttgccgg	ttctaagagc	aatccctgaa	atcctgggct	530640
ccaagtccca	ttcccaaagt	atgcaactga	tggtgtgtac	gagaaatctc	tttataaagc	530700
tctgtcttat	ccttttcggg	atttataggt	aaggaaagcc	gagatctata	cctagatggc	530760
aatgtgtgca	taacattcac	ccagggaaca	gtacctaacg	aagtccctag	ggcctgctgt	530820
aaaatttttac	cctcccttaa	gtaagaatcc	ttcccataac	agccgaccat	aagggtcaaag	530880
tgtttcgtat	cttcgccctc	ggcaccctga	ggttccaaga	cggaaaagaca	ctgaacttca	530940
gaatgtagac	ctagagaacg	gagctgtttt	tccttatcag	aggagatatc	ccctaccac	531000
tcctnattaa	aatcgataag	aagatataga	gttgtcttgg	atttgggata	gagttgaatg	531060
acctcattcg	ccaagcgtac	taaatctctc	tggtcttcag	gactgacgag	atctatacca	531120
acaatagcta	tagagtccaa	ctgaggagta	ggggcataac	tataggatct	ggtgatgcga	531180
ttgcgaactc	tagaaaaggc	tttgccaagc	tcgctaacat	gaactccctt	atcgagttaa	531240
agaacctcac	tagaggccat	atctgcataa	ggattctctt	gatattgccc	gtggacttta	531300
tctagatctt	caacctcgat	agttttccta	aggctcttta	gctgattttc	gattctagaa	531360
atatgatctc	ggcccccgat	cttttctact	ttcagtatat	gagcaatata	tgaagggaac	531420
ccagggtgtg	agactccctt	ctcgaagcaa	tgagagatca	accaatcgac	ttccataaca	531480
agatgccctc	caatggggat	ggccttaatc	accctaaag	cgaagtgggt	aattcgagaa	531540
tataaaggac	gtgagaaatt	aaacgcctgc	acaaagtgat	gacgaactac	agaaaaccaa	531600
ccatgtaagc	aatgagtcac	aagaaattta	cgttttagatt	caaaagtaca	aggaatttaa	531660
atgatgtgcc	aaaaatacaa	aataaacaat	ttgtattaga	catcaagtac	actgaaaata	531720
aaacgctctt	gttgagcacg	ttttcctaac	aaatacgtta	tcgattctta	ggggaaatag	531780
gttctgacaa	ttagatttga	gagactctgt	tatgagagag	agaccatagg	cacaaagaca	531840
cgctgtaaa	gcagagtatc	ctgattcaaa	gcttagacat	tgcgatcgt	tatcctcaaa	531900
ccgtcgaaat	ttctttgtct	ctatttgttg	gctcctaagt	gagcttcctc	ctctggaatt	531960
ggagatattt	ctgaaggagc	tctgctaaga	gtcgatccta	gagattcaac	agcttcatct	532020
aatgctgtga	aatctataga	caattgcgcg	gattgctgcg	tttctagatt	cccctgagga	532080
tctttttttg	cgttgttagg	tagtgatgta	cagtagtaaa	gagttgttcc	cctaaccgcc	532140
gtctctcaat	agagagaagt	tctggcatac	gggatctcca	tatagactgg	cggattgcag	532200
catctaaaga	acaagcgaag	ttctgttgcg	ccgtcagctg	attacaaacg	taaatctcgc	532260
tctcgtcttg	atccaaagca	gcttcttggt	tctgttttct	aacttctctt	ttccaaagac	532320
catgctttct	attccacaga	ttagattctc	gctccaaagt	taagacttct	tccatcataa	532380
agttcgcgca	tcctgacgta	tagacatcga	cagcatagca	ctctttacca	caaagcatct	532440
cttcagacgc	caaatgcaaa	cagcggtat	ctccttgaga	tactgaatcc	tcacagaaaa	532500
tcattggtaaa	ggctttctct	tgagaacttt	catttaagat	cctacgttct	tctacacaca	532560
tgctattaga	tctaaaggca	aaaatattga	agtgcgaata	ccctcgacac	tctagctcca	532620
taataaagtg	ttggaagctt	ggctcctcct	tccagtcggt	acccacacaa	gaatcacata	532680
caacgacaac	cacattgcga	tcacttctgc	tcactcctct	aaaaaagcca	aagtgtgcc	532740
ttaagtaagt	tttgctattt	aagataagat	ttagagatat	aggttgcagt	atgggtactgc	532800
tcaactcctt	aggattcaga	aatgccgcta	aaattgtttt	ttgtaaccgg	ggattttcta	532860
agtctgcaag	gtaggaatgc	caataatgcc	cttcagataa	gggagcatgc	acccgttttg	532920
ggtccatcaa	gatccctgac	cgactatctc	caaaccctaa	actaagaacc	gaagagcgct	532980
ctcctacgta	taccaatcga	gaatatagct	gttctttttc	taattcagag	tactctagag	533040

ctttctcttt	atctcccttc	atctccaaag	atgaaaatgg	agagaaatcc	cacaaggatt	533100
gtgaaagagg	cttttgcccc	acatgaatcc	aaggggtttc	ctcccctgac	ttttctaact	533160
cttcctgaat	ctgattcaac	gtaccttgat	cattctcccc	atgatacacc	atccaacagt	533220
cacaagttgc	ttgtttgact	acatcacccct	gattaaagtc	caaacaagca	atcttggggg	533280
ttagttcgca	atcactaagt	aacttccgat	tctttttgtc	catagcattg	cgaccaccag	533340
aagctgttag	atatagagaa	atcgtagcgt	caggatagag	tcttttgagtt	tcattacaga	533400
gacgggctag	atgcaagaag	tcgtcaactt	caaaaggatt	catatcgttt	cctatgatgt	533460
aaatcttctg	cagttttggc	cgtggagcct	gcaaatacgc	ctgtcttaca	cgattacgaa	533520
ttttagagaa	ggcaagccct	aacgttgcac	cttgaacttc	gggatagaga	gtgagaactt	533580
ctacagggtg	gattcccccg	aaaggatgca	caggaatctt	cccatggacc	ttatcctcat	533640
cttcaggagc	cacagcgact	ctctgcctct	tcaaagtctc	cactacacga	gcaatgtgat	533700
cgcgaccagc	aactttctct	gttttcagaa	gactcaccac	atcagagaca	aatgtcggct	533760
tggtcacgaa	actctctaaa	tacctagaaa	cgagccactc	tatcccaaca	ataatgtgac	533820
ccacaacagg	gatccccctg	atgaccccta	atacaaattc	cgtaatacga	gcacaaaacg	533880
gcaaagaaaa	atcaaaggct	cgataaaaag	gctcacgaac	tatagaaaac	caggcagata	533940
aacaagaagc	cataacacga	ctaggaagaa	atacttagga	agaagtattt	taaaaaaaac	534000
ttgaaaaaag	caatctctaa	gatacttagc	gactcctata	gccacaagaa	attcgctatt	534060
tttaaaatta	gaaagaggag	acctgagaaa	ggttgtaaaa	agcgcttaga	tacaactatt	534120
tagaatccta	tcctggaaat	cagaaatcta	cggaatacta	gtgtagaaag	aacaaatata	534180
gagagagtc	tctaaggagt	ttgtgcactc	ctggggtttg	tgaaattaag	atattcctag	534240
gcaaaccctt	cctggaatcc	taggtacatg	gaccaaggat	tccatctgga	gataagaaat	534300
ttctctagta	tttttacttt	ctaactgcct	tcatttttgcg	aggaatcagg	gttactatct	534360
ggattaggaa	cgggatgcgt	aggatcattg	cctgaatctg	cagggaactc	ggctggggag	534420
acttgaccca	tgcgatctag	ctcttcgaag	ctgataacga	cctcatgttc	ttcggtagtt	534480
cttttcccca	tattctcatt	acgctcctga	ctccctaaat	aggaaaatat	cgcagttaag	534540
aaactcctcg	ctagtgcctt	tctttccata	gtaagaagac	ctttcgaacg	gaatctccag	534600
atcgctgtgt	ttaccacagc	atctagagaa	aatacaaaat	tctgttgtgt	agtgagcatg	534660
ctgctcaatt	gatcctgaga	ataaattact	ggttctctgg	cttcttctcc	tgcttcatct	534720
tcgacacgtg	cctcccattg	tctatattca	atagcctgag	gactctgcat	ctcagaaaac	534780
tgaatgcagg	aacatccaga	ggcacaataa	tctgctacgc	tggggagatc	cttagcaacc	534840
ataccttctg	cagctagctg	caaacaacgg	aaatctgctg	cactaatggg	atcttcaa	534900
aagatcaatt	tgaaagactt	cccttcagaa	cgatctccaa	agaactgacg	ttcttttaca	534960
atcattttcc	tgattttata	ggagaaaatg	ttcaaatagc	tatatccaga	catttgtaat	535020
cttctgggtc	gaatgttcat	tgagtcagga	tcaagatctt	ctggacgagg	agttccgtgg	535080
gcaagggtaa	ctatgtttct	cccttcttgc	tgaccgcgaa	caaggcggaa	aaataacgag	535140
tccaattcta	atggcaatct	agcgatattg	aatgctacag	gacgaagatc	ctcgctacta	535200
agattgccag	gatctaggaa	aggcgaaaag	actaaagttc	gtagatcctc	attttctata	535260
tccgcaagg	aggaatgaca	ataatgccct	tgggatagag	gagcatagat	tctatctggg	535320
tccatcagga	gtcctgcac	ctctggtttt	aatcccaaac	caagcatata	ctcaggtgga	535380
tacgatcgac	tcagttgtcc	gtacaaggaa	tccttatccc	cctcactttc	agggagttct	535440
ggtggcgatg	ttgggtctgt	agattgtctt	gtatgtgagt	atgaagtaaa	gtttgggtggg	535500
taataaaaa	cctttgtgtc	ttcagtaaca	tgaatccaag	gaattggatc	tgactcttc	535560
cctagacact	gctgaatata	ctgcccgtct	atattatgct	gttgctctcg	tgaataatag	535620
ccaatccaaa	gttcgggatt	ttcaggagag	ccagcgtcgt	cttctttact	gtccttgcac	535680
tggatttctag	agtcgagacc	tgagttatgt	aggtaactgt	tcttctctgc	agtagttgta	535740
tcgcacatct	gagattcgcg	attcaagcct	gtcaaatata	gacaaactaa	cgcttcagga	535800
tgcagtctct	gcgtttcatt	cgcgagactc	acaaattcgc	agaaatcttg	aggagtttta	535860
agtttcgaac	ccacaataga	aatcgtacgt	atctcgggtc	ggggggcctg	taagtacgca	535920
cgagtcacgc	gcgtgcgaat	cggagaaaa	acagtatcta	aagttccccc	tctttctccc	535980
ggcttaagtt	ttaaagtttc	ctcggatttt	aaacgaccaa	aaggacagac	aggaaacttc	536040
ccatgcacct	tatcttgatt	ctcaggagtt	atgggtcccc	tttctctttg	caatatctcc	536100
gccactcgag	atatatgac	tcgacctaac	gccttctcag	tctttacaat	ctgaacgaca	536160
tctgaggtaa	aggaggacct	agtaataatc	ccggcaaacac	aggaagaaac	taaccactcc	536220
atccccatga	caatatgtcc	tacaataggg	atggccttga	tgacccttaa	agcaaaattc	536280
gtaaccctag	aacaaaagg	acgagagaaa	tcaaacgcct	taacaaaatg	ctgtcgaacg	536340
gtagaaaatcc	aagaagaaat	atagggaaat	ggcatnncaa	caaaaaaat	aaaattagaa	536400
acaaaacaatt	ttaaataaca	acatagaaaa	tatcaattaa	attgaataaa	cagcttttaa	536460
atatttttag	tattattttc	tttaataaac	taataaccaa	ctacttttga	agtcctagct	536520
tggattttaat	atcctcatct	aggggtaaaa	taagaaacag	cccttagatt	cgagcagaaa	536580
tttcagtcag	attctattca	ggaaaacctc	agattgtttc	agagtcagga	gaattcgaga	536640
ttctgaggga	atthagtttt	cagggagccc	tttgcaagga	acttttaagg	tatcagacaa	536700
acgttactca	tcttcgtgca	tgctagtcgg	agatgctgtt	gccccgtag	cggtcgaagc	536760
tgctgttgca	tcttcgtcat	catcagaaga	gcatctttct	tgtagagcct	gctctaagg	536820
ggtaaagtcg	acagaaaact	taaagctttt	cttggttctc	tgagatccca	aaatcccgac	536880

dataactctga	atatattcct	ctaagctgac	tttgatttct	cttcctaaag	cctgactttc	536940
aacataaaat	aaattgagtt	tctcttgtga	tctccaaccg	gcctgtttta	ttacagcgtc	537000
taaagtaaat	aagaagttct	tctgtgccac	gatttttatca	cacatatagg	ctctgaaata	537060
ttctctgaaa	gaaacactac	cttcttctct	caacttgttt	gtagaagttc	tccaattcct	537120
gagcccagga	tgcatttgga	ttttcgtaga	ctaagacttt	acatccccga	gcacatgcat	537180
ccgcggcac	aagagaactg	gagactaaaa	tcctatccga	ggctaattgt	aaactacgga	537240
tatcttcgct	acctaaagga	agatctgtaa	tcctgacagt	aaaggaccgt	ccttgagat	537300
ctcgcccttag	aatctgacgt	tcctgaacct	tggagactcc	ttcggggctc	accgagagaa	537360
tgtttagata	cgaataacct	gattctctta	agtcttcttc	taatagagac	aatgcctctg	537420
gggacaatcc	ttcttccaga	agttttgcat	cattacaaac	aacagctacg	tgcttttctt	537480
tctcgtcgtg	cagaacacga	gatagaaact	ctgaccatct	ctgtccaaac	gaagagttgc	537540
caaagtttat	agagacagaa	cggaaatggt	cgctagttag	atttttaggg	tctagaaacg	537600
ttgacagaag	ggaacgacgt	agctctttgt	tttgcaaact	taaaagatag	gaaggacacg	537660
agtacggtga	agataaaggc	gcgcaaacc	tatagggatc	cagaagccac	cctgacagg	537720
aattctgaat	tcctagattc	agcttataat	gatcctaac	agacataaac	agagaacaa	537780
acgtggagaa	ggattccagc	ttattccatc	ttttcttttt	acctatttct	ggggaatgat	537840
cgcacggaga	gagcttctct	tggtcttggt	attgcacgga	aatggaagg	gtctcttcta	537900
gagcaaagtt	tagaagatgt	tgtatcacct	agggatcttg	gacttcctga	tctttcccgt	537960
aacaggtaat	cataaaatcg	acagtagcga	cttctggcac	tgaagggaag	cctgcactcg	538020
taagggatat	actctctatt	ttaggggtcta	aacctagagc	tcggagttgc	cctttttcct	538080
cttcagaaat	ttcacagtcc	cagacatctg	ccaagttctt	cgctaaatag	agcttcactt	538140
tagtatgggg	atagtgattc	tgacgcctat	tagcaagacg	cacgaaattt	atgaggtccg	538200
cagaatctcg	gagaccaaaa	cccacaagag	caagatcttg	aatcataggt	ttctctacgg	538260
acctatagcg	ataggttaac	ctactacgaa	cgcttgacg	tgctcatct	acagtagaga	538320
gttcttcaat	cagggagaa	gttggacaat	ttctgtgggt	gtgatctcta	cgaagggatc	538380
ttctgggggt	ctcccggtga	ctttgcctag	atcttcttgg	gaaatgggga	ctctcaagct	538440
acttaaatag	gcttctaggg	gagctaaaca	attatgacct	cggtgttgtt	ctactttaat	538500
agcactagag	acatcagaag	taaacattcc	atgacgaacg	gtgtgtctgg	gaatccagga	538560
aatcaaccac	tcgattccca	tgacaatgtg	tcctaatacg	ggaattgcct	taatgatccc	538620
caaagcaaaa	tttgtaatcc	gagaacaaac	gggatgggtg	aaatcaaagg	cgtttacaaa	538680
atgctgtcga	acgacagtaa	accaagaaga	aatacttgga	caagccacag	tagaaattta	538740
tgtataaaaa	ttttaacaaa	gttattttaa	tcaaataaga	cattaaaaac	aataagtatc	538800
taattatgat	aataatattt	ttaaaaacgt	ttttatttga	aaaataaaaa	gtcagtgtaa	538860
agagttcaag	ctttcataaa	atttttctat	acaaaagaat	cggtgggatac	ctaagagaaa	538920
aaacctcgat	accctctata	gacaactaga	caataagaac	cctcgatacc	ttcaaaaaac	538980
ccagaatgac	ctaagaaaaa	agaagaatct	tcaaaaaaga	gctctgctgg	actaataaaa	539040
aggttcatca	aaacaaacac	cttagaaagg	tgtgtctaat	tagttcccat	caatctgcga	539100
tttcggttgc	aagattgcga	tcttttagtc	tctgtattgt	tctcctcaga	aggtgcactc	539160
tgagctgagc	cacaagctgc	acacacagcc	tcgtctaacg	tagcaaaact	cacattgaca	539220
ttacatgcga	cttgaggctg	tatagtcccc	tcaactaaga	gactgctgcc	gatataacct	539280
tctaaagcac	gtcgcagtgc	atctcctaaa	gcctgacttt	ctacagcaaa	aagatcccgt	539340
tttttaaact	tccacatggc	ctgttggtat	accgcattga	gattgaatac	gatgtccttt	539400
tctaaaacta	ctctcgtaga	tgctgagacc	cctaaaggct	ctcctggaat	cccctgacgt	539460
tgaagatcgc	ctgccctgtc	gatgtttcta	tagaacgacg	catactgttg	cgcccactct	539520
tgctcgggat	cctcatattc	taagatctta	cattcagaag	cacaggcatc	agcagcatcg	539580
agagcactaa	gaaactaaga	tcctatctga	cgctagctgc	aagtgtcgga	tatccgaact	539640
cccttcagga	agatcagtga	ggattacagt	gaatgacctc	cccgaaggat	cagaacttaa	539700
aattctacgt	tccttaacac	acgtgcgttc	ctgactcact	gaaacgatat	tcaaataaga	539760
ataacctgac	tcttccagtt	cgttctctaa	tagagataaa	gaatgtgagg	gaaaactcct	539820
ttttataagt	tgtggattat	tgacagactac	agccacatgc	ttttctgttt	catcatgtag	539880
aacacgagat	agaaaactcag	accacctctg	acccaaagga	gagtttccaa	agtttatgga	539940
cataggacgc	ggatttccct	gaccagaatt	gttgggatct	ataaaagcgg	ataacaagaa	540000
acaacgaagc	tcttcacttt	ttaaatctaa	gaggtatgag	gggcaggaat	actctccaga	540060
taaaggagcc	gaaaccctaa	gaggatctaa	aaatactcca	gaggcaaaat	cttccattcc	540120
caagtgaaca	catatcttat	cacatctagg	gttagacagg	gtggtatacg	tttgaagatg	540180
ctcctgctca	ctccaaggga	tcctctgate	gggtgcccgt	cctccttgag	aaccaggaaa	540240
gaaatagtag	ctataaaaaag	gatcgtcagg	tctataggtt	acagaaatcg	cagggatatg	540300
ttcggaagaa	agattgagta	gactctttat	agagtccacg	tctctgacgg	actgttgttt	540360
cccgtataaa	ttaatgagaa	gatcacagga	aggcaagttc	tcggattgaa	gatatttctg	540420
gagcaggaga	gcggggggccg	acacacattt	gatttttagca	tccaaaccta	gagagcggag	540480
ttgctgttct	ttttcttgag	aaatcgtacc	gtcacactga	ttccatatct	tttggataga	540540
gattaaataa	agttttatct	gagtttgggg	gtactagttg	tgtatgccgt	tagccagacg	540600
aacgaaatcc	acctgatctt	cgggatctaa	aatgtcaaaa	ccgacgagcg	taagacaagg	540660
gacttccaga	ggagtgactc	gttgatacgc	cttggttact	cggttgcgga	ttccataaaa	540720

cgcgcgacct	agctctccca	gatattgatg	aggaaccata	ttcagatttt	cttggggag	540780
cctgtcgcga	acataatctc	tggagacctt	cccatggatt	tttccctaaat	ctccttcagg	540840
aagtcgaacc	ctaagctgtc	tcaagtactg	ttccacccaa	gcaaggggat	tataacctcg	540900
agttttttct	attttcacga	tactagcaac	gtcagaagta	aatgccgggt	tcccaaacct	540960
tcgtgcagaa	catgtggaaa	ctagccaact	taccctata	acaacgcac	ctaaaatggg	541020
aatagccttg	atgaccccca	aagcaaaatt	tgtaatccga	gaaccaagag	gacgtgtaaa	541080
atcaaaaagcc	ctaataaaaat	gctgcttaac	tgtagatata	caaatagaaa	tatagcatgc	541140
cataggatca	aaccaacatt	gaaaatgaaa	gcgtacgcag	gctatataaa	gatttaaaaa	541200
aagatagaaa	attaactatc	ttttaataag	aacaacacga	tagtttttat	ataaaaaaatt	541260
gaattctatc	gcaactaatt	aagagtcttc	aagatccgaa	ggatgatcat	ctgaaggatc	541320
ctcagaggta	gagggaaacat	cttcacacga	acctgggaag	agcgcctctt	taagaggaga	541380
acagtctgcg	ataatctctt	tttgtatgaa	cgggcctttc	gatgtttttt	cgtgagagtt	541440
tgtgacatat	tcaaggtacg	atacgataga	tggcaagcac	tgtgttttca	agtctagggc	541500
ttcacactct	ttatctatca	agctgggatg	tttatgagtc	cataccgctt	gctttatagc	541560
ggcgtctaac	attggaatga	agtgtctcgt	gacagtcact	cgatcacaga	atgctaagaa	541620
tccttcccag	aagggtttttg	aagggagcgg	gagttctcca	gactctagga	tccttgatt	541680
cgcctgcgta	atcagtttaa	attctcttga	gttaaatcct	gctgatacgt	ctacagcatc	541740
tgcgaaatcg	gcgtggcgac	tgaagttcc	aggtctccaa	tttgtatgat	cgattttcaa	541800
gagcttgcat	cttgacgat	aggcatctac	aagatcaaac	tctctagaga	ccatgatcct	541860
ttcagaagca	agttgtaaac	tacgcagtgc	tgtatcccct	agatataaaag	cgcaaatcac	541920
tgtaaaataa	cgcctgaag	ttccctctaa	ttccttacgg	aataaaagct	gaggactact	541980
atctccgtga	caagaaaata	tattgaggta	ggagtagtcc	ttagagttca	attcctctac	542040
taatttgcat	acttgggttg	cgggtaagga	gagaactcct	ttaaaaacca	cgacgacgtt	542100
ttttcccggt	tcacacagta	agaccatcga	gaggaaatct	ttctgttgta	gaggagaaaa	542160
agaatctcca	acgtttatag	agacttgag	gagttctcct	gctgagatat	tctgaggatc	542220
taaaaacatc	gataatatta	aatcctttta	atgttgatcc	actagatcta	caagatacga	542280
gtggcaatag	tgatcctcag	atagaggggc	gcagagcatt	ttttcatcga	aaaggaatcc	542340
gagttcctct	tcgagactga	accatagaca	cggttggtaa	tgctcattcc	cacgagatag	542400
aaatgtgtat	agctcttttag	catcctgccc	gactccttgt	ttcatcatag	agtctacgaa	542460
agcattcgag	gtctcatcaa	taggaattcc	gactgtggat	atattgactc	tgggagttct	542520
acagtttgga	gttcccagga	gctgtccgt	tttttcgtag	ggagaggaca	gctacgactc	542580
gtgtgcacgt	agatggagag	atcgaagggc	tcactctctg	gaacagcatc	ctcgtgaaa	542640
aaccacaac	ggatgtgcac	attttctaca	tgtaattttg	agagtacagc	actttgattt	542700
acattcttgc	ccataaagaa	tcttaaatat	atttgcgatt	cagaatagat	acaactcata	542760
taagagatta	gccgctctag	gatcttgga	ctttctgaat	cgagaactcc	tatatagacg	542820
atggcaattc	tatgtaggtc	gggttgcccta	gcacgactgt	attctgtagt	cacacgggtg	542880
cgtagtggag	caaataatag	aaataaattt	agagctgtcc	cctcagagaa	caactgtagg	542940
aacttgagac	tttggtatct	aaaaaaaagg	agctgaaggc	agatctccgc	gaaccttccc	543000
ctcgtctcta	ggctctaatt	agagcctttg	tctctttaga	atatcttcaa	ctcgacttct	543060
atggctgcta	cccacgacgt	gttctactcg	cacgatctga	tccacatcgg	aaggaaaattc	543120
tggttttttt	atcctagaga	ggagccagtc	cagccctaca	tacaactgcc	caataatagg	543180
aagcaatgca	atcactccca	aagcaaaatt	agaaattcgt	gaacacaggg	agcgagtaaa	543240
atcaaatgct	gcttgaaagt	gctgttgac	cttcagatac	caaagagaaa	agtaataact	543300
cattaaaaat	gagtctttta	aaaaatactt	tactttaaaa	aacagaaaaa	atctattatt	543360
ttctaataat	caaaatcagc	aaaaatctat	aggaatagag	ataagtggct	cttatgagta	543420
caagtctccc	cgatggctct	ttgtttttat	ctctaacaga	ccctcggtgt	ttcggaagag	543480
ttcctagggc	atcccctagg	gatataagga	ggctctccga	tcccaaactc	cacaagctcc	543540
ctaaaggcaa	acgacctga	gaacccaaaa	ctgctctaag	caaagtatgc	aaagagcttg	543600
atcctctgac	tacttgctgc	cattttccaa	agtatgatgt	acgtttacta	aaactcttgg	543660
actcgcattt	tattgtgaaa	aaaggaaatt	aaaatcgtct	tgtcttaaat	aagataactt	543720
taaactactc	ataattagac	actataaaac	aaattataga	caaaaaatct	agcattgatt	543780
tattcagaat	atttctttct	atttgtgaac	gagtatgcgc	tttttttgct	tcggaatggt	543840
gcttcctttt	acttttgtat	tggctaata	aggtctccaa	cttccttttg	agacctatat	543900
tacattaagt	cctgaatata	aagcagcccc	tcaagtaggg	tttactcata	accaaaacta	543960
agatctcgca	attgtcggga	atcacaatga	tttactcttg	gactataagt	actatcggtc	544020
gaatggagg	gctcttacct	gtaagaatct	tctgatctct	gaaaatatag	ggaatgtctt	544080
ctttgagaag	aatgtctgtc	ccaattctgg	cggggcaatt	tatgctgtct	aaaattgcac	544140
gatctccaag	aatcagaact	atgcatttac	tacaaacttg	gtctctgaca	atcctacagc	544200
cactgcgagg	tcactatttg	gtggagctct	ctttgccata	aattgctcta	ttactaataa	544260
cctaggacag	ggaactttcg	ttgacaatct	cgctttaaat	aaggggggtg	ccctctatac	544320
tgagacgaac	ttatctatta	aagacaataa	aggcccgatc	ataatcaagc	agaatcgggc	544380
actaaattcg	gacagtttag	gaggagggag	ttatagtggg	aactctctaa	atataagagg	544440
aaattctgga	gctatacaga	tcacaagcaa	ctcttcagga	tctgggggag	gcatattttc	544500
tacccaaaca	ctcacgatct	cctcgaataa	aaaactcata	gaaatcagtg	aaaattccgc	544560

gttcgcaaat	aactatggat	cgaacttcaa	tccaggagga	ggaggcttta	ctaccacctt	544620
ttgcacgata	ttgaacaacc	gagaaggggt	actctttaac	aataaccaa	gccagagcaa	544680
cgggtggagcc	attcatgcga	aatctatcat	tatcaaagaa	aatggctcctg	tatacttttt	544740
aaataacact	gcaactcggg	gaggggctct	cctcaactta	tcagcagggt	ctggaaacgg	544800
aagcttcac	ttatctgcag	ataatggaga	tattatcttt	aacaataata	cggcctccaa	544860
gcatgccctc	aatcctccat	acagaaacgc	cattcactcg	actcctaata	tgaatctgca	544920
aataggagcc	cgtcccggt	atcgagtgt	gttctatgat	cccatagaac	atgagctccc	544980
ttcctccttc	cccatactct	ttaatttcga	aaccggtcat	acagggtacag	ttttattttc	545040
aggggaacat	gtacaccaga	actttaccga	tgaatgaat	ttcttttctc	atttaaggaa	545100
cacttcggaa	ctacgtcaag	gagtccttgc	tgttgaagat	ggtgcggggc	tggcctgcta	545160
taagtcttc	caacgaggag	gcactctact	tctagggtcaa	ggtgcggtga	tcacgacagc	545220
aggaacgatt	cccacaccat	cctcaacacc	aacgacagta	ggaagtacta	taactttaaa	545280
tcacattgcc	attgaccttc	cttctattct	ttcttttcaa	gctcaggctc	caaaaatttg	545340
gatttacc	acaaaaacag	gatctaccta	tactgaagat	tccaaccga	caatcacaat	545400
ctcaggaact	ctcaccttac	gcaacagcaa	caacgaagat	ccctacgata	gtctggatct	545460
ctcgcaactc	cttgagaaag	ttccccttct	ttatatgttc	gatgtcgctg	cacaaaaaat	545520
taactcttcg	caactggatc	tatccacatt	aaattctggc	gaacactatg	ggtatcaagg	545580
catctggtcg	acctattggg	tagaaactac	aacaatcacg	aaccctacat	ctctactagg	545640
cgcgaaataca	aaacacaagc	tgctctatgc	aaactgggtct	cctctagggt	accgtcctca	545700
tcccgaacgt	cgaggagaat	tcattacgaa	tgcttctgtg	caatcggtcat	atacgggtct	545760
tgcaggactc	cactccctct	cctcctggga	tgaagagaag	ggtcatgcag	cttccctaca	545820
aggcattggg	cttctgggtc	atcaaaaaga	caaaaacggt	tttaagggtat	ttctggtcca	545880
tatgacagg	tatatgtcta	ccaccgaagc	aacctcttct	caaagtccga	atttctcttt	545940
aggatttgct	cagttcttct	ccaaagctaa	agaacatgaa	tctcaaaata	gcacgtctc	546000
tcaccactat	ttctctggaa	tgtgcataga	aaatactctc	ttcaaagagt	ggatacgtct	546060
atctgtgtct	cttgcttata	tgtttacctc	ggaacatacc	catacaatgt	atcagggtct	546120
cctggaagg	aactctcagg	gatctttcca	caaccatacc	ttagcagggg	ctctctcctg	546180
tgttttctta	cctcaacctc	acggcgagtc	cctgcagatc	tatcccttta	ttactgcctt	546240
agccatccga	ggaaatcttg	ctgcgtttca	agaatctgga	gaccatgctc	gggaattttc	546300
cctacaccgc	cccctaacgg	acgtctcctc	cctgttagga	atccgcgctt	cttggaaaga	546360
ccaccaccga	gttcccctag	tctggctcac	agaaatttcc	tatcgctcta	ctctctatag	546420
gcaagatcct	gcaactccact	cgaaattact	gattagccaa	ggtacgtgga	cgacgcaggc	546480
cactcctgtg	acctacaatg	ctttagggat	caaagtgaag	aataccatgc	agggtgtttc	546540
taaagtcact	ctctccttag	attactctgc	ggatatttct	tcctccacgc	tgagtcacta	546600
cttaaacgtg	gcgagtagaa	tgagatttta	acaataagt	accaaacag	aaagattaag	546660
gaacctctag	tgtcaaagac	tcctcctaag	tttttattct	atctcggaag	tttcacagcc	546720
tgcatgttcg	ggatgactcc	tgcatgttat	agtttacaaa	cggactccct	tgaaaagctt	546780
gctttagaga	gggatgaaga	gtttcgtacg	agctttcttc	tcttagactc	tctctccact	546840
cttacaggat	tttctccaat	aactacgttt	gttggaaata	gacataattc	ctctcaagac	546900
attgtacttt	ctaactacaa	gtctattgat	aacatccttc	ttctttggac	atcggtctgg	546960
ggagctgtgt	cctgtaataa	tttcttatta	tcaaattgtg	aagaccatgc	cttcttcagt	547020
aaaaatctcg	cgattgggac	tggaggcgcg	attgcttgcc	agggagcctg	cacaatcacg	547080
aagaatagag	gacccttatt	ttttttcagc	aatcgagggt	ttacaatgc	gagtacagga	547140
ggagaaaactc	gtgggggtgc	gattgcctgt	aatggagact	tcacgatttc	tcaaaatcaa	547200
gggactttct	actttgtcaa	caattccgtc	acacactggg	gaggagccct	ctccaccaat	547260
ggacactggc	gcatccaaag	caacagggca	cctctactct	tttttaacaa	tacagcccct	547320
agtggagggg	gtgcgcttcg	tagtgaaaat	acaacgatct	ctgataacac	gcgtcctatt	547380
tattttaaga	acaactgtgg	gaacaatggc	ggggccattc	aaacaagcgt	tactgttgcg	547440
ataaaaaata	actccgggtc	ggtgattttc	aataacaaca	cagcgttatc	tgggtcgata	547500
aattcaggaa	atggttcagg	aggggagatt	tatacaacaa	acctatccat	agacgataac	547560
cctggaacta	ttcttttcaa	taataactac	tgcatctcg	atggcgaggc	tatctgtaca	547620
caatttttga	caatcaaaaa	tagtggccac	gtatatttca	ccaacaatca	aggaaactgg	547680
ggagggtgctc	ttatgtctct	acaggacagc	acctgcctac	tcttcgcgga	acaaggaaat	547740
atcgcatctc	aaaataatga	ggttttcttc	accacatttg	gtagatacaa	cgccatacat	547800
tgtaaccacaa	atacaactt	acaacttgga	gctaataagg	ggtatacgac	tgcttttttt	547860
gatectatag	aacaccaaca	tccaactaca	aatcctctaa	tctttaatcc	caatgcgaac	547920
catcaggga	cgatcttatt	ttcttcagcc	tatatccag	aagcttctga	ctacgaaaat	547980
aatttcatta	gcagctcgaa	aaatacctct	gaacttcgca	atggtgtcct	ctctatcgag	548040
gatcgtgcgg	gatggcaatt	ctataagttc	actcaaaaag	gaggtatcct	taaattaggg	548100
catgcggcga	gtattgcaac	aactgccaac	tctgagactc	catcaactag	tgtaggctcc	548160
cagggtcatga	ttaataacct	tgcgattaac	ctccccctga	tcttagcaaa	aggaaaagct	548220
cctaccttgt	ggatccgtcc	tctacaatct	agtgctcctt	tcacagagga	caataacct	548280
acaattactt	tatcagggtcc	tctgacactc	ttaaatgagg	aaaaccgcga	tcctacgac	548340
agtatagatc	tctctgagcc	tttacaacaa	attcatcttc	tttctttatc	ggatgtaaca	548400



gcacgtcata	tcaataccga	taactttcat	cctgaaagct	taaatgcgac	tgagcattac	548460
ggttatcaag	gcatctgggc	tccttattgg	gtagagacga	taacaacaac	aaataacgct	548520
tctatagaga	cggcaaacac	cctctacaga	gctctgtatg	ccaattggac	tccttagga	548580
tataagggtca	atcctgaata	ccaaggagat	cttgctacga	ctcccctatg	gcaatccttt	548640
catactatgt	tctctctatt	aagaagttat	aatcgaactg	gtgattctga	tatcgagagg	548700
cctttcttag	aaattcaagg	gattgccgac	ggcctctttg	ttcatcaaaa	tagcatcccc	548760
ggggctccag	gattccgtat	ccaatctaca	gggtattcct	tacaagcatc	ctccgaaact	548820
tctttacatc	agaaaatctc	cttaggtttt	gcacagttct	tcaccgcac	taaagaaatc	548880
ggatcaagca	acaacgtctc	ggctcacaat	acagtctctt	cactttatgt	tgagcttccg	548940
tggttccaag	aggcctttgc	aacatccaca	gtggttagcgt	atggctatgg	ggaccatcac	549000
ctccacagcc	tacatccctc	acatcaagaa	caggcagaag	ggacgtgtta	tagccataca	549060
ttagcagcag	ctatcggctg	ttctttccct	tggcaacaga	aatcctatct	tcacctcagc	549120
ccgttcgttc	aggcaattgc	aatacgttct	caccaaacag	cgttcgaaga	gattgggtgac	549180
aatccccgaa	agtttgtctc	tcaaaagcct	ttctataatc	tgaccttacc	tctaggaatc	549240
caaggaaaat	ggcagtcaaa	attccacgta	cctacagaat	ggactctaga	actttcttac	549300
gaaccgggtac	tctatcaaca	aaatcccaa	atcgggtgtca	cgctacttgc	gagcggagggt	549360
tcctgggata	tcctaggcca	taactatggt	cgcaatgctt	tagggtacaa	agtccacaat	549420
caaactgcgc	tcttccgttc	tctcgatcta	ttcttggatt	accaaggatc	ggtctcctcc	549480
tcgacatcta	cgcaccatct	ccaagcagga	agtaccttaa	aattctaaaa	taaaagaacg	549540
ataaaattga	aatctttaga	attaacaact	atccgatgag	ctacgttagc	ccaatcggta	549600
gaggactccc	tcaaaattta	aatatagaaa	atcattcaaa	tatatgagtt	tactaactct	549660
gtaatatcca	acatgttaat	aagcatattt	aaatataaat	ttataaactt	ctagacaaca	549720
aattgatgat	tttttatgac	aaactctatt	ttcatatcaa	agtttggatg	tttatgcgac	549780
ccatttgtct	cagcatttta	tcactgcgc	tatgttgttc	cttatcagga	aatgaagtc	549840
ctaacctcgc	ctcttgtcag	atgtctagaa	aagacatctc	tgctttccac	acgtctccaa	549900
gcttccgtct	caatgtaact	ccagagccct	tggtttcttc	ctttcgtccc	tctaactctc	549960
ttaatggatt	cggtcacgat	ataaccaggg	acatcacaat	tacaggaaac	tctatcaatt	550020
ctgttataga	ttataactac	cactacgagg	atggaggcat	tcttgcattg	aaaaatttgt	550080
tcatttctga	aaataaagga	aacttaagtt	ttgaaaggaa	tagctcccac	agttctggag	550140
gggctctcta	cagtgttcgg	gaatgctgga	tttctaagaa	tcagaactac	tcgtttattt	550200
caaatgcggc	ttccttagct	actactacaa	cttcaggatt	tggtggggct	atacatgcac	550260
tagatagcta	tattacaaat	aacttaggag	aaggacaatt	cttagataat	gtctctaaaa	550320
atagaggagg	aggtactctat	gttgggggtga	gtttatcaat	cacagacaac	ttaggtccta	550380
tcgttatcaa	gaaaaatcaa	acattagaag	attccagctt	tggaggaggc	atcttctgca	550440
gagccgtaaa	tatagaaagg	aattatcaaa	acatccaaat	caatgataat	gcttcaggac	550500
aaggggtggt	atattttctg	ccctaggagt	cattatctct	tcaaaataag	aaattataga	550560
gatcagcaat	cactccgcat	cctcaattaa	cacagcatca	ggaaaactat	atcccgggtg	550620
tggcgggtatc	atgtgtacct	ccttagtcat	tgagaacaat	cccaaaggct	ttatctttaa	550680
caataaaaacg	gcagcactta	gcgggcggagc	tatacacacg	agatctttca	tcttccaaaa	550740
taacgggtccg	acagcattta	ttataaactc	tgcgacttca	ggaggggctc	tcatcaatct	550800
ttctgggtata	ggaagtactc	ctcaaaaattt	cttctctctc	gcagactacg	gcgatattct	550860
atttaacaat	aatacaatca	catcttcttc	tcctcaaccc	ggatatagaa	atgcactcta	550920
tgctgctccg	gggattaact	taaaactagg	agcaagacag	ggttataaaa	ttctctttta	550980
tgatcctata	gatcacgatc	agacgacaac	agatcctata	gtatttaatt	atgaacccca	551040
tcaccttgge	accgtgttgt	tttccggaat	caatgtagat	tctaacgcaa	caaateccatt	551100
gaacttccta	tcaaaatttt	ctaactcttc	acgacttgaa	aggggtgtgc	tcgctattga	551160
agatcgggct	gctattttct	gcaaaaccct	atcgcaaat	gggggcattc	tcggtttagg	551220
aaacgcagca	ttaatcagga	cgaaaggccc	gggaagctcc	ataaatttta	atgcaatcgc	551280
gatcaatctt	ccttctattt	tacaatcaga	agcctcagct	ccaaagtctt	ggattttatcc	551340
tacattaaca	ggatccacct	attctgaaga	cacttcttct	actatcactc	tctcaggacc	551400
cttgactttt	ctaaacgatg	aaaatgaaaa	cccctatgat	agcttagatc	tctctgaacc	551460
tcgaaaggat	atccccctc	ctctacctcc	tcgatgtgac	tgcaaaaaaa	atcgatactt	551520
cgaatctcat	tgtagaagcc	atgaacttag	atgagcacta	tggatatcag	ggaatctggt	551580
ctccctattg	gatggaaact	acgactacaa	caagctctac	agtaccggaa	cagaccaata	551640
caaaccacag	gcagctctac	gtagactgga	ctcctgtagg	ataccgcct	aaccgggaac	551700
gtcagcgaga	accttattgt	aataccttat	ggcagctcgc	ctataacgct	ctgttaggaa	551760
tcgcacatctt	acttccacaa	aacctcaaa	agcatgacct	tgaagcctct	ctgcaaggac	551820
tcgggcttct	aattaaccaa	cataatcgcg	agggacgcaa	aggcttccga	aaccatacta	551880
cgggctatgc	agcaacaacc	tcagcaaaaa	ctgcagcacg	acatagtttc	tctttaggat	551940
tcgcacaaat	gttctccaaa	actagagaac	gtcaatctcc	aagtacgact	tcctcccaca	552000
actactttgc	aggactccgc	ttcgacagtc	tcctcttcag	ggacttcac	tctacagggc	552060
tatccctagg	ttatagctac	ggagatcacc	atatgctttg	ccactataca	gaaatcttaa	552120
aagggctcgc	caaagccttc	tttaataacc	acactttggt	agcctctcta	gactgcacat	552180
tcttaccagc	tagaatcacc	cgcactctcg	aactccagcc	ctttatcagt	gccattgctc	552240



tgcgctgttc	ccaggcctcg	ttccaagaaa	ctggagacca	tataagaaaa	ttccatccaa	552300
aacatcccc	tacagatctt	tcctctccca	taggcttccg	ttctgaatgg	aaaacttcac	552360
atcatatccc	catgctatgg	actacggaaa	tatcctacgt	acctacccta	tacagaaaaa	552420
atccagaaat	gttcacgaca	ctactcatca	gcaatggaac	atggacaaca	caagcaactc	552480
ccgtctccta	taattccgta	gctgcaaaaa	taaaaaatac	ttcccaactt	ttctcaagag	552540
taaccttatc	cttagattat	tcagctcaag	tctcctcgtc	aactgtaggt	caatacctta	552600
aagctgagag	tcattgcaca	ttttaaccac	aaagaaaaaca	tcaaggaata	aacagtgcaa	552660
aataacagat	cccttagtaa	atcttccttc	tttggtggag	ccttaatttt	aggtaaaact	552720
acaatactcc	ttaatgcgac	tccgttgtct	gactattttg	ataatcaagc	aaatcaactc	552780
acaacactct	tccctcta	tgatactctt	actaacatga	ctccctactc	tcatagagca	552840
acactttttg	gagttagggg	tgacactaac	caagacattg	tcctcgatca	ccagaattcc	552900
atagaaagct	ggttcgaaaa	cttctctcaa	gacggcggtg	ctctctcttg	caaatacactt	552960
gccataacga	atacaaaaaa	ccaaattctt	ttcctaaata	gctttgctat	taaaagagct	553020
ggtgcatgt	atgtgaatgg	taatttcgat	ctttctgaga	atcatgggtc	catcattttc	553080
tctgggaatt	taagctttcc	taatgcaagt	aatttcgctg	atacttgtac	agggggagct	553140
gttttatgtt	cgaaaaatgt	tacaatctca	aaaaatcaaa	gaaccgcata	cttcattaac	553200
aacaaggcaa	aatcttcagg	aggagcaatc	caagctgcaa	tcataaacat	taaggacaac	553260
actggccctt	gcctgttttt	taataatgct	gcaggcngaa	cagcgggggg	cgcgttgttc	553320
gctaatagctt	gtagaattga	gaataattct	cagcctatct	atTTTTtgaa	taaccaatca	553380
ggtctgggtg	gtgcaataag	agtacatcaa	gagtgcattc	ttacaaagaa	taccggttct	553440
gtgatcttca	acaataat	tgccatggaa	gcggacatct	ctgctaacca	ttcctctgga	553500
ggggctatct	attgcattag	ttgttctata	aaagacaacc	caggaattgc	agcctctgat	553560
aataatactg	cagcacgaga	tggaggtgct	atctgtacac	aatctcta	tatacacagac	553620
agtggctccg	tctatttcac	aaacaatcag	ggaacttg	gcggcgctat	catgctccgt	553680
caagatgggtg	catgcacttt	atTTgtgat	cagggagata	ttatttttta	taataataga	553740
cacttcaaag	atactttcag	caatcatgtt	tctgtaaact	gcacgcgtaa	tgtctcatta	553800
acagttggag	caagtcaagg	tcattctgct	accttctatg	atcccatact	acaaagatat	553860
actatacaaa	actctatcca	aaaattta	cctaataccag	aacacctcgg	aactatcttg	553920
ttctcctcag	catatattcc	ggatacatcg	acttctcgtg	atgacttcat	ttcacatttc	553980
agaaaccaca	ttggactgta	caacggcaca	ctcgccttg	aagatcgagc	agagtgga	554040
gtctataaat	ttgatcaatt	tgggtgggact	ctacggttag	gcagtagagc	tgtgttttct	554100
acaacagacg	aagaacaaag	tagcagtagt	gtgggttctg	taattaacat	caataatctt	554160
gcaattaacc	ttccctctat	cttaggcaac	agagttgctc	ccaagctatg	gattcgcccc	554220
acaggttcat	cagcaccccta	tagcgaagat	aataacccta	taatcaatct	ctcaggacct	554280
ttgagcctac	tggtatgacga	gaacctagat	ccctatgata	ctgcagacct	tgcccaacct	554340
atcgcagaag	ttcctcttct	gtatctctta	gacgtcacag	ctaaacatat	taatacggat	554400
aatttctacc	ctgagggtct	aaataaca	caacactacg	gctaccaagg	cgttttggtcc	554460
ccttactgga	tcgaaaca	cacaactctt	gatacctctt	ctgaagatac	tgtgaatact	554520
ttacatcgcc	agctttatgg	tgattggaca	cctacaggat	ataaggtaaa	cccagaaaac	554580
aaaggagaca	ttgccctatc	tgcttctg	caatctttcc	ataacttatt	tgcgacacta	554640
cgttatcaaa	cacagcaagg	ccaaatagca	cctacagctt	ctggagaagc	tactcgactc	554700
ttcgtgcatc	aaaatagcaa	caatgatg	aaaggattcc	atatggaagc	tacgggttat	554760
tctttgggaa	caacctcaaa	cactgcttct	aatcatagct	ttggtgtaaa	cttctcccaa	554820
cttttcagta	atctctacga	gagccactcc	gacaattccg	tggttctgca	tacgacaact	554880
gtagcgctcc	agatcaataa	tccttggtg	caagagagat	tctctacatc	tgcatctcta	554940
gcctacagct	acagcaacca	ccatatcaaa	gcatctggat	attctggaaa	aatacaaacg	555000
gaaggcaaat	gttatagtac	gacattaagg	ggcggtctct	tcttgcctct	tatctctaca	555060
atggcgatca	cgacctctcc	acttcaactcc	ttttatccaa	gcaattgccg	ttcgttctaa	555120
tcaaactg	tttcaagaaa	gtggagataa	agctagaaaa	ttttctgttc	ataaaccctt	555180
atataacctg	acagtcctct	tggaattca	gagcgcttgg	gaatccaagt	tccgtcttcc	555240
tacctattgg	aacatagagc	ttgcttatca	gcctgtcctc	taccaacaaa	atcctgaggt	555300
caacgtgagt	ctagaatcta	gtggatcgtc	atggctccta	tcaggaacca	cccttgctcg	555360
caatgccatt	gcttttaag	gaagaaacca	aatttttatc	ttcccta	ttcgggtgtt	555420
cttagactat	caaggctcgg	tatcctcatc	aacgacgaca	cattaccttc	acgcaggaac	555480
gacctttaag	ttttaaaagc	atgttatata	gacaatgcaa	cctgtaagaa	ccaaatagag	555540
agtagtgaac	actctctacc	atcatgaatc	ttatgggaga	agctaaggga	aatccacaga	555600
tacgtttccc	ccataaaaat	taagaacccg	atacatcctc	actagagatt	cgaaagaact	555660
acttaa	taagcattcg	actctccacg	aggccatcct	ttttgtagta	agattttcgt	555720
tgtagctaca	agtcctcccta	agggctctag	atattctgat	tctccgtccc	cgggtctgt	555780
tggaggaaca	atactctctg	cttcgaccat	aacagcactc	acgctctcgc	taagcaaagc	555840
ggctcttact	tctgggtccaa	accctgggct	cactctaagc	gaaacattag	tcaatgtatt	555900
ctcgggtctt	ggaagtgtag	cagggggcct	gccatgaatc	catgggatct	catcataaat	555960
aggctctaca	ggagaagcgg	aagcaccg	tgacctctcc	tgtaaaatc	tatctatatt	556020
tctctgagta	aatggattat	cttcaggagt	attagcatat	atgggttcat	ccaagtcgcc	556080

tctaggagag	ggggaacggc	tcatactctc	ataatcactt	tcacctgcac	ctgaagcacc	556140
gctcatatcc	tcataaatgc	tcccctcctc	actcatagca	ggtgaaggaa	ctggaggaag	556200
aggcacaccc	cgtctatttg	gtgagctgct	tcgtacgcga	tctgaagacg	gagaacgtga	556260
gcttccagac	gatcctggac	gtgaaggaag	atcatagata	gcaggagttg	ctaactctagg	556320
tgtcatgtag	atgttcttgt	ctttagatgg	ttcagcagag	gttataggaa	cttcataatc	556380
tccaaaaaca	tcctcttcca	actctcgcgc	aggactccat	ctaggggaac	taggaacgtc	556440
atagattcca	tcttttctac	gaggaacatc	atagaaaata	tgatcatctt	ccataacaat	556500
aaaactgacg	gaactgtctt	gactccaacc	tctcactatg	ggagcagaaa	tcgaaatttc	556560
cggggtagctt	gattctgaac	tctccttggg	tttagcaccg	tgcttatgtg	cccatcctac	556620
taaggcattc	atcaatggag	aatcttcacg	tggacttcca	tttctgcgtg	gaacgtcatg	556680
cggagagccc	gttctttcag	tttcatcaat	ttctgaagga	gacccaccg	acatcgagtc	556740
ctcttcagaa	gaagtacact	cttctcctcg	gcacgtgcaa	caacgaccca	ctgcttcagc	556800
agctgcatga	cgagcaatac	gcaacctgtg	caagatggac	cctagaatgc	ttaaaatcat	556860
tcctaaaaga	gaaaccagag	cctcgcgaat	ctgattccat	aatctttag	accagttttc	556920
ccgagttctt	tgaggatctg	cagctcctcc	gatttcccca	taaataggct	cttcttgaga	556980
aatcagagtt	ggattattgt	ctatcggagt	tggattatcg	tctaaagaaa	aactcaatcg	557040
agcatgggac	aaagcagctt	ctaaatcgct	ggcagttctc	tctaataagg	tttgaagaga	557100
gtctccatca	ctcatgagtt	cttgaagctc	aggatctgtc	agttctgaac	agaggggaatt	557160
gatctcatca	ctagtttcta	cccccttaaa	acgagcttct	gctagagata	ccgaagattg	557220
tggtgcctcc	atatagccgc	attggaattc	tgtaatttgg	atcagctgtt	gtatggtaac	557280
tgtggcttct	gctttttcct	ctggagtcga	ctgatcatta	ctttgtatgt	cagagagctc	557340
ctgacgtaaa	ctactcaaac	ggagggttag	ctcgtagaga	cttaaaggct	cgctgtctgt	557400
aggtggagcc	ccactaggaa	gtactatgag	atcgcgaact	gtctgtacca	accgacccaa	557460
accgctctgt	ttttttactg	aaggaagaga	aaataaacgc	tgagggttctg	gtccagaaga	557520
gggttctctga	accccttgag	aaggattttc	gcctgaaaca	ctcgcgtcct	ctgccactcg	557580
ggcttctgta	gcagcagcac	ttgatgaatc	gacatcccgt	ctctcatccg	cggtgatggg	557640
ttttgataat	ctaacaaaag	cttgctgcgt	ttcacgcgct	tgactcgtag	actctgcgga	557700
aaaaaagttg	ccaaatgatt	ttaaggccct	gtctacccca	gaacgtacgc	gagaaaaaaa	557760
tcccgggcta	gaagctgccc	aagaagagct	ctgagactcc	tgatcttctg	gtagaaaaga	557820
ggaactgcta	tgtatatgag	aagatcctga	agctccttcc	tctccatggt	cttgaggagg	557880
cagggaatcc	ctgtggctgc	caagtctctc	cttagggagag	ggcgatcgac	ttctatcccc	557940
attatcttta	ggtggaatct	ttcctaatac	actagatcct	ccgattcctg	atgccataaa	558000
cacttccata	aaagaataat	cttttttctg	aaacaattta	attttattaa	aaaacaacaa	558060
aaatgctttt	aaatatatta	aaataatcaa	catattgaag	agtttttaatt	aaaactcttc	558120
aagtttccct	tgcgcataga	gaaacagtga	gataacgact	actgtccctc	tgaggcaaat	558180
gatctagcta	atcctaagcc	ttgttgaaatg	acaggatcag	tcacattgcc	tgattccaat	558240
ttttcaagac	tctggggcatt	tctgttactc	atttctgcag	ctctacgagc	gatctcttcc	558300
gcaaaaagata	agctaggtgc	agccgatgga	tttgaaacgc	cctcttgctc	cacaaacccat	558360
tgtgtattac	tttctgatgc	aagatcatct	acagctgatt	cacgtcgtgc	tgaacttaat	558420
cttgaagcaa	ttggccctaaa	gaagctcgtc	accgcttgga	atatgctaac	tacaaaatcc	558480
cgtaacgctt	tccatgctcc	ctgcgctgca	gatccctcta	ccccacctgt	ttcgggagct	558540
tccgcagtct	ctgctggggc	ttgcgatcca	tcttgaggta	cgatggatgc	atactccaca	558600
gaatcactac	ctacattgga	ttctacgaaa	gtaataagat	cctccacagt	aggaggttcc	558660
tgatgagtea	attgctccat	gcgtgcaaga	agagattgca	ccctagaagc	cacctctggt	558720
gacacttggt	ctggagctac	tttttccaaa	ttttctaaag	ccttacgcag	atgttttgct	558780
gctttattca	cattagaaaag	atcaccttcc	gtgaagaac	agttctgata	558840	
ttccctgggtg	ctgatctgat	tgacactgca	gcctgtctct	cgaacgccga	aaccttctct	558900
ttagcgtcac	ctaaggctcc	ctgaactgta	gacgtcgtct	ctcgaactcc	tgataaaaaa	558960
gaagaactct	tcgaagaagc	ctctgcttct	tcggaacgcc	tttctttttac	agtatcgccg	559020
gcagaatctt	cgccctgagt	tgttaaatca	tcttcggaag	cagaacgctg	gaactttcct	559080
ttaatatcac	ctagggcacc	atgaacttta	gacaccgctc	ctcgaactcc	tgataagaag	559140
gaagaactct	ttgaagaagg	ctctcctcct	tcagaacggc	tatcctctgt	agaatcttca	559200
ttagaatcgt	gtcctactcg	atcaagggtca	ccatcagaat	aggaacgttt	catcttccct	559260
aaatctgcct	ctggattttc	agatcttttc	tggaatcgat	ctctaaagcc	ctcgagtcca	559320
ggaagacgtt	ggccatggtg	cacatgggat	ggaagacgtg	gactagaaac	ttcaggacgc	559380
gcttgagggg	tttttttaaa	gaccccttta	acgcctttcc	aaattctctg	aagtacccca	559440
gaacgtcctg	aagttggaga	atctccgggt	tctttgacag	atggcaaagg	aattttatca	559500
gtcccgccta	actgggcttt	tctctcttct	attgtagggc	cctgacttgc	aagactactg	559560
tcactactgc	taactgtatg	ttcccctaag	ttgtcttttag	gacttacttt	tccatcctca	559620
ctattccttc	tattaggagg	aatgggggaa	ggagatcttg	agccgcctac	gccaccaact	559680
gccataattg	aaccttaaaa	tgataaatta	tttaataaaa	actattaaac	aaatgttata	559740
ataaaaaata	ttttaaaaaa	aaaatataaa	ttaaaaataa	caaaaagaat	gctgattata	559800
taattaagta	aactactaga	tgtaaaagag	aaaataaaat	tagagaaggc	agacaagctc	559860
ccaaagctcg	aggatcttac	attcaaggac	ctggcctaag	cagctccatc	tatatctaca	559920

tccacatcaa	taaaatctac	gggaccatca	agatcaaata	gatgatcgtg	gctagcagca	559980
agagcctcaa	caactaaatc	cgtagcaatg	gagcgcattt	tacttttcagg	accatagaga	560040
agctcacggc	gattacgtcg	acgctcatag	agcttcacaa	gctcatcata	gagccagttg	560100
acaaacttcc	tcattaaaat	cgatcccgcg	attcctaacg	tcgatcctcc	aagagcaaga	560160
ataccaggaa	cgataggagc	aaatgcaggg	accagggcaa	gaagcatgat	cccagttcct	560220
acaccaagta	agattccacc	aacaagggcg	ctgttcactt	ccccaccctt	ctcaaaattg	560280
cgaacctctt	cacgaattgc	agcgtcagtc	ttctgaatct	gttttttgta	gactgtcttc	560340
cacatttggg	taaattctcg	atccgaggca	atcactccag	actcaattaa	gaactggcgc	560400
acccgctttt	tattttttgc	ttctttccaa	cgtaattttac	tgatattcaa	tcttgctttc	560460
agttggtagg	cgacgtagga	aaatcctgag	gaaaccatag	ggagtgttac	agaagcaacc	560520
gccgatccta	cagaagcaac	aaggagaact	tgcatgactg	tcaatccacc	aaatcccgtg	560580
actatgaagg	cagcaatact	tgctaagagc	aagagtgtcg	caagagcaaa	gatgaccttc	560640
tgtcttgtcg	tcagggaaag	cctcgtatcg	atttcttccg	cagagatcct	cgtctctgca	560700
atccccctcg	aatctggaac	ttctatcaca	gattgggaag	tttactcttc	ttccacctca	560760
ctgggggggca	atttttctaa	gcgaatgtct	ttcagggagg	tgtctacaaa	aagatctttt	560820
ttttcttgag	taagcagaaa	ggctctccac	tttccgatac	tactatggag	tatcgtttgc	560880
aaaaccgtcg	taagccctat	agaaattaaa	gggggagcta	aaataatagc	aatcgtttgcg	560940
ggagcgcctc	ctagcaatac	cgttcctgca	atggcaagga	gaatccccaa	aaccgcaaga	561000
ccaacgccaa	tagtggcaat	tgacaacgtg	atatagtgtg	attttttcgc	ctcttttata	561060
gtttctgctt	ctgtaagctt	ctccccctta	gcaacttttt	cagaacggaa	aaacttagta	561120
taaatataat	gactgaagct	tgctaattgt	gtttggcttc	ccccgggaata	cgcactggat	561180
cccaagctac	ccacgagacc	cccataccct	ccaggaacaa	aattcgcccc	caccttcctg	561240
accaaaccga	tgacagtaaa	tccagtcctt	acagctaaag	cacttttgat	tctgctcgac	561300
tcttgcatcc	tgggggacat	atagtctcgg	accatataaa	ccaagctctt	cattatagaa	561360
aatccaccaa	taccacgccc	tgaaatggcg	attccaagaa	gaatagcctg	aggaactccg	561420
ggagctaaga	cgggtcaaagc	gacaacaaca	acagaaaccg	ctaccagcaa	aacaaccagg	561480
ccagcaaata	aagtcacgga	atgggtgaaa	atactttttc	gcaatcctgt	atcttcaggga	561540
ttgctaggaa	ctaggggaatt	tggtactggc	gagagactcc	ggctattttgc	aagaagagaa	561600
gttttctcag	ttgcattaga	caaagacaaa	tatcggggat	cgttgctaata	tggtgatgta	561660
gacataaaaag	aaataactaat	aattattttt	ataattaaaa	ataatcaacta	561720	
caccacaaaa	tagaacaatc	ccacaacaat	ttacaataaa	agtattttaa	tttttagaaa	561780
aaagtaacta	aatagatcac	agtagctaaa	ggagggagct	ctatatccaa	accccaagcg	561840
accccttggg	cttgacagac	cacaggagcc	cgattttccct	tccctgagcc	tccaaaagac	561900
tcatcatcag	tggtgagaag	gagttcacaa	tgcttttacac	cttcacacct	taaaacatag	561960
gaaggaaaag	tactcgcact	gaaatgatgg	acacagagaa	gcgccgaaga	acgatttgctg	562020
cctgcaaate	tataataggc	aatgacattg	ttttctatat	catggaagtc	tacccaatgg	562080
aagcactctt	gagagctctc	ttgcatccat	aaatagggtt	ggtgaatata	caacgcattc	562140
aatgcagaga	cacagtttctg	caaagttttg	tggtagtgtg	gattcaaaaag	ctcccaatct	562200
aagggacgat	caggagacca	ctcgccgtat	tgtccgaatt	ccccacccat	gaacagtaac	562260
tttttcccag	gcaaacagat	ctggtagctc	aagagcactc	tcatttgagc	aaatcgggtc	562320
caggtatccc	cggggaagctt	attcactaag	ctgccccttac	cgtggaccac	ctcgtcatgc	562380
gagagaggaa	gaataaaaaga	ctcttggaag	gcataccaaa	ggctaaatgt	cagatctttc	562440
tgatggtatt	tacgatatac	gggatccttc	ataaagtaat	gaaagggtatc	gtgcatccaa	562500
cctaagttcc	atttgtaate	aaaccccaga	cctccctgat	ctacgtcctt	agtgactcct	562560
ggaaacgctg	tggaattcctc	tgcaaagggtg	agcactccag	agaactcctt	atgaattaca	562620
gaatttaagt	gtttcaaaaa	ttctatatag	tctaagttct	ccttacctcc	atagatgtta	562680
ggcgctccatt	ctccatcttc	acggccataa	tcacgatata	gcatagaggc	cacagcatcc	562740
acacgtaagc	catcaatatg	catcttatcg	agccaaaata	aagcactccc	tagtaaaaaag	562800
ttggtcactt	catgacgact	gtagtcaaag	gtaaacgtat	tccagtgggg	atgaagagcc	562860
tgactatgcc	ccgtgtactc	gtagagaggc	tccccatcaa	aagaggcaag	agcaaacgca	562920
tctacgggaa	aatgtcccgg	cacccaatct	aaaataatac	caatattttc	tttatgtaga	562980
tagtctacaa	aatactgaaa	ctcctggaga	gtcccgtatc	ttgatgttgg	agcataatat	563040
cccgctcactt	gatagcccca	agattcattc	aggggatgct	ccgtaatggg	aagaagctcc	563100
acatgagtg	agtgcatttc	cttgcaatag	ctagcaaggc	gatgcgccat	ttcgctgtag	563160
cttaaggggc	ttccctcctg	ccattggccaa	gagcctaagt	gcacttcata	gatcgtgacg	563220
ggcccttcac	tctgcttcga	gcgcctctcc	atccaacgat	gatcactcca	agagtagctc	563280
tcagaatccg	caacacgagc	tgtaccctgg	ggtggaggat	caaagctctt	cccataagga	563340
tctgttttta	caatcacatt	ccccgattgg	gtaacgattt	cccacttata	ccgtattccc	563400
tctcccaagc	ctggggacgaa	aagctcccag	atccccctgat	cggaaatttt	acgtagagga	563460
ttgacaaggc	catgccaaaa	attaaaaatct	ccgactacag	agactctctg	cgcattgggga	563520
gccccaaagaa	caaagagcac	ccctgagatt	ccttgaactt	ccatagggat	tgccccctatg	563580
cgttcataaaa	tgcggtaatg	cgttcctcta	tggaaataaaa	agaatcaaat	ttctcccccac	563640
agaggagaaa	acgcataagg	atcatgagcg	agaagtccat	tctgatgata	cacacggtaa	563700
tccccgtgtc	cgattccttt	gggaacggat	aagaaaaaga	gccccgaacg	ataagctaca	563760

gcgtggtgaa	gctctcctag	aagttcaata	gcaaccgtat	gcgcccctgg	acgaaaaata	563820
acaatatgat	ctgaagaatc	ttcagaagca	aggatcccta	agagttttatg	gggatctttc	563880
tgctgctctg	agacgagcag	atcaagatcc	caaggatgga	tcagttttatc	aaccatggaa	563940
ggctatctat	ttatgaaaac	aatcccataa	atatgtggtt	cctgcttttta	tctccagagt	564000
ttctcctaaa	gaaagtctct	tagatccaga	gagacgtcgc	tccgaccatt	cccgaaggcg	564060
cgcactgcat	agtgaagaac	aaaactttta	aaatacctcg	ccactatatt	ctgcatggag	564120
ctcgacctga	cggatagttt	tcttagtcca	gacgatagac	aaagtcccaa	gattaggaag	564180
ggcaacatga	atcaagcggc	cacaaggaaa	ttcaggaggt	aatgcaggaa	ggatctctac	564240
tagctgtccc	tggtgtctca	gaaaaatatc	ttggatcata	ccaaagctat	acgagagaag	564300
ctcaaaagga	actccccct	ctggatctcc	atcttggggg	aggattcctt	ggaactcttc	564360
atcatagctc	ctaggaagaa	agcactctga	aaatcccgca	agggctatgg	agagtaacgc	564420
aggagcaatc	tctgtagttt	ccctatgtaa	aactctttga	tgggcagtct	ttaccaagct	564480
accgatagcc	gtcgtctcta	gatcccgata	ggatccctta	ggagccatag	cggcgaaaacg	564540
gaaccatagg	ggaagaattt	ctttaagatc	acgacgacaa	cggacctttt	gccaatctgc	564600
atgcttatgc	accccaagag	ataacagggg	ccctgcttgc	gctgccgaag	gcagtttccc	564660
tttgatagat	tggtgtcact	ctcccagggg	aaggagataa	tacttgtagc	gctcagaagt	564720
cactgcaagc	ccccacgat	gtaaatcttg	gaaaacagca	aagcgtttta	aaggcccttg	564780
cacctgtaag	gtctgtcat	ttaagatttc	gtgtttcgaa	gaaaatagac	gccacagggt	564840
aggaaatacc	tgagcatata	acaaagatcc	aggaataggg	agtttttgct	ctgggaccat	564900
agtatagggc	ttaaaatggt	gcattatata	tatcatacaa	tctcccacat	cagcccttct	564960
tcctctaccc	tatcaagacg	cacagaaaact	agagtgttga	tagctaccgt	tcctacaaca	565020
gggaaagaaa	ccttttcaaa	ataaggagag	tgacctgtag	caacctgccc	cgttactttc	565080
tcaacaagca	cctctgtagt	ctctcctaaa	cgcttccatc	ctcttttctg	gcctaccctc	565140
ttagcaacct	cagcaagata	cttcttctc	tcatagatca	cctgattggg	aatctgatta	565200
tcaaaagtat	atgccttagt	acgacgacga	gcactgaaag	ggaaactatg	cactttaata	565260
aagcctacat	cttcaataat	tctcaaagta	tcttcaaaat	cttgatcact	ctctccagga	565320
aatccgacaa	tcacatctgt	agtaaaggca	tagcgaggat	cagaagcacg	gaacttctct	565380
acacaatcta	aaaaatctcc	gcgagaatac	ttccggttca	ttctctttta	aattgaattc	565440
gaccccgatt	gaagaacaag	gtgtgacgaa	ggacaagtgt	gacgcgatga	ggtgatggca	565500
cgggtgcagat	cttcagtgt	atcatcagga	tctatagagg	aaattcgaat	cctctcaatt	565560
ccaggaatct	ggtccacctg	ttcaatcaaa	gaggctaatt	aacgctctcc	atcgcaataa	565620
tctccaacct	aaatcctgc	aattacaact	tcgcgatata	ccttggctctac	aaccctgctg	565680
atttcagcta	aaatcttctc	agcaggacga	gaaaccgaac	gcccccgcaa	ataaggaata	565740
atgcagtacg	agcaaaaaaga	attacagcca	tcttgaactt	taataaaaagc	tcgagacttt	565800
ccctcaaaac	tatggatctt	gaactcaggg	aaggctcgat	cataggaaaa	aattttttct	565860
ataagtcggg	atttttcttt	attggaacaa	agcgtgcatt	gccgatccaa	agaagcaaaa	565920
aactctttgt	cagattcccc	caaacaacct	gtgacaacaa	tatgtgctgt	aggggtctga	565980
cgacataact	gacgcacagc	atgacgaccc	gaactctcag	cagaagctgt	gacagcacac	566040
gtattgatta	tgcataaatc	tgcagggatt	tcagaattcca	ggacctcttg	gtaacctaaag	566100
atagtcaact	ggtcgcgata	tgcttggacc	tcatactgat	tcacccgaca	gcctaaacag	566160
accagcttaa	atgttctctt	gacttccgca	accgtcatat	acctctagag	acttcaatag	566220
atttagcgat	gagtggctat	tttaaaatat	cactcttttt	ctcactaaca	aagattcgat	566280
gtcctagaag	aaaactacct	aatccccgaa	agaactctcc	aagacggggc	ctctaccctc	566340
gtcatctcca	caatcttcag	ggaaaacata	agaaataaaa	ggacgaaatt	tcttttgcag	566400
ctccttagga	agatacgctt	caacaactaa	aaaatcttct	tgataacctg	acgaggccac	566460
aaccccgcca	tcgcaaagtt	ccgtaaaatt	tccatatctt	gtataaggaa	aattcaaagt	566520
cacatgcaaa	cttttctcct	gaatgatttc	cgtcataaga	ctaagaagat	tctggatccc	566580
ctccccagtt	tttgcgaaa	tcaatacagg	aagaggagag	agcaaacgta	atttcatagg	566640
gatacttctc	tgagggaagcc	gatctacctt	attcaacaca	gtaatgatcc	taggcttttc	566700
aatcttcaac	tcttgaaaga	gatcgtaggt	cgtctgtaca	tgctctaaag	ctaaaggatg	566760
cgaagcatcg	acaacatgca	gaagaacatc	ttcatggaaa	gctgcttcta	aagtactttt	566820
aaatgctgct	accaaagtat	gaggaagttt	tcgaatgaag	cctacagtat	cagtaagaag	566880
gacatgacgg	cctcctggaa	gtacgcattt	gcgcgttttg	ggatctaaag	ttgcaaatag	566940
cttgtcttca	acatacgtat	cagcagccgt	cagcaaatgt	aatagggtgc	tcttccctga	567000
atttgcatac	cctatcaaag	caaaggtagg	aattcctcgt	cgagatttta	ctttacggcg	567060
ttccgcacgc	tgtttgatca	cagctttcag	ctgtgctgac	agcttatgga	tacgctcacg	567120
gaccattcta	cgggtctagct	cgatctgttt	ttctccttcc	cccttaacaa	agcctccgct	567180
acctccccca	gatttttggc	gagataggtg	cccccaaagt	ctcttaagac	gaggaaggag	567240
ataacgtgct	tgtgcaagtt	ggacttggat	atttgcctct	gcagtaaggg	cacggctgga	567300
aaagatttcc	aaaattaact	ccgtcctatc	caaaacgaca	aggccaaggc	gtttctctaa	567360
attccgttgt	tgggatggag	tgatctcctc	atctatgatc	aaagtcccta	tagagggaaa	567420
ctctttcaag	atttcttcga	tctcctccaa	cttccccaca	ttgatatagg	tggaagctga	567480
gggtgttttt	aaaatccaag	aacgggtctc	taaaacagaa	ataccacagg	aatccgcaag	567540
tgagatcaac	tcgtctaaat	gttcttcaac	gacctgagaa	tctgtcttat	tttgatagga	567600

agccacagct	aaagcttgag	agggatcctg	ttccttacga	ggcaagtcga	acctggcccc	567660
taacgaattt	ccgaaagatt	gagaaccctg	ttccccgggc	gtatctatag	tgtccaaagg	567720
acctccatgc	catcataagc	aatgtgacc	tctggatgct	ggtcacgctc	tgcttctaaa	567780
cagtggtga	tatgtgtaat	aattaaattc	tttatccctg	catgattcgc	aaaagctttg	567840
gcttcttcta	cagtaagatg	cgaagatttg	tgccccgaa	aaggaatagg	agtttccgat	567900
ggacccgcag	acaagatcaa	tgtctctaca	ttatctaagt	aactgaaaat	ttttgcatca	567960
tagctacaga	gatctgtaag	ataagcaaga	tttccaaaac	gaaaaccctg	tacatggcac	568020
gacttttgat	aataggaaac	ataagtatag	ggaatgccct	gaaattccctc	ctgcccacag	568080
tcctcattca	agattgtaaa	ctctaaaact	gcgggaagtg	aagactctac	attcggagtg	568140
gcgaagagat	actcttttagc	cttgttttaa	aatctatagg	tgcttgacga	aaggaccaa	568200
ggcaacgaac	gctgcgtgac	tatgtaccac	gcacgtaaat	catcaatacc	accgatatga	568260
tcgtagtggtg	gatgggtcag	aaatacccca	tcgagctcgg	aaaccctcgc	aactaacatc	568320
tgcgtagcga	aatcagggcc	tgcgtaaatc	actagagtct	tgttttgata	ttgaatgagt	568380
accgaagatc	gtaaacgatg	aatccctgtg	ttttgacaca	ctctacatga	gcaaacggcg	568440
acgggaattc	cttcgggatt	tcctgtgctc	aaaaatacta	atttccctat	agattcactc	568500
tgaatatctc	ttaccatacc	aattgctcat	ctggaaacac	aagcaaacaa	aaataattag	568560
tcagtctctt	aactttggat	cttaaagtca	agaagttgct	agaaccccaa	tttagaatcc	568620
tctatagctt	tttaaaccat	agtttccaag	tatctatcct	taaaaatttt	cgagagggat	568680
ctcgtgcagc	gcagtaaaag	attcatgaga	aaatgtgaga	aataactgac	gaacacgctt	568740
agttatctct	gcgtgatcca	ttaggtaact	ttgtaatcgg	ttgagataat	gcacagggtg	568800
caggatactc	tgtgatcaca	gaatagtttt	gggaatgtgc	ctgtatctga	cgacaatgac	568860
attgcgttat	atattcgtgt	gaaagattga	gccactcacg	gactctccct	cttcccaagg	568920
acgccatcaa	gatcgcaaac	aagcataaaa	tggcaccaac	ccctccaatg	atacagggaa	568980
tcacccaagc	acttaatccc	gcaatcaaag	gggcttcaac	cattaccccg	acaatcagac	569040
ctgcaaaaat	acacaacca	ccaaagaccc	aactcacaat	agagcagatg	tcaaaattcc	569100
ttacttgaga	acagagctcg	tacattgcag	actccagctg	cggagctccc	ttaccacagg	569160
gctccaaagc	ccataaagaa	gtaatggggc	catgtacggg	taggccttga	aattttatgtt	569220
gcttacaacg	caagacctgc	aagataacctg	taggaggagc	cccttgacac	tcaactacaa	569280
taacaggaac	aacataggga	ctaacgacct	cagcacataa	ctgacaatag	aaatacctat	569340
ttttgtattc	ttcaatatgt	ccagcaccag	gataacatgg	caaagaacct	aacatgcaat	569400
cttgttctct	ctttgatata	aattcaccta	gtctcccaga	gattccccaa	gaaattcnnt	569460
catccgatta	aagacaggaa	aagattcaaa	taaaggcaat	gctcctaacc	acattctttg	569520
gggaacggct	gtcaaataca	tcaaagcttt	caatccttga	aacgacacgc	cctgtgctgc	569580
caagccatga	acaagcataa	ccgcagcctg	ttcacttaaa	acatctctag	gattcaatac	569640
tttttgtcca	gactgtaaac	gactcgcaaa	ttgagataac	atagaatcca	agccttgcaa	569700
acaaacggtg	taatcggcct	gatcttctag	agagatttctg	gtaccgcgaa	cacagtctag	569760
caaaacagcc	caatctatca	aataggataa	aggatattca	tacaaactgc	agaggaaacc	569820
tgactcattt	tctaagattt	cagtgttcga	aagaatctgc	tcacgaatct	gcctacgatc	569880
taccctgacc	acagaacctat	atttgtcaaa	gagccgcttc	atagcaggaa	cagaagaga	569940
aaaagcaata	aataggttgt	ctaattctttg	atttgcgctc	tcataacatt	tttctccctc	570000
agcacagtta	tatccccaat	ctaaggacat	tgcgtttatc	aaatcgagct	tctgaaaata	570060
gcgagagaga	aatgtttgta	tttgtgcttc	atagcgggcg	acatcgatcg	ctgtctctgg	570120
gagctttctt	tgcaagctct	ctagatggcg	atgtaaaaac	ttctcaaaaa	atgaagacga	570180
ccaaatgtag	gtaagaaaag	aatcctttta	gaagcgtctg	tcgggatttt	ccaacgcaa	570240
aagaagatcg	aattgcgcca	aagcatcctc	aggagaacat	tcttctctgc	gacagctaaa	570300
taccccgctc	gcgtctacac	taaaggaacc	tgaatctgcc	caatccatca	aaggagacgt	570360
tgcttgtaaa	agctctccgt	agcgaatcaa	tttcaaaaata	tcaggagagt	aatactgctc	570420
ttctatcaaa	aagagtagaa	gttcctcggc	gtgcgcagtg	acttcaggac	taagatccac	570480
tcccagtaag	ttccactgtc	tcactaaatg	taaaatgata	ttgatgtgga	cacaatcttt	570540
ctttaacagc	gaaagtgtcg	tagatagggg	ctcaagtttc	aatatatattt	gtaaactctg	570600
atcaatatct	aaagatcgat	ccttagaatc	aacaatcaga	gattcgtgga	gatccctcgc	570660
taagaacaag	gaaatcaact	cggaaacgcca	atactcattc	cctaagacat	cttgttgtgt	570720
agtccactcc	ttttgcgcaa	caatttcttg	aggagtcgct	tctcgactag	gttctaaagt	570780
cttgccataa	acgagaccgg	agacagcaaa	aacgatagct	aagcttaaaa	gtaaacattc	570840
aagagcaaac	ccgaggacca	cagccacaaa	tccgacctgt	gggaaaatga	caatcatagc	570900
aataaaaaat	aaacagctca	aagcccctag	gactaaagct	gcgtaataca	ttcgcgatgt	570960
tcgttcagta	aatctttcgt	tggaggagtt	agcctctcct	acagaagtag	atgaagttac	571020
aggaacagag	gttgccataa	gaataccctc	tattcgtaag	caacttcaga	aagttgccat	571080
ttcttggtta	aagattgaaat	cacccttctg	ctctttaaat	ctgtaatcgc	ttgttgaaatc	571140
gtttgtattt	cttcaggacg	atcttttagta	cgccgagacc	acagcccaac	acccaacatt	571200
caggagggag	ctctaattctt	gttgcaacaa	gattagggaa	gtctttaaga	acgacacgtc	571260
ctaccgaggg	ttctagaacg	gcaaccggag	atttcccata	acgaacttcc	ataatcacct	571320
ccaaggtgct	atcaaaaagaa	cggacacaaa	ttccgggctg	agataaaaaga	taatgtcctc	571380
gaaacgttcc	tgtctgaaca	gcaacagaag	aatgctgtgt	taggggaagc	acaggggtct	571440

ctaaagaccg	cttagaaacc	accatcagct	cttgaacctc	atcgccataa	tagggaagca	571500
gggcgatttc	cttctgacgc	gaaggagtaa	tggacattcc	tgctaaaatt	gcacgcgatac	571560
gatgtttttt	taaatttaaa	attaaagcat	cgaaagcgaa	ttctctaact	tccaattgct	571620
tgccaagttt	ttcactaatt	gcctttgcca	aatctatatac	gaaacctaca	acttccccct	571680
gagcatccac	atactcaaaa	ggaggatatg	tagcattcgt	acctacaatc	cagatgcgat	571740
ttcgatcgat	tttagactca	caacttggtta	aagataaagg	cattataaaa	ataaatgctc	571800
taaaaaaacg	gcctatttgt	tttatcatga	aagtttgccg	tctatacgct	aaattctatc	571860
atgtgttaaa	gtttacataa	caaaaaataa	tacatcaaac	tcgaaaaagt	tttaactttg	571920
aataattttg	attaaaaaac	gagcaatttt	tgaacgtatg	tttccaattc	ccccaccaca	571980
ttgcccggcc	aataacaaga	ataattttta	ccacttaacg	actgatacta	aagacctctc	572040
gttacttaga	attctacgta	ccataggata	cgttctgctc	catatcatta	ctcttggttt	572100
gcttcttctg	attcactact	acaagcatca	tcgggttgctc	agaaaagaag	gcttgccaac	572160
gcctcccact	cttcccaaag	gaccagagcc	aaaaactata	gaaattgcca	aacaaccgcc	572220
taaggatggt	gaagacaaaa	aacccgatgt	tcccaagccg	ggcacgccgc	ccccagagga	572280
cacacccccg	cctcccccca	aagctccttc	accagcgagc	ccaaaagtcc	ctaaaacaac	572340
ctgctgataa	aaagccgact	ccaccaccag	aggccctccc	tcctcccgtg	cgggttggtc	572400
ccccatgcc	tctccgcca	tctagtcaag	gctattggca	atgcttaa	cgcatggtga	572460
gcatggtact	aagacgagcg	cctctgcctc	ttcctgccat	gcaagttgat	ccaatacttg	572520
gcgactttaa	ccctcatttc	gtagcttctc	atcccaatcg	gattaataac	gaaccgatgt	572580
atttccaaat	aaaacagttc	aagaaaatcg	cacaaaatcc	ggatcttctc	caacaacacc	572640
ggcgacttgc	gcaactctct	cttgaacagg	ctctctatct	aaatgacaat	tactaccttg	572700
tgaatgtacc	gggagatggg	aactgctttt	atcgctgcta	tgctgtagga	tggctatctg	572760
ctctctacga	agagagcagc	agaaatgata	ttgtctttga	gcagggaagcc	acacgtctcc	572820
ttgacctgcc	tttcgctccc	tcttctccgg	caaatgcgaa	tctttgtgca	gaaatggctg	572880
aactccttca	gttatgcagt	acttattgct	ccttcataga	cctctatgac	ggggtgattc	572940
tttctcagaa	acacactgca	actctgatag	cctttctaag	aaaactctct	gcatatgcga	573000
ttcgccaaca	aatcgagctc	tcaagtaatg	aagaaacagc	gagagcctta	tttatttctg	573060
atatgcagga	cgatctcctc	cccagtggtc	tggaatttct	tgctgcaaat	cgtccctatt	573120
cggaattggt	ccaaaatctc	attgatcatt	ccgcacaccc	tacatgcaat	ctagagacaa	573180
actctttctt	ctcttggaac	atctgcccgc	tctctttctt	actgatgcag	agcttcaaaa	573240
gatgtctcca	gaagatcaac	aacttcgaaa	gcaatatgaa	agagaaatag	gagaggcttt	573300
tgctaagctg	agtcgacgca	ttgctgattc	aggggtggat	actgagagat	tcaatgctat	573360
agtcaaaagt	cacctccctg	aagcaatccg	atgtcaatac	tctcgctttc	ttgcaactat	573420
agaaaacaga	cgatctgggg	atctcccttg	gtctccagct	ctttctttct	ttgcttttct	573480
atgtacctgc	ccctctgtaa	gatttcacaa	actctgcgct	actttctaca	aatcattaga	573540
ggatatcatt	atagcgtccg	cgcccccca	acgctctata	caagagatct	tacanataag	573600
taacgcctcc	ctcagctacc	ttaatgaaga	tttagattct	tcttggaac	gagagggtgat	573660
ttcttctaac	atcatgacta	tccttacgac	tcatgagagt	ttgacgttag	agagctctat	573720
gcctcaactc	gaaacactac	ataaacgcgt	agcaaaccta	ttaaagaatg	taatatccac	573780
atcctttgaa	acccctcctt	taagcaatca	gccggattta	ctttcaaate	ttgtaaacaa	573840
gctatttagtc	gcaattcata	gtaagcttga	attaaaagag	cacttcaata	ctgtctgctc	573900
ggcaagaagt	ttacgtttta	cgcgtgatga	aggcagtggt	ctctcacaag	agcaggacct	573960
cctctataca	caggcagtag	agctcttatt	ctttatttta	cagcatcctc	aagtgaataa	574020
tcgtccagaa	actaaagatg	ccgttaaaga	gttaaaaatg	cttctacttc	cttttctaca	574080
atatgccttt	aaaaaagtag	aaaacgaaaa	gaaactccaa	aaacttctac	gttccattct	574140
agggtctcta	gtactcaagc	ctccagcacg	ctatccttca	accccttcta	ataaagataa	574200
agagacgttc	tgcaagtctc	ggtcacgaca	tcctgaagtg	atgggttttag	atcccatact	574260
tgaaaagaac	tgtatgcagt	ttctacgagc	tactttccca	aattatcaac	tggaaaccga	574320
ggccatactc	ttagaaaaag	aaatcgaaag	taccttttag	aatgggtgga	acgttttttt	574380
aacacgggtta	aatctcttcg	gatcaaaact	gggttcgcct	tcttctccca	cagctttaag	574440
tgatcagttt	tcgaaatctt	ttttaatctt	ttgtttcctt	aacaactacc	ctaaacttct	574500
acaaaaaaag	actccgctag	ctgctcgatt	agacgctttc	caaagagagg	cttctcatag	574560
atttacacaa	gtaaaagata	agcttttact	ttcgtaaaaa	tacgggtttcc	ctctagctac	574620
agcgactata	aatcaatact	ctagagctcg	agatcagttg	atttgtaatc	tcttaaaaaa	574680
cacggctaca	gcactctgat	gtttctgtcg	ctctggtttt	agacaatcac	tgataggcta	574740
cctccactcc	ctaagttcta	atgaactcgg	tgatattctg	gatgacgtca	aagagcaagc	574800
tgaggctaac	gacgtcgctg	ctatgactac	tgtacctttg	cagccgtttg	ctggtttgtct	574860
gatcatgtct	gatcgagata	ctgtctcaga	agaaaatatt	gaaaactttg	ttgcgatgca	574920
tggattttta	aatacaattt	ctccggaaag	agacgctcgt	atcttcttaa	tccgcttccc	574980
caaccactac	ggttgtctct	tgcttagaaa	ccctagaact	gaagatcaga	actcaaaacc	575040
ggacagctca	aatccctagt	tttgcatgag	gtacttatcc	ttacgtttac	ctatccctca	575100
ccgcgcaccc	tcaaacagca	tcctgacgag	gtccataacc	ttcctatttc	tccaaatcta	575160
tcgtttggag	aaggatcgcc	aatactgac	gcaggcccc	gcacctaga	aagttacgag	575220
catacagctc	cttcagctct	tacagttaaa	gaagcaggag	ctcaggtatt	ccgaggatca	575280

atcagaaaac	cacggacaag	cccattttcg	tttcaaggat	gggagaaaga	gtgtgtgctt	575340
tggcataagg	aagcacagag	catccatggg	ctccctacag	aaaccgaagt	tttagatgtc	575400
cgagatgttg	aaattactgc	cgaacatgtg	gatatcctcc	gtatcggagc	caaaaacatg	575460
cataacaccc	ctctttttaca	agaggtcagc	aaatcacatc	gtccgattat	cctaaaacgc	575520
agtccagcag	ctactcttga	agagtggcta	tgcgcagcgg	agtacatcct	tgcttcttct	575580
ccctcctgtc	ctggggtaat	cctttgtgaa	cgaggaattc	gtacctttga	gcactctacg	575640
cgctacacgc	tagatctcaa	taccgtgggt	ctccttaaag	agatctcttc	tctccctgta	575700
attgtagatc	cttcccacgc	agcggggaag	cgttctctag	ttcttccctc	cgctctgtct	575760
ggctctctcg	taggtgccga	cggctctgat	atcgaagtgc	atgcacaccc	tgaaaaggct	575820
ctttgtgacg	cgaagcaaca	gatcacgccc	gaggagcttc	acctatttgc	taaaaagcac	575880
ttctgcccac	cagaatcacg	ggctcatgcg	atttcttgaa	atcggttgat	gattctcaaa	575940
taaaagagac	taaaaaatct	tttattttgag	aactcttaaa	ttaaacttaa	ccaaatactt	576000
ttaaaaaagt	tattagaaat	tttgttttat	tatatttaat	ataaatattt	ttattgaata	576060
gtaaaacta	ttttcactat	ctaacagcca	attggaagaa	cgccaacacg	cgtctttctt	576120
tggaggttta	tgataaaaca	agcgtgtaaa	ttttaccttt	tacagtgttt	actttgctct	576180
ctgtattggc	tattaaagta	ttgcagaaag	cttcttaagg	gcactcttca	ccattctgaa	576240
gagacgctct	atcaagccct	gctctcctct	cttatcgacc	tgctctatca	gttaaaacag	576300
cttcccgcgc	ctacgaatga	ataataaaaa	ataaaacgaa	cccccttctt	tcttggaana	576360
gaaggagagg	tatcagattc	taaacacaac	ttaaaaaact	gacgatctct	tactaagcgc	576420
aacctatcag	atctaagaga	aacctaaaca	actcaggatc	tatttttagtt	atatcttctc	576480
atgcagtggg	tatctaagtt	tgcgttttga	ctttgttttt	ccaagtgtatc	tcaataaatc	576540
ctacaaagga	aaaggcgact	agagaacctc	cccaagccaa	tagctcccc	aacctcccc	576600
aagagactat	ctgaacccat	ccatagccca	gagcaccac	gagcactcct	gccaagcag	576660
cagctccgct	cacacggcga	cctttaggag	ctagaagata	gaaacccaca	gggactgaaa	576720
gacaacacac	tgacaggcta	tagcttaaaa	tcaagacatc	tacgatgttt	gtaaaaccaa	576780
tagcaacaag	aggagctgca	accgccaaac	ccaatactaa	ataacgataa	taaggggctt	576840
tcaacgtagg	gtattcttca	gcgattagct	ggcttacagc	attcataaga	gagtcgcg	576900
tagagagaat	cgcaacgccg	atggcagcag	ccatcacagc	tgctagtgtg	ggattgcaaa	576960
aatatgcaat	ggtatcaatc	agagggcatc	ctgctttaag	gcctgcttta	gctcctaaag	577020
aacctaaaaa	taaagggata	aagttaaaaa	gaagaagaac	aaggcctg	cctacagcgc	577080
cccattgcaa	gcgttttggg	gaggaggcag	ccacacacct	ttgcaccata	tcctgtctca	577140
caagcataaa	gagcataggg	atgaatatcc	aattggaaaa	cttcgcacaa	ggaagtgtat	577200
ggaaaggatc	caacacagac	aaggatttag	ggacagagag	ccatacagaa	acaccacaga	577260
cgagcaccgc	aataagaaga	aatcctgctt	ggatcacatc	agtacgtacg	accccgcgaa	577320
accctcctgt	tgaggtatag	gatgctaaga	caatccaaaa	tgctacgggt	acgtacttgc	577380
caaaagggaa	gctgctaacc	aaccgatcta	aagcaatcac	ctgagcgacc	aggatgaaaa	577440
ataaggaacc	tgccgataat	aaaaatgcga	tcttacggag	cttttttagaa	ccataaaaaca	577500
cttcaaagat	agagactacg	gtcgttaact	atccctctgc	caaccgcttc	ccggggccca	577560
ttcctaagaa	aatcaaccct	aaagcgactc	ctaaaggata	aagaatcccc	ccataaccat	577620
aacagaaggc	ctcttcagca	gccccaaaga	gtacaccgcc	accgatttgg	gtggcaatga	577680
atgtcatcat	caaaggaaag	attttttaac	tccttctctg	aagaaaaatg	ctctcgcat	577740
cttctacctt	tttgctacca	cgacgtccca	cgtacaagca	gattccctga	atagctatca	577800
ggaaaaataa	aaataatgaa	aaattcataa	aataaagaac	tccacaacct	aaatganana	577860
tatttccctt	aagcaagcta	cgggtgctgag	cttaaagata	gaaatgctag	gaaaattagg	577920
agtgggtgat	gagataacgt	ccagaataac	gaaatcttaa	cgagaataga	gattcaaaaa	577980
acaaatctga	ttttatatac	aggttgtgca	tgacatacag	gctctgagct	tacgctcttc	578040
ataaattata	aaagctacca	gataaaaaatc	tataacaaag	ttttctatct	ccaaagactt	578100
aaaaatgaaa	gaataaagtc	agtctgaaaa	attatttttta	agaaatagaa	attacaactg	578160
cgtgggtttt	cttctatata	ttgaataatt	ttattaatat	ttatttgaaa	atagagaaaa	578220
gagcaccgcg	tgctgcactt	cgcagcgaag	gagcttcgtg	atggcagcag	tctagaagaa	578280
aaggcacagc	atcaagattc	tcagaaaaag	caacgctctc	taagattgct	aatttatctt	578340
gccaacggct	gtcattataa	agttgagaga	ccctctgtag	ggaagcttga	tcttttttct	578400
gacatagcga	ggctaacgct	ccttccaact	ttgctgcaaa	gcaagcatct	gtaaccaa	578460
cctcagaagt	tttcacatct	ccctcttccc	agaacattcc	agaaaaaaag	ctccatccct	578520
gagcttgaag	tcctgaaagg	aacgttgctg	ttacagcctt	ggcttggtga	tagcgagcta	578580
ctgccaaaag	gcgaatgagc	ttcctaccaa	tctcacgttt	aatcatatcc	gaatatagag	578640
ggaaggatc	accacgtaaa	ttccattgtg	catcccataa	gaaatactct	atagccagc	578700
acatttcagg	attggagagg	tagcgagcaa	tcacatctcc	agctctttca	atatcttcac	578760
ggctcacaag	aagcaaaaatg	gagaggttcg	cagcagcctt	tcgagaagaa	aggctctcca	578820
aatgctcctt	tgccaaaagg	actccatgga	ttcctaaaga	gcagagagcc	gccgaagctg	578880
cctcacacac	aagagggtga	ggagagcgca	accctcaacc	agagagtctc	tgcccaagg	578940
gtctccatgc	agatggagaa	gtgcagcagc	ttgaaaacgt	acttttgcaa	atggagaagt	579000
gcacatcata	tgccgcactt	tactaagaaa	ctctttgtga	ttctgtagct	gatgactcca	579060
agctaaagca	gaaagtaaga	gagactcctg	cacttcagga	tgctctacag	ataagagttc	579120



tgtaaaaaatc	tcagtagtct	ctggcaacat	accgttacgc	aacacttcac	aagtgaacaa	579180
cgcttgatca	atategtcct	tagctacacc	cgtctctaga	aattgagaag	agagttccaa	579240
gcaagccttc	cacgcctctc	gacgttctac	actatctaca	agtttggtct	cagcacgctc	579300
tcttaaaaaat	ggcaatagct	cctctatctg	taaaagagcg	accacctgat	atgctgtaat	579360
ccgaacatga	atagaatcat	cattacgggc	aagctctaca	atggcctttt	ttaaactttc	579420
agagccatag	ttcacagcaa	cctgaagagc	caaagatcga	acaatagcac	tgctatcatt	579480
acaactttgg	agcaggagag	ggaccaagcg	aaaatctcta	gcaagcccaa	tagcaaggac	579540
actcacagca	cgaacgggtca	cggaaggatt	ttcgattccc	tcacgcagaa	cttgaatccc	579600
aaattcttct	aagacatcgc	gatcatgagc	taactctgga	taggaaatct	gacacttctt	579660
aaaacttcta	aaccaatcat	caaaagaaga	attttgagcc	agagccctta	aaactagctt	579720
agcctgaagt	aaagaatact	ctttagactc	caaaaggcct	atgccctctt	ctgaaacttt	579780
tgcaaaatct	tggatcaaca	attgataacg	gagggactcc	gagccgaaca	aggatccaca	579840
gaaacaaaag	aaaattaggc	tatagcacct	aaaggacgcc	cacctaaaag	atgaatatgt	579900
aagtgaataa	ccgcctgtcc	tccttcagca	ccgttggtga	taaccacacg	atacccatcg	579960
gcaattccaa	attctgcagc	aagctcttgc	acgatcttgc	cagcctctgc	cattaaaatc	580020
atctcatccc	ctgggatatc	ctgaaatcgt	ggtataggtt	tttttaggaat	gataagaaga	580080
tgaacaggag	cttgaggaaa	acgatctttt	atagctatga	aattttcgtt	ttcaaatacc	580140
ttttcacaa	ctatcaatcc	atcgataatt	tgtttgaata	ctgtcatatg	atccctcgat	580200
cttgtaacgt	taaccgcaaa	gcacgttggc	aactttctct	atttgtccat	acagaaagga	580260
aaagaccttt	atggcagaac	acagccccag	gaatccctga	tactttggac	aactctttac	580320
ctaacaaaac	tgcccaattc	tcagggaaag	gaacacgaac	ttccatacgg	cgatctaaat	580380
tcggaggaat	ccctcgtaaa	atccattgat	cgcaggaagg	aaaacaaaac	aaagctgcag	580440
ggtgcttctc	tccccctaaa	aaaaagaaat	tttcttgcca	tgctaaagga	cgatcaaaat	580500
ataaacacat	atcctcggtt	tccatgctct	ctctgacaat	ccccctacaa	actcgatcat	580560
actgaaactt	cttccttagc	cgacacaaaa	agtcgatggt	aaaatgcaaa	gcacaagaaa	580620
aatccgcac	cgaattagtt	tcttcttctc	cgcgaggatt	ataaatttta	ataatatcag	580680
aaaacgaaca	aatccctctc	ttagagaaga	atctgccatt	atcttggtca	tccacacccat	580740
gtaccaaaag	gttggttaag	aaatgatatt	cttcacaatc	catataacca	aactctttaa	580800
gataatgcag	aatcatacct	gcactactcc	aagatccatc	ataagagact	tgatgatgat	580860
caaaacgctt	gttttctata	gaataaacac	caccgacatc	acaaacatat	tcacatttct	580920
ataatacgac	aggatctcga	gagcgtataa	ttttattttc	atccacaaga	tcgaaaataa	580980
taaggagagc	acacgctgtg	acctcatccg	catggaaaga	accatcgtga	gtaccaatgc	581040
ttcttggaat	ctgcatacct	actatcctcc	ttagccaatc	ctccattgta	accagagaga	581100
aataattctc	aattgcaaag	actattcttt	acattttact	caatctctcc	aagagaaaag	581160
ttctgcccta	ttttctaaga	aacttttttc	ctaaaattcc	cttccacaac	acaattttct	581220
cgttccaaga	ccccctcctt	gacaaattgc	acaaaattat	aacaacaagc	agaatgaagt	581280
ccttgtagga	aattcttctg	gaaacgctag	tcttagaagc	gcaaagaggg	accttaccta	581340
ttgcttttaa	ctttaaaata	cgatgaatta	tgtataacct	actccacgcg	catcatgatg	581400
cagcctcccc	agacggacga	ctcgtttccc	atttgaaaaa	actctcgccc	cacatttacg	581460
aaggagaggt	ctcattgag	aatattcctg	cgtactttct	tggatttcat	ctgcctcaac	581520
agtgatatac	agtaaattta	aaaagtctct	tagcccaact	aggtgtcgaa	gccgttttaa	581580
accacttgga	gctaaataaa	gcccgaagag	aagctcgtct	acacgttctc	ttcatgagcc	581640
aagatccctat	agccactgct	aatgttggag	ctcctaggag	cctggaggtt	ttgtctgcaa	581700
gctctttgct	gctgatgatc	gccgactcgt	acgttcgcct	tggttatctca	acaggatggt	581760
tacgcacaca	gaccgtacag	gatctccgct	cctacgcttt	gggaaaaaac	ttgagcactt	581820
catcactcta	gagatcatta	atgatcggtt	tggtgtcttc	cttccgatcc	ttccaggaac	581880
aatctgtttac	gaagagacaa	tttatgggtt	ccttccccta	atgagcaaat	cactcacgcg	581940
tccccattta	aaaatacgta	agtttcttcc	tttgatatca	atggtaacag	atcgtcctcc	582000
cgttcccga	gatcataaaa	ttcttctcat	aaagacagag	cctctgcaca	tccgaaccgt	582060
atttgcaaga	gtcgttcagg	acttactccc	ccaagggtct	cgtcacaccg	cagcggatat	582120
tctcgaaact	accacacaag	aatctggaga	tatttatgaa	ttctacggca	gcacttcaga	582180
acctattgag	agaatacctt	tagaattttt	tactcttgag	ccttacaaaag	agcattcgtt	582240
tttcttctat	agagatatgc	tccaggaaac	cttanaatct	cctcaagagg	tatttcgtgt	582300
ttttgaatcc	ataccggaag	gcgaaaatca	agctgcatg	tttatctcca	aaggtagatga	582360
gcttgcttga	gctctcccaa	gactcttgga	tcatacaaac	tcgaatctcc	ccatcagatg	582420
aaagacatgc	tagggaaatt	caaaagcaca	ttgaagaccc	aaccttggtt	ccctttttta	582480
aaagccatgg	aaacagatca	tatcacaaag	caaggagttt	tattttcccg	ctacttccct	582540
tcagcatcgc	tgaaggcat	gttctctctc	aactactctc	gctattacct	gcaacatata	582600
tattttcaga	ttccctctcc	cacttctgga	gagtttttct	cgaatcgaga	tcgctctttc	582660
cttctcgatc	tatatatttg	aggaattttc	gtattttggg	cagacttaga	atcgaaacga	582720
ctcttacaat	acatcaaacg	cagaaataaa	gatgtgggca	tgtttgctcc	taaacatcaa	582780
gctgaacagt	ttgctcaatc	ctactttata	ggaattcatg	gttccctgct	aatcgctggg	582840
gattatgatg	agtttctccg	tgagctcctg	acaggaatgc	atactcttcc	tcagcaattc	582900
acgatcccg	aatttccacc	acagacaccg	ttagcaatcc	ttacaggagg	gggttctgga	582960



gctatggaac	tcgcgaatcg	tgtagctaca	gaactctcca	tactctcttg	tgggaatcta	583020
attagcttgg	ataccacgaa	tgcctatgta	gaagctaaaa	tgagctatgc	tattcctgat	583080
cttttagaac	gtcaggccga	cttccatgtc	gaccttgctg	tatttggtat	cggaggcatg	583140
ggaaccgatt	tcgaactcct	tctggagctt	attagtctca	aaacagggaa	aaaagctctt	583200
gttcccgtct	tcctaatacgg	acctgtagac	tattggaaat	ccaagatcac	agctttgtat	583260
aattccaatc	atgctgtagg	aaccattcga	ggttctgaat	gggtacacaa	ctgcctattc	583320
tgccctatcct	cagcaaaaggc	aggcattgca	atcttccgca	gatattctcaa	tcatacgctg	583380
cccataggac	ctgaacacccc	tgtccctgaa	gatgggtttt	ttatcgttta	gaatccatag	583440
gtaagacgga	aaccgtagta	attacacggg	tcacgaatga	attggccttc	tttagaaaat	583500
ccctgatgat	attctaaaac	agcacggatt	ttccttccga	tttcttgaaa	tttggcccac	583560
tccatgccta	aaatatagct	ttgatccaag	ccaaatttct	gttcttccca	acaacggaaa	583620
tgcatcgcgga	aaatcggttg	tgcgtggaga	tttcttcttc	tcagaccaa	aggctctgagt	583680
tccgcacccc	attcacagta	aaacggccgc	tcaggaaaag	taagatccct	acttacaata	583740
taaccgcagc	cgccatacaa	gcggatctgt	ggtgtgtaac	gaaacgaaat	gaagagatcg	583800
acgccctcat	cactcaaat	aaatcttggg	aaatttggat	gcgtaagaat	aaactcatct	583860
cctaaatggg	acgagaggtg	ccacaatcga	aacctaaaac	tccattttatc	tatagccctt	583920
gaccagagtc	cggcaacaaa	gaaatctgaa	tttaccatgc	acgattcagg	atgatctaaa	583980
tcaaaaactg	agaagactcc	tccttgaatt	ccgaaatcac	aatctacatg	gaatcgagaa	584040
acatcaaaaa	gacgcaggag	aataaaatct	ccccaaaaga	tggtagcacc	taccgatctc	584100
cccacgacct	tctcattaaa	acgaatgcca	gcactgtttg	taacctgacg	aggatctgca	584160
atcaaaggag	aaaacaaaa	ggtattttga	ggtaaccata	ccccttcttt	gcgcgagaaa	584220
attggcattc	ctaaagtttt	ctcttttagg	agtaagggac	gctccgcaga	agactctcgt	584280
atgcattcac	cataaggacg	ctcgcaaatc	tccacagcac	atatgaaggg	aagatcccta	584340
acaaagtggg	taatggcttc	tgataaaactc	gaatctacag	gcaaagagaa	aagatacgct	584400
ctattcttct	caataacaac	ttgcgtacgg	ctatctaaaa	aatgcatgtc	caaaagagac	584460
tgacacataac	ctgtaagata	acagtcgttt	tcatagtctc	agagatgatc	cggcagctga	584520
tccgaacgta	aaacagactt	agtttcgtat	ttgcaatcgg	ggcaciaagg	ctctccccc	584580
gcgatgccac	ccacaaaagag	taccaagaag	ctaaagagcc	aacaaaacca	agaatatgcaa	584640
gagtgaanaag	ctgtcttcat	cgtaaagaca	tggtatagag	aagaaagtat	ttatttcgca	584700
atattgtata	gcaattctta	aaactaagag	accctaactc	ttttcattga	tctttccgat	584760
ctgtgaagag	aggaattcac	aacagacctc	caaacatctc	catgtagaat	cagcttggtt	584820
ccttctagaa	tctccgttga	aaatccactg	gtcttctctc	tatggattcc	ctcccttcta	584880
ccgcagagac	ctaaaactct	gaaccctctt	aatgaagaga	aggagggatc	tcagctctga	584940
tccggattag	ctgtctttcc	aatggacgtg	cttgcccttg	gggtctttgt	ttccaggctt	585000
tttcaagatc	cctttgggtg	tctctataaa	tgagggtctc	gcattcttct	gttttctctc	585060
tacaccactc	tgttttggac	tgcgtgtgta	agttcgcaaa	cgtatgtaag	ggtgcgttgg	585120
agaaaaactt	gagggagaac	gcttcttgct	tccacgtcct	gtaaacgttc	taatccattg	585180
aacaaatctg	ccaacgaatc	ccttgcttgt	cttcgaatga	gaaccttctg	tcttggatta	585240
tttgaatggg	gcttctgaaa	tgcccttgac	cttcttctct	aaagaagctt	tccccgtctt	585300
agaacccgag	gtcaccccaa	ctgaagcact	cttatgcttt	ctacgaatcc	caccacgacg	585360
atgcaagcga	gagttccctg	aaaggggtac	atcctttttc	ccatcttctg	gagaaggatt	585420
cctaccccta	taacttccat	aaggattgac	ccttatcata	attacctaaa	aaattttttc	585480
aaatcttatc	ctttaattat	agtgaagcaa	ttagaaaaga	tttaaaaaac	ttttaataaa	585540
cagaattata	aatatatctt	aataattaac	cgaaactaca	gagcactcct	tgcctttata	585600
gaggcggtta	aggnnaaatc	agaaaatggc	tatccaaaaa	gctggggctt	tcttaagatg	585660
tcttccaagt	gaatcacgcc	cttacctgga	gcacgctatg	cgtagaaatc	cccacttttc	585720
tcttctcaag	cctcagtatc	tattttctga	aattagtaaa	aagcttgctc	agtttctgca	585780
ggagaatcca	gaaatctctg	tcatagatct	ttctatcgga	gatacgacac	aacctctctg	585840
ccgctctatt	actcaggcaa	tcaaagagtt	ctgcgtttct	caagagaaac	aagagacctc	585900
tcgtgggtac	ggcccagaaa	ccggattaga	aaaattacgc	acaaaaattg	cctctgaagt	585960
ctatgaaaa	agaatctccc	ctgaagagat	ttttatttctg	gatggtgcca	aacctgatat	586020
cttccgtctc	ttttcttttt	ttggctcaga	aaagactcta	ggctctacag	atcctgtcta	586080
tccagcttat	agagacattg	cccacattac	aggaatccgc	gacattatcc	ccctagcatg	586140
cagaaaagaa	actgggttta	ttccagaact	tccgaaccaa	caatccctag	acattctttg	586200
tctatgctat	cctaacaacc	ccacaggaac	agttctaacc	tttcaacaac	tccaagcact	586260
tgtgaactac	gcgaatcagc	acggaaccgt	tcttattttt	gatgcggcct	atagcgcctt	586320
tgtctcagat	cctagcctac	ctaaaagcat	cttcgaaatc	cctgaagcaa	aatattgtgc	586380
tatagaaatc	aactctttct	ctaaatcatt	aggctttact	ggcatgcgcc	ttgcctggaa	586440
cgtgatccct	aaagaactca	cctatgacaa	taacgaacct	atgatcaacg	attggaaacg	586500
gctcttttgc	actacattta	acggagcacc	tctcctcatg	caagaagcag	ggtattacgg	586560
cttagattta	tttccgacac	ctcccccat	ctctttatat	ctaaccaatg	ctcagaaact	586620
taaaaaaagc	ttagaaactg	caggattctc	agttcatggg	ggcgatcatg	ccccttacct	586680
ttgggtagaa	ctccctgaag	gaatctctga	tgaagaagcg	tttgatttct	tcttacatca	586740
gtatcatatt	gcagtgactc	ccggccacgg	ttttggttcc	tgtggacaag	gatttggttcg	586800

tttctccgct	ctgacacaac	cacaaaaatat	cgcttttagcc	tgtgaccgcc	tctgtaccgc	586860
ttcactaaaa	gaaacgatgg	ttcttgcgatg	acaatttctac	gtaaactctc	tcagtactta	586920
ttttttctttt	ctctgttttg	ctcttttcac	tatgtagcca	cttgtgggtc	tcaaccagat	586980
agcgtctcct	ctcctaaaaat	cgcaatttttc	ttatcctttc	cccattcccc	attagaagat	587040
tgcagtaaaa	gctgtataga	aaccttgaaa	gattttgaga	accttccctga	aattgtttgtc	587100
ctaaatgctg	aagacagtat	cgtaaaggct	aggaaaattg	ctcgctcctt	acataccgat	587160
aaaaatgtcg	tggcgattgt	caccttagga	actattgcta	cgaaggctcat	gagccacatt	587220
gaaacacaga	aacctgtgat	ctatgccgct	gttcttgatc	gcgaaagcct	aacctctcct	587280
aaaaacacaa	tgaatatcta	cgagtggaat	gacactctag	acatcaatca	atactgcttt	587340
gctatacaag	ccgtagctac	caatgcacaa	tctatcgtgt	attttaaacc	ctccgaacct	587400
ttccccctcag	atctccaaaa	agaaattgtt	aagaaactcc	atgcttcagg	aattgagggtc	587460
attgagatct	ctattacaag	cagtacattc	aaaacccgga	tacgccaggc	tatcgacaag	587520
cgccccctcag	ctatcttcat	tccccctctcc	ccactttctc	ataaagaagg	caccgcattc	587580
cttcaggaaa	tccctcaaaga	gaaaatccct	atcattaccg	acgatacctc	cttaattttcc	587640
gaagagcctg	cattgcctgt	agcgtggatt	acaaaaaatc	aggaaaacaa	atcgcaaaaa	587700
attgtgcacc	acctactcta	taacaatcac	gatgtggaca	gcctgcgtaa	aatcattgct	587760
caacgcctgt	cacctacaac	cacctttaat	gaagatatca	tcaagtactt	aggaatcaag	587820
cttcataaaa	cagaacgcaa	ccagttctta	tcttttaaaa	gcaaaaaatt	ggaaaaatct	587880
gagaaagggg	aaaacgtagc	tgtgagttag	gctatacgtc	tatatgcaaa	gaaaaaataa	587940
tgtcttgaac	tctgttagga	agaagaaact	ttttctttcg	agaagtctct	cctgcaatta	588000
aagtgcacac	acgcttcggt	aaggataaag	cttttgctaa	taaagaaatt	acagcatcat	588060
tggccttacc	cttttctggg	ggttcggtaa	cacggacctt	caaagcttgt	ccatcaaagc	588120
ctacaatttt	gttctctttg	gcttttggag	tgactttaac	ctctaagatc	catgacatcat	588180
ccaaaacaac	cctctgaaat	atttaagcag	ccgttctgtt	cttttaacca	ttccgctaaa	588240
gtatgtagac	aaatccttgg	agcccaatga	tacttcaaga	ctccttgagc	aaatccaggt	588300
ccagcaagat	catagctttc	ccctttgaaa	aactgcccga	ccctgcaagc	atctaaaccg	588360
ataaagggtt	gactacttac	aaataacacg	cgtcccggaa	acgcttcttg	ataagaacgg	588420
aataaaaagta	aggtgtcctt	acgattcgca	accacacgat	tttctcttgg	ctttgctaga	588480
agaaatgtca	ctctgactcc	tgaagtacta	tctcgccatg	ctctaggtaa	aagcatttgc	588540
atccaaacaa	atttggcaac	ctcttcttca	gaagagggag	taactcgggt	accagattcc	588600
cagttctctt	cagtagggaa	aggattgtac	cgagaatcaa	agaaatgctc	ttgttcttca	588660
atagactgat	agcgccctcg	ctctccacat	agaaaaacga	ttttcttaaa	gcgcacgccca	588720
cgctgccact	ctcgcaccaa	aaaatctaa	cgctgacgta	gcgctggcaa	aggcccgccca	588780
aaaactacag	cacaatcata	cgttgcagaa	tacgaaggca	cagcctgagt	catatgtaat	588840
aaagacaaat	cgttatagaa	agcatgctca	tctttaacct	gacagataga	gactaactct	588900
ccagaaaaac	gttcttcagg	agtcagtacc	caagcagacg	aggactcgat	taaatcctca	588960
acattctcag	cttcaggaag	tccacaaact	tctagtaaac	gattgactac	aggaatatac	589020
ttatcaatag	aacatcttga	tttcgcttgt	taccaaggac	aacacccaac	agaaatgagc	589080
gccgtcattg	cgaacaatgc	cactaccatc	cttgcttttc	ttctattcat	aaagggcgcc	589140
ctccttaatc	ggcaatatta	gacgccacca	tataacaaaa	attcaaaaaa	aacaataaac	589200
aaaccaccgc	aatttgaact	ataaaaaatg	gactgggtga	gagtaaaagc	tggcaattct	589260
gattcgatag	tttctactca	gaagagatca	ttctttatta	taactccgtc	tcttctctac	589320
tatcagagtc	ttgcttatca	cctcgactag	gttggttacg	gccatctcca	tggggagatt	589380
caggatgtat	agactctccc	tcagctctca	caatcatctc	ttcctcagat	aagtccagatc	589440
gccgagaaa	gcgttctctc	cttgtagaac	gctctccgga	agaagacctc	tggcttctct	589500
gagaagcatc	gggattatgg	aaaggcaaac	accccagccc	aggcaaaagg	ttaatccgtc	589560
tcactatcca	catcaaaaac	aacacgatgt	tgctatagca	actcgaaata	aaacctacaa	589620
aatcgcgcca	aagacgcagt	aattcattga	gcaattcttc	acagcaagac	aaactttctt	589680
caaccctagg	atcagacgaa	gattccgttg	ttccctgaag	agtcgcgaat	tcttctacag	589740
taggtagatt	cactttcttg	atctggacaa	gcatactgtc	agcagtaagc	accagtcgag	589800
gaatccccct	ctcacaagaa	agagaccaat	taccttcagc	gtctacatca	agccctaacg	589860
aaccagatg	ctcaagaacc	ctatcattat	tgtcaaaccg	cagggaaaga	tcttcacgac	589920
tgagtcacctg	tagcttgtga	tgtacatctg	ttaacttact	taaaatgaga	tgagccttcc	589980
catgaaactg	gttcgcagtg	cctaagacag	cctcgtaatc	gctacgaaat	aattccagcc	590040
tcgctatate	cgcattatcc	ccagcacctc	gagttctcag	tcttctcggt	gaagattttcc	590100
atgcccgaag	acagtttttc	aactctgact	gaaagctagt	gaaaaggagc	tgggcacctc	590160
taaggctcgt	taaaagctct	ccaacacgct	ctacaagtga	tgagatctga	tcagcaaccg	590220
cccgactcga	agaaacttca	gctacaatct	cgtctacctt	cggattactc	gccgtttctt	590280
cagatgaggt	ccccacacct	tcaggaagag	aaagttgagt	gactatagga	agagccacag	590340
catgcgtggc	ttgcgcctca	tctgaagaaa	caacattttt	gttttcttcc	gtagatttcag	590400
gagaagttac	ctcttctgga	ttcgggggtt	cagagctttg	atttactgac	gacatagtag	590460
tacaattaca	aaaataaaa	attaataagt	atacacttaa	ttataagttg	agattattaa	590520
atttctaaat	aaaaacaaaa	atataattaa	aataatacat	aatcctgacc	ccaattgtta	590580
agttaagaac	ccaacgcaaa	acattgatct	agaaaaatcc	ctgtgttaag	atacctcctt	590640

catagctaaa	ctaaatctac	tagcttaaaa	gactctcgat	ataaaatcgc	aatagcctgt	590700
aattttttct	atagactctt	gacgatcaat	cactgaagat	aacagcccta	ctctatgaaa	590760
acgtctcaac	tcttttataa	gacttcaaaa	aatgcaaata	aaagcgctgc	tgtgctctca	590820
aacgagctcc	tagaaaaggc	aggataccta	tttaaagtaa	gtaaaggagt	ctatacctat	590880
acacccctgt	tatggcgctg	ggtctccaag	atgatgaaca	tcattagaga	ggaacttaat	590940
gcgattggag	gtcaagaact	tctactccca	cttctccaca	atgctgaact	ttggcaacat	591000
acagggagat	gggaggcatt	tacttcggaa	ggactgctct	acactctcaa	agaccgcgaa	591060
ggaaaatctc	attgcctagc	tcctacacat	gaagagggtca	tctgctcttt	tgttgacaaa	591120
tggctctcct	caaaaagaca	acttctcttc	cacctttacc	aaattgctac	aaaattccga	591180
gacgagattc	gccctcgatt	cggtctcatt	cgctctcgag	agctccttat	ggaagacagc	591240
tataccttct	cagactctcc	cgaacaaatg	aacgagcaat	atgaaaaact	ccgctctgcg	591300
tatagtaaga	tctttgatcg	tctcgggtctt	gcctatgtca	tcgttacagc	tgatggaggg	591360
aaaatcggca	aaggaaagtc	tgaggaattt	caggctcttt	gctctctagg	cgaggacacg	591420
atctgcgtca	gcggttcccta	tggagctaat	attgaggctg	ctgtctccat	tcctccacag	591480
catgcctacg	atcgcgagtt	tcttcccgtc	gaagaagtgg	ccaccctggg	gattacaaca	591540
atagaagctc	tagcaaaactt	cttctctatc	cccttacata	aaattttaaa	aacccttgct	591600
gtaaaactct	cctactcaaa	tgaagaaaaa	ttcattgcca	ttggaatgag	aggagatcgg	591660
caagtcaacc	tagtgaaggt	cgcttccaaa	ctgaatgccg	atgatattgc	tctagcttct	591720
gatgaagaaa	tcgaacgcgt	tctaggcaca	gaaaaaggat	tcacgggtcc	cctaaactgt	591780
cccatagact	ttntcgcaga	cgaacaacag	tccccaatga	cgaactttgt	ttgtgcgggc	591840
aatgctaaag	ataagcacta	cgtaaagtga	aactgggagc	gcgacctctt	cccccccaa	591900
tacggtgact	ttctactcgc	tgaagaggga	gacacatgtc	ctgaaaatcc	tggccatcct	591960
taccgcattt	atcaaggcat	agaagttgct	catattttca	atctcgggac	acgctatacc	592020
gatagttttg	aggtaaactt	ccaagatgaa	cacgggcaaa	cccagcagtg	ctggatgggg	592080
acctacggca	ttggagtcgg	aagaacatta	gccgcttggt	tagaacagct	tgccgacgac	592140
cgtggtattg	tttggccaaa	agcactcgct	cccttctcta	tcactatcgc	ctttaacgga	592200
ggagacactg	tatctcaaga	gcttgccgaa	actattttatc	atgagctaca	aagtcaaggc	592260
tatgagcccc	ttcttgatga	tcgagatgaa	agactcggat	ttaaacttaa	agacagtgac	592320
cttatcggca	ttccttataa	gcttatttta	ggaaagtctt	accaatcttc	gggaatatte	592380
gaaattgaat	cccgatctgg	agaaaagtat	acagttctcc	cggaggcctt	ccctacttgg	592440
tgtcagaatt	ccttagccta	gctctttgat	cgctgccctc	ctcgtaaaaa	agttagcatt	592500
cattcaattc	gagtgcataa	ttctcttgac	cttctcgggt	tcttttcccta	taatgctctc	592560
agttacgatt	gttctagtag	gactcgagat	ggctagatcc	aaagtctcaa	agcgagattc	592620
aaaaatcctt	gatatcctgt	ttgctacaac	agagttgtac	ctaaaaacag	ggcagcctgt	592680
agggtctaaa	acttttaaagg	aaagtttttg	ctctgatttg	agtacggcaa	ctataagaaa	592740
ttactttgca	gaacttgaag	ctgaaggatt	cttaaaaana	aatcatactt	ccggagggaag	592800
aatccctaca	gacctagcat	tacgtcacta	tgtagatcac	caagaagaat	gcccagaagc	592860
tgagattttc	gccccatttt	ttgataagnt	cagtcngctt	ccctagcgaa	agtcgcaata	592920
ttatcaggga	cttacaataa	gctacggaac	ttcttggaga	aatcctagac	ctgcctacgt	592980
ttttttcttc	cccacgcttt	gaaaatgatt	ccgtaaccaa	tattcaaatt	acacaggtcg	593040
ataagcaaag	agctgtcacc	atcctctcta	cggagtgttg	tcagatcttc	acagacaccc	593100
tatggctgcc	tgaagcttgc	gatactcttt	ctatcaaacg	tatagaaaaa	ttcctgcaga	593160
actacatccg	aaagctcccc	acaaatgagg	aactttcgaa	aaaagaagaa	cacctgagca	593220
tgtccctcta	taatgagggtg	gttgtccgct	atctaacacg	ctactgcaac	tttagtgaag	593280
aagatctcta	tcaaacagga	atgtcgaaac	tactgaaata	cgaagcggtt	aaagatcctg	593340
aagttctagc	tctaggactc	tctctttttg	aaaatcgag	acaaatgtgt	gagcttctaa	593400
atataggaat	gcataaagga	agagctacag	cggttcatagg	gaaggagctt	tctgatattt	593460
tagggacctc	gaatccagga	tgttctgtaa	ttactattcc	ctatttatatg	aatcgctctc	593520
cactcggagc	tttaggtatc	ctaggcccga	tcaatcttcc	ttataaggaa	gctcttccct	593580
tgctcaaact	atgtgcgaat	aaaataaatg	aaaccctgac	acaaagtttc	tacaaattta	593640
aactatcctt	cagaagacca	ctcacctcta	actgtaagct	ttcgaatgag	cctattttta	593700
gaacggagta	ctcttctata	aaactattac	cctctaagga	gacgttatga	cagatacccc	593760
acctgaaaaa	gaggaacaac	acgaaagcaa	tgttcaaaaac	gaaaatgaag	ttgaacattt	593820
gcaacaggaa	atcgctcacc	taaaaaccga	attaaaagaa	aaaaacgata	agtatctcat	593880
ggctctagca	gaatctgaga	attctagaaa	acgcttcaaa	aaagaacgcc	aagaacttat	593940
gcagtatgct	ttagaaaata	ctttaataga	ctttctcaat	cccatagaaa	gcatggagaa	594000
agccctcgga	tttgctacac	aaatgtccga	cgatgtaaaa	aattggggcc	tcggattcaa	594060
catgattctc	aaccaattca	aacaaatctt	cgaggaaaaa	ggtattattg	aatattcttc	594120
aataggccaa	aagtttaacc	ccttctctaca	cgaagcgggtg	caaacagaag	agacttctga	594180
agttcctgag	gggacgattt	tagaagagtt	tgcaaaaggga	tataaaatag	gagaacgccc	594240
gattcgggta	gctaaagtta	aagtcgctaa	agctcctact	cccaaagaaa	ataaagaata	594300
gaataaaccc	ctagagatta	ggtaccaaac	atgagtgaac	acaaaaaatc	aagcaaaatt	594360
ataggtatag	acttaggcac	aacaaactcc	tgcgtatctg	ttatggaagg	aggacaagct	594420
aaagtaatta	catcatccga	aggaacaaga	accacgccat	cgatcggtgc	cttcaaaggt	594480

aatgagaaat	tagtggggat	tccagcaaaa	cgtaagcag	tgacaaatcc	agaaaaaact	594540
ctcggctcta	caaaacgctt	tattggccgt	aagtactctg	aagtagcttc	ggaaatccaa	594600
accgttcctt	atacagtcac	ctccggatct	aaaggtgatg	ccgttttcga	agttgatggc	594660
aaacaataca	ctccagaaga	aattggcgca	caaactctaa	tgaaaatgaa	agagacagca	594720
gaagcttatc	taggcgaaac	tgtcacagaa	gcagtgatca	ccgtccccgc	atacttcaat	594780
gattctcaac	gagcatccac	aaaagatgct	ggacgcattg	caggtctaga	tgtaaaacgt	594840
atcattccag	aacctaccgc	agcagctctt	gcctacggaa	tcgataaagt	cggtgataaa	594900
aaaatcgctg	tcttcgacct	tggtggagga	acttttgata	tctccatcct	agaaatcggt	594960
gatggcgctc	tcgaagttct	atctacaaat	ggagatactc	tcctcggtgg	agacgacttt	595020
gatgaagtca	ttatcaaagt	gatgatcgaa	gaattcaaaa	aacaagaagg	cattgatctt	595080
agcaaagata	atatggcctt	acaaagactt	aaagatgctg	ctgagaaagc	aaaaatagaa	595140
ctttcaggag	tctcttcac	agaaatcaat	cagccattca	tcacaatgga	tgcacaagga	595200
cctaaacacc	ttgcattgac	actcacacgt	gcgcaattcg	agaaactcgc	agcctctcta	595260
atcgaaagaa	caaaatctcc	atgcatcaaa	gcactcagtg	acgcaaaact	ttccgctaag	595320
gatatcgatg	atgttctctt	agttggaggt	atgtcaagaa	tgcccgcagt	gcaagaaact	595380
gtaaaagaac	tcttcggcaa	agagcctaata	aaaggagtca	accccgcaga	agttgttgct	595440
attggagccg	caattcaagg	tggtgttctt	ggcggagaag	ttaaggatgt	tctacttcta	595500
gacgttatcc	ccctatctct	gggtatcgaa	actctaggag	gcgtcatgac	gactctggta	595560
gagagaaata	ctacaatccc	tacacagaaa	aaacaaatct	tctccacagc	tgctgataac	595620
cagcctgcgg	ttaccatcgt	agttctccaa	ggagagcgtc	ccatggccaa	agataacaag	595680
gaaatcgga	gattcgatct	tacagatatc	cctccggctc	ctcgaggcca	tcctcaaact	595740
gaagtctcct	tcgatatcga	tgcaaacgga	attttccatg	tctcagctaa	agatgttgcc	595800
agcggtaaag	aacagaaaaa	tcgtatcgaa	gcaagctcag	gacttcaaga	agatgaaatc	595860
caaagaatgg	ttcgagatgc	cgaatttaata	aaggagaag	ataaaaacgt	cgtgaagctt	595920
cagatgctaa	aaatgaagcc	gatagcatga	tcttcagagc	cgaaaaagct	attaaagatt	595980
ataaggagca	aattcctgaa	actttagtta	aagaaatcga	agagcgaatc	gaaaacgtgc	596040
gcaacgcact	caaagatgac	gctcctattg	aaaaaattaa	agaggttact	gaagacctaa	596100
gcaagcatat	gcaaaaaatt	ggagagtcta	tgcaatcgca	gtctgcatca	gcagcagcat	596160
catcggcagc	caatgctaaa	ggtggaccta	acatcaatac	agaagatttg	aaaaaacata	596220
gtttcagta	gaagcctcct	tcaataaacg	gttcttcaga	agaccataac	gaagaagctg	596280
atgtagaat	tattgataac	gacgataagt	aatcaaaatt	ttcaatttaa	gtttctctat	596340
tcccactctc	ataaggaggt	gggaaacttc	cttataaaac	gaaaacagtt	ccattctctt	596400
attctctgat	caaggagttg	caataacaga	gcttctttag	tacaattggc	tttgaatttg	596460
agactgctcc	tttcataatc	acaaaaccca	cttaaaaggg	aaaattttgt	tgagccactc	596520
agttcacgag	tgaaactacg	ggatttctcg	ttcaatgtcc	taaacttaca	ggcggagccc	596580
aattgttgaa	aaaaccaaaa	agaaaaccag	ggagaagaac	atacggtaaa	tccttgaaga	596640
tttttattcc	aggaacccta	tttgttcattg	ctagaaaagg	tttcggtttt	gtttctcccg	596700
acaaccccgga	agaataccca	tttgatattt	ttgttcccgc	ccgagattta	cgcggggctc	596760
tagatggtga	ccacgtgatt	gtctccgtgc	ttccctatcc	aagagacgga	caaaaactca	596820
aaggcactat	caaggaagta	ctcgcaagag	gaaaaacaac	actcgtagga	acgatcacct	596880
cactagtcag	tcccacatca	gcacttgcct	acacaagcat	gtcgggatcc	caatctttta	596940
ttccagtaga	actccttccc	ggacgcactt	acaaaatcgg	cgatcgcat	cttctgagca	597000
ctcctccctg	ggtagataaa	ccccagaag	gagcctctcc	agccttaca	atgctcgaat	597060
ttattggcca	catcaccaac	gctaaagcgg	actttcaggc	aattcaagcc	gaatataacc	597120
ttgccgaaga	attcccccca	gaggtcattg	aagaagcaag	ccttttctct	caaaananat	597180
taaccaaggt	tctccaactc	tcgcaaagat	ctccgtgatc	tctctgtttt	caccatagac	597240
tcttccacag	ccagagactt	cgacgatgcc	atctccctca	cctacgatca	taataacaat	597300
tacattcttg	gtgtacacat	cgcagacgtc	tcccactacg	ttaccccaca	ttctcaccta	597360
gacaaagaag	ctgctaaacg	ctgtaactct	acatatttcc	cagggaaagt	cattcccattg	597420
ttgccatcag	cactctctga	taatctctgc	agcttaaaac	caaacggtga	tagactcgct	597480
gtatccggtat	ttatgacgtt	tacaaaatca	ggtcatcttt	cagattacca	gattttccgt	597540
agcgtcattc	gaagcaaata	tcgtatgacc	tacgatgaag	tcgataacat	cattgaaaag	597600
aaacactccc	acccctctct	aaaaatcctc	aatgagatgg	ccactctaag	taaaaagttt	597660
tccgatatcc	gtgaagaacg	tggttgcat	cgctttgtcc	tcccctcagt	cactatgtcc	597720
ttggataatc	ttcaagaacc	cgtagctctg	atagaaaacc	accagacctt	ctcccataaa	597780
ctcatcgaa	agttttatgt	taaagcaaac	gaagtggtcg	cctatcatat	ctcccataaa	597840
ggcgtttctc	taccttttctg	tagtcacgaa	cctcccaatg	atgaaaacct	actcgccttc	597900
caagaannng	caaaaaacat	gggctttgat	atcacgttca	ctcccacaca	aagaacctga	597960
ttaccaatac	cttttgcaaa	ctacgtcagc	aggacatccc	ctagagcaag	ttctacactc	598020
gcagtttgtc	cgaagtatga	aaacagcctc	ctactctaca	gaaaataaag	gtcattacgg	598080
acttaagctc	gactactaca	cccactttac	gagttcccata	cgtagatata	tcgatcttat	598140
tgttcacagg	cttctcttca	accccttatc	tatagaccaa	acgcacctcg	aaattactcg	598200
aagagcatgc	tctacaaaag	aacgagtatc	cgcaaaagca	gaaaattctt	tcgaaaacct	598260
caaaaaaact	cgggttcataa	ataaattttt	gcaagagcaa	cctaaaacta	cataccatgc	598320

gtatatcatc	actgcaaatc	atgaaggact	ctcattttgta	gtgaccgaat	tctgccatga	598380
agggttcatt	gcagcagcag	aactccctaa	agaatattcc	ctaaagaaaa	acgctcttcc	598440
agaatctatc	ccagataaaa	tgaaacctgg	agcttctaga	aaagtcacta	ttgattccgt	598500
gaatctcctt	acgcaaaaaa	tcgtctgggtc	tatagcgaca	accacagaag	ataaacctaa	598560
gaaaataaag	aaaacgcctt	ctaagaaaaa	aggaacgaaa	aaaagagcct	cgtaacgtgc	598620
tacaagaaca	tttttttcta	tcggaagatg	taattacact	agcgcaacag	cttttaggac	598680
ataaactcat	cacaacacat	gagggctctga	taacttcagg	ttacattgta	gaaaccgaag	598740
cgtatcgtag	ccctgatgac	aaagcatgcc	acgcctacaa	ctacagaaaa	actcagagga	598800
acagagcgat	gtacctgaaa	agaggctctg	cttacctcta	ccgttgctat	ggcatgcac	598860
acctattgaa	tggtgtcact	ggacctgagg	acattcccca	tgccgtcctg	atccgggcca	598920
tccttctctga	tcaaggcaaa	gaacttatga	tccaacgcgg	ccaatggaga	gataaacccc	598980
cacaccttct	caccaatgga	cccggaaaaa	tgtgccaaag	tctaggaatc	tctttggaaa	599040
acaataggca	acgcctaaat	accccagctc	tctatatcag	caaagaaaaa	atctctggga	599100
ctctaacagc	aactgccccg	atcggcatcg	attatgctca	agagtatcgt	gatgtcccat	599160
ggagatttct	cctatcccca	gaagattcgg	gaaaagtttt	atcttaaaata	atcttaagct	599220
gtatagttaa	gaaacaaatg	cccatttcct	catatcttgc	aggagaatca	tgaaaaaata	599280
ctttattaca	ggacttggtta	ttctccttcc	tctagcaatt	actattgcta	ttgttactat	599340
gatcatgaac	ttcctaacc	aacccttcgt	aggcttggct	tcggaattct	ttgacgaaat	599400
ttagctttta	tactaaacat	agagctcttc	taaaattcgt	attgcaaate	atcttactct	599460
tcggtctctt	tttcgccaca	gtgctcctag	gttctctcac	gagaattatg	atcttttaaat	599520
ccctactctc	tatctacgac	aaaatcttac	accgaattcc	catcattaaa	acagtgtata	599580
aagctgcgca	acaagtcacg	actaccatat	ttggatcaaa	atcaggatcc	ttcaaacaag	599640
tagttattgg	tcctttccct	aacgcaaatg	ttcaatgcac	cggctctcgt	cgtaggagacg	599700
caccacagat	atgctgcaca	ggagaaaagg	aagacgaccc	cctcgtcacg	gtcttcaccc	599760
caacaacacc	caacccacc	tcagggtttc	ttaccctatt	tagaaaaatc	gatatcgat	599820
tcctagatat	gaaaatcgaa	gatgctttca	aatatattat	ctcctgtgga	gtcctctcaa	599880
cccccatggc	atgccccctg	tctcccctcc	ctgacgagct	acaccaagat	caaggcagct	599940
aaaagacgtc	atcttcttga	aaaaaaaact	ttcttttact	atcctttttc	ttataaagta	600000
ctccgtatcc	tcaattttccg	ttgtctggag	aaattaaaaa	attcaatatc	gagttattta	600060
tgacacgaat	gagtaaacaa	gctcggcgca	gagcgaaaag	tcctaaaaaa	cgtaaaccta	600120
agtagcccat	tgtgcatcca	gcgccagtcc	aagaattgta	tataaattgc	atcgaatgc	600180
attgagcacc	agtgatagca	tttttatccc	gaaaataggt	taattttctag	agtagaatta	600240
tgtctcgaca	tcgtagttat	ggtaaactctg	tcaaaggggt	taccaaaga	aatgttttga	600300
agcgttttga	gcgagtagaa	gtcttgcgta	agttgggccc	ttggaatgat	agtacagcga	600360
aaaaagtcac	agggtttac	aagaccctca	ttttaaaata	agtttgtttt	tctctatggg	600420
aatttcatte	gcgtgacgca	agaaaagatc	aaaatacatg	tttccaatga	gcaaacatgt	600480
attcctatte	atgttggtttc	tgtagagaag	ctgggtctta	cgctcttaga	gcacttaana	600540
gtaacancta	atganatttt	tatctacttc	ctagaagata	aagctcttgc	agaactccat	600600
gcataaggta	tttgctgatc	cttctctaac	agatcagatc	actctgccta	ttgatgctcc	600660
cggagatccc	gcttatcctc	atgttttagg	agaagcattc	attagcccac	aggccgctct	600720
taggttttta	gagaacacat	ccccaaacca	agaggatate	tacgaagaaa	tctcgagata	600780
cctcgtccac	tctattctcc	atatgctcgg	atacgacgac	acctcatcag	aagaaaagag	600840
aaaaatgaga	gttaaagaaa	atcaaatect	gtgtatgtta	agaaaaaaac	atgctttgct	600900
aacagcttaa	catgctccat	attcttttag	ccatattctg	tattcttcta	ttcctagcct	600960
tcgggcttac	gcaaccgtcc	tgtcacggat	cctcaaaatt	cctaaaaacc	ctaaaccaac	601020
gcttcttcac	agataaagga	agagagtate	ccccctcccc	cagtgtcctc	acaattctcg	601080
ccacgtgctc	ctgcatcctc	tatggagctc	tcgggacaaa	actctatacc	ctcctccctc	601140
caaaaacagc	tcacaaagat	ctcctattct	ggccccata	ctctctaagc	gccctgatag	601200
cttacggatt	cctcccccca	tggatctcta	caaaagtccc	taaagaaacc	accgcccacc	601260
tccgttttct	agcttcggta	ttccaactcg	gtctcttccc	actgcaactg	ctcttttaca	601320
gacgccgccc	taaccaacaa	gtacgatctt	caacatcatt	tcaaagccag	ctctccgaag	601380
ccctctccgc	ttttgataac	ctcattgtcc	gtgaagtcat	gatcccaaaa	gtagatatatt	601440
tcgcacttcc	cgaagaaact	acactacaag	aagctctggt	tctcgtaagc	gaagaaggct	601500
acagtgcgct	tcctcggttat	aaaaaaaact	tagacaacat	cacaggaatc	cttcttggtta	601560
aagatctctt	actgctctat	acaagcagcc	acgacctcag	ccaaccata	tcctcagtag	601620
caaaaccccc	attctatgcc	ccagaaataa	aaaaagcctc	ctctcttctc	caagagttcc	601680
gacaaaaaca	tcgccatcta	gccatcatag	tcaatgaata	cggattcaca	gaaggcatcg	601740
ctaccatgga	agatattatc	gaagaaatta	taggagagat	cgcagacgag	cacgacgtac	601800
aagaaaatac	tccttataag	aaaatcggaa	gctcttggat	tgtagatgga	agaatgaata	601860
tctccgacgc	tgaagagtac	ttcaatttga	aaatcgatca	tgaaaatagc	tacgatacac	601920
taggaggaca	tgtcttccat	aaagtgggtg	ctgttcccca	aaaaggaatg	cgatccatc	601980
acgaaaactt	cgtataagaa	atcattacct	gcacagaacg	aaatgtcgga	aaactaaaaa	602040
tcacaccaag	aaaacgtaaa	ttcaatatct	cctaagaatg	taaacatcct	aggaccgatt	602100
tccttgcaat	ccacgatccc	atcctgcctc	cccccaatcg	aaattctcaa	acatcaccaa	602160

tåaaaatctc	tttgcaaaaa	agctaaagat	ttatcagagt	gaaaacttaa	gctcccgtat	602220
agttaggaga	actatctaga	tgagtgatat	ccaaaaagaa	gaacacggct	caacaacaat	602280
ctttcatctc	cacggaaaa	ttgatggaat	ttcttctcca	gaagtacaag	aaaatatatta	602340
ccaatcccta	gcagctggat	ccaaaaatat	cattctcgac	tgtgctcacc	tcgattacat	602400
gtccagtgca	ggtatccgag	tcctactgca	aagctaccat	caagtaggac	aacattctgg	602460
gaaaattgtc	ctgactacag	tcccaaaaac	catagaacaa	actctctatg	ttacaggatt	602520
cctttcttac	tttaaaatat	tcaatactgt	ggatgaagcg	atacaaacac	taaacaaga	602580
cggggattga	gaaaaacctc	actgttagta	tatgatggcg	cttttaagtc	atataaagcc	602640
tcctctttac	tatgcgacga	tctgtttgtt	acgttaaccc	ttcgatagct	cgagcagggc	602700
aaattttctac	ttggaaattt	ctttattccc	ttgccacacc	actaccagct	ggaaccaa	602760
gtaaatttga	cttagcagga	agtgggaaac	ccacagattg	ggaagccccc	gcgacagatc	602820
tctcccaa	tagaaacgta	atctacgcag	aatgccaga	aggcgaaatc	atcgaaacaa	602880
cgcgcattcc	tgtaaaagac	aatcccgttc	cacaattcga	gtttactctc	ccctacgaac	602940
ttcaagtagg	agaaacccctc	actattgtca	tgggagcctc	tccaaacccat	cctcaagtgc	603000
atgatgctgg	gaacggagcc	caacttttcg	cacaacgtgc	caaacccttt	tacctctaca	603060
tcgatcctac	aggagaagga	aactatgatg	aacccgatgt	cttctctatg	gatatccgcg	603120
gaaacgtcct	aaaaaaaata	gagatcttta	ctccctccta	tgtcgtaaaa	aacaaacgct	603180
tcgatatcac	cgtgcgattt	gaagacgaat	tcgggaacct	caccaacttc	tctcctgaag	603240
aagacccgaa	tcgagctttc	ctacgagcat	cttagagaaa	atttaaattg	gcagctcttc	603300
atcccagaaa	caggctttgt	tattcttcct	aatctctatt	tcaatgagcc	tggaaatttat	603360
cgcacccaat	tgaaaaacct	ctctacacaa	ganattttca	tctctgcccc	tatcaaattgt	603420
ttcgctgact	ccgccccgaa	tcttatgtgg	ggtctcctcc	acggcgaaatc	cgaacgcgtc	603480
gactctgaag	aaaattattga	aacttgtatg	cgttatttcc	gagatgaccg	cgctctgaat	603540
ttctatgctt	cttcacatt	cgaaaatcaa	gagaacctct	ctccagatat	ttggaagctc	603600
atcaatcaaa	ctgtctccga	ctttaatgaa	gaagatcgct	tcatcacact	atccggattc	603660
caatatagcg	gagaacctca	tctcgaggga	gtgcgtcaca	tccttcatac	caaggaaaca	603720
aagtcccaat	cgaaacacaa	agaatacaaa	catattcccc	tcgccaaagct	ctataaaaagc	603780
actgtcaacc	acgacatgat	ttctattcct	tcggtcacag	cttctaaaga	acatggtttt	603840
gactttgaga	atttctaccc	cgagttcgaa	agagttgtag	aaatttataa	tgctggggga	603900
tcttcagaaa	ccacagccgc	tctaaacaac	cccttcctca	tccaaggtaa	agatagcgaa	603960
gacccctcgag	gtacagtaat	tgaaggatta	aagaagaatc	tcgcttcg	atttgttgc	604020
gggggtctcg	acgatcgagg	aatttataaa	gactactttg	actctccgca	agtgcaatat	604080
tccccagggt	tgacggctat	catttgtaat	aaatataccc	gagagtctct	tgttgaagct	604140
ttattcgcac	gtcattgcta	cgtacaaca	ggacctagga	tcgtcttaag	cttcaacatc	604200
acttcagccc	ctatgggctc	cgaactctcc	acagggtcga	aacctggact	caacgtcaac	604260
cgtcacatct	ctgggtcatgt	ggcaggcact	gccctactca	agactgtaga	aatcatccgc	604320
aatggcgaa	ttctccatac	cttcttcccc	gatagcaata	acctggacta	tgaatacgat	604380
gatatggtac	ccctaagttc	agtgacccta	aaagatccaa	acggtaaagc	accttttcta	604440
ttctactatc	tcagggtcac	tcaggcagac	aatgctatgg	ctggagttc	cccaatctgg	604500
gtggatttaa	attaagaac	tatccatctc	aaggatttct	tatgatgaca	ctttttctcg	604560
taatctgctg	tgccacagta	ttgttaggtc	tagggatggg	tattctactt	gtagggtccc	604620
atttgcttgg	caggccctc	tctaaagggt	gtcaaaaacc	agattgctgc	caaaaaaaaa	604680
catgtgacaa	aacagagcac	tgtgctacaa	aatctcgaga	gaatagtaca	tcaaagtgtt	604740
catcaaata	cgacgtgcct	cccacagccc	cctaaaactt	cccccccta	ctccatattc	604800
gaaaaactgg	atgcccaaga	acgattaagc	agtgaagacg	ctcttcatct	cctcctcctc	604860
acgaataaag	aagatcaacg	cacactctgg	aattttgcag	accaagtctg	caaacacagg	604920
gttggcgaca	ctgtatacta	ctcctcaacc	ttgtacctct	atcctacaaa	tttctgtgac	604980
ttcagctgca	aattttgctc	tttctatgca	aaacctggag	accctaaagg	atggctctac	605040
tccccagatg	atcttctaca	gcaaatecaa	aatataaaaa	ctccaattac	agaagtacat	605100
atcggtgggag	gctgtttccc	ctcctgcaat	ctgcaatact	attccgatct	atttactaaa	605160
atcaaagagt	acgatcctca	gatccatate	aaagctctta	ctgccattga	atatgcctat	605220
ctctcagatc	ttgataacct	ttctattcgc	gatgttcttc	tcacattaaa	agatgcgggt	605280
cttgattcca	tccccggagg	aggagctgaa	atcctcgtcg	acaaaatacg	taatttctta	605340
gtccccaac	gcctttcttc	ttctgatttt	ctcaacatcc	ataagatggc	tcatacaatg	605400
ggaatccata	gcaatataac	catgctctgc	tatcataaag	aaggacctga	agacctcgct	605460
accacatagg	taaaagtccg	cgacttacaa	gacgaaactc	agggctttta	aaacttcata	605520
cttctaaaat	tcgccaaga	aaataatgtc	ctaggaaaaa	gattaagaaa	atcaggccag	605580
gggtcatgcca	tcctctctaaa	atctttaa	gcagtagccc	gaatcttctt	agacaacttt	605640
tccaatatga	aagccttatg	gaattaccta	ggtattgagg	cagctctaga	cctcctttcc	605700
tgtggtgcta	atgacctttc	ttcaacacat	atgggggaaa	aggttttcca	gatggcctca	605760
tctaaagaac	ctattaaaat	ggacgctgag	ggaatggcgg	ccctcatcac	acaacaaggg	605820
agaacgccat	gtctaaccaa	ctccagccat	gtataagctt	aggctgcgta	agttatatta	605880
attcctttcc	gctgtcccta	caactcataa	aaagaaacga	tattcgctgt	gttcttgcct	605940
cccctgcaga	cctcctcaac	ttgctaatac	aagggaaact	cgatgttgct	ttgacctcat	606000

ccctaggagc	tatctctcat	aacttggggg	atgtcccccg	ctttggaatt	gcagcaaacc	606060
aacgtatcct	cagtgcacac	ctctatgcag	ctcccacttt	ctttaactca	ccgcaacctc	606120
ggattgccgc	aacttttagaa	agtcgctcct	ctataggact	cttaaaagtg	ctttgtcgtc	606180
atctctggcg	catcccaact	cctcatatcc	taagattcat	aactacaaaa	gtactcagac	606240
aaacccctga	aaattatgat	ggcctcctcc	taatcggaga	tgcagcgcta	caacatcctg	606300
tacttctctg	atttghtaacc	tatgaccttg	cctcgggggtg	gtatgatctt	acaaagctac	606360
cttttgtatt	tgctcttctt	ctacacagca	cctcttgga	agaacatccc	ctacccaacc	606420
ttgcgatgga	agaagccctc	caacagtctg	aatcttcacc	cgaagaagtc	cttaaagaag	606480
ctcatcaaca	tacaggtctg	cccccttctc	ttcttcaaga	atactatgcc	ctatgccagt	606540
accgtctagg	agaagaacac	tacgaaagct	ttgaaaaatt	ccgggaatat	tatggaaccc	606600
tctaccaaca	agcccgactg	taaaaagatc	ttcgattcca	tagcgagtaa	gtatgatcgc	606660
acaaatacaa	tactctcttt	aggaatgcac	catttctgga	atcgctcttt	gatccagatc	606720
ctagggtcgg	gatactctct	cctggatctc	tgcgaggaa	caggaaaagt	cgcggaagcgt	606780
tatattgccg	cacaccctca	agcatcagta	actctcgtcg	acttttctct	agcaatgctc	606840
gacattgcaa	aacaacacct	tcccagggc	tcttgcctct	ttattcatag	cgatattaat	606900
caactgcctc	tggagaatca	ttcttatccc	ctagcagcga	tggcctatgg	cctcaggaac	606960
ctctcggatc	cacataaagc	cctacaagaa	atctcccag	tgcttatgcc	ttctggaaaa	607020
ctgggcatte	tagagctcac	acctccaaaa	aaaacacacc	ctacctatag	tgcccataag	607080
ctctatttgc	gtgctgtcgt	cccctggatt	ggaaagtctg	tttctaaaga	tcccagcgcc	607140
tatagctatc	tcagcaaaaag	tatccagcaa	cttccaaagg	accacgatct	tgaagaccta	607200
ttctctaaat	caggatttta	tattgcgaaa	aagaaaaaat	tgttcctagg	agcgggtacg	607260
atttggctac	tagagaaaca	ataaaactag	gaggatctcc	aagcttgggtc	gcaaggagct	607320
ccctaagatt	cgtggagtgc	tctacccac	gctaaactaa	aatggtaaac	ctacctctgg	607380
gaagactctc	atcagcaaaa	ctcccgacaa	gcttcgtcct	gacacaactc	ttaaatcgct	607440
gttttagcat	agcagtcttg	ctaggttcgt	tatcgataat	aaaagcacc	tcttcatccg	607500
aagactcaaa	gaactgcata	atctcaccag	aagcaactaa	actctccaaa	agctctacaa	607560
gctcggtagc	tctttcacca	actcctctaa	ggacaaatct	cccaaacggc	tgattctccc	607620
aatatccaga	aatacgtcca	gcctgcacca	gacctcgcag	taccgaccga	atctctccag	607680
cttgatcagg	atggtcatac	caaccttcga	ttccaggctc	taggaccggt	agccccctaa	607740
agagaatctc	ctcatcagaa	gccacaaaa	attccgttaa	gatgttattt	ttaggtctag	607800
actcgaattc	cgatttaaag	aggtctagtt	ttgacgtagg	aagaggttta	gctgtacagc	607860
tctccctac	gttaaagctt	tgcaagagcc	atgccactaa	agaattgaat	actttaatac	607920
gtgcttgtga	ctgagttgcc	gccagccctc	gggcaagaat	catattccct	aactctttgt	607980
ttaagaaaat	ttcttcta	ccttctttct	ttgttttaaa	gaaaaattta	tagagcctct	608040
ccgaccaacg	ccaattcgta	cgccaattct	caggtaaate	aggaacgtgt	ttctgtattt	608100
catccttaga	aagttcataa	tcagctaaat	agccattata	caagtccaac	tccatacgac	608160
gcgcacgagt	agcttctaaa	atcagacttt	tttcttcac	tgtaaacatc	acctcaggtt	608220
cttttagcgg	ctctggatag	ggaacatttt	gaactacaag	cgcataacct	agagaaaaac	608280
tcgggtcctc	ctctgtccct	ggtgtagaat	ccacggtagc	ctcagccgcc	gcagcctctg	608340
aaaacccaga	tgtggtgtct	gtagttcccg	aagctgcagg	catgggtatc	gttgatttcc	608400
ctggagctac	aggtgaagac	tctacagtct	cggaagctgc	aggtatctct	tgagtaggat	608460
tggcgttcac	aggaaccatt	tccgaatcca	caataacagc	gtccttacta	cctaaacttt	608520
taggaaactt	taggcgcttc	attgtttctt	ctaaccacac	tagccgctcc	tcagaaccaa	608580
ggataggggc	ccactggacc	aaagtactac	atagccggcc	gtgggtcggg	gaaatttgag	608640
aaacttgtgg	ctcaagagaa	cgtatcccaa	tagcggggcc	agcctcctca	taatacattt	608700
tcacagagag	ggtatccac	tgcaaagcaa	aaggacgcct	ttgaagaata	cataatttta	608760
atatgtcatc	caatcccga	attatagaaa	aattcttttt	agcaaaactc	ttacccttcg	608820
caccggaagt	gtgctgcggg	acaaagaaa	gccttatagg	caagcgctca	ttaggaacta	608880
aagtagggaa	gtcacagagc	ccccttgcca	ccatacatat	gtaataggcc	ttcgcgatag	608940
ccctccccag	gacggctagg	ataatcttca	cgaaccatga	cactcggaat	gatatcgata	609000
ttcttcaatc	ccattttctc	tataatcaac	ttagagtggg	tcaaccggta	gcaatctacc	609060
atagcaaaat	gggcgtcgta	atcagagcgg	aaagcctcac	aaatcgattt	gccttcctta	609120
gtcctcagcg	atgaccttg	tttttcaata	acaaagcaca	aagaactgac	gtgaggccta	609180
aaatcccga	tcaaacaggc	ccaatccacc	aaaggctcgt	tcgggtggctc	agggctgaaa	609240
tgctccataa	ataggaata	tttagcagct	aaaggcatgg	taagaccatg	gttctgaaat	609300
ggagagaata	acgtccttac	tataggaatc	tcgcctgtgc	ctaaagatga	tcgtcctaaa	609360
tcccaatggc	ggacccctc	gtagtaaagc	gagcgagcgg	gcttgtgaat	ctcaaaagct	609420
ctcttatttt	gccggtaact	cgtaacagtg	ctataagtaa	gataacttat	aattgcaacg	609480
tcaccaagaa	gtgacatcac	aaaaagaatt	aaccccatat	ccgtaaaaga	ggtcgccaag	609540
gccataatgc	ttggaatcaa	actagagagg	gccacacaaa	ccaaaatgat	caacaatgcg	609600
cataaaaaga	tgacacttgc	ccgaactaga	cgtgtgtctca	actgattctg	actcgtatcc	609660
tcaagatagc	tctttaagct	acaggtaac	cgagtcggct	ctattcttcc	gcagctcagt	609720
agtgatgaca	tgatgaacta	ttcactgttt	cttaaattag	ctttaaaaat	tttaacagtt	609780
ttttaattaa	aaaaatgact	aataataaat	agctattggt	aaaattttta	caaaacaata	609840



aatagaaata	agaaagattt	gtaataagat	catgtaaaaga	agcaataaga	acagcgtcta	609900
aaaataaact	acttcacaaa	atagaagatt	aagaagattt	tttgcggcct	cgcttgctcc	609960
ccttcgtctt	agtgaccact	ttctcatcat	catcaccaaa	gaaatctcca	gtagaaagag	610020
agtcgtaacc	aagcttagcc	gaaagctctt	taagagaagc	aaacctctct	gaaagattgg	610080
taagattcag	ctgggtcttca	acacgagtcg	aaccgcgcga	gttagcaaga	aattcttctt	610140
ccgtatcaaa	tttttctgag	aaagtaattg	aagaggggtga	agtaatctcg	ggtaagaaaa	610200
ggaaacgacg	agcagcctga	gggacttttg	tataaatatc	actcgaaatt	gttggttctg	610260
tttctacctt	agcagattgc	ttcggaggac	ggcctcgttt	cggacgaggg	tttaatgctt	610320
cattggaata	gtaaatctta	gctttgttcg	acaacaactg	acgcgcttga	gtgatttctt	610380
tccccacctt	ggcatcaaac	aaatgtattt	tcaactgttc	caaaacattc	tttgtgaaat	610440
ctagatcttc	ttcaaagaca	aaatggaact	tattattgctg	aagccattct	ataattcgaa	610500
ttcgagaacg	ctctacataa	aattgctgct	acttttctaa	ctctgcctcg	tgatcataaa	610560
taaactctaa	aaactgctca	cgggcattct	tggattgcaa	aatctcaagg	aacttttctt	610620
tggtatcgat	atcataaatc	ttttcattga	taaacgtttc	catgattttt	tttacttcat	610680
aaaacgtcaa	cttcggaatc	aaacaatacc	gctcggcatt	ctcttctaata	tcttggtaaa	610740
tcttatttag	atcctcttgg	tctttatcta	aactctatga	gagaataaac	ccttcaaac	610800
gatctaaata	aaagtccctc	tcatcgtcag	acttagagaa	tgcatccata	agacgaagga	610860
ttcttaaaag	aagtgggttt	tgtggtacag	gatacgtcat	cataaattac	gattatagaa	610920
aaatcccagt	tagagagcaa	gatctatccc	taaacaagat	tttaaaatcc	ttgcatgaca	610980
aaatcaaaaa	tcacatctaa	ttataaatct	ctagttacag	agccctgaag	atatacccgt	611040
cccctatttt	gactcacagt	cataagctct	ccaccccaag	tatggatttg	gatcgactcc	611100
ttccatccat	aggagtttga	cacaacaaga	gcagaagcta	gagccctgt	tccacaagct	611160
gcagtttccc	cttcgactcc	acgttcgtaa	gtacgaacgc	gcaactggca	atgtcccagt	611220
atctgaacaa	aattgacatt	caccccatct	ggagagaagg	tctgatgata	gcgaagaaaa	611280
ggacctaaaga	tagaaagatc	taaagtagaa	atctcaggaa	gaattacgac	agcatgaggc	611340
actcccgat	ggatacaaac	gatctctttg	ggaagaggat	caggacgcga	ctccaatcga	611400
tgaacagaag	ctctccaatc	tgcgagagtc	atatctacaa	gcacacgac	ccaagaataa	611460
aaatatcctg	aatatagacc	actatccgta	gatacagaga	tgtccgattt	tcccttctga	611520
gaagctaagt	gagcaatcgc	acaacgcaag	ccgttaccac	acatcgttgg	acgtgatcca	611580
tccgaattaa	aaataatgag	ttgcgcatca	gcacaagaag	agggcttta	atataaaaaa	611640
ccatcaaccc	tcgtctcttg	gcataagaac	cgaacatctt	caacctcagg	aagtgtttca	611700
ccaagaagga	aacgatttcc	tgctccagaa	tagataaaat	atthagagat	cggtgaaagga	611760
gaataaaatg	ccatccaata	aaccaaatac	cttagcttcg	ttggctgtca	tccacatctc	611820
tctatcgata	gccttttcta	tgatatctcg	agggtgattt	gtcgctctca	catagacatc	611880
tataatgcga	gcttttggtt	ttaaaatctc	tctcgcatga	atgtctaaat	cggttgcttg	611940
accggtaatc	ggtccaccta	ttgaagggtg	atgaatcata	attctagaat	gaggagtgtg	612000
aaatctcctt	ccaggagctg	cacataaaat	caataccgag	cccatagaag	ctgccaaccc	612060
tgtcacaaca	gtagtgcg	gtgagggtta	catttttaatt	tgatcccaaa	cagcaaaaacc	612120
tgcgtccaca	gatccccag	gactattgat	cacaaaaaat	ataggctttc	caggatcttt	612180
taattccaaa	taccaaagct	ttttaattgc	atcggaagca	cttttctctg	ttacaggctc	612240
tgagaaaaat	actctgcg	cttccaataa	ctctttttct	ataatatcac	gtaatttatg	612300
aacttccccg	tctgccataa	aataatgtct	ctcctaacta	aactaaagct	tctaaatcaa	612360
tttcagggta	gagcgggaaa	cgcagcaaca	agttgcgaac	acgatctcta	gcttcctg	612420
ctatggcttc	aggaagttcc	cctttatttt	tcttagaact	cccttcaaca	tggcaactta	612480
aacgaatatt	tcgcaatact	ttcacaataa	tatctgcaac	ttcttccatt	tcatcgatac	612540
ccatacccaa	agtcgttagt	gcaggggttc	ctaaacgtat	acctgaagt	tcccacttac	612600
caatagcatc	tgaaggtaat	gaattccgat	tcacagcaat	tctacggaa	ctcaagatat	612660
cttcagcaat	ttttccagaa	atgcccaaag	aacctaatac	aatcaccatc	atgtggttgt	612720
ctgttctctc	cgtcaaaaga	cgtagcccat	gacttaaaaa	tctctctgct	aatcgacgag	612780
cattatttac	aacctgatga	gcgtatttct	tgaaatccac	agagagagct	tccttcaaa	612840
ccactgtttt	agcagctatc	acgtgaggta	gaggacctcc	catcatcaaa	ggacacgcct	612900
tattgagagt	gctttcatac	tctcgagttg	ccaaaactaa	tccccgcga	ggaccgcgta	612960
atgtcttatg	cgttgtttgt	gtcactatat	ctgcataagg	aataggattt	tcttcatcaa	613020
caaacactcc	cccagcaact	aggcctgcaa	aatgcgccat	atctaccac	aagacagatc	613080
cacaatcttc	tgcaatctgt	tttaaaactg	caaagtttaa	tcttcgagaa	taggaagaat	613140
atcctgcgat	cagtacctta	ggtttatact	ccttagctaa	ccgggagatc	tctgcataat	613200
caaaacactc	cgtatccgga	ttgacatcat	aggggaagca	acgcataagc	ttagacatca	613260
catttaaacg	tacgttccca	tgggtcaaat	ggcctccaga	atttaatgaa	ggctcctaagc	613320
aaacacaaga	agacatttca	gccttaagta	gagtgtattc	ttcttctgtt	aattcggtta	613380
cagttttata	acctaaactta	ctgacagctg	ggccttgga	tttgtgcgtg	agaatggcca	613440
ttactgccag	taaattagca	tcagccccag	aatgaggctg	aacacaagcg	caatcccgag	613500
caaaaagtgc	tttcgctgtc	tctacacact	cccactcaat	agcatctaca	ttttcacac	613560
aggaatagaa	acgcttaaag	ggacttcctt	cacaataact	atctgtgagc	aagttcccca	613620
tagccaactg	cactgaaagt	gaagaatagt	tttcagaagc	aatcatcttt	aaatgggaac	613680



gctggctctt	caactcatca	atgattctct	ccccaatgga	aggaaacgca	tttaagagat	613740
ggtcaagagc	tgctaaatac	gctgtcgaag	ctaaactttg	tccctttttc	cccgaagcat	613800
tttctaaaaa	cttatgcaac	aacgaaacca	ccgcaaccac	ctttgtaaat	atttccacta	613860
ttgcgaattt	cttaaatttc	tcaaaaaactt	ttagcaagga	cttctaaaga	cgaagcctta	613920
atagagagaa	cctctaagtc	cagaaaaaac	cagcctagct	ttcaaagtga	aaaatgtcaa	613980
tcaacgcatg	atcaagaaga	actaagggaa	aaagaaaaat	tattttcaat	atatcccttt	614040
gaaggtacaa	aaacttaggc	agccttcctt	ttaccgaaa	agactcatga	ccctctactt	614100
aggattgaat	caaaaaaccg	ctcgtaaata	ccaagctcat	tatttgccca	ttctaactct	614160
cttcccctat	gcaaaaaagca	ctccacaaaa	taagcgtgct	cttcaattcc	ttccacaagc	614220
aaacccatgtg	attctcacaa	gtccctcatc	cactcaccta	ttcctttcca	gaatgacttc	614280
tcttctttct	aaggccactc	taaaaacaaa	gacctacctc	tgtataggag	agtcacacaa	614340
agaaagactt	ctctctttcc	ttggacaagt	gaagtacgta	gtagcaactc	aagaaatcgc	614400
tgaaggcatc	ttcccattgc	tacaggcact	gcctctctca	gcccgcattc	tctaccccca	614460
ctcctccctc	gcaagacctg	tgatcagaga	atttctttac	aatcgattta	cttttttctc	614520
ttaccctcac	tacacagtga	agccgcgaaa	acttaaaaaa	aataattttat	ctaaatacaa	614580
aaaaattatc	ttcacaaagcc	cttcaactgt	aagagctttc	gccaaaatct	ttccgcgatt	614640
tcctgaaaaa	acctactggg	gccaaaggaag	gatgaccttg	caggagtttc	aaaagtcttc	614700
ctctcaaaaag	caggtatctt	tgttagaaac	gcttggaag	tccaggacat	ctccgtgaca	614760
aaaaagaccc	cactacttta	aaatgcttta	tgctccgaaa	aaaacttaat	ttttaatagt	614820
ttatggcttc	ttcagctact	cccggttttg	atggaacggc	tccctctcta	tttccccag	614880
ctactcgtcc	tcgctataat	ttcaagcttg	ccctcttcgt	tactattgcg	attgcactcg	614940
tctggatagc	tctgattgct	accaccatag	ctattgggct	atgtatccac	cctttgtgct	615000
cctttatctt	cctaacagca	attcccttat	actttatatc	tcgctatatt	tgctccact	615060
acgcacgcaa	tgtctacata	gctctagatg	tcgtccccga	tcattctaaa	ttgcaagaca	615120
tgcgctctca	ctctccaatt	ttctcggatc	gataaacaaa	aatttggtta	aattatagaa	615180
agtattttac	aaaaaaaaatg	ttatgtcagg	accctcacgt	actgagagct	ctcaagtttc	615240
tgtactatcc	tatgtgcctc	gggataaaga	aattgtcctt	aaaaaacagt	ttaccatagc	615300
aaaaatatcc	actcttgcaa	tcctagcttc	tttagcttta	ggagcttttg	tggttggaat	615360
ctctttaacg	atagtattag	ggaaccctgt	atttttggtt	cttctcatta	ccacggccct	615420
cttctcagtt	gtaaccttct	tagtctacca	ccaaatgacc	tcaaagggtat	cttctaactg	615480
gcagaaagtt	ctagagcaaa	acttcaagcc	tttgggaaaa	gcgtggcaag	aaaaaacgt	615540
agactgcnac	tcaaacgaga	tgcaatttta	caataatcac	ctgaacccta	agttcaaggt	615600
agcgatacaa	acagatgcgt	ntcaaccatt	tcagcctact	ttcttaactg	gacttagagt	615660
gatcgaaaaa	aatcaatcca	cagggatcat	ctttaatccc	gtaggcccaa	cgaatctgat	615720
cgacaacact	gcaacgaacc	tctctactat	cctttactcc	accctaaaag	ataaaagcgt	615780
gtgggataca	tgcaagcaac	gcgaaggggg	tcccgcacaaa	ggagaagacc	ccttttcccc	615840
taccgaagtg	agagtagtaa	aacttccaaa	cgaagctcta	gatcaaacgt	ttaatctaaa	615900
tttaagctct	gcagaaaaga	aaagtattct	tcggaccttt	ttaggccacg	tatgctggcc	615960
taaatctgaa	gagttacca	atcagcaaga	atattatcgc	caagctttac	tagcgtacga	616020
gaactgcctt	aaagcagcta	tagaaagtca	tgcaagcaatc	ggtgctcttc	ctctctttac	616080
ttcggctctat	gaagtgcctc	cagaagagat	tcttcctaaa	gaaggcactt	tctattggga	616140
caaccaaact	caagcgtttt	gcaaacgcgc	tttattggac	gctattcaaa	atacggccct	616200
acgctatcct	caaagatctt	tacttggtat	actccaagat	ccttttaata	ctatagaatc	616260
acaaagtcgt	tctgaggagt	aacccaaagg	gtttcaccaa	caacccttta	taaagtttag	616320
ctaaaaattt	tctcaacatt	taaaagtata	tttttatttt	ttactaaaaa	tgattaaatg	616380
cgctttggaa	gtgttcttac	aggaacaatt	tacaagtaaa	aattatatga	atggctagac	616440
attagttcta	agaaaagggc	atttcgcttg	ctcaaattta	taagaatttt	ccttacaaaa	616500
aaacatgcct	tacttcttgc	ctaaaaagag	gtaaaactgta	tttttcttca	catgtatcgc	616560
attcctaaac	tccatagtga	tttttggtct	tcttaggaaa	cttaagtaag	gaataatttt	616620
catgcatgac	gcacttctaa	gcattttggc	tattcaagag	cttgatatta	aaatgattcg	616680
ccttatgcgc	gtaaagaaaag	aacatcagaa	agaattggct	aaagtccaat	ctttaaaaag	616740
tgatattcgt	agaaaagttc	aggaaaaaga	actcgaaatg	gagaatttga	aaactcaaat	616800
tcgagatgga	gagaatcgca	tccaagagat	ttctgaacaa	atcaataaat	tagaaaaatca	616860
gcaagctgct	gtaaaaaaaa	tggatgagtt	taacgctctt	accgaagaaa	tgactacagc	616920
aaacgaagaa	cgctgcctct	tagagcacca	gcttagcgat	ctcatggata	agcaagctgg	616980
aggcgaagac	cttattgtct	ctctaaaaaga	aagcttagct	tctacagaaa	atagtagcag	617040
tgtcattgaa	aaagaaaattt	ttgaaagcat	caaaaagatt	aatgaagaag	gcaaagcttt	617100
gcttgaacaa	cggacagagt	taaagcatgc	gacgaatccc	gaactactca	gcacttatga	617160
gcgtctatta	aacaataaaa	aagatcgcgt	tggtgttcct	attgaaaatc	gtgtctgcag	617220
tggttgtcat	attgttctaa	ctcctcaaca	cgaaaatctt	gtaaganaga	aagaccgact	617280
cattttttgc	gaacattgct	ctcgaattct	ctattggcaa	gaatcccaag	tcaatgctca	617340
ggaaaattcc	acagcaaaaac	gtcgtcgtcg	tcgcgcagct	gtataaagtt	aatcggaaga	617400
gaaaggcaac	cgctgtttat	atttctcaaa	aaatataaag	agaggaaagt	ctggacttca	617460
taagagaaga	tactggagaa	attccagggg	ccgtaaggct	acggaaagtg	caacagaaaa	617520

càctccgcta	taaaatttat	tttatagaca	ggctgaaaat	tcctacttta	ggagtaggag	617580
ccattaaggt	gacttaatat	gcatgcaaac	cctatctgaa	gcaagagaaa	aaagcttttt	617640
gtgtctgcaa	atgtgagagg	aattcctccc	ataggctttt	tcgaaatcgc	ttgagggatc	617700
tagtaatagc	ccccctagat	gaatgggtgc	ccttaggata	gttcgcaaga	gctatcttat	617760
agacagaatc	cagcttacc	tctcttcgga	tatttttctc	atattctcaa	agtagaccag	617820
ctttgggcta	agtgtgcata	tgcaacaagc	cagtcacatg	tcggttctcc	tcgttatcta	617880
aaacaggaag	aacagctaca	ggactactag	attccataag	ttgcaaagca	atggcaatat	617940
ccgaatcttc	agtaatacat	cgaggatttg	ccgtcatcac	cttctccaaa	gataacgaaa	618000
gcacctcccc	cccataaggaa	gctaaagaac	gccgtaaatc	tcggtctgta	aaaattccca	618060
taagtcggaa	ttgaggatct	actatacaaa	cacaaccaca	accgtaagca	gaaaagacct	618120
ctaaagaaaa	actcacttta	tctccaagat	gacagaaagg	tacctctgtc	tttggaaca	618180
taaaatcttt	aaccttacca	ttagccttca	tcccaacctg	cccactagga	tggtttttgc	618240
cgtacgtaga	taaagaaaca	ccacgactat	gaaaaaggag	catagctaaa	aaatctccaa	618300
agatcatttg	gcatgtcgtg	gaattttag	ggattaaatt	aaaaggatct	aattcagcaa	618360
cagagggtaa	aataacgact	aagtccgaga	gagccgctaa	attagaataa	ggcatggaag	618420
taatcgcgac	aagaatcgcc	cttcgactct	ttagatgagg	aaccgtatct	agtaactctt	618480
gggtttcacc	acttttagaa	aataaacata	caatgtctcc	aggactcaca	agaccaagat	618540
ccccgtgcag	aagatccaca	ggagaaaaga	acagagcagc	ttcacttaaa	gattggagtg	618600
tagccactaa	ttttcgtgct	acacatccac	ttttccctac	accagaaaaa	aatacccatc	618660
ccgaatgacc	gagtattttt	tctgctaatt	gcattgcctc	tttgggttga	aaggcttgga	618720
aaaaaaaaatc	tacagcttct	ttttgcttac	ctagaatgtc	ttggcatacg	tcagtagaaa	618780
tcacgcgggga	aggcattcgg	ttctcttttg	attggctaca	ctttagccca	tcgtaacaga	618840
ctccaaacga	tttttcaatg	agggttaaaaa	ctcactgcgc	taaataccat	ccaatactct	618900
atggtcaaag	gtaagtgtca	catagaccat	tttgcgaatg	gctaaagaat	cgctacacg	618960
gacgacaaca	cgtttttgta	ttgtgccaat	tcctaaaata	gcaacttcag	gataacgtat	619020
gatgggcatc	ccaatcaaag	ctcccgtcat	tccaaaattc	gtgacagtaa	cgctgccatc	619080
ttgcacttca	ctaggatcca	atttatttaa	ccgagccctt	gaagatagat	ccgccaaggc	619140
ctttgcaata	cttactaaac	cgcgatcttg	acaattgtgg	atgacaggaa	caacaacccc	619200
ttccttattg	aggttcacgg	caacgcctac	attcacagat	ttcttcataa	caatggtagt	619260
cccatctaag	gaaccattca	ataaaggaaa	ctgccttaaa	gtctgagcta	aacactgtac	619320
aatgaaactt	gtaatcggtg	gcttcacccc	atgcgtatct	aagaagcggt	ggcgttcacc	619380
agaaatcaga	ttcataagat	ctgtgacatc	gacatcaaca	accaaagatg	cgtagggaac	619440
ctcatctgaa	gacttgagga	gagaagaagc	tattgcccgga	cgtagcggag	acataggaat	619500
gcgattcact	tctccttgaa	atatttcggg	aatagaaact	tggtgcgatt	ctgaaatata	619560
cgcttctaaa	tcctgacgag	tcactcgtcc	ccctttcccc	gtgccggcaa	tcttttgagg	619620
gttatcaaga	ccaatgcctt	cacgttgagc	taaactcagc	acggcaggag	aaaaccatac	619680
cgaagaactg	ctggaacccg	cctccgactt	tgtttcacaa	gaagtccagag	gacatgaggt	619740
gctctcatca	tcagcttcgg	aaatctcctc	aagctctatc	aatcctaaaa	catccccaga	619800
agcaacctcg	tctcctcat	tgacgcagaa	acgcaccagt	cgccctgctt	taggagagg	619860
taattctgta	gcaattttat	ccgtagatac	ttcaatcaga	ggctcatctc	tagctacatg	619920
atcacccaaa	ttttttaacc	aacggactat	agatcctccg	gaactcgtct	ctcctatttt	619980
agggaaatcgg	aactcaaata	tcattgtatcg	ttaccttcta	tgtagtttca	acgctttcct	620040
gtttttattga	ttcataagga	gaaagctctc	cttctccaga	agctacataa	gtagcaacta	620100
cagcatcccc	aagaatatct	atgggtgtac	ctacaatatc	ccttaaccgg	tcaatcccag	620160
caagtatagc	gataccctgg	ataggtaaac	ctacagaggc	taatacggaa	cccagagtaa	620220
tcatacctcc	tccaggaaca	ccggcactac	ccacggcaga	gaatgttgcg	gtaactacca	620280
ataataacag	actgctcaag	gatagcggac	aattgtatgc	ttgagcaatg	aaaaccgctg	620340
ccataccctg	aaaaattgca	gttccattca	tattcacagt	ggcgccctaga	ggcaaaaaca	620400
aaccagaaac	ctcagcggac	actcccaaat	ttttagaaac	acaacgcatc	gttacaggta	620460
aagtgcgaga	actactcgct	gtagataccg	cgcaagaaat	cgcatccatc	attgaagaga	620520
gaaacttcga	aaaggacatc	ttgcaaccaa	aacgcacaag	tcccccaaaa	acaagcgtag	620580
catggaacaa	acacgccaga	tagtaagcaa	tgataaaattt	gcctagctgc	caaaggactc	620640
ctaaaccatg	atttcccgaa	atccatgcca	tgctagctcc	cacaccatag	ggagcaaaac	620700
tcattgatcat	atttaccatg	cgcaacatga	tttcagaaaa	accatcaata	aaacgctcga	620760
cagggcggcc	acgtttctca	gaaagccgaa	gggcaaatcc	taagaaaatc	gcaaaaataa	620820
taatttgtaa	tatattccct	tcagcaaaaag	agcgtacagg	attcgatggg	aaaacttgag	620880
ctattataga	aagaaaatac	gccgctgttt	tgtttgaaatc	aatgacagta	acggccgaat	620940
ccatagattg	ggcctgggca	aaatcacacc	catttctctg	agagaaaatc	caagcaaaac	621000
acaagccaat	cacaatagct	agtgcgtag	tccctagata	gaggccgaca	cttttaatgc	621060
caatgcgtcc	caattttttc	atatcgctaa	tggaagcgat	tcctaaaacc	attgagcaga	621120
acactaaagg	atacactacc	atgctcaata	gatttaaaaa	gatgtctcct	ataggtttta	621180
aaaagatggc	tttatcttct	aaaactaaac	ctaaggtaac	cccagacaaac	aatccaataa	621240
agatcttcat	ccataatttc	attagttacc	cctggtttta	tgtatttggt	caatcaggtt	621300
gagaagagaa	agtgtatcgt	cttgattcac	agaaaggcgc	atttccacct	tagctatcgg	621360

caataaaactt	acctctcctg	ataatcgagg	aagcttttaca	ctatctttttt	ctgtacataa	621420
caacccttgt	ccttggcgca	tggccatttg	ctgacaaaag	taattttaatt	ctttttttgt	621480
tattgctgcg	tgatcaggca	ataaatactt	tcctaaaaata	tgaattcctt	cttctctaag	621540
catattcaaa	aacccttgag	gaaaccctaa	accacaaaaa	acccccacac	gcaattctcg	621600
aagagcctct	ttaggaatac	gctctccggt	atgggtccaa	actacagaag	ctattgtagg	621660
tttcacaaag	atctgggggg	cattcgaaac	acgttttact	acagtcccag	cctcttttcc	621720
accgccattt	acaataatgg	catccacagt	cttcaatcga	agaggaaaaat	cccgaagcct	621780
tccttttaggg	aagaaggcac	gtcctcctaa	aggatcctga	ccattcacta	cagcaatttc	621840
tacgtctttg	tgtagtttac	ggtactgaag	accatcatct	aaaaggagaa	taccaaattt	621900
ctctgcagcg	cgtgctgcag	agatcctccg	gtccttatgc	acccatacgg	atccctctgg	621960
cagttttctct	gccattaata	aaggctcgct	ccctacatag	gacgcagaat	ggactttcga	622020
gtctacaaca	gtcagtttct	tttgccgact	cgactggctt	ttatagccac	gcgacagtac	622080
accgcaagaa	taccctcgaa	gcctcaaage	ctctgctaac	cacaatactg	ttggagtcct	622140
tcctgcccct	ccaacaacga	tattgcctac	actaatgact	gtagaacgcg	cacgataaag	622200
agtagaccag	gaaaatcgat	tccaacatgc	caccaagaat	gcaaaaactt	tggaaaagaa	622260
ggaacctaac	cagccccatc	ccaaaatacc	ctcaaggcta	atagctatgg	tgacacggcg	622320
ataaaaagaga	aagagtgtgg	aaggaaaaccg	ttttttcatt	gttcctcttt	taaacgcacg	622380
aattttctttg	cacgaaaatc	atgcttttta	aaagatcaca	atcttcgccg	tattacaaag	622440
aatgctagta	ttgcagaaga	aaagattaaa	aatcaagttt	acaaagctta	attaaaaaat	622500
tgtgttaaac	aaaaaactaa	tataattaat	ttgatctcaa	aaagaaaaat	ggtgtactaa	622560
ttaacccaac	gttgacgaac	aacttcataa	gctacagcag	ctacagatgt	agcgagattc	622620
aaagaatctg	attccccctaa	cataggaaga	gcgatttcag	aaaaatcttc	agaaaaccaa	622680
tcctcagtc	aaccatcttt	ctctgaacca	aaaaccaaag	ccgtgggacc	aagataattt	622740
ttagaaaaat	acatagtttc	agctcgagga	gatgtgacaa	aaacagtcca	gccttctctg	622800
ttgaacaact	ccttcccttc	ctctcttgaa	atagagagga	tgggaagaga	aaagacagct	622860
cctaagaag	agcgcaccac	attaggattg	tacaaatcta	caataggatt	gcataaaaatc	622920
acaccgtcaa	caccagcacc	atcagctatt	cttaaaatag	caccgacatt	cccaggtttt	622980
tccacctgct	caataataag	atagaaaggc	tgagcatttt	tacgttggat	caaaaaatct	623040
tctttattcc	acactctctt	ttgtatcacc	gcgacgaaac	tatcgtgatg	ttctttaaaa	623100
gaaagttag	ccaaagtcca	gtctaagcaa	tataaaatct	ttgtagaatt	tctttttaac	623160
tcataataaa	attccttttc	ttttcttgaa	agatgtgtcg	aacaaaaaac	atgctgacac	623220
aggtagcctg	tgcgtaatgc	tttctgaatc	tcacgggctc	cttcaactag	aaaccaagaa	623280
ctttttctac	aacgagaccg	ttttaagct	agagcctctt	taactagagg	attatgtttc	623340
cctatgcaat	ccattgaaca	aaactcccag	aaggcaaggc	tcccacacct	tctccacaaa	623400
aaactttccc	acaagaccac	gcttcagaaa	caaggttgg	cacctacgcc	tagctatagc	623460
ccttaaaaac	tctgggggat	gtcctggagt	atgagagggt	aagagaaaaat	aagaagcgct	623520
atctgcaaga	agcttcgaac	acaaagaaaag	caaaggaaaag	agatctttat	ctattttaaa	623580
tacttcccca	tcagggtccgc	gaccatagct	tgggggatct	aaaagaatca	cttgatattt	623640
cttattttctg	cggatttctt	tttttaaaaa	agaaatcaca	tcttcaataa	cccaaaaaat	623700
acgtctctca	ggaaaagcat	ttttctctac	atttctttgc	gcccacgta	ccgctgcctg	623760
cgaagcatct	acatgggtca	cacgagctcc	acacttagct	gcaaaaatag	aaccgcggcc	623820
tgtataagca	aagagattca	atacctgacg	ttctttgtgc	ttctcaatgg	cttgtttcaa	623880
agcggggccag	aaccccatat	gttcaggaaa	tacgcctaga	tgcccaaagg	gggttctctt	623940
caatagacaa	cgcacatcag	aaaatgcgac	ctcccattct	tcaggaagac	gcttaaaatt	624000
tttccatgct	cctcttttct	cttcacgaac	atactgcaat	tgcgcctgag	accatagttc	624060
aggctgctt	tttggccaaa	cagcaatact	tgaaggacga	attaaagtga	caggaccaaa	624120
acactcta	ttgttcccg	ccccactatc	gagcaattta	taatccataa	ctaattcttc	624180
cctgatgagg	ctaaaaatag	ttttactgtg	tctacctgta	tctttgttga	catatcgatc	624240
tcgatattga	ctcttttctc	ttcccttttc	tttcttaaag	tcgtcctttg	aagagtctca	624300
ggaatcaatc	ccacagaaaa	cgtatcacta	tcaactgaca	ctagcgttaa	gctgacacca	624360
tcaattgcaa	taaacccttt	ttcaaaaagg	tactgagata	attcttttga	accacggaaa	624420
taataacgat	tttcttttat	caagaaaatc	tctgctgttc	caaaaacatg	cccagagagt	624480
aagtgacctc	caatcgagtc	tcccattttt	aatgcagcct	ctaagttcac	ttgatcgcta	624540
catctttttt	ctcccaaagt	cgtacaagct	agagttttctg	gaatcacatc	aaaaaagatc	624600
ttactttcat	tgcgtgatgt	taaagtcaaa	cagactccat	ctacggctac	gctatccctt	624660
gtaaccagag	gggtgacaaa	tagtggcggtg	ctcttaattc	ctaaactcag	accatttctt	624720
tgagcttcaa	aaaaacacac	ttcaccta	tcttgaataa	ttcctgaaaa	catcccaccc	624780
catttaacaa	cagaatcttt	acaacaaaag	ctttcctaga	gtagagtatg	ttttttctgt	624840
ctcaataaag	aaagcaattt	tgcacagaaa	tttaagataa	tacgaatccc	taaagccgtt	624900
tcttttagaga	agtatttctt	ctacccttga	tttcttagaa	aaaaactttg	caactatagt	624960
ctcttatatt	tatcctgac	taaaaattctg	gtttttctta	gactacctta	acctaggagg	625020
tagtctccat	gcagtgctct	ttttgcaatc	atggggaggt	gaaagttata	gattcaagaa	625080
acgtccaga	agctaattgca	ataaaaacgcc	gtcgggaatg	cttaaaagtgc	tcccaacggt	625140
ttacgacctt	tgaaccggtt	gaacttactt	tacaagtact	aaaacgtgat	ggtcgctacg	625200

aaaattttca	agaatctaaa	ttaattcacg	gtctgaacgc	agcttctagc	cacacacgga	625260
ttggtcaaga	ccaagttcat	gctatagctt	ctaattgttaa	atctgaactc	ttaggtaaac	625320
aaaataggga	aattttctacc	aaagaaattg	gcgaactagt	aatgaaatat	cttaaaaagg	625380
ctgatatgat	tgcctacatc	cgatttgcct	gcgtttatcg	tcgattcaag	gacgttggtg	625440
aattaatgga	agttttattg	tcagcaactc	cagatatgga	aaaatagttg	aattttataa	625500
ggagcaaggt	tgtgccgtta	tcagatgacg	aaatagaaca	gtttaaaaaa	agacttttgg	625560
agatgaaggc	aaagttatcg	catactctag	aagggaacgc	tcaagaggta	aaaaaaccta	625620
acgaagctac	aggatattct	cagcatcaag	cagaccaagg	taccgacacc	tttgatcgga	625680
ctattagcct	tcaaaagcact	acaaaagaat	atgagcttct	aagacaaatt	aatagggtctc	625740
tagaaaaaat	taatgagtct	tcttacggga	tttgtgatgt	cagcggagaa	gaaattcctc	625800
tcgctagggt	gatagccatt	ccctatgcta	ccatgacagt	caaagctcaa	gagcagtttg	625860
aaaaaggact	cctatctgga	aattaagttc	tatggcaact	cgttttcgta	gcacactatt	625920
agtgattact	ctgtttgttt	taatcgactg	ggtcaccaag	cttggtgtct	tattacaata	625980
caaagatctc	caaattttta	cgcaccccac	cttatatact	catagttggg	ggcgggtttc	626040
attttcaatt	gctcctgtat	ttaatgaagg	ggctgcttcc	ggtctctttt	caaattataa	626100
atatttctta	ttccttctgc	ggatatttgt	gattctttggc	ctcctggcct	atcttttttt	626160
taaaaaaaa	tctatacaat	ctacaacgca	gactgctcta	gtccttctct	gtgcaggagc	626220
tataggaaac	gtcggggata	ttatctttta	cggccacata	gtcgatttca	tttctttcaa	626280
ttataaacia	tgggcattcc	ccacctttaa	cggtgccgat	gtattgattt	ctcttggcac	626340
tctgtctcct	gtttataaat	tttattttcc	tacaaaacaa	actgaaaaaa	agagataata	626400
tagatctctt	caagagaagc	taagatatgt	ttttaaaact	gttatgaacc	gtcttctatc	626460
gcttttatcc	gtctttgatg	attttttctg	gtcctatgtg	gcctttatcc	taatcattgt	626520
tctaggtgta	agtttttctc	ggaagtccgc	attttttcaa	ttcacgaagt	tctctcagtt	626580
ttgcaagctt	ttcogttatt	actctcagaa	tccctcaaaa	agagaaacaa	agcaaggtgt	626640
ccatcctcta	aaagtatttt	ttgcctccgc	aggcggaat	atcgccatag	ggaatgtcgt	626700
aggaattgtc	acagcagcat	gtatcggtgg	acccggggct	cttttctggg	tgtggattgc	626760
tgggatcttt	ggttctattg	ttaaatatcc	tgaggtctat	ctcggaatca	agttccgtaa	626820
gttagatcgt	gatggcgtct	atcagggcgg	gcctatgtat	tttcttataa	aggcgttcaa	626880
aacccctgtc	gtgtctgtta	ttgttgcgat	tcttctctgc	atztatggag	tggaaatcta	626940
tcaattttca	gtcatcactg	acagccttgc	ccactgttgg	aacctaccta	aagtctatcc	627000
gatgttaggt	ctactcttcc	ttgttttcta	tgcaattcga	ggaggcttgc	agcgtatagg	627060
aaaaatttgt	tctatagttc	ttcctttctt	catgctctta	tactgtgcc	tatccctcta	627120
catcctcggt	caagagtttc	atacccttcc	acacctactt	tccacagtat	tttcttctgc	627180
atttaaaggt	caaagtgtcc	ttggaggatt	tgcaggctgt	actgtagcca	ctacgattca	627240
tcaaggaatt	tcacgagcag	cctattctgg	ggatatcggt	ataggctttg	actccatcat	627300
tcagagtga	agttctgcta	aagatccctag	cacccaagcg	caactcagta	ttgttgggat	627360
tgccatagat	aacctgatct	gtactctgag	tcttctcatg	gtgcttgctt	cgggctcctg	627420
gtctctggga	ttagagaatg	cttcccaagt	agtagaacac	actctagcaa	gctacttccc	627480
tatggtgaag	ttcttctctc	ccaccttctt	ctttgttaca	ggctatacaa	ccatctactc	627540
ctacttctcg	gttgggaaga	agtgtgcaaa	gtttctttac	ggaaacacag	gggcaagat	627600
ctatactctc	tatggtcttc	tgattcttcc	cttattttgt	ttcctcagcc	aaaacacagc	627660
tttgttgatc	atgtctgtat	ctggagccct	actcctttgc	tttaacctct	taggagtcct	627720
catcttaaga	aaagaagtta	tcttccctgc	aagggtctgt	tctctcacag	aaacttctct	627780
ttctacagaa	taaaaaattt	accttattca	tacacaatga	gataagaagt	tttaattttt	627840
attaataaat	taaaagatta	gttttagaaa	aaaacacttc	ataaagtaaa	ataaaagaat	627900
aaaagttgta	attaattttt	ttacttttta	tggataacta	tctcctcgga	agcttgattt	627960
tctgttggtg	acttctatca	atagggatgt	gcacgatttt	cgtgatgacg	atctgctttc	628020
tacgcccaact	caataaaatc	cttaaaaaca	tccatcggtg	gactacaatt	ttaaattttg	628080
aggctaagat	cctagctcct	ttgatgttag	ggaaaaagct	tctctgtgga	tggctaaaga	628140
aaagaaaaaa	tcgcggctct	ctgtctgaag	acattgacga	actcttagat	gagaaaaagc	628200
agagaagctg	gaaaaaaaac	ttagaccaag	gaattaaatg	gtgcgcacac	tggctcctcat	628260
ttggaaagtg	tttcgtaata	aagattaaaa	cattgaggga	tatcgttatg	ttcaggaaca	628320
accacaaaacc	taaaaaaact	aagtgcacaa	gatttccgtg	gctacggggg	gttttatctg	628380
gtggattcat	agctacgtta	ttaacatgct	tgttttactc	caaaagtggc	gtccaaactgc	628440
ggaagaaaaat	cctcaaagta	aaaaactctg	gggcaaaaaa	aagtagagtg	ttctttaaaa	628500
attccaagca	acataccaag	tcattcgtaa	aacaagcgaa	gttgctagct	aagaatatct	628560
cacacgaact	tcaagatttt	aaaaagggaa	tcctcgacga	caaagattag	agttgctatt	628620
aagaagctct	gtatgattga	gatattctct	cagggtcttt	tttcatttaa	aagcacataa	628680
atagaggctc	tctccgagaa	atgccattct	cgagtcaact	ttttatttcc	gtgtatttat	628740
ttttctgttc	tatgtaagtt	tagatctgta	taaggctata	acttattagg	actccgacat	628800
atgaagcaga	tgcgtctttg	gggattttta	tttctctctt	ccttctgtca	agtttcttat	628860
ctacgagcaa	acgatgttct	cctccctcta	tcagggatcc	attctggaga	agaccttgaa	628920
ctctttactc	tacgcagttc	ctccccaaca	aaaactacgt	attctctacg	caaagatttt	628980
attgtttgtg	attttgcagg	aaattctatt	cacaagcctg	gagctgcatt	cctgaactta	629040

aaaggcgatc	tattttttat	aaatagcact	cccctagcgg	ctcttacctt	taaaaacatt	629100
cacttaggag	ctcgcggtgc	tgggctcttc	tcggaatcca	atgtgacctt	caaaggcctg	629160
cactctctcg	ttctcgaaaa	caacgaaagt	tggggaggcg	tcctcaccac	atctggcgac	629220
ctttccttca	taaataatac	cagtgtgctt	tgtcaaaaaca	acattagcta	tggacctgga	629280
ggagcgctac	tcttacaagg	aagaaaaagc	aaggctctct	ttttcagaga	caatcgagga	629340
acaattctat	ttctgaaaaa	caaagccgtg	aatcaagatg	aatcccatcc	tgggtacgga	629400
ggagctgtaa	gtagtataag	tccctggctcc	cggattacct	tcgctgacaa	ccaagaaatc	629460
ctattccaag	agaatgaggg	cgaacttggt	ggagccattt	ataacgatca	gggtgccata	629520
acttttgaga	ataactttca	aaccacaagc	tttttctcta	acaaagctag	tttcggagga	629580
gctgtctata	gccgctactg	caatctctat	tcacagtggg	gcgataccct	attcactaaa	629640
aacgctgctg	caaaagtagg	cggacatcca	tgcggattat	gttcatataa	gagactgtaa	629700
aggaagcatc	gtctttgagg	agaactcagc	aacagctgga	ggggcaatcg	cagtaaattgc	629760
agtttgtgac	attaatgctc	aaggctcctg	tcgctttata	aataactctg	cgtaggact	629820
aaatggtggt	gctattttata	tgcaggctac	tggatctata	ttgcgcttac	atgcaaatca	629880
aggagatatt	gaattttgtg	gaaataaagt	acgatcgag	tttcattcac	atataaatc	629940
cacttcaaat	ttcacaata	atgccattac	tatccaagga	gcgcctcgag	aattttcgct	630000
cagcgcaaat	gaaggacatc	gcactgtgtt	ctatgatcct	ataattttctg	caacagaaaa	630060
ctataactct	ctgtacatca	accatcagag	acttttagaa	gccgggggtg	ctgtgatctt	630120
ttcaggagca	cgcctatctc	cagagcataa	aaaagaaaat	aagaacaaaa	cttcgattat	630180
aaaccagccc	gtacgtctct	gttctggagt	cctttctata	gaagggggcg	cgattcttgc	630240
tggtcggtct	ttttatcaag	aaggaggtct	tcttgctctc	gggccagggt	ctaaactgac	630300
cactcaaggg	aaaaattctg	aaaaagataa	aattgtcatc	acaaatttag	gattcaacct	630360
agaaaatcta	gactcttcgg	atcctgcaga	aatccgagct	acagaaaaag	cctctattga	630420
aatttctgga	gttcctagag	tctatggtca	cacagaatct	ttctatgaaa	atcatgagta	630480
tgcttccaaa	ccttatacaa	cttcgattat	tctatctgcc	aaaaaacttg	ttacagctcc	630540
ctctaggcca	gagaaagaca	tccaaaatct	catcatcgct	gaatctgagt	atatgggcta	630600
cggctatcaa	ggctcatggg	aattctcctg	gtctcctaac	gacactaaag	aaaagaaaac	630660
cattatagcc	tcttggaactc	ctacaggaga	attttcttta	gatccgaagc	gccgtggatc	630720
tttcattccc	acaaccttat	ggtcgacatt	ctctgggctg	aatatagcat	cgaatatcgt	630780
gaataacaat	tacctcaaca	actccgaggt	catccccctg	caacatctct	gtgtttttgg	630840
aggccctgtc	tatcagatta	tggagcaaaa	tcctaaacag	agctctaaca	atctcttagt	630900
tcaacatgcg	ggtcataatg	ttggagctag	aattcctttc	tctttcaata	ccatattgag	630960
tgctgcactt	actcaactct	tctcttcttc	atcacaacaa	aatgttgctg	ataagagcca	631020
cgcgcaaaata	ttgataggga	ctgtatctct	taataaaaagt	tggcaagcac	tatctcttag	631080
atcttcatct	agctatacgg	aagactctca	ggtaatgaag	cacgtattcc	cctataaagg	631140
gacctctcga	ggatcttgga	gaaactacgg	atggctcggg	tctgtcggca	tgtcttacgc	631200
ctatcctaaa	ggaatccgct	atctaaagat	gactcccttt	gttgaccttc	agtatacaaa	631260
gttagtacaa	aatccctttg	tggaaacggg	ttatgacctt	agatattttt	cttccctcgg	631320
gatgacgaac	ctatctctac	cgataggtat	cgctttagaa	atgcgcttta	taggctcgcg	631380
ttcttcccta	ttcttccaag	tcagcacctc	gtacattaaa	gacttacgtc	gggtcaaccc	631440
acaatcttca	gcttccttgg	tgttaaatca	ctacacgtgg	gatatccaag	gagtcctctt	631500
agggaaagaa	gctctaaaca	ttaccttaaa	tagcacgatt	aagtacaaga	ttgtgactgc	631560
ctatatgggg	atttctagca	cccaacgaga	aggcagtaac	ctttcggcaa	atgctcatgc	631620
aggcctctcc	cttagtttct	agaagttagc	actatagaaa	taaaagaaga	cttaaaaagc	631680
gcgtgggtat	cattcaaaca	cgcgcttttt	tatcccttgc	ctaattttatc	catctgattt	631740
atctatcact	tatcgagttt	gtgaatatat	ctgataggtt	ttcctctatg	aagtggctac	631800
cagctacagc	tgttttttgct	gccgtactcc	ccgcactaac	agccttcgga	gatccgcgct	631860
ctgttgaaat	aagtaccagc	catacaggat	ccgggggatcc	tacaagcgac	gctgccttaa	631920
caggattttac	acaaagttcc	acagaaactg	acgggtactac	ctataccatt	gtcggtgata	631980
tcaccttctc	tactttttacg	aatattcctg	ttcccgtagt	aactccagac	gccaacgata	632040
gttcacgcaa	tagctctaaa	ggaggaagta	gcagtagtg	agctacatct	ctaattccgat	632100
cctcaaacct	acactccgat	tttgatttta	caaaagatag	cgtgttagac	ctctatcacc	632160
ttttcttttc	ttcagcttca	aatactctca	atcctgcact	cctttcttcc	agtagcagcg	632220
gtggatcctc	gagcagcagt	agctcctcat	catctggaag	tgcattctgct	gtgtgtgctg	632280
cggaccacaa	aggaggcgct	gccttttata	gtaacgagc	taacgggaact	ttaaccttca	632340
ctacagcact	tggaaatccc	ggctccctga	ctcttcagaa	tcttaaaatg	accggagatg	632400
gagccgccat	ctactcgaag	ggctcctctag	tattttactgg	tttaaaaaat	ctaactttta	632460
caggaaatga	atctcagaaa	tctggaggtg	ctgcctatac	tgaaggcgca	ctcacaacac	632520
aagcaatcgt	tgaagccgta	acttttactg	gcaacacctc	ggcagggcaa	ggaggcgcta	632580
tctatgttaa	agaagctacc	ctattcaatg	ctctagacag	cctcaaattt	gaaaaaaaca	632640
cttctgggca	agctgggtggt	ggaatctata	cagagtctac	gtcacaatc	tgaacatca	632700
caaaatctat	tgaattttatc	tctaataaag	ctctgtccc	tgcccccgct	cctgagccca	632760
cctctccggc	tcaagtagc	ttaataaatt	ctacaacgat	cgatacctcg	actctccaaa	632820
cccagagcagc	atccgcaact	ccagcagtgg	ctcctgttgc	tgcgtaact	ccaacaccaa	632880

tctctactca	agagaccgca	ggaaatggag	gcgctatcta	tgctaaacaa	ggtatttcga	632940
tatccacgtt	taaagatctg	accttcaagt	ctaactctgc	atcggttagat	gccaccctta	633000
ctgtcgattc	tagcactatt	ggagaatctg	gaggtgctat	ctttgcagca	gactctatac	633060
aaatccaaca	gtgcacggga	accaccttat	tcagtggcaa	tactgccaat	aagtctggtg	633120
gggggtattta	cgctgtagga	caagtcaccc	tagaagatat	agcgaatctg	aagatgacca	633180
acaacacctg	taaaggtgaa	ggtggagcca	tctacactaa	aaaggcttta	actatcaaca	633240
acggtgccat	tctcactaca	ttttctggaa	atacatcgac	agataatggt	ggggctattt	633300
ttgctgtagg	tggcatcact	ctctctgac	ttgtagaagt	ccgctttagt	aaaaataaga	633360
ccggaaatta	ttccgctcct	attaccaaaag	cggctagcaa	cacagctcct	gtagtttcta	633420
gctctacaac	tgctgcatct	cctgcggtcc	ctgctgccgc	tgacgacact	gttacaacg	633480
cagcaaaaagg	aggggcttta	tatagtacag	aaggactgac	tgtatctgga	atcacatcga	633540
tnattgtcgt	ttgaaaacaa	cgaatgccag	aatcaaggag	gtggggctta	cgttactaaa	633600
accttccagt	gttccgattc	tcatcgccctc	cagtttacta	gtaataaagc	agcagatgaa	633660
ggcggggggcc	tgtattgtgg	tgacgatgtc	acgctaacga	acctgacagg	gaaaacacta	633720
tttcaagaga	atagcagtga	gaaacatgga	ggtgggctct	ctctcgccctc	aggaaaatct	633780
ctgactatga	catcgttaga	gagcttctgc	ttaaattctga	atacagcaaa	ggaaaacgga	633840
ggcgggtgcga	atgtccctga	aaatattgta	ctcaccttca	cctatactcc	cactccaaat	633900
gaacctgcgc	ctgtgcagca	gcccgtgtat	ggagaagctc	ttgttactgg	aaatacagcc	633960
acaaaaagtg	gtgggggcat	ttacacgaaa	aatgcggcct	tctcaaattt	atcttctgta	634020
acttttgatc	aaaatacctc	ttcagaaaat	ggtggtgcct	tacttaccca	aaaagctgca	634080
gataaaacgg	actgttcttt	cacctatatt	acaaatgtca	atatcaccaa	caatacagct	634140
acaggaaatg	gtgggggcat	tgctgggggga	aaagcacatt	ttgatcgcat	tgataatctt	634200
acagtcctaaa	gcaaccaagc	aaagaaaggt	ggtgggggtt	atcttgaaga	tgccctctac	634260
ctggaaaagg	ttattacagg	ttctgtctca	caaaatacag	ctacagaaaag	tggtgggggt	634320
atctacgcta	aggatattca	actacaagct	ctacctggaa	gcttcacaat	taccgataat	634380
aaagtcgaaa	ctagtcttac	tactagcact	aattttatatg	gtgggggcat	ctattccagt	634440
ggagctgtca	cgctaaccac	tatatctgga	acctttggca	ttacaggaaa	ctctgttatac	634500
aatacagcga	catcccagga	tgacagatata	caagggtggg	gcatttatgc	aaccacgtct	634560
ctctcaataa	atcaatgtaa	tacacccatt	ctatttagca	acaactctgc	tgccactaaa	634620
aaaacatcaa	caacaaaagca	aattgctggt	ggggctatct	tctccgctgc	agtaactatc	634680
gagaataact	ctcagcccat	tatttttctta	aataattccg	caaagtcgga	agcaactaca	634740
gcagcaactg	caggaaaata	agatagctgt	ggaggagcca	ttgcagctaa	ctctgttact	634800
ttaacaaaata	accctgaaat	aacctttaaa	ggaaattatg	cagaaactgg	aggagcgatt	634860
ggctgtattg	atcttactaa	tggtcacct	ccccgtaaag	tctctattgc	agacaacggg	634920
tctgtccttt	ttcaagacaa	ctctgcgtta	aatcgcgag	gcgctatcta	tgagagagact	634980
atcgatatct	ccaggacagg	tgcgactttc	atcggttaact	cttcaaaaaca	tgatgggaagt	635040
gcaatttgct	gttcaacagc	cctaactctt	gcgccaaact	cccaacttat	ctttgaaaac	635100
aataagggtta	cggaaaccac	agccactaca	aaagcttcca	taaataattt	aggagctgca	635160
atttatggaa	ataatgagac	tagtgacgtc	actatctctt	tatcagctga	gaatgggaagt	635220
attttcttta	aaaacaatct	atgcacagca	acaaacaaat	actgcagtat	tgctggaaac	635280
gtaaaatttta	cagcaataga	agcttcagca	gggaaagcta	tatcttttcta	tgatgcagtt	635340
aacgtttcca	ccaaaganac	aaatgctcaa	gagctaaaat	taaatgaaaa	agcgacaagt	635400
acaggaacga	ttctattttc	tggggaactt	cacgaaaata	aatcctatat	tccacagaaa	635460
gtcactttcg	cacatgggaa	tctcattcta	ggtaaaaatg	cagaacttag	cgtagtttcc	635520
tttaccat	ctccaggcac	cacaatcact	atggggccag	gategggttct	ttccaaccat	635580
agcaaagaag	caggaggaat	cgctataaac	aatgtcatca	ttgatttttag	tgaaatcggt	635640
cctactaaag	ataatgcaac	agtagctcca	cccactctta	aattagttatc	gagaactaat	635700
gcagatagta	aagataagat	tgatattaca	ggaactgtga	ctcttctaga	tcctaattggc	635760
aacttatatc	aaaattctta	tcttggtgaa	gaccgcgata	tcactctttt	caatatagac	635820
aattctgcaa	gtggggcagt	tacagccacg	aatgtcacc	ttcaagggaa	tttaggagct	635880
aaaaaaggat	atthaggaac	ctggaatttg	gatccaaatt	cctcggttc	aaaaattatt	635940
ctaaaatgga	cctttgacaa	atacctgcgc	tgcccttaca	tccctagaga	caaccacttc	636000
tacatcaact	ctatttgggg	agcacaaaaac	tcttttagtga	ctgtgaaaca	agggatctta	636060
gggaacatgt	tgaacaatgc	aaggtttgaa	gatcttgctt	tcaacaactt	ctgggcttcg	636120
gctataggat	ctttccttag	gaaagaagta	tctcgaaatt	ctgactcatt	cactcatcat	636180
ggcagaggct	ataccgctgc	tgtggatgcc	aaacctcgcc	aagaatttat	tttaggagct	636240
gccttcagtc	aggttttttg	tcacgccgag	tctgaatatc	accttgacaa	ctataagcat	636300
aaaggctcag	gtcactctac	acaagcatct	ctttatgctg	gcaatatctt	ctattttcct	636360
gcgatacgg	ctcggcctat	tctattccaa	ggtgtggcga	cctatgggtta	tatgcaacat	636420
gacaccacaa	cctactatcc	ttctattgaa	gaaaaaaaata	tggaacactg	ggatagcatt	636480
gcttggttat	ttgatctgcg	tttcagtggtg	gatctttaaag	aacctcaacc	tcactctaca	636540
gcaaggctta	ccttctatac	agaagctgag	tataccagaa	ttcgccagga	gaaattcaca	636600
gagctagact	atgatcctag	atctttctct	gcagctctt	atggaaactt	agcaattcct	636660
actggattct	ctgtagacgg	agcattagct	tgccgtgaga	ttatttctata	taataaagta	636720

tcagctgcgt	acctccctgt	gattctcagg	aataatccaa	aagcgaccta	tgaagttctc	636780
tctacaaaag	aaaagggcaa	cgtagtcaac	gttctcccta	caagaaacgc	agctcgtgca	636840
gaggtgagct	ctcaaattta	tcttggaagt	tactggacac	tctacggcac	gtatactatt	636900
gatgcttcaa	tgaatacttt	agtgc aaatg	gccaacggag	ggatccgggt	tgtattctag	636960
ggtatacaat	taaagatttt	atgaaattga	ggatacggag	agagtgggat	tcgaaccac	637020
ggtacgcgtt	aacgcacaca	cgctttccaa	gcgtgctctc	taagccactc	ggacatctct	637080
ccatatttat	agattttcca	ggcaaaaaga	cttgccgaga	acatatctta	acctttccat	637140
ttttatcaac	atccgtctta	ctatgagaat	tttttcctaa	gatcacccgt	tcttaggata	637200
ttcgttcttt	attaaaaatta	tgccccaata	gaataataga	tcattcttatc	aaactgcttt	637260
tgatcatgcat	aaagtaatag	tttttnatttt	ccttacccta	tattcgttaa	aaagtatttg	637320
gaatgatgta	atagataagc	cccatgttct	tgtagtatac	gccccctata	aattcctagt	637380
tgaacaaatt	gctgaagaga	cctgttttgt	ctatgcgata	gttacgaatc	actatgatcc	637440
ccatacctat	gaacttcctc	ctcagcaaat	caaggagtta	cgacaaggag	acctttgggt	637500
ccgtatagga	gaggcatttg	aaaaaacttg	tgagagaaac	cttacctgcc	aacaagtcga	637560
tctttcccaa	aatgtctcgc	tgattcaagg	aaagccttgc	tgtaatcaac	ataccacgaa	637620
ctacgacacc	cacacttggt	taagccctaa	aaaccttaaa	gtccaagtgg	agactatcgt	637680
taccacttta	agtaaaaaat	atcctcaaca	cgcgactcta	tatcaaagca	atggagagaa	637740
acttctgtta	gctttggacc	aactcaatga	ggaaattctt	acgattacct	ccaaagcgaa	637800
acaacgccat	attttagttt	cccatggagc	ctttgggtat	ttttgccgtg	attacaattt	637860
ctctcagcac	actatagaga	aaagcagtca	tggtgagcct	tctcctaaag	atgtggctcg	637920
cgtatttcgt	gacattgaac	agtacaaaat	ttcttctgtg	attcttctcg	aatactctgg	637980
aagacgaagt	agtgtctatgc	tggcagatcg	tttccacatg	catactgtga	atctcgatcc	638040
ctatgcgga	aataacttg	taaacttaaa	aacctatagc	acgacttttt	ctagtttatg	638100
acaatacgaa	tctctgtctg	aggcctagct	ttccgttacg	gaagcaaggg	accgaatatc	638160
attcatgatg	tttctttctc	tgtctatgat	ggcgacttta	taggaatcat	aggaccaaac	638220
ggagggggaa	aagcacctta	acgatgttaa	ttttgggctt	gcttactcct	acattcggat	638280
ccttgaagac	tttcccttcg	cattccgcgg	ggaaacaaac	ccattccatg	atcggttggg	638340
ttccccaaca	tttctcttat	gacccctgtt	ttcctatctc	agtaaaagat	gttgcctctc	638400
caggaagatt	gtctcaactc	tcttgcatg	nnaaatataa	anagaaagat	tttgagctg	638460
tagatcacgc	gttgataat	gttggaactt	ctgaccacca	ccaccactgc	ttcgccctc	638520
tctcaggagg	acaaatccag	cgtgtacttc	tggcaagagc	cttagcctcc	taccctgaaa	638580
ttttaattct	tgatgagccg	acgacaaaca	ttgatcctga	caatcaacaa	agaattttta	638640
gtatcctaaa	aaagctcaac	cgtacgtgca	ccattcttat	ggtaactcac	gatcttcacc	638700
atacgacgaa	ttactttaat	aaagtttttt	atatgaacaa	aactttgact	tcattggcag	638760
acacttcgac	cttaacagac	caattttgtt	gtcatcccta	taaaaatcag	gaattttcat	638820
gctctcctca	ctaataccgtg	attcatttcc	ccttcttatt	ttacttccca	cattctctagc	638880
ggcattagga	gcctccgtag	ctggcgccgt	tatgggaacc	tatatcggtg	taaaacgtat	638940
tgtttcaatt	agtggaaagta	tatctcatgc	aattctagga	ggaattggcc	tcaccctatg	639000
gatacaatat	aagcttcatc	tctctttttt	ccctatgtat	ggagctattg	taggagctat	639060
ttttctagct	ctttgcatcg	gcaaaagatc	cacctgaaat	accaagaaag	ggaagactct	639120
ttgattgcga	tgatttggtc	tgtgggcatg	gcaattggaa	ttatattcat	ttccaggctt	639180
cccaccttta	atggagagct	catcaatttt	ctatttgga	acattctctg	ggtcacccct	639240
tcagacctct	atagcttang	aatctttgat	cttcttggtt	taggaattgt	ggtcctttgc	639300
cacacccggt	tccttgctct	ttgctttgat	gagaggtaca	cggcttttaa	ccattgttct	639360
gtacagctgt	ggtatttcct	acttcttggt	ctgacagcaa	tcacgattgt	gatgttgatt	639420
tatgtgatgg	gaacgattct	gatgcttagc	atgctctctc	tacctgttgc	tatagctgtg	639480
agattttcgt	acaagatgac	acgaattatg	ttcatctcgg	tcctcttgaa	tatcttatgt	639540
tctttttctg	gaatttgcat	cgctactgt	ttagatttcc	cagtaggtcc	tacgatatac	639600
ttgctgatgg	ggttangtta	tacagcgagt	cttgtgtgaa	gaagcggtac	aatccgctga	639660
cgcttctctc	tgtaagtcct	gaaatcaata	caaagtata	gctagggaa	cgcttttgga	639720
agctttggag	gcattcttcc	tgctcgtcag	gaagaagatc	atcaatttta	tttaaagcta	639780
ccagcatatc	tttcttttca	aaatctggct	gatgagagt	gagctcgtgg	atgagcgttt	639840
ctaagtcttc	ttcgggagag	tttctctctc	ttttggagac	atcgataaca	aatagcagta	639900
aaagagtgcg	ctcaatatgg	cgaagaaaat	cgagtcctag	gcctttgttt	tgatgagctc	639960
cttcaatgat	tcctggaatg	tcagcgataa	tccagggttt	ttgatacaaa	cgatctttac	640020
aaaggactag	gccccaaagag	ggggccagag	ttgtgaagg	ataggctccg	actttcactt	640080
cggtatgtgc	gagtgtatta	aatagtgtgg	actttcctgc	atttgggaa	cctaccaaac	640140
cgatatcagc	aatgagctta	agttctaact	ctacctgacg	gatttctccg	ggttttctctg	640200
gggtggcctt	tgtaggggct	cggtttactg	aggtcttaaa	gaaggatatt	ccttttctctc	640260
cctttctctc	ttggctcact	aggagacgct	ctccatctac	ggtaaagtca	tgaaggattt	640320
caccagtctc	agcatcacga	agcaggggtc	ctgtagggac	agaaactatt	agatctttac	640380
cactgcgtcc	tgtgcgggta	ttttagcttc	ctgactgacc	gtcggggagcc	ttgagaaagc	640440
ggatatttct	ataagcttcg	aaagaatata	cacttgtggg	ggcttctatg	attacggagc	640500
cgccattgcc	accattgcct	ccgtaaggcc	ctccttttag	aaggatattt	tcctttctctc	640560



aagcaacaac	gccgtttccg	ccctttccag	cacgcaattc	taaggtaatt	tgatctacaa	640620
acatgattac	gtttttatcc	ttcttcaaac	aaaaaaagct	cgatttgatg	cctgagcaaa	640680
aaaccgagct	tttttaagt	ttctgaaaaa	tcgaaaaata	ggaactaaag	ttgctcagga	640740
acaacagaga	tataagtacg	attcgtcttt	ttcattacta	caataccatc	gactaaagcg	640800
aatagggtat	catcacgacc	acgacctaca	ttttgtgcag	gattccatcg	ggcccccttc	640860
tgacgaacga	gaatacttcc	tgtagaaact	ttttgcccag	cgccccactt	aaccccaagg	640920
cgcttcgatt	ttgaatctct	accgtttcgg	cttgccccct	gtccctttctt	atgtgccata	640980
actctaaact	ctctagcttc	tgtttatatc	aatatctcac	ggattttcac	acgaagggtac	641040
ttctgacgat	gtccgtgttt	acgatgataa	tttttgcgtt	ttttatactt	ataggcgact	641100
actttttctc	ctttaacatg	agaaagatat	tcggctttta	cttgtgcgtt	cgcaatcgta	641160
gggcttccta	gagaggcttt	agttccatcg	aatacaaaaga	ggacatcttg	aaaaatgact	641220
tctttatccg	aagcaacttc	ccctagtaac	tcgacatcaa	tcacatcgcc	tgagcgaacc	641280
tgatattgct	tgcttccctg	ttggattact	gcgtagggct	ccatcaattt	tttccttatg	641340
aatctttcaa	tgcttaaagt	taagcgctgt	ttgctaagtt	acttttagcaa	acttaaggat	641400
tatacaaaat	ataaagtctt	ggattatagt	ttttaacccc	tcggagagcg	ctatcctcaa	641460
gcggttatgg	ccagagccgg	gatcgaaccg	acgacacaag	gatcttcaat	cctctgtctt	641520
accatctgag	ctatctagcc	at ttgtactc	agttatcata	ggaaaacatt	cagtttaata	641580
tcaatgagat	ttcgaattct	tcgcctctct	ttttgctatt	aaggagtatt	tctcaagaga	641640
gtgcttcgat	gtagcgagaa	agtttgacaa	attactggaa	taatgcgtga	at tttagaaa	641700
ttttgtagta	tcttctgtga	aagaaattct	taaaaaaaac	atataccagg	tagttatgga	641760
tagagacaat	gaggttcccc	tgcccaaagcc	caaatggatt	taccgtacag	gtattgggtca	641820
agacagccac	cgctttctcc	cagaaagttc	cacgaagccc	tgcat tttag	gtggatcat	641880
ttttgatcat	tgcccaggat	ttcaggcaaa	ttccgatgga	gacattatct	ttcatgccat	641940
ttgtaatcgc	tttccctcag	taactaataa	aattatttta	ggaaagggtg	ctgatgagct	642000
tctccaaaca	cggggaatta	cagatagtgg	gatttatctt	gaggaggctt	taaaatctct	642060
gaagccta at	caaaagattt	ctcatgtcgc	tattacgatt	gaaggaagtc	gacctaaatt	642120
tctctgtaag	ctatctgcat	tacgtcaaaa	tattgcccag	gttatgaact	taacacctac	642180
ggatattggc	attactgcca	cttctggaga	gggtttgagt	gactttggct	gtggagatgg	642240
cgttcagtg	ttctgctgt	taactgtgat	ggaatactgt	gactaataga	cgtaacaac	642300
gtaacgatgt	tcctttctga	gggaggctag	agtactcttt	cctaagattt	cgtctaagc	642360
gtgttttact	tctatgccta	agactttacg	ttcacagaca	aagaaaaacc	ctccctcttc	642420
ataggccctt	cttacctcat	ctttttgaa	cctaagaaga	tcttgaacat	agactttttg	642480
gtctctctct	cttgagaagg	ctaaaaagag	tttttagttt	ccttctctct	ctgcatgggt	642540
ccagaattct	cgataataga	agttcacttt	ttctttgcgc	tcacaaaaaa	atagtaaatt	642600
at ttctctgg	tctttattga	aaaggcgctt	ctctaggaag	gctttataag	gagcgattcc	642660
tgttccagct	ccgatcataa	ctaaggggtt	cccttcagtc	tgtgtagata	gagtgaagtg	642720
ttttgtagg	tgtacgaata	tgtaggcaga	atcgttgacc	tgtagtctgc	tacatagaaa	642780
ggacgagcaa	actccgaagc	gtttttgata	ttttccagga	taggaaacgt	gttttaccaa	642840
tagctctata	cttttgggat	gtagatctgg	tgaggaggct	atagagtaga	aacgaggcaa	642900
taaagggaac	acactctcag	cgaagagttc	tattgggatc	tgaggggcgt	actcttgaat	642960
ggcatcatac	agtgtaatct	taggatcttt	gtctgggaaa	aaggaattta	gctttgctgg	643020
aatttaatac	agatcaacat	agccttggat	aaat ttttgg	gcagaaactt	tttcagaagt	643080
tttttttacg	ttgacaagg	tcgttgggga	atagccttag	aagctggaga	acgtgttcgg	643140
agacctcttt	agaattctct	ggtaagactc	ctaaagcatc	gcctacttta	taggatatag	643200
tcgtatcatt	gctatcaaag	accatgcgg	agatgggac	gctatcggtt	atggaatcgg	643260
aacaagaaa	tagctcacgc	aatactagag	gaacttgctg	agccttaaac	tttcttgta	643320
ggtagatctt	ttatagacaa	gcttgaatta	agccgctttg	at tttaatat	caactcctgc	643380
aggaagtgt	aacattttca	aagcatcgat	agtttttctt	gtgggatcta	aaatatctac	643440
aagacgtttg	tgagtacgaa	tttcaaactg	ctctcttgat	tttttatcca	catgtggcga	643500
acgcaataca	gtatagactt	ctctttttgt	aggcagagga	attggctcta	caacacgagc	643560
tcctgttctt	ttagcagttt	caacaatatc	tgctgtggaa	cgatctagct	gccccgtatc	643620
gaatcctttc	agacgaatac	gaattttttg	cttttgcgtc	ttcatacatc	ccttacttct	643680
taacaatctc	ttcttgaatt	ttttgaggaa	ccttagcaaa	gaatgctgg	tccatgggtg	643740
atgttgacg	tcctgaggtc	aatgatctta	aagatgtcgt	gtacccaaac	at ttcgctta	643800
gaggtacctc	agcattcact	tgagccattc	ctcgagaaga	ttcttgtcct	aaaattttgc	643860
ctcgacgacg	gttgaggctc	ccaataacat	cgccaagatg	atcttctggg	gtaattactg	643920
ctaccttcat	gattggctct	aagattacag	gcttcgcttt	tctacaggcg	tctttaactg	643980
ccatagaccc	acagatctta	aatgccattt	cactagaatc	gacttcgtga	tacgaaccga	644040
aaacaatact	taccttaacg	tctacaagac	cgtagccagc	caggactcct	gtgttcaatc	644100
cctcttctat	ccctttaatt	actgcaggga	tatattcttt	aggaatgaca	cctccgacaa	644160
tcttactgac	aacttcggtg	cccttcccag	gttcggttag	ttctatttcg	aggcaaacgt	644220
gagcatattg	ccctcgacca	ccagactgct	tcacgtattt	gttttacta	tttcgctgt	644280
cagtaattgg	ttctttataa	gaaactgtcg	gttttctctac	gttagcttca	actttaaatt	644340
ctcgatcat	acgatctcga	agaatatcta	aatgaagttc	ccccattcca	gaaatgatgg	644400



tctgtcctgt	ctcttcattt	gttgagacac	ggaatgtagg	atcttcttct	gataaagaac	644460
ttaatgcttg	agcaagtttt	tctctatccc	cttttagactt	tggctcaata	gccatatcga	644520
tgacgggggtc	tggaaattct	atacgttcaa	gaacaatttc	tgggttatcg	tcacacaagg	644580
tatctcctgt	gacagaaaac	ttcagaccca	cgcaagctcc	aatatcgccc	acagtaaact	644640
catctctatc	tgtacgctca	ttagcgtgca	tttctaaaag	gcgagaaatc	cgttcttttt	644700
tatcttttgt	agaattttaa	atggcgagacc	ctttttttaag	agtgcctgaa	tagattcgga	644760
taaatgtaat	ccgacctacg	tagggatctg	tcatgatttt	gaaagctaga	gctgctagag	644820
gtccatcacg	tcttggctct	aaactaattt	cttgatctgt	tttaagattg	attccgcgga	644880
tatttctctg	atccaaagga	gaaggcaacc	acttgacaat	cacattgagc	agttgttgca	644940
cacctttatt	tttaaaagcg	gttccgcaga	gtacaggatt	gattttattc	tcaatgactc	645000
ccttacgcat	aacctgatgg	atttcatctt	cagtaatgct	atcgggatct	tcaagaactt	645060
tcatcatgaa	agcttcatta	ctttcatcta	tagtagcgag	ttcttccaaa	agattcgctc	645120
gcaattctgc	acaacgctct	ttgagatctt	cagaaatctc	tttttcttcc	catttttgctc	645180
ctaggggtatc	atctagaaaa	taaagagctt	tttgagagat	tagatcgacc	atgccgacaa	645240
actggctttc	agatccaata	ggacagtggg	cagggaaagc	attcgctccc	aatttctctt	645300
tcatggattc	cacggcgaca	aaatagtctg	ctcccatacg	gtccatttta	tttacgaaag	645360
caatccgtgg	aacaccgtat	ttatctgctt	gtctccaaac	agtttctgat	tgaggttcca	645420
cgccagatac	ggcgtcaaat	acggctacag	caccatcaag	aaccggaaga	gaacgttcta	645480
cttcaatcgt	aaagtcgacg	tgtccaggag	tatcaataat	gttgattttt	gcgcctagcc	645540
agaagacagt	agttgcagca	gaggtaatcg	taattcctct	ttcttgetcc	tgggccatcc	645600
agtccatggt	agctccgctt	tcatgacttc	accgattttg	tgagttcttc	cagcatagaa	645660
aagaattctt	tctgtagtgc	ttgttttccc	agcatcaata	tgagccatga	tgccgatggt	645720
tctaattgca	cttaaatcga	attcttgatt	gtctcatgaac	ttgttatttt	ttccgtaatt	645780
taactaatct	taccacttat	aatgtgcgaa	tgttttattt	gcttccgcca	tacgatgggt	645840
gtcttcacgt	ttcttaattg	ttgcaccctg	tttgttgaag	cagtcaatca	gttcggtagc	645900
aagtccaact	tccatagact	ttccagggtt	actacgagcg	tgtttgatga	tccattgcat	645960
cgctaaacaa	ttcctacgtt	cgctagcaac	ttcaacaggc	acttgataag	tagcgcctcc	646020
aacacgacgg	gaacgaactt	ctaaaatagg	ttttgcatth	tctaaagctt	ctccaaaacc	646080
ttcaagcaca	ttctctaaat	ttaatttttt	accgaaacgc	tctagagcag	agtagacaat	646140
tttctttgcc	acacttttct	tcccattgcat	cataaccttg	ttgataaatt	tttctaagat	646200
cacgttgcca	tagataggat	ccccagggat	atcgcgcttt	tcagcggagt	gccgccttga	646260
catatacatt	tacctctatc	ttataaatct	cgaccaagaa	cttcgtatga	ttacttaggc	646320
cgctttgctc	cgtaccgtga	acgactttgc	tttctatttt	ttactgctgc	acaatctagg	646380
gtgccacgaa	caatatgata	acgaacacca	ggcaaattct	tgactctacc	gccttggtatc	646440
aacacaatgc	tgtgctcttg	aagatttgtg	ccttcaccac	caatataggc	aatgacttcc	646500
tgcccgttag	atagtcgcac	ccaagcaact	ttccttaaag	ccgagttcgg	cttcttagga	646560
gtttttgttt	ttacttgaag	gcaaactccc	cgtttttgtg	ggcacttctg	caaagctggg	646620
gatttcttct	tagctagact	tgacttaact	cttttacgta	ttaattgatt	aatggtgggc	646680
atgtattctt	ctcgtttcaa	cctcactact	acaagcatgg	aaatatagag	taaggctctc	646740
tttgttggca	agggttattt	ttcagatgaa	gagggaacgt	atcctgcttg	aatttaaaaa	646800
aatgctatct	ttttctagac	gaaccgtttt	tttacttttt	aaaagaaatt	ttagctgtaa	646860
cgaacttatt	ctaacctatc	tctttggaga	gaagaatttc	gtattagggt	tctcctaattg	646920
aagactgtgc	acaattaaag	cagtattcca	taagagccgc	gatttatgta	accaaagaga	646980
aatcctaata	tgggtctctg	taaatcttgg	ttataggtaa	aactactttc	tttgcttgtt	647040
tctatgatgt	gaatagaatc	gttggtataa	ataaaaagca	aaggtagcgt	gtgggaaagc	647100
aattgcgtan	ttgagctagg	tctgggatgc	ccgcaagnat	tttagcggag	tcttcagata	647160
ggaaaagaac	ttgaacgtag	tttagaagag	accaaaaagc	accgagggaac	gtgggtcacga	647220
cttgtgagtc	acaaagatca	acaagcgtgt	ggttattctt	tcttttggtc	tctttcagaa	647280
acttttctat	actatccccg	tagagaatca	attgcccatc	caggagtgtg	tatccctgat	647340
tgcataggca	agtatttggt	tctatgccct	tttctgcttc	tttttccgag	tagagcaggg	647400
tatctgggtg	gttaggacaa	cgtaaaacta	atcttagatc	cttgggttgt	tttagagcgg	647460
gtccgttttc	tttatttgcc	attccctcag	cgtaagtttc	tccgttacgc	atacataaaa	647520
tacctaaate	ggagagatgg	gattgggaaa	ggttttagagg	ttcttttcgt	ttgaaactga	647580
tagaggcttc	tggaaatttt	tccttatata	tcaaaaaaat	ttcttttatt	tttgcgttat	647640
tagtgcgaaga	aatgggtcct	atttgcaggc	cgcactgggc	aacaaagtc	tcattcgttg	647700
tgaggataat	atctatgaaa	ggaatcccta	gcactgttaa	acaggtcgat	gtttcccgag	647760
agaagctttc	tgaagctctt	agagggaaga	cggctcttcc	caagataaaa	attataagga	647820
atctgaggac	aacgcgccac	atacaacctc	agtaaaaagta	gaactcctat	tactaaacta	647880
aaagtaagac	tttattttta	gtgttttctt	accttcttct	ttgtataata	cttgtttatg	647940
tacggtttat	gtacgaagga	aaatcacgca	tggcatcgcc	cactccagga	caattgcatc	648000
tacagcaaaa	agtagaatca	aaggcctatg	actatttcag	cagcctcgct	atgattgcta	648060
cagcttttgt	attttttatt	gttgccttta	ttcttctcgg	attgagtctg	cttccctcagg	648120
tcttctctcc	cttttcagga	gcgtatttta	ttatcggttc	tttttttagct	tttattgcgt	648180
taggggattct	tcttattaat	tgcgtctgcy	atctcaaaaa	gtaccttacc	tctgtcttagt	648240

ttacaacctc	gcaaagcttc	ttttttttat	tacaaaagtt	ttttcctgac	taagctgttt	648300
gtaataaatt	agttttctac	atctataaga	aatctgtgct	aaagcccttg	ggcttcgtgc	648360
cgatgttacg	aatatccatt	aacattaaat	agatgttcgt	aatgaaaaaa	cttgctccgtc	648420
tatgcgtagt	tcttctttct	ttacttccga	atgtattatt	ttcttcggat	cttttacgag	648480
aagagggcat	caaaaagatg	atggacaagc	tgatcgagta	tcatgtcgat	gctcaagagg	648540
tttctacgga	tatactctcg	cgttctttat	ctagttacat	tcaatctttt	gatcctcata	648600
aatcttatct	ttcaaaccaa	gaggttgca	tttttctaca	gtctccggaa	acaaagaaac	648660
gtctcttaaa	gaattataag	gcaggcaact	ttgctattta	tgcgaacatc	aatcaattga	648720
ttcatgagag	tattcttcgt	gccaggcagt	ggagaaacga	atgggttaag	aatccaaaag	648780
agcttgattt	ggaggcatcc	tcatatcaga	tatcgaagca	acctatgcaa	tggagcaaat	648840
cttttagacga	agtgaagcag	agacaacgcg	ctctactcct	ttcctatctt	tctttacatc	648900
ttgctggagc	ttcttcctct	cgttatgagg	gtaaagaaga	gcagcttgct	gctctgtgtc	648960
tacgtcaaat	cgagaaccat	gagaatgtat	atttaggtat	caacgatcat	ggtgttgcta	649020
tggatcgga	tgaagaagcc	taccaattcc	atatccgtgt	tgtaaagct	ttagctcata	649080
gcttagatgc	acatacggcg	tatttcagta	aggacgaagc	gttggcgatg	cgaatccaac	649140
tagaaaaagg	catgtgtgga	attggtgttg	ttctgaagga	agatattgat	ggagttgttg	649200
ttagagaaat	cattcctggg	ggacctgcgg	ctaaatctgg	ggatcttcag	cttggagata	649260
tcacttatcg	ggtggatggc	aaggatatcg	agcatctttc	tttccgcggg	gttttagatt	649320
gtttacgtgg	aagtcattgg	tctactgtag	tcttagatat	ccatcggtgg	gagagcgatc	649380
atacgatcgc	cttgagaagg	gagaaaaatcc	ttttagaaga	ccgtcgtgtg	gatgtttcct	649440
atgagcctta	tggagatggt	gtgattggga	aagttacgtt	acattctttt	tatgaaggag	649500
aaaatcaggt	ttctagttaa	caagatctac	gtcagcgcgt	tcagggatta	aaggagaaga	649560
accttcttgg	attagtttta	gatataccgag	aaaatacggg	tggattttta	tctcaagcga	649620
tcaaagtttc	tggtttattt	atgaccaatg	gcgttggtgt	tgtatctcgc	tgatgtgatg	649680
gtaccatgaa	gtgctaccgc	acagtatctc	ctaaaaaatt	ctatgatggg	cctttggcta	649740
ttttagttatc	taaaagttcc	gcatacagcag	cggagattgt	agcaciaaact	ctccaagatt	649800
atggagttgc	tttagttggt	ggagatgagc	agacctatgg	gaagggaacg	attcagcatc	649860
aaacaattac	tggagatgcc	tctcaggacg	attgttttaa	ggttactgta	gggaaatatt	649920
attccccctc	tgggaaatcg	actcaacttc	agggagtaaa	atccgatatt	ttaattcctt	649980
ctctctatgc	tgaagatcgt	ctaggagagc	gttttctaga	gcataccctta	cctgcagatt	650040
gctgtgataa	tgtacttcac	gatcctctca	cggacttgga	tactcaaaca	cgctcttggt	650100
ttcaaaaata	ctatcttcct	aatctacaaa	agcaagagac	tctttggaga	gagatgtctac	650160
ctcagcttac	gaaaaacagt	gagcaaaggc	tttctgagaa	ttcgaatttt	caggcatttt	650220
tgctcgcagat	aaaatcatct	gaaaaaacgg	acctatccta	tggttccaat	gatttacaat	650280
tgggaagagtc	gataaacatt	ttgaaggaca	tgattttatt	acaacagtgt	agaaaaataat	650340
tactgttgct	ctttacatct	gatctcgtac	gtggaaagta	gcatacccaag	ttctaggatg	650400
cttgtgagat	gaacgtctaa	acgcgagcta	ttttacttac	taaaggtgaa	agtacaggan	650460
ttccgcggcc	atcattaagt	actgggggtan	tagccctaga	ggtatttccct	tctgttttca	650520
catggccaaa	aatcttattt	gagttattaa	ggatcccatc	atcgagctga	tcttctaaaa	650580
cacctgcccc	tttttggaaa	accatgagtt	tttcagatgt	acaagcttca	tcaaaacata	650640
atgatgtaac	tagtaactta	atcaatccta	tggcagcagg	aataatcaac	caaaatgcat	650700
ttgcccctaa	ctggctatgg	aagataaaca	tacatgctaa	tccagcaaca	accaaagaa	650760
ttcctaaaac	gagcagggtg	atttggcaag	ctctggattg	aaagagcttt	gattcacgta	650820
taggttgaat	aaattttgtc	tttgcccatc	ctatgagtag	attcaccatt	cctggactgg	650880
acgtaattgc	ttgtagacca	gcggtgacac	tccccgatgc	tgctatttcc	tctactatgt	650940
ttagcacaga	ctcaggagca	gctgtcctgt	ttcctgttcc	tcctacggga	tgtagatttg	651000
atgacatacc	gttctcctag	tgtagtccct	aaagaagcag	gttacactag	gaaaacatta	651060
attaaaaatt	ttaattacat	acctaaaaag	atgggctttt	aaaataaatc	ttaggatttc	651120
agaaacttaa	ataatatctt	tgattaagaa	actctacgat	tggattgaag	agcttataaa	651180
acaaaaaaac	cgcttttagta	cgtaagggtac	taaagcggta	cttctttgaa	agctatccta	651240
aagcagagcg	gaatatcgct	ctgcttttagg	ataattcctt	agaatttaat	acacgtgggt	651300
attttctgtg	tctgatactg	gtgaagtcag	tgtatcagaa	gaaagaatag	cttcgccgcg	651360
agcatctccg	ggagcaatac	ctttcaaggt	aacagaaaaac	tctacagatt	ccttagaacc	651420
gagtttaggt	aaagcgtcga	aaacaacggg	attacctgaa	atcgttcctt	tagttggacc	651480
tgaagaagct	attggctgaa	gttcttttga	gaacttcaag	attaaagata	cgtagtatac	651540
ttcagcagaa	ccacggttag	ttacacagat	acgatagaca	gtattttctc	ctacacagat	651600
aggatcattt	gtgtctaata	cgcacatatg	ggtagctgca	agacctttcc	aatgtgttgt	651660
tgtttctgcg	caagatgtac	atgttccgca	gttagactca	ctagttactg	caacttgatt	651720
tgtgaatctt	ccaggaactt	gagctttcac	tacaagttta	aactggaggg	tttctcctgg	651780
gcacatttct	ttaatacgcc	aaacaacttt	attacagcag	atctctccac	caggagcttc	651840
gagtactgta	acaccagaag	ggagtgtatc	ttggatcacc	acatcatgaa	gaaccaagtc	651900
tccaggatc	gatactgaga	tagagtatc	cacaggttta	catacgtaag	accaatcagc	651960
accagagata	tttacttgta	cacaaggctc	attaacaact	gtagttacat	ttgcagaaca	652020
tttgtgtcca	ccgcagtaag	ttacagtagc	aacgttagtg	atttgacctc	ttctttgagg	652080

gcagaactca	actgtaaata	cctttttatc	gccaggtctc	atgtctccta	agttaaaaga	652140
gagaactcct	tgaccagatg	catgagaata	gccatcgga	acaggattat	ctacagttac	652200
gttacgggca	atagcagatc	ctgtgttcac	tacttcgatt	ttgtagcata	cagggcatct	652260
taggcaagca	cagtcaggtc	cttcttgctt	aatacaaatg	gctgggtgac	cgcatttagt	652320
ataagaacgg	agctctgggc	aagcacatac	agtagcagct	gtgaagcagc	aaccttcttt	652380
aagaggtttt	acccatacag	taattttgca	tttatctcct	gcaccaggc	gatcgatttt	652440
ccagactaat	ttcccatcac	ttgtaggagt	tgtttctgga	tcactgctta	cgaattcagc	652500
ttcgcaagg	agctgttggt	taatcacaa	atcaacacaa	tcttttttgc	ctatagcaag	652560
gatttcaata	gggtaaggag	atcctacagt	agcgtattct	ggaacggact	ggcaaatttc	652620
tacgttgcaa	tcacgttcta	cttttacaga	atacaatctt	ccgtagcaag	actcttgctg	652680
agcctctaca	ggttgacatc	gtccctcttc	acagggataa	aattctttat	cacaaaaagc	652740
accacggctt	ttttgttcaa	ctgggtgttt	atctctacgg	acaagtctaa	ccttcttcgc	652800
tgatcatagga	acaggtgctg	gctttgtttc	cgcactagcg	acgatcttag	taatcagaga	652860
ctctgctaca	gcggcctcta	taccccgctc	ggcaaagcaa	ctcgccatac	tcgttagcgc	652920
aaggaccgta	actactcgtc	tgatgagttt	ggacataggg	atctcctatc	gcatgtttat	652980
ttttttcttc	tgccatcggg	tagaatgttt	tgtaaaactct	tacctcaac	atgtgggttt	653040
attatctgaa	ttaaggtagt	caggaattaa	ttcatctcct	aactacctga	tcaatttaag	653100
taaacagtta	agagaactct	ccttactgtt	tgcatctgcc	atcaggtgat	gtacaacctt	653160
taacttggtg	gctttgagag	ttacactctg	ttgaaccaca	tggattagaa	caagaaggaa	653220
cgtaggaccc	acaagcatta	ccgccgcaag	atctttcttt	ttttcttatt	acttcacaag	653280
gattgcaaga	agaggggtgc	caaggatcct	caaaaaca	atctacaatg	cggcagcagc	653340
tacttaagct	aactactcca	caaaacattg	cagcaattaa	aacagctttc	ttcataagtt	653400
tttaactcct	ttctaattag	aaaacttacg	tgtcttattt	attactgaaa	attcaacaaa	653460
acttttaata	attaataaag	cacgttccca	tgaacaatat	tacaaatgaa	aataaaaaatt	653520
ttatcaatta	ttttttctag	ataaatcttt	ttggtattaa	aactcttttt	agaaaacact	653580
atttactaaa	agataaacct	ataattttca	aaaggaagcg	tcacagggaa	tttgaggaaa	653640
ctgaagaata	aaaagaataa	tttgtttaat	aactaatggt	ttatttcacg	agactttttc	653700
acttattttc	tatatataaa	acacataaga	ttcacaatca	acgagttgaa	gtagaatgat	653760
tgtaaatccg	cacaatcaaa	tcattgaatt	ataacaaaat	aatttcgtaa	cattaaaaaa	653820
taaaaacgag	ggggaaatga	aattatttta	cttttgtaac	attattttcc	tgacatctct	653880
atttctgta	agctgcacgc	acacgcctcc	tccacgtagt	tatatctctg	ctcaaggaag	653940
aacgcccctc	gtcaataaag	cgcattcctt	agaattcttt	ttagcaagat	ctgtctttaa	654000
cacgtgttat	aatacgaact	tatagcctca	caaatcacga	tcaagagaga	ggaacgcagg	654060
actactctgg	gatagagctg	cgttgtagat	tgtcttcgca	acgactcaaa	caggaagtgt	654120
ggttatgaat	agaaaccgcg	gtggctgttt	cgcttagcta	gcagccacgc	acattcatgc	654180
gaccgatatt	tagagatcga	aagtagcctc	ttcgaagtct	tctcgttgca	tgaacttatc	654240
cacagttgca	gcgagcttct	taggaacgcc	tcctaaaagc	ttttctgcat	acacaagacg	654300
tgctctcgct	cgaggtttcc	ctaaaatctc	tatagagtca	aagagaggga	gccccgtgct	654360
tttcccagta	attgccacat	aaagcagtg	gatgatggct	tttttatggg	ggacattgaa	654420
tgcttgagct	aaccatttag	atccgaggta	acacgtctct	ttcgtccatt	gatcgggttt	654480
ctcaagatat	ttgacatagc	tatagagaag	gatagctgct	ttctctggag	aaagggcctg	654540
tggtaggagt	tcctcaacac	ggtactctaa	caatcctgag	aaaaagaacg	aggtgaggtt	654600
gataaactcc	gcaagagttg	taatccgaga	ttgacagagg	ggaaggattt	ttaagaaaaa	654660
ttcgtcatta	agtagccaac	cctggagttc	ttttaacaag	cactctggcg	aacctctgtg	654720
ggtgaggtaa	tgcttattca	tccagtcgag	cttttgata	tcaaaaactg	ctcctgactt	654780
tccaatacgt	cgaggattaa	aagtttctat	aatacgtctc	agagaataga	cttcttcac	654840
cccttccata	ctgtaaccca	tgagagtcag	gaagttcaca	aaggcttctt	tgacataacc	654900
tgagtcgcgg	taataaaaaa	tcgaggtagg	gttctttctt	tttgaaagtt	ttgttccatc	654960
ggggtttaga	agcaggggca	tatggagaaa	gacgggaggc	tcccagccaa	aagcttcgta	655020
gagtaggaga	tgcttaggag	ttgaacttag	ccactcttcc	cctctgagga	cgtgagtgat	655080
gccccatgag	tggtcgtcaa	ttacattagc	aaagtggtag	gtggggaatc	cgtcagattt	655140
tactaggacc	tgatcatcga	catctgccca	aggaaacacg	actcttccct	tgtataatc	655200
ttcgaaaaca	cattcccctg	ataagggaac	tttaagacga	atggtgtagg	gctgacctgc	655260
tgccctcgtg	gaggtacac	cttcgggaga	gaggtacctg	tacctgcgat	cgtatcccc	655320
acgataacgg	aggggtactg	ccacagcgcg	catttctgcg	agttcttgag	gggttgcaaa	655380
gcacttataa	gcgcaatctg	tctttaaaag	tgtctcaaca	taccttgat	agattttcgt	655440
gcgttctgac	tgacgatagg	ggccataggg	gccgcctaca	tcagggccct	catccccatt	655500
gatcccgcac	caacgaagag	ctgagaaaaa	atcttctctg	taatcttggc	gactacgtgt	655560
tctatccgta	tcttcgatac	ggaggatcat	tttcccttta	aatcgttttg	caaagatttc	655620
attaacacaga	gccatatagg	cggtagctac	atgaggatct	cctgtaggtg	aaggagctac	655680
cctaacacgg	acattttccc	aattttctat	tcttttatcc	ttagaccaga	gagacttcac	655740
accctgaaaa	cggctatttc	ttcaagggaa	atcctctctg	cagaaatgca	taaatccaaa	655800
aataaaagaa	actccttaat	ttaataaaaa	attaaggagt	ttctcaaaaa	aatcacgaaa	655860
ggatattttc	ccacccttag	atcggggatc	gcctttaaa	tatcagaaag	aagtagttaa	655920

tcaacaatgt	tgtaagtaga	aaatcgaaaa	atcgagagcg	agttagttag	attcaggaaa	655980
aatttcagta	ggagggttcga	aatttgagagc	ctgatgttct	ttcgggttcag	ctccttttag	656040
tttttttagct	gcttgcttac	tcagatactc	attcttatat	ctttcaatct	cagatacgtg	656100
aattacccaa	gcggctccct	tacgctctcc	tcgtatgggt	cccgtacgag	ttgcatagta	656160
gaccttctgc	acagggtattc	ctaaaatctg	agcaacctga	tttatggagt	agcatccttt	656220
accgttatcg	aaaacaagct	ctccttgata	aagagatttc	tttcgagagt	aacgggttacg	656280
tttgactctt	tccaaatctt	taatatctat	ttcccagcgc	gtctcttttag	aagcttttag	656340
ttttttctgc	ttaattgcca	cataaattgc	ttgcctagtg	acgttatgta	atttagcagc	656400
ttgagtgc	gaaacccatt	ttgtatctga	gtctttgata	tcctcaattt	cttctctttc	656460
ttctctttct	tctaattcgt	agcatccctc	atgttggttcg	cacgccataa	gctagcatcc	656520
cctccccctc	aacatatttta	caattaaaac	aaccgtaaca	gttagtttct	tccttggttt	656580
tagaagtttt	taaagaagca	ttttcctaaa	aaaagcttta	ttaatcaagc	ttttttgtta	656640
atacaaagtt	tatgttttca	gattaaaatc	ttaataaatc	gtaagcagga	ttatgaatta	656700
ttaatatttc	tttacgttat	aaaaaatagg	tattcttaaa	aaaacacgcc	ctgaatatcg	656760
ccagggtacgt	ttttctaatc	ataacgtttt	tcttaagtag	acaagacaaa	ataccagaa	656820
ccaacaaaa	atctactctt	tttcttttcc	tgaacgaagt	attttttttt	aattttcctt	656880
atcgggtcagc	agtttacaga	agccagggat	aaggaaacta	caaagatttc	tttactcttt	656940
taaaataaag	ctctcgattt	ttgatttaaa	tctgcgatga	accttaggaa	actcattttt	657000
ggttttaaag	atgagtttct	aattatcgaa	atgtcttcga	atatgacctg	caacttcttt	657060
aatcacatca	tcggaaagga	tatgatcgtg	tcttagaccg	gtctgagcta	cagggatttt	657120
cttcctgaa	cactcttcca	agtttttagg	atctaaaaat	gggtctgcga	agcacgtctc	657180
ttttttgaac	aatccatccc	cgataagatt	accttgggaa	tccttgccat	aaataaagag	657240
ttctgggcaa	tgcaagtcct	tgtctctctt	ttcagaatta	atattccaat	gggtaagatt	657300
cgccagccaa	actcctagac	ttccaataaa	ctgttttagca	acggctcctg	tagagcgagc	657360
tcctcgatct	ttaacgacaa	accaacggac	gctatcactt	ccgtctgcga	tctctttact	657420
taatgcttcg	gcttgaacac	tagctcctaa	agaatagcca	taagcaacga	tttgacgcgc	657480
ctgaggtcct	gcgggttcat	ctctaagata	gcgtacgcac	gcttgataag	atttgactac	657540
attgtttctt	gttatattcc	cttggtctct	catgactcct	gggtaattga	agattaaaaat	657600
gttggtattga	gactcttcag	caatacggaa	tatccagtc	ttttcccctt	gcagcactgt	657660
cctatactct	aagcaatcgg	agtttccatt	ggagattaac	atccatcgat	ctggcttagc	657720
attgggaaga	cgtaactcca	atccgtcaat	aaagacctcg	tcatactgta	agcaaaccct	657780
tcgcacagag	gagacatgat	cttggaatga	agcggagaaa	agacgcgcgg	cgtaagcttg	657840
tcgcaataaa	ttagagtccc	tgcatatggg	tctaaaaatc	cacctctctg	caccaagaag	657900
aataaaattc	tgacatatct	tctgaaggac	ccagaaaaga	cccaagggaa	taaagaagat	657960
taagccgaga	agaaatttca	caacacccca	tatgatctca	agaagacgat	aaaggtaagg	658020
atgagcctgt	cgtttctccc	aagaagttct	cgctgtctcc	gaagaaaaca	tggcgatcga	658080
aggtttagga	tgcatatcca	atatagctgc	gtgttggtcc	cttgcaatag	ctattgacat	658140
tattacctta	taatttcatg	cagaatgtag	tgagcaaact	attatagtgg	aaattattga	658200
ataaaccaa	aacaaaagcc	gagtttat	atattaatat	aagtaattat	tttaatatga	658260
tcgacctcga	accatttagat	agattaggtga	cgacctcat	ctagaaaaga	acattcattt	658320
attatgataa	tgaagtaaat	cttttacttg	caatgaacaa	agaaccaatc	gaatgaaagt	658380
tagcgggtctt	tttttagtct	gaaaatctag	gttctgagga	aatacggaaa	tcctcggaaca	658440
gcagggtgat	gactcccgat	ccagaagttt	gggacaagcg	gggtgtgtaa	gcaatctcaa	658500
gagggtaatg	ccaacttgct	tttaatgcac	cagcgtgtct	tcctcagaccg	aagcgacacc	658560
ctcaagattt	ctttcttttt	ggcttaagta	gagtttgaga	tggtttccag	gcaatacttt	658620
tggatagcgt	acctggcgca	cttttgaata	gaagatagcg	atcagattcc	ccttcccaaa	658680
aggctcgaat	agttccatag	aagctaggag	atcataatct	atagcatcaa	aatccgcata	658740
agcatcaatt	tcgagatgag	gaagtgtgtc	acctttttta	agagaagagt	tcacgagatg	658800
aacgaatttt	tttttaaaat	cttcgacttt	atcttctctc	ataatcacgc	ctgctgcaaa	658860
gtcgtgtccg	ccgtaagata	aaaggagcga	ggagcatttc	tttaagactc	cgagtagagg	658920
aaatgacctt	atagttcttg	ctgatccctt	tcctaattcct	cgttggatag	cgatgattac	658980
cacaggtttg	ttataagctt	tagcaagacg	cgctgagata	atagggatga	cacgagcatg	659040
ccatgccgtg	gatgaaagaa	ctatagcagc	ctgctttaa	atctcaggat	tactatttaa	659100
tatctcttgg	acattctgaa	atacctcagc	ttctattctt	tgcttttctc	tatttatatt	659160
atctagctcc	ataattagag	catctacacg	ttcatcatct	tgggtgagta	aaagttcaac	659220
acctttttgca	gggtcgtcca	accgtcccaa	gctattgagt	tttgggtgca	tcttcaagac	659280
aatatctgtc	gaagtgactt	cgcttttttc	tactccacat	aatgcgcaga	gtttattcaa	659340
tcggggtcgc	gcgcctctgg	caatttcttt	aatcccatag	cgcaccataa	cacgggtttc	659400
ccctagcaaa	acaccgacat	ccgtgatggg	tcctaattgtg	actaaatcga	gtaatttttt	659460
cagggtacct	tgactcttgg	ggacaagatt	tctggatatt	agtgcgttca	gtactcctct	659520
tgcgagctta	aaagcaacgc	ctacgcctgt	gagttctcga	ttcgggtagg	tatgatcccc	659580
taatttagga	tttaattgaa	ctacgcagtg	gggaattttt	cctgtcggca	tgtggtgatc	659640
tgtaatgac	acatcaatgc	cttgctttgt	aatatactc	acctcttttc	ctgcagtaac	659700
tccgcaatct	acgggtgatga	ggagtgtaat	tccttctctt	ttcaactttg	caatgagtgt	659760

ggaggtctct	ccatgttgct	tgagtatcgc	accaagaaaag	aagtagctaa	cgtggacatc	659820
aatatctctt	aaaaattcga	ccaggagagc	gacgcctgtc	atgccatcga	catcgctatc	659880
tccataaatc	atgacgtgtt	ctttacgac	tctagccagg	agcaggcgtt	ctacagcctt	659940
tgacatatct	aggaagagtc	caggatcata	aaggctcgac	agatggctgt	ataagaactt	660000
atggatttcc	tgaatcgttt	ggaatcctct	tgagataaaa	atctgagcca	ctgtgggagg	660060
caagtgaat	tctttgataa	tcattccaag	aaacgcagga	tcttccttgg	gatgagccca	660120
gagcaatcct	gctgcagaag	cattatctga	atttgtcata	aatttaatac	cacaggggcc	660180
tttgggacta	aagteccaaa	ggagattttt	atattgctac	acgttagatt	aagtttaacg	660240
gtactttatt	tgagcgattt	tctttacgga	ccataaacia	caacagaggt	ggtgcaatat	660300
aaagagacga	taaagttcct	agaagaatcc	ctatggtcat	aataaatgca	aaattaaaga	660360
cagaggagcc	gcctataaac	aaaagcatta	acaaaactga	tagagttgta	gctgttgta	660420
ttaccgtgcg	gctgaacgtc	ttttgaaggg	catcattaac	taaaacatgc	ataggggtaa	660480
acaggttcgc	ttggcgatct	tcacgaatac	gatcaaaaaa	gatcaaagta	ttgtttaatg	660540
aataccccaa	tacagtcatt	aaagcaccaa	tggcttgcaa	attctattga	attttcttca	660600
aaaagaaatg	tgctataaac	aagactgac	aggtgcacaa	aaggtcatga	attaaagcgc	660660
atacggcact	gaaagcatat	tgccattcaa	agcgcaaaact	cacatagagc	aagatgattg	660720
ccaaagctcc	taaaagcccc	atggtcgcct	gataacgcat	tttcttcgat	agtttgctgc	660780
ttacctttga	ccaaaaattt	tgctgttctg	ttagagtttc	cgtagagaaa	tctaggcctg	660840
tttctgacaa	caatcccaca	gctaacgcca	gctcatgac	gttaatttta	ggagagaggc	660900
tcgtatctgc	tttagtatag	cttaaagctt	tatcactaaa	atagattttg	atcttttctg	660960
aagatccaaa	tgtttgtaata	cggaagcttc	tagaagaaaag	accagcttcc	tgtagtttat	661020
gcacaacttt	gccacgcatt	tgagcaacat	cgctgatgcc	atgctctttt	ggattaaagg	661080
taaaggcata	ccctccttta	aaatccattc	ccaaaacgga	attccaggct	ccaaaccgga	661140
gagcaacgca	acctaataaga	aaaacacttc	cagaaacagc	ccaaagtttt	ttgcatcctc	661200
tcaagaaatc	atgctttatc	cccacgaact	tattcatcat	atgcaactgt	gtatgttggg	661260
tcttattcat	ccacagcatg	aagaaaaatt	tagtcatgaa	aagagccgta	aacattgaag	661320
agaaaattcc	taaaatcaat	gtcaaagcaa	accctttaat	aggccctgta	tctaggaaga	661380
aaagaagtgc	tgaggccaat	actgtagtca	agttagaatc	aaaaatggct	ccaaaagcct	661440
tggtatatcc	tttttctaca	gattttttta	gactttgaga	caataaaaaa	tctctcggga	661500
ttctttcgaa	tacaagaaca	tttgcactta	cggccatccc	catagcaaga	acaatcccag	661560
cgagtcctga	caaggtgagt	ggcgcatcca	aatactgtag	agctgccag	ataagcaaaa	661620
gattcagaag	aacagctccc	gaagcgatga	cgctccaaa	tctataatat	acgctcatca	661680
aaacaataag	cattgccaag	ccacagcatg	ctgagataat	gccttggtga	cattgttttt	661740
tcccaagatc	agaagagatc	gtctcttcac	tgagaacctc	gggaacaaaa	gacatcgctc	661800
cagattttta	atctgaggcg	agtttgctca	cttcacggtg	ggtaaatttc	cctgagacac	661860
tggtcatgatt	tttcaatggg	acgtttaaaa	tagggctgtc	gaccatataa	ccgtcaatca	661920
ctacagccat	acgccatcca	cggtttgtag	aatattgtcc	attagcagtg	ccgctgctcc	661980
cctcctgaca	atatgcgga	gtccatgtgt	ggaaactctc	tgtaggagaa	agtttctctg	662040
ccattttctt	agggtttgta	tctttgactg	aaaaatttaa	aacataacct	tcccctgcag	662100
caaattcttg	acgaatgtct	tttagggaag	ctccatctaa	cgcataattt	ctaaaaacaa	662160
tgactaaagg	atttgctttt	tgttctgcat	cttttccaat	agcaatcata	gaaaacgctg	662220
tatctaaatc	tgctgaaggc	gtttcgcac	ctgaaggaga	gaacgccaac	ccctcacttt	662280
taagcttagt	aatggcctca	tggaactttg	gaggcacatc	gacttctctc	ttaaataagg	662340
cgtagcgaa	ggtattgatt	tcttcgggag	atgtctttcc	ttgagcttga	gaggtaaacc	662400
aaagatagtc	taaaaatctt	tgcaacttct	agcgggaagc	gctgtaagaa	gagaacctct	662460
cattcaccac	atggaaactc	atttttgagg	tccccaagat	ctcagatgag	gagatcgtag	662520
aagatcctgg	cacactgaga	tgaatgtaat	ctccctcacg	gcgaagtctg	atttcagata	662580
ctccaagttt	atttaatcga	gcacagagct	catccgaaac	tttaagaata	tcttccttat	662640
cggtagctg	ctttccctga	tgatctttta	aagagagtag	cagctgacgc	ccaccaacaa	662700
aatcaatacc	aagacgtagt	atgttctccc	cacgagaaaa	ttttctcatg	ttgagtttca	662760
tattttctaa	gaaaagattt	tgataaggaa	tcggagcact	caaacgttcc	tgaagatcca	662820
tagaacactt	tgctgttcgg	tattgctcat	gccaacgcac	taaatcgctt	tgacgattct	662880
tctcgatttg	gtttacagtt	gcaaggcgat	cttgaatgtc	tttaactttc	aaaaaggcac	662940
agccctcttt	ccctatgaca	aatccctcac	cccatacatc	tagaaattgc	tgcaaggggt	663000
gccggatttc	ttaagacttga	tcttctccta	gagtcacagga	aatcgcttct	gtatgagaaa	663060
aacagttata	gagattttgt	agatcttttt	cgaaactttg	gagttcttta	ccccctccct	663120
gttgatattt	cgcgacgata	gaacggagtc	ctttcaataa	gatgtaaacg	gagccttttag	663180
aaaagtgttt	gcaatctgta	ttgggagaaa	agatgttaaca	gccaaaactt	cgctttctct	663240
aggttgacga	cagaaaacag	gaaaattttc	tggaatcagg	tcacaagatt	cagctgcagg	663300
cctatgcaaa	gttaatgccg	tgagatgttc	tgcgattcct	tgagcaaac	gctctccctg	663360
gagaataatc	tttccctgag	tatcttttat	catccattgg	aaggaaaaatc	cggtgttata	663420
atcttctact	tgaacagtta	agttctttaga	gagcttttgt	ttttcaacag	ccaaacgact	663480
gtcaaaatct	aagcgtttgt	ctttagacaa	agacgtacgc	tgtgctaaca	aatcagaatg	663540
tagtgtcagg	aaaattttac	gttccttagg	gcaatactct	atggaactaa	aaaataatga	663600

ggactcacta	caatctaate	gaagcccttc	aatataaggg	caatctaate	tacgaatgca	663660
tgcagtttga	gaaagagttt	catatacact	cttgagtagc	ttttgatctt	caacatcgat	663720
tgctgcgtcg	tttgacaacg	aagacaggcg	tgataaaaac	gcaagtctat	cttggttgga	663780
agaaaaggac	tggtggcaaa	acgctgaaag	tcgcgaagaa	aaaacctcaa	atcctgaaga	663840
aagggttctg	gcatactgta	acaattgttc	tttaggtgcc	gtttcccaga	tagaggggta	663900
actacaagaa	cagtcttttt	gtttcggaca	agtacatgca	gaatagactc	gttgcaaaat	663960
acttgaggcc	atctcttgtt	catttttcgga	agaataggaa	acaaaagaaa	aatcactttc	664020
tactaaggaa	gtatttatag	agcttgctac	ttgtattaca	tggtcgtcgt	gttctcgact	664080
atagccaacc	acatggagtc	ttgcagactt	tatgggaacg	ttaggctctc	catgaacgag	664140
gttcccagata	aagtcctctg	catcttcacc	tcttttaaaa	cgcacactga	caatatctgg	664200
aatcgcagga	tggtgttgta	tggtcccacg	taaatgtagg	gacgaaagga	tcgctgagac	664260
gcgagggaatg	acatccttac	gaacttgctg	ggcctgcttg	gtaaaagatt	tgatttatatg	664320
ttcgggtctcg	tttccatcta	ttttcttatc	cagaggtttg	gcgtaatat	aacatgtagg	664380
caaaaacgtaa	tacaaagcca	aagcaaacac	gcaaataatg	atagcgaagt	ttcgcttaac	664440
cttctgtttc	attgcaccgc	tctacttttt	attaggaat	attaaaacca	aaataccagt	664500
tgaaaaaaa	atcgtcaaac	gaagaggagc	cctccacctt	caaagagagc	tctttattct	664560
gtatctttta	caaaatacta	tttttaattt	tcctaaaatc	tctatctcaa	aagggtcaaa	664620
ttcaataaaa	actaggcaaa	agtatagctc	tcttggtcgc	caacaaaacc	agaaagcgaa	664680
ataggagtta	cactatgcgg	ggttgaggag	tgatgagggg	aaaaatacag	tgaggttggg	664740
cttggtgggat	ctgtgaaaat	aaactttatc	cgaatggaat	cttggttctc	ttctctcatt	664800
cgttttgccca	cctgctctgc	agagtagagg	aaagcggctt	gtgagagcag	ttttaggttt	664860
tcctgttctt	ctttagggag	tgcatcagga	actccaagga	taggagttag	tacgtagatc	664920
gtatgttttt	tcactatatt	aggatgcgcg	atttgatcta	acacagtaaa	aaatgcttta	664980
gtataggcat	cgatataaca	tcttccctga	ggttccctgg	ctgcgtcaga	aatatttaca	665040
taaatcgcg	tttttaggatg	cgtgcgggtca	ctagcttggt	cttctgagct	ccaggaaatg	665100
actttaggat	ccaaatattg	ctgttctctt	ctttggattt	cagagagcaa	cgaagacact	665160
acagaaggat	ctatagcaaa	agttttgctg	gataaggagc	ttttttcgat	cccctgtctt	665220
aatgcgatct	gatccatttc	ttggatcaga	aagatactgg	tatttctatc	ggattttttc	665280
tggaatatct	tagtaacgat	ctcctgggag	ccttcgcaga	tctctacttg	gggacagcct	665340
ggatgatagt	agcatccggg	tcgtattttt	ttccaagact	gcaagagaga	gaggcatcct	665400
aaccaattta	taggtttttt	aaagacctta	gtttctcgaa	atagaggagc	ctgaatcgt	665460
gaccatccct	tagagtattg	taagtacgca	aaccttaaaa	gaaccaatcc	cagaatcata	665520
agacctatgc	acgggaaaat	ggtttgacat	acccagcagc	cgaaggcagc	acatcctaac	665580
aacgccaaac	caaaaacaagc	taaaacaccg	cccagtatct	tcttcggcag	gttttgtgca	665640
ttggggacgt	agtggacatt	gccntcctcg	gccgccacca	aatgaccatt	tgagtgggaa	665700
tcaaactctga	aatggatatg	cgaggaaatt	tcatactacg	aagcatcctt	ttagaatttc	665760
tttttatttt	taataaaaaa	ctagaatcga	atagaattgc	actaatatta	acaaaacaaa	665820
aaattaaaaa	acaaaagagt	ttgtttcaaa	attttcattg	aaaaataaaa	agaacactaa	665880
aattgttttcg	aatttgaaaa	aatgaatgtc	aacttgtcaa	gatattctag	tttcttctac	665940
tatgaacact	aattttttct	actcctttgc	tcgtcatgag	taagccgagt	atacttagat	666000
taggaggatg	cctaagaagc	ccttgatttc	atttgaagta	agaactctca	aaaattttct	666060
tcttgagaca	ccgatctgct	tagagaatag	aatacagcct	ctccctactg	ggatggctgg	666120
ggaaaaatcc	tttgtgattt	ttgtcttagg	taagtgaacg	aattctcctt	tcttaaaaat	666180
aggttcgaaa	cgttggttct	gagaacgaat	tgtgacttac	gccctaataa	atgatcctgt	666240
agacttgctt	ttagctacca	acaatgctga	atccaagtct	ccctctctac	agcgccttcc	666300
caacctatgt	gctatcatta	tggaaggcaa	tcgcgatggt	tacaaaaagc	atagggagga	666360
gtgcggccac	acacacacgt	caggtcatta	ttatggcgct	aaagtccctc	caaatatttt	666420
aaatgcgggt	cttgattttag	gaattaaagt	tcttactctc	tatacgtttt	caacagaaaa	666480
ttttggggaga	ccaaaagagg	aaattcaaga	aatatttaaa	attttctata	ctcagttaga	666540
caagcaactt	ccttatctaa	tggaataatga	aatctgctta	cggtgtatag	gagacctttc	666600
caagctccct	aaaggcatcc	aaacgaaaaat	caacctatgt	agtcgcatga	cggcatcgtt	666660
ctcgcgttta	gagctcgtat	tagctgtcaa	ctacggtggc	aaagatgagt	tagtccgtgc	666720
atttaaaaaa	ttacatgttg	atattctaaa	taaaaaaata	tcttctgacg	acctttcaga	666780
atctttgatt	agctcatact	tagatacttc	aggacttacg	gaccccgact	tacttatccg	666840
tacagggggt	gaaatgcgtg	tcagtaattt	cttattgtgg	caaatagcat	atacagaact	666900
atatataccg	gataccttgt	ggccagattt	tacgcctcaa	gatttggttg	aagcgattaa	666960
cgtataaccag	caaagatcaa	gacgaggggg	gaaataggtg	cttaattcaa	ataagtttaa	667020
atcgaagacc	ggtgcatacg	gtgattttat	tcagcgtgtt	gttggttcatt	cgtagtagt	667080
tacatttttg	gttcttcttc	tctatagttc	cctatttccc	ttacttctt	ttgctctagg	667140
gtttattacc	gcgacttggt	gcgctgtagg	aacttatgag	tactcctcaa	tggcgaaagc	667200
caagatgcac	tatccattaa	gcacgttttag	tgcgatcgga	tcttttttat	tttttagcatt	667260
aagttttctt	tccattcggt	ggggacacag	tctcccagga	tcttctcgatg	ctcttctctg	667320
gaccttgctt	attgtttggg	tcgtgtggag	tatctttaga	gttcgaaaaat	ctacaatcgg	667380
cgctttacag	ctatcaggag	tcactctctt	ttctattttg	tatgtaggga	ttccgatacg	667440

tttattcttta	catgtccttt	atagctttat	tcatacccaa	gaaccctatc	ttggaatttg	667500
gtgggcttct	tttcttattg	ccacaactaa	aggtgcggat	atcttcgggt	atttcttcgg	667560
taaagccttt	gggaataaga	aaatcgcccc	acaaattagc	cctaacaaaa	ctgttgtagg	667620
ttttgttgca	gggtgttttg	gagccacgct	cattagtttt	attttctttc	tacagattcc	667680
cacgaggttt	gcgagttact	tcccgatgcc	tgcgatttta	attccttttag	gtcttgcttt	667740
aggaatcaca	ggattttttg	gagatattat	tgaatccata	tttaagcgtg	atgctcattt	667800
gaaaaatagc	aacaagctca	aggctgtggg	tggtagctg	gataccttag	actcactgct	667860
cctgtccacg	ccgattgctt	acttattttt	gctcataacc	caatctaaag	agttttattg	667920
atgatttatca	ctattgatgg	gccttcagga	acaggaaaaa	gcacaacagc	gaaagcttta	667980
gccgaccatc	ttcattttcaa	ttactgtaat	acagggaaga	tgtatcgcac	tttagcctat	668040
gctcgtttac	aatctccctg	ggcgacgctt	cctttaacta	aatttttaga	agagcctcct	668100
ttttctttta	cctttgctac	aggccaacct	ttagagtcgt	tttttaattg	tcatcttctt	668160
acctctgaat	taacaactca	agaagtttgc	aacgcagcat	cggagctctc	tcaacttcca	668220
gaagttcgtg	cattcatgca	agatttgcaa	cgaagctatg	ctcagcttgg	caactgtgta	668280
tttgaaggaa	gggatattgg	atccaaagtc	tttcccaacg	cagattttaa	aatttttcta	668340
acttcaagtc	ctgaagttcg	tgcgcaacgg	cgttttaaaag	accttcctga	agggactcct	668400
tctcctgagc	aattgcaagc	agagcttgct	aaacgtgatg	ctgcagatgc	acaacgcgct	668460
cacgatcccc	tagtcatccc	tgaaaatgga	attgtaattg	actcttcgga	tttgacaata	668520
agacaagttc	tggagaaaat	tttagcttta	ctatttcgaa	acgagctatg	attttccgca	668580
tttgtaaatt	tttcacgtgg	gtagcttttt	ctcttttcta	taagctaaaa	gtttatggag	668640
tgaaaaaaaaa	ttttattaaa	ggtcctgcta	ttattgcagt	aaaccataat	tcttttttag	668700
accccatagc	attgcacatg	tgtgtccatg	agtgtattta	tcacctagca	cgggcctcct	668760
tatttaatat	cccctgggta	tgggaagcaat	gggggtgttt	tcccgtgctg	caagacgaag	668820
gaaactctgc	ggcattttaa	attgcctctc	ggctctttaa	taaacgaaag	aagttagtga	668880
tctatccaga	gggggctcga	agccctgacg	gtcaactcca	gcctggcaag	gtcgggtattg	668940
gtatgatggc	tgcaaaatct	agagttccga	tcatccctgt	ctatattagg	ggaacttttg	669000
aagcttttta	ccgtcatcaa	aaaattcctc	atgtttggaa	aacgatcacg	tgtgttttcg	669060
gtactcccat	gtattttgat	gatattattc	aaaatcccga	gatcaaaaaat	aaagaaacct	669120
atcagatcat	cacgaatcaa	actatgaaca	aaattgccga	gctcaaagca	tggtatgaat	669180
cggggtgcaa	aggagacgtc	ccctaaactt	atgtcgacat	tactttctat	cttatctgtg	669240
atatgttctc	aggcaatagc	aaaggcattt	cctaactctag	aagattgggc	tccagaaatt	669300
accccgctca	caaaagaaca	ttttggccat	tatcaatgta	acgatgcat	gaaattggct	669360
cgtgttttaa	aaaaagctcc	gagggtctatt	gctgaggcca	tagtagctga	gcttctctca	669420
gagccttttt	ctttaattga	aattgctgga	gcaggattta	taaactttac	cttctctcca	669480
gtattttctaa	atcaacagct	agaacatttc	aaggacgctc	taaaattagg	atttcaagtt	669540
tcccaaccta	aaatnattat	cattgatttt	tcctctccaa	atattgctaa	agacatgcat	669600
gttgggcatt	tacgtcttac	aattattggg	gatagccttg	ctaggatcct	ctcatctgta	669660
gggtcatgat	tacttagact	caatcatatc	ggagattggg	gaactgcatt	tgggatgttg	669720
atcacctatt	tgcaagaaaa	tccctgtgac	tatagtgtac	ttgaggatct	tacgagtctt	669780
tataagaagg	cctatgtctg	ctttactaat	gacgaagagt	ttaaaaaacg	ctcccaacag	669840
aatgtggtag	cattacaggc	taaggatccg	caagccattg	ctatttgga	gaagatctgt	669900
gagacttcgg	aaaaagcctt	ccagaaaatc	tatgatattt	tggacatcgt	ggttgaaaaa	669960
cgcggagaat	ctttctataa	ccctttcctt	cctgaaatta	tcgaaatct	agagaagaaa	670020
ggccttctca	ctgtttccaa	cgatgctaaa	tgtgtatttc	atgaagcctt	ttcgattcct	670080
tttatgggtc	aaaaaagtga	tgggggctac	aactacgcca	ccacagatct	tgtgcgatg	670140
cgctatcgca	tagaggaaga	tcatgccgat	aagatcatca	ttgttactga	cttaggtcag	670200
tctctacatt	tccaactcct	tgaggctaca	gcaattgctg	cgggctatct	acaacctgga	670260
atattttctc	atgtaggctt	tggccttgct	ttagatcctc	aagggaagaa	acttaaaacc	670320
cgctctggag	aaaacgtaaa	gctccgagag	cttctagata	ctgctattga	aaaagctgaa	670380
gaagcattgc	gagaacatcg	acccgaactt	acggatgagg	caatccaaga	aagagctccc	670440
gtcattggaa	tcaacgctat	aaaatacagt	gatctctctt	cccatcgcac	tagcgactat	670500
gtcttttctt	ttgaaaagat	gctccgcttc	gaaggaaaca	ccgccatggt	tctactgtat	670560
gcctacgtgc	gaatccaagg	aattaaacgt	cgttttaggaa	tttctcagct	gtcattagag	670620
ggacctccgg	agattcaaga	acctgctgaa	gagtttgctt	cattaacttt	gctacgcttc	670680
cccgaagcct	tagagagcac	aattaaagag	ttgtgtcctc	attttcttac	agattatctt	670740
tataatctca	cccataaatt	caatgggttc	ttccgtgaca	gccatatcca	agactccccct	670800
tatgctaagt	ctagactgtt	tctatgtgct	ctagctgaac	aagtcttggc	tacagggatg	670860
catctcttag	ggctaaagac	tttggagagg	ttgtaagttc	ttcctgttcc	atatcaaaga	670920
tctgaatttt	agctccgagg	cttctgagct	tgcctaccca	atttgatat	ccacgatcta	670980
gaagatgagt	gttctcaata	atagagcctc	ctccttctgc	aatcagtgct	gccatgacat	671040
aggcaaatec	tgctcgtaaa	tctggaatga	ctaaatgcga	ggcccataaa	ggcgtcgccc	671100
catgaatcac	agcgtgtgta	ggaaaattcc	cgatagcata	acgacatgcc	ttggtactta	671160
agcactgatg	aaaaagctga	cactcagctc	ccatgtgctg	aagaccatga	aggtagccga	671220
ggcgattttc	atggacagtc	tcatggatta	ctgaagatcc	ctgagcctgt	gatagtagaa	671280



ctgcgaaggg	ttgttgccag	tccgtcagga	accctggatg	aacatcggtt	tccaagacaa	671340
cacctccac	caagggggt	tcttgaaaa	attctattcc	cgactcggag	acaaaaaatc	671400
ctccgcctat	ggagcgcaac	atcttgagga	agggaatcag	aagtcttctg	ttagcatttc	671460
ggacgaaaac	acgtcctcca	gagacaaccg	cggccattcc	aaaagagggt	gcttcaatct	671520
tatctggaag	gatgggtgtg	tctacagagc	cgagacctcc	agtgccaaaa	atatctatcg	671580
tacgatcatt	atcggtagtg	atatccgccc	ctgccttttg	caaaaagagc	accaaactta	671640
agatttcagc	ttcgagagct	acatttttta	taaccgttct	tccttttagca	tgaattgctg	671700
cgagtatgag	atcttctgta	gcccctacag	aaggataggg	tagatgaata	taattccctt	671760
taagacctcg	aggagccttt	gcgtagtata	ccgaactatc	agaggaaatc	tgcacaccaa	671820
gttggttttaa	cccttcaaaa	tgaaagttaa	aggctccttc	tcctatagca	tctcccccca	671880
cagtgggaac	atagacacct	tcagggcaac	gccctaacag	cgctcctaata	aaaaggatgg	671940
ggatcctatt	gacatttgaa	aatgtgggag	gaactcttgt	gcattgtatt	tcgggagtat	672000
agatttccaa	aacctctgtt	tccttatccc	aagaaacatg	tgctcctagc	gacttgcata	672060
actctacagt	taaggaaaca	tctcctatat	cggggacatt	ccgcagtgtg	cacttctgat	672120
cagaaagtaa	agaagcaaca	agcagcttag	ttgcagcatt	ttttgctcct	gaaactttta	672180
cctcaccatt	aagtctacca	caaccaaaata	cttgagcaat	ctgcattctc	cgttccccct	672240
tggcatcaaa	atcactaaaa	gaaacgttaa	ccttctcgaa	ggttttattgc	cattcaaact	672300
ttttccttag	atcaaagtta	cttaattcaa	aatgattaaa	atattaaaaa	aatattactt	672360
tgatatttta	aaaacaaana	cagagataaa	tataattaat	attatttaaa	atataattaa	672420
tagaattaaa	aattatttat	ttctcaaaat	agattatggc	agctcctatc	aaccaaccat	672480
cgacaacgac	tcagataact	caaactgggc	agactacaac	gacaacaacg	gtaggatcat	672540
taggagagca	ttctgttaca	acaacaggat	ctggggcagc	agcacaacaa	tctcagacag	672600
taactctaata	tgagatcac	gaaatgcaag	acattgcaag	tcaagatgga	tccgcggtaa	672660
gcttttctgc	tgagcactct	ttttctaccc	tccttcagga	gactggaagt	gttgaggcta	672720
cagcacaatc	cgctcaatct	gcggggctat	tttcattatc	aggctcgata	caaagaagag	672780
attcggagat	ttcttctctc	tctgacggca	gttcgatata	tagaactagc	tcaaacgcac	672840
cttctggaga	aacaagcaga	gctgaaagta	gtcctgatct	aggcgacttg	gatagcttat	672900
caggaagcga	gcgcgctgaa	ggagccgaag	acctgaagga	cctggagggt	tacctgaaag	672960
tacgattcca	cattatgatc	ctaccgataa	agcgtctatt	ttgaacttct	tgaaaaatcc	673020
tgcagttcag	cagaaaatgc	agacccaaa	gaggccactt	tgtttatgta	gatgaagccc	673080
agaagtagtt	tcatttttgt	ccgcaatggt	gactgggtcaa	ctgctgagtc	tataaaagtt	673140
tctaattgcaa	aaaccaaaaga	aaatattact	aagcctgcgg	acttagaaat	gtgcatcgct	673200
aaattctgtg	tgggatatga	aaccatccac	tcggattgga	cgggacgcgt	aaaacctaca	673260
atggaagagc	gctcgggagc	cacaggaaat	tacaatcatc	tgatgctcag	catgaaattt	673320
aaaactgctg	tagtctacgg	tccttggaat	gctaaagaat	ctagtagtg	atatacaccc	673380
tctgcatggc	gtcgtggagc	aaaagtagaa	acaggctcga	tttgggatga	tggtgggggc	673440
ttgaaaggca	ttaactggaa	aacgacccca	gctccagact	tctcctttat	aatgaaact	673500
ccagggtggag	gggctcactc	gacgtctcat	acaggctcctg	gcactccagt	aggagctact	673560
gtggttccta	atgtgaatgt	caacttggga	ggcattaaag	ttgatctggg	tggcatcaat	673620
ttaggtggaa	ttacaacgaa	tgctactaca	gaagaagggtg	gtggaaccaa	cataacatct	673680
acgaaatcca	catctactga	tgataaagtc	tcaataacat	ctacaggatc	tcaaagtacg	673740
atcgaagaag	acactataca	atctgacgat	cctgggtcagg	gagaggatga	taacgcaatt	673800
cccggcacaa	acacacctcc	tcctccagggt	cctccgcca	atctaagcag	ttctcgcttg	673860
ctgactatct	cgaatgcgtc	cttgaaccaa	gtcttacaga	atgtccgaca	acatctgaat	673920
acggcttatg	attcgaatgg	taattcagtc	tcagatctca	atcaggattt	aggccaggta	673980
gtaaaaaaca	gtgaaaacgg	agtgaacttc	cctactgtga	ttcttcctaa	aactactggc	674040
gatacagatc	catccgggtc	agcaaccgga	ggagtcactg	aaggcggcgg	tcatatccgt	674100
aatattatcc	aaaggaatac	acaatctacg	gggcaaaagt	aaggagcaac	acctacacct	674160
caacctacta	tagcaaagat	agtgaacttc	ctgagaaaag	caaagtgaag	ttccagctct	674220
gtgctaccac	aaccacaagt	agctacgacg	atcacccctc	aagcgagaac	ggccagtaca	674280
tctacaacga	gcataggaac	cgggacagaa	agcacatcta	caacaagtac	gggaacggga	674340
acaggaagtg	tctccacaca	aagtactggc	gtagggacac	caactacgac	gactcgatct	674400
acaggaactt	cgggcgacaac	cacaacatca	tcagcttcga	cacaaacacc	ccaagcgctt	674460
cttccctctg	ggaccaggca	tggtgtctaca	atctccttag	tgcgtaatgc	tcaggaagg	674520
tctattgtat	tatacaagg	gggtcgatct	caaagcttcc	cgatccctcc	ctcagggact	674580
ggaaacacaga	ataatggggc	acaattgttg	gctgcagcaa	gtcaagttgc	ttccacttta	674640
ggccagggtcg	tgaatcaagc	agctacagca	ggttctcaac	cctcctctcg	tagatcttcc	674700
ccaacaagtc	cacgaagaaa	atagctcttc	gtaatctagt	tgagaaaggc	aagtccgtag	674760
aagtgaatag	ctaaaatacg	aggctcctgaa	acttaggaca	tggtgtggta	gacgtcatcc	674820
acatcttcga	tttgctctag	ccaatcaata	agagctaagt	ttgcctcgcc	atctttctca	674880
tcacaatcta	ctagacgcaa	gggaagataa	atcaacctgt	cttcactaca	agtcgcaccc	674940
tgactgataa	gtttctcttt	aacggaggga	agttcacttg	gagcacagat	cactaagaag	675000
ttttcttcac	cttcgggtatc	gagatcctca	gtcctcgctt	ctatagcata	agaaaaattt	675060
actttctcat	ctatagagct	cttagcgaca	gtacacgccc	ctttccttgc	aaaattataa	675120



agtagcgttc	cagggttctac	aagagaaacct	ccacgtttat	ttatagcaat	gcgcatatca	675180
gaagccgtac	gggttcttgtt	atccgtcatt	gcttccacaa	taattcccac	tcccccatga	675240
ccatacagct	cataggtaac	ctcttcaaag	ttcttttgct	ctgcagaagt	tgctttcttc	675300
aaattccctt	cgatattctc	attagggata	ttattttcct	tagctttctg	tatcaccata	675360
cgtaatcgcg	cattggactt	agggtcagct	ccccctaatt	taacagctga	aatcaactct	675420
ttaataatac	gagaaaaaat	cttgcctttt	ttatgatctg	ctctttcctt	gcgatgtttc	675480
gtattggccc	acttactatg	cctgccata	tctccacct	actctttttt	tataccctcg	675540
caataaataa	gcgtttgcct	tttcccaagc	aacagcacga	tcatacaagg	ggaaacgttg	675600
ttcgtattct	ttaaactttt	taccatgaaa	aatcgaacgt	cccgatagag	aatactctct	675660
agggactaca	ctatgaacca	tttcatgata	cacaagatat	tccataaaaa	atcttgggat	675720
ttcctgccga	tctaaagaac	gatgaattcg	aattaaactgt	tcattttcat	gaaacaatcc	675780
caagacaaca	ctcttgccct	ttctggtagc	tttccttccg	aaccaaccaa	tctgtaaacy	675840
cagtgcacct	tgaataaact	gcgcattcaa	ttcctcatag	atctcctgca	aatcatagat	675900
ctttcccggg	cagtagtcta	ctgggaatga	aggacgagca	agaaccctgt	gcgaagatag	675960
gaacgtcttt	tgacgacatg	ggaagcgaaa	taccctatag	agataacttg	tcagataacg	676020
ttggaaatta	tgaagtactg	tttcaaccat	aacgatagga	tgtctaaaac	ctctttctgc	676080
gctctataga	tcccttttcc	atagtagttt	tagcaagata	gccgatttca	tctttataaa	676140
aacgggtttg	ccttctact	tcgacaaatc	caaaacgttg	gtagagatgc	agagcaggat	676200
tgccctcata	gacttcaaga	tagaggacct	caagcttaaa	tcgctctctc	gccaaatgaa	676260
taagattggt	tagcaaggcg	gtccctatgc	ctttattacg	aaactcttct	ccaacaataa	676320
tggaaatcag	cgcattgatg	gaaaccttaa	cataagggtt	aagaaccaa	gttgccactc	676380
cagcaacatt	cccattgtac	acagctgtta	agctagaatg	ataacgatag	aatcctaccc	676440
agaaattttc	agcttcacga	atttctgctt	ccgtttggat	gggaaatcca	cgtaaaattt	676500
taggatcatt	cagccatttt	agcatatacg	ttgcatcgct	aggaagagtg	taccgtattt	676560
ctaactctag	aattcctgta	ttttgctttt	ctgctgtcat	gaaacnctc	caaactctgc	676620
caaataatgt	ttaataaatt	catccaatag	ctcgccgtcg	agcatcgctt	ggacattttc	676680
tgtttcatgt	cccgtacgta	catctttaac	aagagtatag	ggctgaaata	cgtagttgcy	676740
aatttgagat	ccccaaagca	tttctttttt	atctttgcga	tcaagagatt	gcttctctaa	676800
acgttcttgt	aaaacctgct	gatacaactt	tgcttgtagc	atcttcatac	agctctcacg	676860
attctgtatc	tgactacgtt	cattttgaca	tgaacaacag	actccagaag	gtaggtcgct	676920
gactctgact	gcggattccg	taacgttgac	tggttgtcct	cctgctcccg	aagaacgaaa	676980
cgtatctata	gtaaatcat	taggtcgtat	ctcatcttaa	tctntcatca	atctcaggga	677040
agacgtctac	agaagcaaag	ctagtgtgac	gtttcccatt	actatcgaaa	ggtgagatac	677100
gcaccaaacg	atgtactcct	cgctctgcct	tgccataccc	ataagcatac	attcctgaaa	677160
actttacagt	aacatgctta	attccaacaa	cttcaccatc	taagcgatcg	acaacctcta	677220
aggcccatgt	atgtttcgtc	gccccatcgg	aatacatacg	aaacagcatc	tctacccaat	677280
cacacgactc	cgtcccacct	gccccagcat	tgatcgtaag	gaaacaagag	ttcttgcctg	677340
cctctccgga	aagcaaccgt	tgcgctctcc	aaacagcaag	tttcttctca	caaaagagaa	677400
attctttctc	taagtcttca	caaactcgag	ggctctcaag	agcatcgcca	tcctcgagga	677460
aaaactctat	agcatctatt	ttgcttttta	attcctgata	ctcttggatt	tgctgtctca	677520
gacttacaat	ctgttcagaa	atctttccag	catgaacact	gtcttgccaa	aaattttctt	677580
cggaactttc	ttcttctaaa	acttgaagtt	ctttttgttt	tttatcgagg	tcaaagagac	677640
ctcgagctta	aagatatttc	cgtgcgaagt	gcttccaaac	gcttgtctaa	atcttctctg	677700
attactctta	ccaacctacg	attccaatca	agattctaga	aaacaaaagc	caataaagtc	677760
aattagagca	aggacttctt	agagcttcta	tgacttaaac	aaaaaccaag	actttttctt	677820
ctttttggag	agaaagttct	ttgttatatc	ttttctaaag	actccccttg	acgctttcta	677880
aatagaaaag	gtaaaagaaa	ttccactttt	ttgttttgac	gagaaacctc	tctgagagat	677940
aaaaaagttg	ggatgaagag	ctcaggtctc	ttcttaccac	ctttactagg	agtcaccaat	678000
gagtcaaaaa	aataaaaaact	ctgctttttt	gcatcccgtg	aataattcca	cagatttagc	678060
agttatagtt	ggcaaggagc	ctatgcccg	aaccgaaatt	gtaaagaaa	tttggaata	678120
cattaaaaaa	cacaactgtc	aggatcaaaa	aaataaacgt	aataatcctc	ccgatgcgaa	678180
tcttgccaaa	gtctttggct	ctagtgatcc	tatcgacatg	ttccaaatga	ccaaagccct	678240
ttccaaacat	attgtaaaat	aaggaatttg	ttcgctgttg	acttaggctt	aagaaagcat	678300
gagctctcat	tctgatattg	taagtacctt	gcccttttag	gcggggatat	aaagtgtatc	678360
ttaattttaaa	atggagtttt	ttctattaag	aaaagaggaa	tacttcaaaa	gcttagtatc	678420
acctataata	ggaaaattct	tgggccccat	aaatagtctc	aagtttctcg	tttttaaga	678480
ccggaaatta	gacaacaaat	agttttatag	tgcttatctc	tatttcttta	gccacccttc	678540
ctattcttgc	cttttcttgg	gcttccctca	ttgaaccgaa	ttggttaaga	acaactgcta	678600
ttccatggag	gcttccaaaa	aaacatgcgc	atttgcattg	tcttcgcatc	gctcagattt	678660
cggatctcca	tttccataag	agagttcctg	agaaaattct	taataaagtt	tccaaatcaa	678720
taaaaaattt	ctctcccgat	cttattgtat	tttgtgtgta	cctcctttgc	cgctgtcgac	678780
ttgaagataa	ggaacgactt	gaaaccttcc	taaatacatt	agaagctcct	ctaggagtct	678840
ttgctattct	aggcaatcac	gactattctt	cgtatatttc	cagaaacact	aaaggagaga	678900
ttacctgtat	ccctgaggaa	aaaagtcgtc	ctatacaacg	cgccatcatt	gctgtaatgc	678960

aagggtatt	ctcctctcct	agctatcgct	atgatcccaa	tctgactccc	caagagcccc	679020
accagacct	cttaaaactt	ctgaagaata	ctcccctaac	tctccttcac	aataccacgc	679080
atgtcattcc	taacactctt	aatattgtag	gacttgggga	tctgttcgct	agacaattcc	679140
atcctgaaca	ggcattcaaa	aactatgatc	cttctctccc	aggccttctc	ctttctcata	679200
atcctgatgg	cataactagg	ctgcaacaat	accctggaga	ttttgtactt	tcaggacatt	679260
cccacgggtc	acaagttact	ttgtcctggc	cgaagtttgc	tcgaaaattc	tttgaaaggc	679320
tgtcaggatt	agaaaatccc	tatcttgcac	gcgggtattt	cgttactaag	gaaggaaaac	679380
aactctacgt	aaaccgcggt	ctcggcggac	taaaaagaat	tcgcttctgc	ccccctctg	679440
aaatctgcta	catcacatgt	tcctatgatt	aagtcttctc	taatacttct	tagtggagga	679500
caagggtacac	gttttggtac	taaaattcct	aagcagtacc	tcctctctaa	tggaaactccc	679560
ttagttcttc	actcattaaa	gatactctct	tctttgccac	aaattgctga	ggtgattggt	679620
gtttgcgacc	cctcatatca	agaaaccttt	caagaatatc	ctgtctcttt	tgccattcct	679680
ggagagcgtc	gccaaagattc	tgtcttttca	ggactacagc	aagtctccta	tccttgggta	679740
atcatccacg	atggagcacg	tcctttttatc	tatcccgcag	aaattcatga	tttattagaa	679800
acagcagaaa	agatcggggc	gacagctcta	gcgtctccga	ttccctatac	cataaaaaca	679860
cgcaatcctg	tgcgcaactc	ggaccgagac	aattttagcaa	taattcatac	ccctcagtg	679920
ataaaaacgg	aaatcctcag	agaggggtcta	gctcttgcaa	aagaaaaaca	gctcacactg	679980
gtagacgaca	tcgaagctgc	tgaatcata	ggcaaaccct	cgcaactcgt	tttcaataag	680040
catectcaaa	tcaaaatttc	ctaccccgaa	gatctaacga	ttgcccgaagc	cctcctatga	680100
ctaaagtagc	tcttcttatt	gcttatcaag	gaactgccta	ttcaggctgg	caacaacaac	680160
cgaatgacct	atcgattcag	gagggttattg	aaagttccct	aaagaaaatt	actaaaactc	680220
gcaactccact	aattgcctct	gggagaaccg	acgcaggcgt	ccatgcctac	gggcaagtgg	680280
cgcatttccg	agctcctgat	caccctctat	ttgcaaagcg	gaaccttaca	aaaaaagccc	680340
tcaatgcatg	tctccctaaa	gatattgtaa	ctcagagatgt	tgctttgttt	gatgataatt	680400
tcctatgcacg	ctatcttacc	attgctaag	aatatcgtaa	ttccctatca	agacttgcca	680460
aacctcttcc	ctggcagcgc	catttctgtt	atacccctcg	ccaccctttt	tctacagagc	680520
tcctgcagga	aggtgcgaac	ctgcttatag	gaactcatga	ctttgcctct	tttgcaaatc	680580
atggcaggga	ctataactct	acagtacgaa	cgatctatac	cctggatatt	gtagataaag	680640
gagattctct	ctccataata	tgcaaggaaa	atggcttcct	ttataagatg	gtacggaatc	680700
ttgtaggagc	ccttttagat	gtggggaaaag	gagcgtatcc	acctgaacat	ctcctagata	680760
tcttagaaca	gaaaaatcgt	agagaaggac	cttcggcggc	tcctgcctac	ggccttctt	680820
tacaccacgt	atgctattcc	tctccctaca	ataactctctg	ttgtgagcaa	tgctctgtta	680880
gcacgtcaaa	cgaaggataa	gagaaaaatt	ccttgccctt	aagttcaggg	taatcttcag	680940
gggtgatctc	cgccatcgaa	ttgatacata	ctaaagtgtc	tggaaatctg	gagagcgccc	681000
gaagcccctt	cacagaatct	tcaaatccta	taactttcat	tccttcacga	gcaaacgtcc	681060
gatacgcgta	gtcataacta	tctccgtaag	gcttagggcg	tgcataaatt	tctcgggtga	681120
cccagaacaa	aaatttattt	aaaattggat	acatagtagc	tagtggtgtc	gtggcatctc	681180
ttggagagtt	agttacaact	ccaaatgttt	tattcaaaga	caagacaagc	tcgatgaaag	681240
cttcgcattcc	aggcatcaga	gcaggacctg	cgtgttctaa	ggacttgtag	taaattctga	681300
gtcgttttgc	aaagatctcc	gccatgtact	cttgtgcttg	gggatattgt	tctataaact	681360
ttttgctaaa	aatttctgtt	cctaaggtag	tatgactata	ataggtagaa	aaatcccaat	681420
gcacttctaa	agaaaattca	gcacaggctt	gtaaaaatgc	acgataaaaa	caaggttctg	681480
tatctacaag	caaaccatct	aaatcaaaaa	agaaaacgtc	ataatcctct	aaatacatac	681540
cactcctcaa	acacaactga	aactcgtcgc	ttaccaacat	actataaatc	caacattgtc	681600
ttaaaaatga	ttttacggat	ctccaccgta	agccttctta	caagttgctc	cttctcgaaa	681660
aattctcgta	cctgtttcgt	cactccagaa	cgcattacct	cacaaaaaga	ctgcccgcgc	681720
cttctccatc	caaaaagcac	tacgatttct	ccccctctct	atgactggat	ctccccaat	681780
agagaggtaa	tcaccgccta	ttctttctac	tgccgaggtc	aaggaaaactc	tatcataact	681840
cccgaagggg	ttctctatga	ttgtgatgga	ctccatcaca	gcataactaa	agaagagttc	681900
cgttatatcc	atcctagatt	gattgaggta	gtacgactct	tgcaacaaga	tcaccctaaa	681960
gtctctatta	ttgaagcctt	ttgttggtcca	aaacactttc	atttttttaga	agcctcagga	682020
atctcactct	ctcaactcca	tctccaagggt	actgcagcta	ccttcgctct	agatcctccc	682080
ctccccatgg	agaaaactctt	ggcaactata	aagaaaactgt	ataaaaaaaa	ctccgatcct	682140
tctctctcta	attttatcgt	tacagaagct	acactgacca	atccagaact	gcgactcacg	682200
caacaagatc	tcggctcgca	tacagaaatt	actgtagaaa	ttctcgataa	tctacaaaac	682260
aaagaggctc	ttcctccgc	ataagagatt	tctcttgca	taattagaac	agaaaaccgta	682320
cattcgtggc	tcactttatg	ccggtgtggc	ggaatggtag	acgcggtaga	ctcaaaatct	682380
actcttagca	ataagggtgtt	ggttcgagtc	cgatcaccgg	cataattctt	tcttttttca	682440
ggttgccaat	aaattgtttt	gtcgtttttc	ttagggaata	ccaaagtaac	accccgattt	682500
cttatgaatg	aaagaaccct	cttgctcttg	ttaaaaaaga	agaagggcct	tttccttgct	682560
attttagatc	ttacgcaaac	agaatcctct	ctaacgactc	cagaattaga	gaaagtctta	682620
aagcaaaaaa	aaatctttct	ttcttgcatc	gatagagttg	atcttcaaat	caagagcttt	682680
cgccatgcct	tctctccga	acttcccaa	gatatccaag	aagagctgga	agaaatccgt	682740
gatgttatta	ttcgtattct	agatacggat	aaacgcaact	atgcacagaa	aaaaaaggaa	682800

tttgggtattt	atgaacgtcc	ctgattccaa	gaacctccat	cctcctgcat	acgaactcct	682860
agagatcaag	gctcgcata	cacaatctta	taaagaagcg	agtgtctatac	tgacagcgat	682920
tcctgatggg	atcctattac	tttctgaaac	aggacacttt	cttatctgca	attcacaagc	682980
acgtgaaatt	ctaggaattg	atgaaaatct	agaaattctt	aatagatcct	ttaccgatgt	683040
tctccccgat	acgtgtcttg	gattttctat	tcaagagggt	cttgaatctc	taaaagtccc	683100
taaaactctt	agactctctc	tctgtaaaga	atctaaagaa	aaagaagtgg	aactcttcat	683160
ccgtaaaaac	gagatcagtg	gatacctggt	tatccaaatc	cgcgatcggg	ccgactataa	683220
acaactagaa	aacgctatag	aaagatataa	aaatatcgca	gaacttgagg	aaatgacggc	683280
taccctagct	cacgaaatcc	gcaatccgct	aagtggaaatc	gttggatttg	cctctatcct	683340
aaagaaagag	atttctctct	ctcgccacca	acgaatgctc	tcctcaatca	tctccggcac	683400
aagggtctcta	aataaccttg	tctcttctat	gttagaatat	acaaaatcac	aaccgttgaa	683460
cctaaagatt	ataaattttac	aagacttctt	ctcttctctt	atccctctgc	tctccgtctc	683520
tttcccgaat	tgcaagtttg	taagagagggt	cgcacaacct	ctattcagat	ctatagatcc	683580
tgatcggatg	aacagtgtcg	tttggaaacct	agtgaataat	gctgtagaaa	cagggaactc	683640
tccgatcact	ctgacctgac	atacatcggg	agacatctcg	gtaacgaacc	ccggaacgat	683700
tccttccgag	atcatggaca	agctcttcac	tccattcttc	acaacaaaga	gagagggaag	683760
tggtttggga	cttgctgaag	ctcaaaaaat	tataagactc	catggaggag	atatccaatt	683820
aaaaacaagc	gactccgccc	ttagcttctt	cataatcatc	cccgaacttc	tagcggccct	683880
acccaaagaa	agagccgcta	gctagaacgc	gttcttgaat	cttcaagacc	acttaggggt	683940
ctcaaagatc	atctacgatg	ttttcttatc	cttgaatttg	ctcttgctct	agtctttcaa	684000
cctccgctct	aagctgtgca	ttttcttctt	gcaatctttg	aagctcgacc	tctagctcaa	684060
atctcattcc	agcatcttct	cgaacaggag	agagaaggct	ctcaaggcca	cagcattttc	684120
tctgagccac	ttcgcaatct	ttgatcgtct	gtgcatgcat	cttatcaaga	gctcgtaatc	684180
cttcttcttg	ctcttctatg	tggtctcgaa	gcttgctgat	ttctttttca	gcttctacag	684240
catcggcaac	cagttgagtg	aattcgttag	atttaaattgc	aagtgttttc	aggagtctct	684300
gattctcttc	cacgagttcg	cggatcttct	tctggctgag	agaagcagaa	tctgtgagta	684360
cccagtcac	gtctcaccg	atctcagtag	gagcagcggc	accctctaaa	tccgctaact	684420
tcttcttgta	ggccatgttt	tccttttgag	ccttctcaaa	gagatcggca	aaatgattca	684480
tactttcttc	taagattttt	tcttttacct	gtttctcttc	ttgaagacgg	ctataccttt	684540
gttgtagctc	tttggaatc	tttctcaact	tttctgctc	cacgcagact	gtcctggtag	684600
tcaagaatga	attgattcag	acgtctaatt	tcttgggttt	gttcgtagtc	ttcctgttgc	684660
tgcttcccta	attcttcttc	ccaaacagct	gctgtcttct	tcagattagc	atctttttgt	684720
tcgagctgct	tctcatagtc	atggaccaga	ctctctaagc	aagccttctc	acttttctct	684780
gcgttgactt	cctgtaaaat	cttttgcata	tctagtctct	gactcagata	tttctcttta	684840
tattcgcgat	agaacagaga	ttgttcgtca	aaagcaatcc	cagtaagtct	cagatcctct	684900
tgtaatcttt	ctaatttggt	attctgctta	cgccaagcct	tctcttggtg	atggattgtg	684960
ccccctcatc	caatccactc	ctgcatagat	ttcagctgtc	tccttaaate	cttctccagt	685020
tgctggcggt	ctgcacaatc	catctctgtg	ccctcacagg	cacgctgcga	agcctcgcca	685080
tcatgagccc	gttgatatat	cttctgagat	tggttaataa	cgttgtaaaag	ccgtccagca	685140
tctcttctgc	tcgtcatcga	tccgactcct	taaatcttgc	accgtctgct	gctgcaaaact	685200
gattagatct	tgtagacgag	aaatctcttt	ttccccctcc	tctgatctaa	ctgtcataat	685260
tccttgaaac	aatcgctcat	aacttctacg	gttaaattct	agccgatcgg	caaccagact	685320
acgcattttc	aagagctcca	gcaagaactc	atacctttcc	tcgtctttta	gatgggcccgt	685380
cgagcgatac	agaatctcct	cttcacgtcg	cagcttacga	tccaacattc	caagacgctt	685440
ttcacagtct	acaaccacct	ggggcacccg	agggctctta	gcgtctctat	cctttaagag	685500
aaactctaaa	agagtcctct	caagaacttc	tctggtctcg	ttctttaaag	cttcaactcg	685560
aatttggtgt	ggttcaggaa	ccggaggagg	ttctctcagg	aggccctgag	aatcataaag	685620
acataaaaatc	aaagccaaaag	caaatataac	ggctcccaaa	gcaatcagac	ctgttccaat	685680
aaacatagga	actgctggca	gcaatcctac	gagtaatcct	ccccctaaaa	tagtaagaag	685740
agcaagaata	ataagactta	ccttaacaat	tgatgatctc	catccacact	gctggactcg	685800
agctattgcc	atctccccct	tttctctcaag	cgtttagcggg	gaaaagacag	gggtggttact	685860
gcctagctct	cttacaaaac	taggatcttg	aaatgtaggg	gattttttgag	cgggtgtttgc	685920
catgttgcta	ctacaatctc	caattgaaaa	attattttggc	ctaaggattt	tacgtcttaa	685980
tgatatttaa	atacaacgat	taaactcgat	ttcttatttt	ataaaaagta	tttgataata	686040
ttttttaaat	tctttctatt	aaattgaaag	ttttgcttca	tttttcaaga	tttagtaaaa	686100
agaaaaaatg	aatccatcca	ggggagagaa	catggcgatt	aaaaatatac	ttgttggtga	686160
tgacgagccc	ctactcagag	atttctctct	ggaacttctt	acctcacagg	gattcatccc	686220
agacactgct	gaaaacttaa	gaaatgctct	ccaaatgatc	cgaagtcgag	actatgacct	686280
tgatcatctca	gacatgagta	tcctgacggc	tctgggtctg	atttaataca	aattataaag	686340
caaagctccc	cccacacggc	cgctccttga	gtcactgctt	acggaagcat	agagaacgcc	686400
gtagaggcta	tgcaaccaag	ggcattcaac	tacttaacaa	aacctttttc	ttctgaagca	686460
ctttttgctt	ttatctctaa	agctgaagaa	ccttaagaac	tagtccatga	gaattctctt	686520
ctacattctc	agacaacacc	agattcacac	cctctgattg	cagaaagcaa	ggctatgaaa	686580
gatcttcttg	ccatagcaaa	aaaagcagct	tcaagctcag	caaatatatt	cattcacgga	686640

gaatcgggat	gcggaagga	agtcctctcc	ttttttatcc	accacaactc	tcctcgagcc	686700
aaccacccct	atattaaagt	taactgcgca	gcaattcctg	aaactctctt	agaatcagaa	686760
ctttttggcc	atgaaaaggg	agcatttaca	ggagcaacta	caaagaaggg	aggacgtttt	686820
gaacttgccc	ataaaggaac	cctcttatta	gatgaaatca	ccgaagtccc	agtaaaccctt	686880
caagcaaaaac	tcctgagagc	tatccaagaa	aaagaaatcg	aacaccttgg	aggaaccaag	686940
accctctccg	tagatgttcg	catcttagcg	acctcaaacc	gaaagcttaa	agaagctatc	687000
gatgataaaa	gcttccgaca	agatctgtat	taccggttga	atgtcatccc	tctacacctc	687060
ccccctctaa	gagaccgaca	ggacgacatc	ctccctctgg	cgaactactt	cctaaataag	687120
ttctgcccga	tgaacaatac	tcctctgaaa	accctctctc	ctaaagctca	agagctcctc	687180
cttaactacc	cctggccagg	caatattcga	gagctctcca	atgttctgga	acgtgtgggt	687240
atcctagaga	acacctccct	actcaccgaa	gacatgctcg	ctttagcttg	atctcctcta	687300
gggggtttttc	ttgtttttct	caatagcatc	tggttaagctg	atcttgcctta	atctctgtat	687360
tcttttaagc	accgatagct	caattggata	gagtaacctg	cttcggacca	gggtggttga	687420
ggttcgagcc	ctcttcgggtg	cgttaaattc	tttttttgaa	taggtatttc	tccttataat	687480
agagctatgg	agaactatct	atcttatcta	ctctcctaaa	gcatacagta	accctaggag	687540
acaagatgag	acctcatcgt	aaacacgta	catctaaaag	cttagcttta	aagcaatctg	687600
catcaactca	tgtagagatc	acaacaaaag	cctttcgtct	ctctatgcct	ctaaaacagc	687660
tgatccctaga	gaaaagcgac	cacctccccc	ctatggaaac	aatccgtgtg	gtgctaacct	687720
ctcataaaga	taagctaggc	accgaggtgc	atgttgtagc	ttctcatggc	aaagaaatcc	687780
ttcaaaactaa	ggttcataac	gcaaaccat	acactgcagt	gatcaatgct	tttaagaaaa	687840
tccgcaccat	ggcaaataag	cactccaata	aacgtaaaga	caggacaaaa	catgatctag	687900
gtcttgagc	aaaagaagaa	cgtatcgcaa	tacaggaaga	acaagaagat	cgccttagca	687960
accgagtggc	ttcctgtcga	aggcctcgat	gcctgggatt	ctctaaaaac	tcttgggtat	688020
gttcccgcgt	cagcgaaaaa	gaagatctcc	aagaaaaaga	tgagcattcg	tatgctatct	688080
caagacgagg	ctatccgcca	gctagagtct	gccgcagaaa	acttcctgat	cttcttgaac	688140
gagcaagagc	ataaaatcca	atgcatttat	aaaaaacatg	acggcaacta	tgctcttatt	688200
gaaccttccc	tcaagccagg	attctgcctc	tgaggactcc	acatcgcaat	ctcaaatctt	688260
cgatcccatt	agaaatcggt	agttagtctt	tactcccgaa	gaaaaagtc	gccaaagggt	688320
gctctccttc	ctaatagcata	agctgaacta	ccctaagaaa	ctcatcatca	tagaaaaaga	688380
actcaaaaact	ctttttcctc	tgcttatgct	taaaggaacc	ctaataccaa	aacgccgccc	688440
agatattctc	atcatcactc	ccccacata	cacagacgca	cagggaacaa	ctcacaaact	688500
aggcgaccca	aaacccctgc	tacttatcga	atgtaaggcc	ttagccgtaa	accaaaatgc	688560
actcaaacaa	ctccttagct	ataactactc	tatcggagcc	acctgcattg	ctatggcagg	688620
gaaacactct	caagtgtcag	ctctcttcaa	tccaaaaaca	caaactcttg	atctttatcc	688680
tggtctccca	gagtattccc	aactcctaaa	ctactttatt	tctttaaact	tatagctaat	688740
catccatgca	gatctgtgtt	accggcggtg	tacttcgcag	ccgcccctta	ggaaaaaatc	688800
atacactcac	cacttttatt	accctgaag	gactctttac	cttttttgca	aagcaaggac	688860
aaacccctcca	atgtgattat	cgagaaaccc	ttgtcccat	atctttgggg	aagtatacgt	688920
tacatcgtaa	tggtctacgc	cttcctaaac	tgaccacgg	ggatatectc	aatgccttcg	688980
aagcaatcaa	acaaacctag	gctctcctag	aagctgaggg	aaaaatgatt	caagctcttc	689040
tggtcttctca	gtggaaagaa	aagccttcgc	ataagctctt	ctctttatcc	ttgaatttcc	689100
tccaccgtat	tcctgaaagc	agcaatccag	aattttttgc	agccatcttt	gtacttaaac	689160
ttctccaata	cgaagggaatc	ctagacctga	ctccagcatg	ttcgctatgc	aaagcatctc	689220
taccctatgc	ctgctatcgc	taccaaggcc	ataaaactatg	taagaaacat	cagcataaac	689280
aagccatctc	catcgagaaa	gaagaagaac	aaatcttaca	ggctatcatt	catgcgaaga	689340
agttttctga	acttctagct	attgcagaat	tcccgattgc	tatagctgaa	aaaatttttt	689400
atctgtttga	ctcgctacaa	gaggaaaaaa	aatcagaaag	aaattcttcg	gaagatccat	689460
atcatgaaat	cctaagactt	tctaaagtag	tccatcccta	ctgatgaagg	acgtgtaggc	689520
ccctagaaat	tataattatc	aaaggtaccg	ctgcaccaa	cctttgaaaa	aaggtgtgtt	689580
ttcctagaat	tcaagaaaaa	ttgagagaaa	taaactccct	aagagaaggt	aattgtaccg	689640
ccctcactag	atacgttaaa	tattaacgtc	acctcagaga	atccaactaa	atcattgtgg	689700
tatattttat	tccatacacc	ccaaccctgt	tttataaacg	tactcccagg	acaaacgttt	689760
ccttttaaaag	aagtttttgt	atttacaatg	acgccaacat	cttttaggcag	ttttaatttg	689820
atagattctt	tctgattaga	aatggtaatg	gtactacttc	tattccattt	gccacggaaa	689880
tccatatcca	tcttgcaaga	actacaagaa	aaattcttag	catagagaac	aggatagact	689940
cccctacact	tgtcacggag	atgaccgaaa	gaaccttgat	aatttaaagt	ctctaattta	690000
gggaactctc	catcgagatt	gaattcgacc	cgtttttttc	tctgcgcctg	gatttccata	690060
ttctccatat	cagggtagct	tttcgaaaaa	tcaaaacggg	gggtgtaaaa	tgattcttct	690120
tcagaaagcc	aacaagggac	agaaagcagc	tgattcccaa	aggaacccga	agcaaaacaa	690180
acaatgaaaa	aaaataaata	tcgacaagcg	aatcccaa	tatgatctcc	atacaaaaat	690240
agtcaaaaaat	aaataataaa	ggaggggggac	atcacgaagc	tattgcaaaa	gaggggactc	690300
gaacccctaa	ggaaagctcc	actaccacct	caagatagcg	cgtataccaa	ttccgccact	690360
tccgcaagaa	gaaactagct	taccgaggct	gtacccttta	cctcaagaaa	aaaagtattt	690420
ccctaccacg	aaaaatcagg	tacattgtcc	taatagctag	aaggagtaaa	gcctaattat	690480

gcgttgcaact	gcctactgta	cagcatctgc	ttataacctc	catgtccttt	tccacctact	690540
taaacccgc	tatcctacca	tcttatctag	agaatatgtt	ctcgcaaac	tagatagtag	690600
acaggcaagc	aaccagttag	cgatcttctt	ccctttcgga	gttgccgtat	tctggggttg	690660
ggaagagtcc	gaagaaatca	aactttttaca	aacaatcggt	acagcatcac	cagaaattct	690720
tccccaaccc	gagatcgatt	gctataactt	tcattacgga	gataaactcc	aaatccggag	690780
ggaccgcctg	acccttgccg	acaccacatt	aaatacaaaag	ctcgccattg	cttttgggtc	690840
ggcgcaatcg	gtaaaactca	caaccttcga	aactacaatc	tataaaaacta	tagaagattc	690900
taaacggcct	ccccagatc	ttgctactaa	aggaaaaatt	tccatgtctc	ggaaagccat	690960
cgcaaaaaag	attggcaagc	tcttcctaga	taaggcttca	gtaaaccttc	attccgatat	691020
cttgatgaa	cctgattttt	tctgggatca	tccagaaaca	caggcgattt	atcgtgacgt	691080
tctcagttgt	ttagatattg	aggcacgaat	caatgttctt	atcgtttgac	tattcttgga	691140
gatgtgttag	aaattcttaa	cgaccaactc	aatcaccaac	actcttcac	tctagagtgg	691200
acaatcatat	ggctgattat	gttagaattt	tctgtagctc	tactcaaaga	tgttttcaat	691260
gtcattttaa	cgtttcttgc	aacagatccc	tgtacgtatc	tgtctactta	ttatctatct	691320
ctaccaatgg	cttatctccc	ctctcttagg	ctcgtgctgt	agattttttc	cttctgttcc	691380
gcactatgca	gaacaagcct	taaaatctca	cggtctctcg	atgggctgct	ggctttctat	691440
aaagagaatc	ggaaagtgtg	gcccctggca	tcctggaggc	attgacatgg	tccctaagac	691500
tgctttgcag	gaagtttttag	aaccttacca	ggaaatagac	ggtggtgatt	caagccattt	691560
ttctgaatga	tcttatccat	aggaatgcca	aacctcttag	ctatcaacca	taaagaatcc	691620
ccgtcctgta	ccacatactc	ttcatcctga	tcttcttgaa	cacgaggagc	ctctaccctc	691680
cgagtgcaga	tgcaaggcca	ctctctacgc	ggagaatgct	gtaatcgaga	gaagaaattc	691740
tgactatagg	gagactcttg	aggcatcagg	cggtgacct	tctcaagatc	ttcatcacia	691800
aattcatgca	aaacaacatc	actatcatgg	acaagcaaaa	gcaaggctgc	cagagattct	691860
tcacaatcta	aataagattt	taagaccttc	tgacgttggt	tagctgaaat	catggaagtg	691920
ggctctctt	cattgcaaaa	atgaaagaaa	cggtcggatc	cgcaacgaat	caccatacga	691980
gctaagtagg	ctactgaaga	ggcctgcacg	tctgcacctc	caagtaacgt	acgcaagtaa	692040
agaaattctg	gagtcgagca	gaaatgatac	aggcaatctt	catctacca	gccttcttgt	692100
accatctttt	ctatcagcaa	aaacaagccc	ttagaagtat	agggatactt	gtggcaacgc	692160
aaatagtcca	aaatcacagg	aaagtcttta	agatcaatat	tccggcaaaa	ccaccgcact	692220
gaagatcctt	tcaactctgt	ataggtcaaa	ggcttcgaaa	gcacaggagt	gatgtctatg	692280
tggtgggaag	ctatcgctac	actcaacgac	caaagtttta	tccggccgacc	atacatatag	692340
cgctcatctt	tgaacaacga	aatcaagtcg	tccaaagatg	cttgagatat	ctcgttttaa	692400
aaatcttcag	aaaggtagac	cttacgacta	cttttcgcaa	tcaaagggtcc	ggaaaataaa	692460
tgcaagcttat	agatgtcttt	acgaaatatg	gcagagtaaa	ataagagcaa	aaaaagcata	692520
ttcaatccca	cactcaggat	caagacttgc	cacagccatc	tagtttttct	tttgaaagcc	692580
atacattttg	cgcttaaaac	tcagttcatt	ctctaggatt	aaaacacttg	ccactataca	692640
caggtcacgc	taaaatccct	cgtaaaaaaca	tccttgcggt	tatcatccat	gcggtattcca	692700
ataactctac	tgcaancata	cttttcagaa	cctcttttca	caaaggaaat	tttagaagcc	692760
tgtgatcata	ttggcataga	anncgagatt	gaaaatacta	ccctatactc	tttcgcttct	692820
gtgattacag	caaaaatttt	acatacgatt	ccccatccta	atgcggataa	actccgggta	692880
gctaccctga	ccgacgggga	aaaagagcac	caagtgggtt	gcggagcccc	caactgcgaa	692940
gcaggattga	ttgtagctct	tgctctacct	ggagccaaat	tatttgatag	cgaaggacaa	693000
gcctacacaa	tcaaaaaatc	taaacttcgt	ggtgtagaat	ctcaagggat	gtgctgcgga	693060
gccgacgagt	tgggccttga	tgaactccaa	attcaggaga	gagctctttt	agagctccca	693120
gaagccaccc	cttttaggtga	agatctcgca	acagtttttag	ggaataacttc	tttagagatc	693180
tctctaacac	cgaatttagg	ccactgcgcc	tccttcttag	gattggcccg	agaaatctgc	693240
cacgtcactc	aggcaaacct	cgatcatccct	aaggaattct	cgttcgaaaa	tctcccgcact	693300
acagccctag	acatgggcaa	tgatcctgac	atttgccctt	tcttttctta	tgctgctcatt	693360
acgggaatct	ctgcgcaaac	ttcaccaatc	aagcttcagg	aatctctaca	agccctcaaa	693420
caaaagccca	taaatgctat	tgctcgatatt	acaaattaca	tcatgctttc	tctagggcaa	693480
cctctgcacg	cttacgatgc	gagtcacgct	gcttttagact	ctctgcgagt	agaaaagctc	693540
tccaccccag	aatctctcac	cctattgaac	ggagaaaaccg	tcctcttgcc	ctcaggagtg	693600
cctgtagtcc	gcgatgatca	tagtctcttg	ggtcttgagg	gtgttatggg	agcgaaagca	693660
ccctcatatt	aagaaaccac	aaccactaca	gtcatcaaag	ctgcctattt	cctccccgaa	693720
gctctccgtg	cctctcaaaa	acttctcccg	attccatcgg	aatctgccta	tagattccacc	693780
cgggggatcg	atccacaaaa	tgttgtacca	gcactacaag	ctgcaattca	ctatatattta	693840
gagatcttcc	ccgaagctac	aatctcccc	atctatagtt	ctggagaaat	ttgtcgtgaa	693900
ttaaaagagg	tcgctctacg	ccctaaaacc	ctacagagaa	ttctagggaa	atctttctca	693960
atagagatcc	tctctcaaaa	gttacagagc	ttaggggtct	ctacgactcc	acaagaaact	694020
tccttacttg	taaaagtccc	ttcctaccgc	catgacatca	atgaagaaat	agatctagta	694080
gaagagatct	gtaggacaga	atcttggaat	atagaaactc	aaaatccagt	atcctgctac	694140
actccaatct	acaaactaaa	acgtgaaact	gctgggttcc	tagcaaacgc	aggacttcaa	694200
gaattcttca	ctcctgacct	gctagatccc	gaaacagtgg	ctctaacaag	aaaagaaaaa	694260
gaagaaatct	ctcttcaggg	ctccaaacat	accactgtat	tgagatcctc	actgcttcca	694320

ggattatttaa	aaagtgtgtc	gacaaaccta	aatcgccagg	caccctctgt	tcaagctttt	694380
gagatcgga	ctgtctatgc	aaaacatgga	gagcagtgtc	aagaaactca	aactctggcg	694440
atcctgtctca	ctgaagatgg	cgaatccagg	tctgtgctcc	ccaaaccctc	tctttctttt	694500
tattcttttaa	aggggtgggt	agagaggctg	ctctatcacc	accatcttct	tatagatgct	694560
ttgaccttag	agtccagcgc	gctctgcgaa	tttcaccctc	accaacaggg	agtgttgccg	694620
atccacaaac	agagttttgc	tacttttaggt	caggtagatc	ctgagttagc	aaaaaaagca	694680
cagataaaac	accctgtgtt	ctttgcagaa	ctcaacttag	accttctatg	caagatgcta	694740
aaaaaaacaa	cgaagcttta	taaaccttac	gccatatatc	cttcatcttt	tctgtgatctc	694800
accttgacag	tacctgaaga	catccctgca	aattttactga	gacaaaaact	tttacacgaa	694860
ggttctaaat	ggcttgaaag	tgtaaccatt	atcagtatat	atcaagataa	aagcttggaa	694920
acacgaaata	aaaatgtttc	tctacgcctc	gtattccaag	attatgagcg	aacattatct	694980
aaccaagaca	ttgaagaaga	atactgtcgt	ttggtagctt	tacttaacga	attgctaaca	695040
gacactaaag	ggactatcaa	ttcatgaaac	aattactttt	ctgtgtttgc	gtatttgcta	695100
tgtcatgttc	tgcttacgca	tccccacgac	gacaagatcc	ttctgttatg	aaggaaacat	695160
tccgaaataa	ttatggcatt	attgtttccg	gtcaagaatg	ggtaaagcgt	ggttctgacg	695220
gcaccatcac	caaagtactc	aaaaatggag	ctaccctgca	tgaagtatat	tctggaggcc	695280
tccttctagg	ggaaattacc	ttaacgtttc	cccataccac	agcattggac	gttgttcaaa	695340
tctatgatca	aggtagactc	gtttctcgca	aaaccttttt	tgtgaacggg	cttccatctc	695400
aagaagagct	gttcaatgaa	gatggcacgt	ttgtcctcac	acgatggccg	gacaacaacg	695460
acagtgtatc	catcacaag	ccttacttca	tagaaacgac	atatcaaggg	catgtcatag	695520
aaggaagtta	tacttccttt	aatgggaaat	actcctcatc	catccacaat	ggagagggag	695580
ttcgttctgt	gttctcctcc	aataacatcc	ttctttctga	agagaccttc	aatgaagggtg	695640
tcatgggtgaa	atataccaca	ttctatccga	atcgcgatcc	cgaatcgatt	actcattatc	695700
aaaatgggac	gcctcacggc	ttacggctaa	catatctaca	agggtggcatc	cccaatacga	695760
tagaggagtgc	gcgttatggc	tttcaagacg	gaacgaccat	cgtattttaa	aatgggtgta	695820
agacatctga	ctgcgcttat	gttaagggag	tgaagaagg	tttagaactg	cgctacaatg	695880
aacaggaaat	tgtagctgaa	gaagtttctt	ggcgtaatga	ttttctgcat	ggagaacgta	695940
agatctatgc	tggaggaatc	caaaagcatg	aatgggtatta	ccgcgggaga	tctgtatcta	696000
aagccaaatt	cgagcggcta	aatgctgcag	gatagtttgc	ggtaatgggt	gatgacaccc	696060
tcatttctaa	acttatgaag	aactcgcttt	cgcaggcggtg	ttctgagggt	ttactgattg	696120
ctaagtatcc	tccactccag	gttatcgctc	actttgataa	taacctagtt	gttaaaacac	696180
atctttcagt	agctcctgtc	ttctcttgtc	tttttttagg	accagcagct	cacaaagcca	696240
tgagggaatt	tgttttatgg	tgttctcgct	atgccaaaca	ggaacatcct	cctttttcct	696300
cgcatttttg	taaagacctc	atccccctac	aatatctcga	aatcctaaac	tgcgttgacg	696360
agattccctt	tggagagcag	caaacctacg	ctgaaatcgc	aaaaaaaact	gatacgcacc	696420
ccaggactgt	aggagccgca	tgcaaaacaa	atccgtttct	gctgttcttt	ccctgtcatc	696480
gcgtcgtagg	aagccatgga	gagcgtaatt	acgtcctagg	gcctgtaatt	cacgagatct	696540
tattgaaatt	tgagaatagc	tactaatccc	cagctataga	tttaagagtc	ttgcagacgg	696600
ggatctaaag	catcacggac	tccgtctcct	atcagagcga	tgcgaatcag	caacatcggt	696660
aataataattg	ctggaggcca	aagaacagca	ctctctgcag	ggaatcctgt	aacaccttcc	696720
ctcataagat	ttccccaa	cgcggaactc	tcttccccca	gacctaaaaa	ggtcagccct	696780
gcctcacagc	taatcatagc	catcatagca	aacggaaacta	aagagatcac	agggacaatg	696840
gcattgggaa	ggatctgatg	caccataata	taatagtggc	tataccctaa	gtttgtagca	696900
gcaagaacat	aacctcggtc	tgcgtgtttc	aacacctcaa	tacggacata	cctactaaac	696960
cctgtccaac	taaaacagcc	tagcaaaaact	gtgttcaata	gcaaaagattt	ctgctgtgtt	697020
atggaaatca	ccagcattaa	gataaacagc	acaggcatgg	tctcccaaat	ttcagtaaac	697080
cgagataaaa	tcatatccac	ggtcccaccg	aaatatccag	aaaccaaccc	gatcataatc	697140
ccgatagcta	aagctatcgt	aatcccaata	cctgcgacta	ccaaagctat	gcgaatgcca	697200
aataactaaag	ccgctagtaa	atctttccga	gtgactctgc	taagctgcca	ccaaggaaca	697260
tacttgttca	tttctcgaga	tccccagca	tcactctccc	aatggaaact	actgaaaaag	697320
gggttaaatca	aaatgcgaag	atcttcagac	tctttctcga	tccacaaacg	cttatcttga	697380
atgaaactga	tgcgctgctg	cagcttggca	tagtcttcaa	gtacctgacg	aatctccaac	697440
aaagattttt	tatagggctc	tgctcggttt	tctacattag	cataagcaat	acaaagggtct	697500
tcagggttgc	cccagttgtt	gtaatcccg	aggcggagct	catgctctat	tctgtcaag	697560
gccatcagaa	acggctcggt	gttgtccgta	gcacgattcc	aagcttgctg	cgccatctca	697620
tagggacgct	gactcttgtc	gttaactctt	gttaactctt	taaggcaaat	gccttcattt	697680
ttcatctcta	agtgaacgaa	tggtggcatc	ggagactgcc	gtttttcttc	aaaagcgacc	697740
tgatacttct	ttacagaagc	ctcttggttc	tttcgatact	ttgccttaat	gagaatcccc	697800
aactgtctcat	acgtactcat	ataccgccgt	tccatctccc	aagtacgtgt	atctttgggg	697860
agcagcatga	ccatctcaga	attcacctta	ctgatgtttt	ctcggacctt	ctcagctcgc	697920
atthttttta	aattctcagt	aacgcgggat	cttgaacttt	cccactatag	gcccagcaaa	697980
aaatcataca	ttgagaaatg	atgcacagcc	ctaacaacca	acgacgtaac	caccccttag	698040
tcaacttaaa	agaaagtatg	aaaaagggaa	acgtgacct	aaaaacgttg	aaaaagagat	698100
ccactgggtt	agtgtaatat	ccagggaataa	acaagtacct	cagtaaagga	aaaaagatct	698160

ctccatgcc	ggtgactagt	aaagggtttac	tactcgcaaa	taaaggagcg	tagatgccaa	698220
tcagagcgac	agaaaataaaa	aattttccatg	ataaagaggc	taataaattt	ttatagtaag	698280
cagatagaaa	acgttgataa	aaggaaggat	gcttctgcat	ttatatectc	cttccctcta	698340
gctgaactcg	aggatctaag	agtacgtagc	aaatatctcc	gagcaaatat	cccactaaag	698400
atagagccga	tcctacaagc	acagaaaata	gaactacatt	gtgatctcga	tttaaaattg	698460
cctgatagaa	gaagttccca	aagccatcta	tattgaatag	ggtttctaca	accaacgccc	698520
ctccaagtaa	cgttcctaaa	tgaagaggct	agagagggtca	ctatagagac	tgcagcattt	698580
ttccctacgt	gcttatatag	aatatcaaac	caacgcaatc	ctcgagcttt	agcagcacaa	698640
ataaaatcct	ggcttaatac	ttctaaaaat	atcgaacgac	ttaatcgtga	ctgtgcggca	698700
agagctccgt	aactcactgc	acagaaaggt	aaaaacccat	gcgacaccaa	gtcaaagata	698760
cgctcctagag	tactgagctc	attaaaaacc	tctggggggcg	aacgtaaccc	agagtaaggc	698820
ataggaattg	tggtaaatgg	aatcgtttta	ttaataacaa	agttatctaa	gatccaggga	698880
accgcaacaa	agacaggaat	agaaaataga	ataaggaaaa	tgaattttag	agagtgatct	698940
atccagcggg	ttcttttcaa	tgccatgatc	ataccaaaaga	tttggcataa	cacaaagcct	699000
acaatcatag	gtaaaattga	caagaccaa	gaacaacgta	aacgcttgat	cacttctgaa	699060
attacagtct	tatgtgcgtc	atttcgtaaa	gttccaaaat	ctaaccgcaa	cacccgggac	699120
atatagcgag	caaagcgagt	ctctaagaaa	aaagtcttcc	agaactgctt	agagctatag	699180
caaaaaactt	ctgttccccc	atgatcttgg	aaccaccctt	ttaaagcttc	caccttagta	699240
tcgagatctt	cttcgttaag	ctgtcttact	aaaaaagcat	tactttctgc	gatctcttta	699300
ttttgagctc	tttggtctgg	gctaagatta	gggcccagcaa	atccttggag	gacgccacca	699360
cgaataaaca	agtctgcagc	aatatggcga	tatttatcat	ctcgcgaaagc	atcgctcagct	699420
tcaaataaca	atgcgggcat	aacaaacttc	gcacaattccc	cccaatagac	taaggactta	699480
gcagcatttt	tcgcacttgg	agtagtatta	tttgcatttg	caagtctctg	gagtgacgtc	699540
tgaatcttct	tatgagtgat	cttagggcga	gtgttaaaaa	aaatgggggag	cgtagggcca	699600
taatgctctc	gaaactgcaa	ataacgggtcc	gggcccttgt	aagagcgcat	cttatcggat	699660
tttccagctt	ctcccaaagc	gtccctagac	ttttcttcca	agacatctcc	aggagccgca	699720
tttaaaatta	caaaatttat	agagacaata	gcaaataaag	tcaggggggat	taaaactaga	699780
cgtttttagga	tgtacttaag	cacggatcct	ccttcttctc	aagccatacc	atagttagct	699840
tgacagtctc	atcctgagct	tcaggaatta	aatctgttct	atgtgtaggt	acgaaaatat	699900
tttttacata	atccttataa	agtaaggaac	aatgtcgtga	gaacaagaaa	gcataaggag	699960
cttctcatag	aataatttca	tggaaacggg	ggtagacggc	attacgttct	ttcagatcgt	700020
atctgtagct	gagtcgtctc	atgattttat	cagcttcttc	attatggaaa	cctacaacat	700080
tcgctgaacc	cttttccata	gcccccttcag	aatgccataa	agccctagga	tcctcaggag	700140
gaattcctaa	acaccatccc	attaaaagag	catcgaaatt	cttttcatca	aaagcttgcg	700200
aaagatcggc	catatctagt	cctagaaggc	tacactcgat	tccgatttcc	ttacaagcag	700260
tagctacgta	atctgcaatg	gtatgagcgg	tgacactctt	tacataatag	cataaacgga	700320
aacggaacgg	gacaatcaca	ccatcgataa	ctttttctcg	gattccatcg	ccatcgggat	700380
ctatccatcc	ctcttcttcc	aggagacgag	ctgcttcttc	tggagaataa	tgccaccctt	700440
cgatctgttt	attataagaa	ggagaactcg	aagcaaaaag	cccactaatc	gtatagcctt	700500
ggccatgcaa	gcactgttcg	ataatcctct	ctctatcgat	tgccatgttc	atagcacagc	700560
gcacctgtcg	gctttggaaa	aataatgaaa	agcaattcca	tcctatgtac	gtatatgtct	700620
gatctgctga	gactgtttca	cggacggctc	ctcccttagc	tacctgtttg	ttataagcgg	700680
agcttttcat	aaaactatag	aaattatctc	tttggttggg	tggaaaggtaa	gagatgtcta	700740
ttttccctgt	cttaaaatct	tggaaatagg	agtctgtgct	ttccttaaaa	tagacgaaac	700800
gcttgtcaat	aagagccgca	agaggatcat	agaagtcagg	atttctagaa	aacacgattt	700860
tctcatcatc	catccctgca	aagtagtagg	ctccacaact	tacaatatag	ttgtttgccc	700920
aatgcatagt	gaagttttgc	gccc aaatgg	aattggttcg	gtaggatatcg	atatctcat	700980
cttcaatgat	tttttccccg	ttagcaaaat	actgatatac	aaatctaggg	aggggctgca	701040
agcttaagggt	attagaaaat	gcagagtaga	gcactttgcg	ctcttctctt	ccttcttcat	701100
tgattaccgt	gtgtgctttc	catctgacta	ctaattttta	atcgttttct	actgagacag	701160
aaaccacatc	ttcataacaa	gagcgcagag	ccactgctcg	catggttgct	acataagggt	701220
tcataacagc	gtcgtagaaa	aacttaatat	catgagctgt	cacaggatga	ggacgttgaa	701280
atacttcgtc	taactgaacg	tgttttggaa	gggccttagg	atctatagga	cgccaaaaaa	701340
cattcggcct	cagatagatg	tgaactctt	tatccccaga	accatcttca	acaagatggt	701400
cttctatttt	cacagcgaga	tctggagaaa	attctctgta	tttccctacg	tggggagaaag	701460
ctaaactaga	atacagagat	cgtaaaaagcc	cacgacatat	caaagccatt	aaaaggctca	701520
ggnntttcngg	tttnccgaca	tgggcagtg	gtaggatacc	atgaggggtg	aaatttggtc	701580
ctagaagttc	aggaagagtc	tgctgtttat	aggggtctag	ggaaagtaaa	ttaggataac	701640
taggatctcc	aaagagtaga	gcaaaaagctt	cgtctctgac	gagcttagga	gcgagcatca	701700
ccccagggtg	cgcagggata	gcttgtgatg	tctgctgttg	tttactacg	cgtgagattt	701760
cacgaatgtc	ttcttgaata	tctcttacgt	taccttttat	cgacttaatg	tctctttcaa	701820
gtaggtctga	ggaccagtat	aacaaaatta	aagaaccggc	gacaatcccc	tttaaaattt	701880
tatctagcac	acatctttta	tacatgtgac	cactctccct	ccgcttttag	aggcaaggac	701940
tcatagggat	ctctccccaa	ccattttaatc	cgaggggacct	tagatgctgc	atagtattaa	702000



aatctctcaa	aatcttatac	aataagtgtc	gcttcgcacg	attaagagaa	catgtttctt	702060
ccttcaacaa	agaggaaaag	gtcttttgtt	gatatttaga	tagcaatatg	atgagctccc	702120
cgtatgccaa	tctgtcttgt	ttgagttgta	aattcactgg	ctgcaaacat	ggatcaaagt	702180
ggtttggcag	catgtttctga	aatctctttg	cttggcataa	actgtattga	aaagattttt	702240
taatcttcat	gtaaccatgt	tatgcttttg	actatgaatg	ggtcaagaaa	tttcagaaga	702300
gagggataag	gagcaaagac	tcttttagaa	attatttgtc	gctacataga	acaaaaacaa	702360
tctccaaaat	tttaataata	gagagttgtg	agtatggaaa	taacttgtca	actcatgggg	702420
gananagaca	aatagagggc	tttcaccctc	ttgtttgtct	tttaaaaact	aaaaactatt	702480
cagcagtatt	ctcttcagaa	ccgccttctt	catctttttc	agtttgagt	tcgctatctg	702540
aagattcgtc	tcgtccttca	tcttcagaac	cttgagcttc	gtcttggtgt	gctgaacaag	702600
attcgtatcc	aaaagcagaa	cctgcaacag	gaagcacaag	agctaaaaga	agggctaaca	702660
ttaatttttt	cattttttatt	ctccttattt	aaaatacgac	agctcaaacc	tgagattggc	702720
caaataatca	gtaacctatg	acaaaaataa	ggctgacgta	aaggtttcca	ggcactatat	702780
aaaaaaaaga	aaataatctg	caaataaaaa	gtataaaaac	aaatggatag	tggtattact	702840
cgcgttggtg	aggaaacaag	taaataccat	agagtaaaa	tataattcct	atgattagta	702900
gacctataac	caatgggata	ggtaaaagcc	ctaaagccaa	acagccatct	ataaatacct	702960
gagcaagagg	ggttcgcagt	aaatataata	cttaccgcag	cagaagcaca	aaaggcaact	703020
aataagccta	gaattgctat	agcactagca	atttcgtaac	gagaacttac	agacaaatcc	703080
gcacgccaa	aaaccctgac	tctattccac	agactgtctt	gccttaaaag	aggataatta	703140
ggtgttattt	cgtccattga	attaatgata	tcgtcggcat	gtattctagg	aaattgctaa	703200
aaaattagta	tttatattca	acaccataaa	atttaataag	tttttgagat	tttttataat	703260
ctcttttttt	tatctcttcg	taaattctta	gaccttttag	attcatacct	tgctgaaaat	703320
aaagtattcc	taactttgac	atcgttttcta	catcattagg	ttttaatttt	aggacaattt	703380
catactcttg	gatttcttcc	ataggcattt	gcaagtcata	atagctataa	gcgagtgtg	703440
cgtgtaccaca	agcgttacct	ggagcatact	catttataat	ttggaactct	tcaatagctc	703500
ttcgcgcgct	tgcaaaaaaac	ttttcttgaa	tctcagcgct	atatctaccc	gaagggatcc	703560
aataattagc	atcaaactct	gggtatttcc	ttggatctgc	gtaaagacca	gaaagagcta	703620
catacgcata	tgctaaagag	acatgcgcac	taagatctac	agggatggct	tgaaccactt	703680
tgatataagc	ttcgcagcgt	ttttggagta	aacattcacg	aaaaagaaag	taatctttcc	703740
aaaaacaaaa	acaactaaat	ttcctaata	gatcatgctt	gggcaagaat	ttgaatatct	703800
cagaaagaag	agagtattct	tgattctgaa	gatttataga	taatttagta	gctgctgccg	703860
ctaaatgcga	ttgctcttct	acaatgttct	gggagcggtt	attgggagga	acgcacctt	703920
gaagatactc	tgaaagcgaga	tcctcaaaaa	aatcaccttt	ccccgaaaga	agatagagcc	703980
gtgtgacaag	gcaaacacaac	aatgtaagaa	aaaaacacgc	aagacagaat	gctggaatga	704040
ctgttttccc	tgagaataga	aagaaatata	gaaaaaaact	gaactcaaga	gcgatgagaa	704100
gagaggctcc	acaaacaaag	aggatctgct	taattaaata	cttaagtaac	tgacgacttg	704160
ttttattaca	taaagcttct	aaattctcct	gaaaacctaa	aggtttcata	aatcctgagt	704220
cctactttgt	taattctaata	ggaaaattat	gagattaatt	gttttaatgc	aatgttttgt	704280
ctccctattt	ttagcaaaga	aagtcaccgt	gacaactcca	gcctatctac	tagctaattt	704340
tggaggacct	cgtcatgcta	aagaccttca	agaattttctg	atttctctac	ttactgtag	704400
agatgttacg	ggcactttcc	ttcccagagt	actgcatagg	catctcttta	ctttcatcgc	704460
taaaaaacgt	gttccgaaag	ttctccctca	atatcaatct	ttgcaaaatt	ggtctcctat	704520
ttattttgac	accgaaactc	ttgcaaaaac	actctctgaa	atcttacgag	cgctgtaat	704580
tccatttcac	cgctatctac	ccagcacaca	tgaaaagacg	ttgcttgctt	tcgctactct	704640
acatacgcgt	cacgtgatag	gtatcccttt	attccctcac	ttcacctatt	ctgttacggg	704700
aagcattgta	cgtttcttta	tgaagcacgt	gccagaaatc	cccatttctt	ggattcccca	704760
atttgggagt	gattctaaat	ttgtctctct	cattacctgc	cacattcggg	atttccttca	704820
gaagttagga	atcttagaaa	aagagtgcgt	ctctctattt	tctgtacatg	gacttcctgt	704880
acgctatata	tctcaaggag	atccctatag	caagcaatgt	tatgaatcat	tttcagcaat	704940
tacgacaaac	ttcaagcaat	ctgagaattt	tctttgtctc	caatcgaagt	ttggtcctgg	705000
aaaatggctc	tccccgtcca	ctgcgcaact	atgtcaaaa	atagatacgg	ataagcctaa	705060
tgtcattggt	gtgccttttg	gcttcatttc	tgatcacttg	gaaactttat	atgaaataga	705120
aagggactac	ctgcctctgc	tacgttctcg	aggatatcgg	gcattacgaa	tcccagcgat	705180
ttatagctcc	cctctttggg	tatcgacttt	ggtagatata	gtgaaagaaa	actctacagt	705240
agttgccgag	gagtttaata	agagcgggaa	aaaacacaca	gggattcgat	aagattttag	705300
ggaagacgat	accgtgtttt	tatagcatcg	tattttctcg	agcgtcgtgt	tttcacaagt	705360
cctgcgttaa	acccttcaag	caaatctccg	tttgtccctt	tcagtattgc	aagccgcaaa	705420
ccatctgcgt	ttaagggttt	tgaaataatt	ttcagtcctc	cttttatatgc	tgtttctatt	705480
agcgcggtca	cttcaattac	aggagctaga	agagcgtcgt	aacaattcga	tgtttaaggct	705540
tccaatgcta	ttggaacatg	ttggtagagg	ctaatacacag	cgtcagggat	attttgagct	705600
acaagaactg	aagagtcaaa	cttatacact	ccaataagac	gacctttaag	atcctctata	705660
gattggtaag	gagagtcttg	agcgacgaca	aggacaggag	ctgtgagtaa	aatgggatca	705720
gaaaattgat	agtgttcgag	catctcaaga	gtaggcaata	cagatgtaaa	tgctccttgg	705780
gtctttttat	catctaaatt	ctcaaagaga	tgcaaccaat	cttgatttac	aatattaata	705840



tttagattct	ctttatagtt	aatctcagaa	acaagatcgt	ttaaaaatgc	gttggtatcg	705900
gatgtataaa	tgccgaattg	ttttggaac	cagggtggcat	cacgacctac	gagaacttct	705960
ctttttactc	gagagcacc	gaaaaagatc	agtcccacag	ccagtaaaca	tattaaaaaa	706020
tttaccttcc	aagaaaattt	tatcttcacg	tttagctgtg	cctcgctgtt	ctgcctcttt	706080
ttgcatcata	ttctagataa	gaaattttta	tccagcgcg	tataaagcct	aatttttaaag	706140
aagaggggatt	cgtataaata	tctgaaaaaa	tagaaacata	taaaaaaatt	atcacattga	706200
aaatcagtac	tttctgatat	taagaaggac	tattcgatat	ttcctcagtc	ttaaggggtcc	706260
ttttccacaa	tatactcagc	aagatatgtt	ttcccaagtt	ttcttcttcg	ccttaggggtc	706320
aaaccttcac	aagcaatctc	ttcatcggag	gcatttctta	ggaatagagt	cccttcagga	706380
ttcaggatgt	ttcccgaaac	aatcttctgt	aaaaggggtt	ctacgtaaca	attacaaagt	706440
tcgtaaggag	gatctatata	gatttagatca	aaggatctct	tttgtttgat	aagtctttga	706500
attgccgatt	gagcatcttg	tctaaagatg	acgacaggaa	gttgttctcc	gagtaaagca	706560
ctattttgtg	gtattaattg	tattgctttt	atagagatgt	ccacgaatac	gacagaagca	706620
gctccacgac	ttagggcttc	aaaacctatc	gctcccatcc	cggcaaaaag	atctaaaaaa	706680
gcagccccct	ctatatcttc	cctacagata	ctgaaaaacg	cttctttcac	taaacctgaa	706740
gtaggtcgga	tatgtggatt	agaaaaatgtt	tttaaggatt	tccctttgta	cttacctgct	706800
aaaattctca	catcacctct	tgaggaaaca	agttttacgta	atcagcagcc	actagtatgt	706860
agtggatccc	tcggatatta	ccgaatccat	ctatagggcg	ttgcacttta	tgaatatgac	706920
caaataggca	tagagagact	cttccatcag	cttctaagaa	ttccgaaata	ggctctggag	706980
taccgtcact	gctgattggg	gggtagtgtg	tcatcacaat	cacctcagtg	acttcttttag	707040
gaagggcagc	aaaagctctc	tttaaacggc	ccaactctcg	gagaaaaatc	ttttcatcct	707100
gttctgtata	agattgttcc	tgagtagaag	gagtaaggaa	attctccttc	ttcacacata	707160
ttgtaggact	atcccacagt	cgcactccta	caacagcaag	atgggggtgt	aacagagcaa	707220
acccttgatt	caaatagtat	agagagggag	gaagtgtctg	tagaatttta	cttgttgaa	707280
cagaactcca	gtaatcatga	tttccacgaa	tcatatactt	cgttcctggg	agatccccaa	707340
taaaggcgaa	atctttatga	gcctctgaga	ggttcatagc	ccaagaaata	tctcctggga	707400
ggagaacaat	atcctctgga	tggacaacag	cttgccattc	agagcaaatt	ttctgatggg	707460
atcctatcca	gggggtctcca	aaaacttcca	tagttttttc	agggacgcct	aaggctagat	707520
gcaaatctgc	caaaccataa	atatgcattt	gaagggagcc	agtgtaaaaa	cgcaattgcc	707580
gtctactgta	ggaactctaa	ccataaaaaa	caaagtgtct	tgaagttcct	atctctagag	707640
cgtcacgact	gaccttggga	gctacacttt	gccctagaag	atatagttgt	caggaaatgt	707700
cgtgccttga	ggaacaatga	taatatattc	tctcacaaat	agctttttat	caggagaatc	707760
atattttaata	tagcccttga	gattctgtag	tttgacaccg	tttccaatac	aacaattctc	707820
atctataatc	gcttttacga	tctcacagtc	tttcccaatt	cctaaagatg	gcatggatgg	707880
agatccgtac	cgagcattgc	ccataattat	agactgatcg	actacagagt	tctctccaat	707940
cttactacga	atccctaaga	cactccgaga	tacatgactc	gtattaataa	cacaaccctc	708000
acataataaa	gaacttgaga	tcatagaatc	cgtaatgatt	gctccaggaa	gatgatgatt	708060
tttactatag	atcattccgt	tatcatcata	acaattcagt	cctcttttct	ctgcctgagg	708120
cttttgagtt	aacgctatat	ttgcttcata	ataagattct	atagttccga	tgtcggccca	708180
atacccatga	taaaggagag	tttgacttgg	tcccgccttc	atctgagctt	ggatgagatg	708240
ctttccaaaa	tcgtttcctt	cttcttcgcg	aagcaaagaa	aacaaactgt	ctcttcggaa	708300
taagtagatg	cccatgtatc	caagaaaagtc	tcctgaatct	tcgggttaact	tatgaatacg	708360
gcgatcttca	gaagaaagct	gaaaacgctt	gagtacttct	ttttcttgag	gtttttcata	708420
gaaatcgatg	agttttcctt	cagaatcaat	atctaagact	cccattctat	aggcatcttt	708480
ttctgggata	ggctggggcaa	caagaacat	atctacatga	gttcgtatgg	ctgtatctac	708540
aatagatcta	aaatccatat	tgtagagctg	gtctcctgat	aagattaaaa	agtattcgat	708600
ttctgtatct	tcgaaataaa	gtaagttttt	tcgaattgca	tctgcgtacc	ctgataccag	708660
atctgggtcac	cctgacgtgc	ttcaggagca	agaagatgta	tctgatcctg	caaaactcca	708720
tgataaaaaat	acgtctttaa	taaagtctgt	tgtagagtgt	aggtaaggta	ctgacctata	708780
acaaaaaattt	ttgaaaaacc	tgcactaatt	gcatgagata	ttggaatata	gatcagctta	708840
taccgtcctc	caaaagatac	ggtaggctta	cagcgacaat	tagtttagagg	agataacctt	708900
ttgccctccc	ctccacacaa	gataattact	ccaaccttat	ctcgataaaa	atgagagctc	708960
tcaaaatttg	aggcctccgg	aaaatcgttt	tctatcattt	gtattcgcct	gttctaattt	709020
aatttttaaat	tagaaacaaa	taaaaaggcc	aacacaacaa	aacaaataaa	ttttgttaaa	709080
taatttaaatt	cttttttaata	aataggttct	agaaattaa	attcaatttc	tgaatttctg	709140
gaaattttgt	ttggcagggt	tagatcacca	ctgcttagct	tcccataagc	gatcaaagct	709200
tttatcagag	tgggtacagt	aaataccgaa	ctgactttta	ttccctgtgg	accaagtggg	709260
tgacacgctt	cttttctacg	atctaagaat	accaatgctt	cacgaactac	cagaccattt	709320
tcttccagtg	cgactgctgt	ctctattata	gatttttctg	aggaaacat	atcattgatg	709380
actaaacaag	tttgtcctgg	agtaaaataac	ccttctactt	taatagcgtc	cgaggggtct	709440
acattctgta	attccttctt	tcgcaataac	atagggatgt	tatattttaa	agagatcgag	709500
gttgctaggg	ttagagcagt	ataagggact	ccgcagagta	agctactatt	gaatgagggg	709560
cggaggcgcc	aaataagagt	tgccactgtc	tggaagaact	ctggagagga	gatcacaaaga	709620
cgcataatcta	catcacagag	agtttcttct	ccgctagcga	gaatatgttt	tccgaacttt	709680

atagctccga	tttgggtatag	aattgctaca	gcttgaccgc	gtaattttgc	atcttcgtag	709740
ttcatcattc	tccagagcct	ccgaccgttt	ttgacaaaat	acaaaaaact	cacttataag	709800
ggaaaacatg	ctaatacgcc	tgtttcttgg	aattttctctt	cccaaaggct	ttcccttata	709860
tttggagcct	cctctagttc	ttgcaacggt	tcaaggaact	caattcgtgg	gaacttatag	709920
tgaggctaca	aaccctttgt	atctcgataa	tttgaatcta	aattaccact	atactcaaga	709980
actactttat	aaagcagtcc	cgtgtaatta	taaactctata	tatagagaga	tacctttaat	710040
tattttccca	gaagtactca	taggaagcac	gccaacacaa	tctactgagt	gacgtcctac	710100
ctaaaagcat	aacaaagatt	aagcaagact	attctttgag	tgacaacaag	aattctgcgt	710160
tactattggg	tttcttcaac	cttcctagca	agagatgcat	ggcgtctata	gtagtaagat	710220
ctgctatggc	ctgacggaaa	aggtagaccc	tttctaattc	actaggatga	tagaggagtt	710280
cttcttttct	agttccactc	ttaattaaat	caatagcggg	gtaggttctt	cgatctgaca	710340
gacgtcgatc	caagacgagt	tccatatttc	cagtgccttt	gaattcttca	aaaatcactt	710400
cgtccattct	ggaaccagta	tcaattaaag	cggttgcaag	aattgtgagc	gatccccgc	710460
cttcaatatt	tcttgagca	ccgaagaaac	gcttaggttt	gtgcaatgca	ctagcatcga	710520
cacccccggt	aagaattttt	ccagaatgcg	gctgaactgt	attataggga	cgtgctaate	710580
gtgttatgga	atcgagtaga	atgaccacat	catttccatg	ttccactaaa	cgacgagctt	710640
tctctataac	catctcagcg	acctgaatat	gcctttctgg	ttgttcgtca	aatgtcgagg	710700
caacaacttc	tccacgaact	tgccgaatca	tatcggtaac	ttcttcgggt	ctttcgtcaa	710760
ttaacaagac	aataagaaca	atctcaggat	tattcacagc	aatcgcggtg	gctatgcttt	710820
ggagaatgac	agttttccca	gatcttggtg	gggctacaat	caatccccgc	tgtccttttc	710880
caatgggggc	ggtaagatct	aagactctct	cagccaaatg	atctttcccc	atttccatca	710940
cgattctttg	attagggtag	aggggggtca	ggttttcaaa	aagtacacgt	tcttttagctt	711000
tatctggagt	agatccgttg	atcttatcta	ctttcaatag	agcaaagtac	ttttctttct	711060
cttttaggtga	gcgtatcgta	ccgataatcg	tatcaccttt	tttgagatca	aatctacgaa	711120
tctgagctgg	agaaacataa	atatcttcag	cagaaggtag	gtaattatag	gttggggatc	711180
tcagaaatcc	aaatccgtct	ggaaggactt	ctaacacgcc	ttcacctatc	agcaattcat	711240
ctggggcgctc	tgacttggct	ttaacaatct	caaagacgac	ctgagacttt	gttagagatc	711300
ctatatTTTT	cacaccgtat	tggcgagcta	atatattcag	ctcttcaatt	cccattcttt	711360
gcagtttagc	aatttttgta	actgtgacag	actcggcctc	ttcagactca	ctggcaacta	711420
cagcacactc	ccctacacaa	gatttttccct	gcatagaaac	gtaagcatgt	tttttcgttt	711480
ccttcaccct	aggcaagatt	tctgaagaac	gctcttcttt	cataatgctc	cctttaaaagc	711540
gtaaaaatat	tcttcaattt	tttgatgtaa	ttctttttta	gttccgttgt	tttcaacaac	711600
aacatctgct	tggtcttaact	tttcttcgac	atttagaaaa	cgcgaaacacc	tttgatcaaa	711660
gtcttcagag	gaacgccctg	ttttcttcat	gaatctctcg	cgtcgaatat	cttcgtttgc	711720
cataacaagg	atcactgaat	caaaccactt	agcatagtgt	atttcgtata	ataaaggcac	711780
ttctgcgaca	aaaaacggat	agttcccatc	ttgaatactt	tgatgatatt	gttccctcaat	711840
aattcgacaa	acttctggat	gtagaatggc	ttccagacct	tgtaatagaa	cggaattgta	711900
aaaaactttg	gctgctatgg	cttgcgcatc	aaacgccccca	tcaactacaa	catccgatcc	711960
taaaagatct	ataacacgac	gacctatgcy	tgtatgaggg	ataaggaaac	tatgcgaaat	712020
ttcatcagca	ctaactacat	aggctcccaa	ttcctgaaaa	acttggcaag	cttcagtctt	712080
cccagaagag	agatccccctg	taatggaaac	ttttaataat	tttaacattc	tgcccaattt	712140
tttccaatta	agatattcac	aactatagga	acggataaag	tcatagctga	ttccatcttc	712200
tctctcacta	gtctttgcat	ctcttctatt	tcttcttcag	gaacctcaaa	taataattcg	712260
tcatgtattt	gtaataacat	acgactcttc	atttgctgtt	gctttattgc	ttgtgaaata	712320
tctagcattg	caagttttat	caattcagca	gcacttccct	gaatgcgagt	atttacagca	712380
aaacgtcctg	aagctgctct	tgagccagga	aattcattcc	aactatcgat	aattctttct	712440
cgacctaaac	tcgtgggtcac	ccgtaaactc	ttagctgctt	gttgatatgt	ttcttcaaca	712500
aaatgagcaa	tttcgggata	acgagagaaa	tatgcttgaa	ttaactcttg	gacttcgcca	712560
atagaaaattt	ttaaaaacttt	tgccaaacca	aaagcctgtt	gtccatacac	gataccaaaa	712620
tttactgtct	ttgcctgcat	tctttgttct	tttgaaacct	gttctaaagg	cacatgaaac	712680
acttgtgatg	cagtaaaagc	atgaatatct	tctcttgact	caaaagcaaa	ttttaatgac	712740
ttatcttggc	ttaaatgtgc	taaaaatctt	aactcaattt	gagaataatc	ggcagataaa	712800
aaataactat	ttttctcaga	taaacgaaaa	gccttcctaa	gtaagattcc	tcgttccgat	712860
cttataggaa	tattttgtaa	attaggatct	cgacaagcta	atcttctctgt	cacagctcct	712920
gtctgatcaa	aagaggggtg	tattctctgt	gtatgggaat	ctacttggtt	cggtaatgct	712980
tttacatatt	tggataataa	tttttcaact	gtccggaaag	ctaaaagtgt	ttcgataatt	713040
gggtgctcag	tacgtaaaagc	ctctaaccac	ctcgacgtg	tagattttgc	cttatctata	713100
gggcgaagac	ctaattcggt	atataaaaata	tctgataaact	gttttggtga	tttttatattg	713160
aatggccttc	cagaaagatc	atagatttcc	tctgtcagta	cggctaattc	tgtttcaaag	713220
agggtctcta	aaatagccaa	ctcctcaaca	tctaaaggca	ctccagctct	ttccatagag	713280
aaaagaacct	tctccaaggg	catttcaata	tcacttaaga	tatgggttgag	attcttacgg	713340
ttgatttctt	ctaaaatagc	gtcttttatt	atgggaagggt	aggcaacaaa	ttcaccacaaa	713400
tattgctcag	gttggtctgg	tagacgacct	ataggcaatc	ctgaatttcc	ccattcctta	713460
gcaaaccggt	gagcagtttc	tgtaaatccg	tgatttacta	aaagagattg	aaaggagatt	713520

tttctctccc	catttgtcaa	gtgctcagct	aaagctaggt	cataagaaat	ttctcgaatt	713580
acaattcctg	catttagaag	agcgtggcaa	tcgcgtttta	gattataacc	atagaaagta	713640
agatcttctc	ttaaaaaaga	atcttttaat	atagggagta	tcttcgtgcc	ttctcttctt	713700
aaggcaataa	aaaatacccc	tgatccctgt	gtcaaagcta	aaccttcaag	cttcaaagag	713760
agaagatggg	ttcctgtata	tgctacagca	aaggcaatgt	cccccccttg	cacaaggttt	713820
aaaatgttgg	tgaggctttc	cgcacctttg	attatctgaa	catcgactgt	cgcagcctct	713880
gtttgcttgg	acggcacaag	agtttttaat	ccttggtgta	tataaaagtg	tatgagtttc	713940
tcttcatcca	caggggtgtg	tggaaaggta	agggactcta	ttggtactgg	gatagggata	714000
ttagaatcca	agagggcaag	ccgtttacta	agcttttaag	tctcctgccg	ttcaactcagc	714060
atagtttgac	ttaatccctt	cacggcgtct	aaatttttcta	aaagtccttc	aacacttcca	714120
aattgtttta	gaagtgtctg	agctttttta	ggcccacaac	ctgggagccc	tggaatgtta	714180
tcagaagagt	ctccaactaa	cgctagataa	tcagggatat	tccctggagg	aatcccataa	714240
cgttctatca	cctcagagat	ccctacaaca	ccttgatctg	cccaaggatt	ccaagctaca	714300
acatgatcgt	ttacaagctg	caacagatct	ttatccgcgg	tgcatagcta	aactttataa	714360
ttctcttctc	tagccttctt	agcaatactt	gcaatcacat	cgtcagcttc	taccgactct	714420
ttttctaagt	aagctaggcc	tattaaagag	cagtactctt	taactagagc	tatttgtgga	714480
gggatgtctt	cgaatttttt	ctgtcgatta	cttttgtaat	cagcataaat	cgcctgacgg	714540
ctttgtttat	tattaggacc	gtcaaagacg	gagatcatgt	attctggaga	gaattctttg	714600
ataagtttat	ttaaagaacg	aataaatcca	aaaactgctt	gtgttgcttg	tccttgatga	714660
tttttcattt	ctggcaaagc	aaagtaggca	cgaagataa	atcctgaggc	atctaataca	714720
aacagtttct	tcattgcata	ttcccttcta	ggctctctta	cagtgcgaag	tagggaggta	714780
tgtatgcagc	gtcatgggat	aaaggcagaa	tatcgtgttt	aatcatgcca	gtaactaatg	714840
gacttgaagc	tgcatgctgaa	gccaccgcgt	tccaccaacc	atcaccacca	gagccaacca	714900
ctctatagtt	atcttcaatc	ttacaaacag	caactatgtc	ttgaaggact	tggtcttttag	714960
ttgcgctcat	aacatcaata	tagccttctt	gtttggcctt	ctctggagaa	aaaatacgtg	715020
ctccgagagt	gtgaactaac	ttctcttttag	taagcagagg	acggttttgt	gtaactatat	715080
caacaaattg	tccgtagaga	aaatcaagag	tcgcttgccg	ttcttctcta	tcatgagaag	715140
tccacgggtg	ataaggattc	attggagcct	tatcttttcc	agctgtcagc	agatcacttt	715200
caactccgta	gcgattttaa	ccttctttta	cattgaagaa	tggtccagaa	cgcactccga	715260
tagaaccgat	aagagaggag	gaggtggcat	aaatttttag	tgcatgagca	gatacataat	715320
agcctcccca	agcacaaga	ccattcacat	aaatataaat	agggaaatccc	ttacgttctt	715380
tccaaaagcg	aagcatagag	ttaaattctat	ctatttcaaa	gacctcgccct	cctgggcaat	715440
ccatatcaat	gacaatacct	ttgacacgat	ctttaagagg	agcttttctca	aatccttcta	715500
aaatattctg	aatcgttttg	gcggtatttt	ttgaagaagc	aattacatct	ttcatttcga	715560
taacagcaat	aatggggggt	gttttcccta	gatcttttac	ttctccttgg	gcgtcaggca	715620
agctaacgaa	ggtagcatcc	ccatttcccta	aagaggaagc	tatgagtgcg	aatataacga	715680
caaaagcaag	aacaactccg	caacacagtc	ctactatcga	taaaaaggct	ttggatacga	715740
agtgccacaa	cgttttcata	acgacctata	aattctagta	aatttcaaaa	tggataaaaat	715800
aagggatgag	cagaaaagct	taaagatgaa	aattataaaa	ttctcatgct	caccgagaat	715860
aacacagagt	ttttctatca	acctacagaa	cagccatttc	ttcttgttct	acagattcct	715920
gggcttcacg	tacgattgaa	gaggaagggt	cttttaggtt	tttcaagggt	gctacagcat	715980
cagcagctct	agagtagtat	tctttaccga	tataggcaac	aaccgcaatc	caaacgacca	716040
taataatgag	aagaactagg	gcgatgacgt	ttaaacttgc	tgcaacagaa	gagaaaataa	716100
caagcagccc	ttggtaaatt	aaagagcctc	cagactttcc	tatccttgaa	acgacaccat	716160
caatcgcggc	tttcccata	tttttatcct	ctggagaaag	tgggataaag	gccatttctt	716220
tggtttgatc	aaagaacgta	aatttcgtcc	ccggggatag	gacattttgc	atccctccag	716280
tccaggcagc	tagagccaga	ggtgtcattc	caagaactcc	cccaaaaata	gagatgtctc	716340
tttttgcagc	aaaaatagtt	ccgaaaaaga	gcagtctcga	aactaacatt	accaatggag	716400
tgactaaagc	accgacagtc	catccccatt	tacggataca	ctgtccggta	aggagtacag	716460
ctgctaatac	agaaacgacg	ccaatgaggg	tagtgattct	actcatatac	ccattgaatt	716520
ctacgtgaga	actgtaaatc	tggctaactt	gatccttcca	aacgacttcg	aatagatgga	716580
tcaccaaatt	ataggatagg	acaataatag	cgagccctaa	taaataacga	gactgaatga	716640
gggtgaagaa	aaggtttcta	gctttggcct	taggtttttt	cttttccctt	agattagcag	716700
tagctgctcc	ctcttctgcc	aagacacgtc	tagatggagg	gatcgaagta	tcaatagtca	716760
aatgatgaat	ccgcctatat	agccagatca	taattaaacc	agaacaagtg	atcagcatgg	716820
tcaagttgag	cattacagag	tgccaggaat	cacatgcaaa	ggagtaggca	acaaatgttt	716880
gtttcccat	ccaataggag	atttctcctg	cgcataattga	ggagagattt	aatcctgtat	716940
tgataagagc	gtaaaaacgg	cccgttccag	taattgtagt	aatctgattg	gctagtcccc	717000
agaacaacat	cgaagaaca	accgaactcc	acagctctga	cattacgtaa	taaatactgt	717060
aactccagta	acggaccatc	acaataaaaac	cacgaagtc	ttgaggaagg	agctcttgta	717120
atttatcagc	gagagagttg	agatgcaggc	tatcccttac	aggataaatg	atcacagcaa	717180
acaggaagaa	aaaaccaagg	aatgcgccca	tgaagcaata	aaaaacggta	tcccaggagat	717240
accgactgcc	taaccacca	tagaccatag	taacaataac	agctcccggg	acaattcccc	717300
aaaccttaag	gaaggggaatc	acttctgccc	cagcatctga	accgacaatg	accagagtat	717360

ctttcatggt	tttcagcagg	cagtagttaa	agccaacgaa	aaacgctagt	agaaatagtg	717420
gaacaaactt	agaaaattct	gatttataaa	taggacaaag	atatgcccgc	agccttgaaa	717480
agggtttcac	ttctgatgac	tgcataaaact	ccttcccaac	tttatggcgt	ataaagactt	717540
atagacattt	agtttacacc	cagaagacat	cgcattgctta	tagctcctat	aatactgggt	717600
acttagcaaa	cggcaaggca	taaattaacg	atcacgataa	aaagagactc	catttttactg	717660
caacgcgccg	taaagttcaa	gcgggttcgtg	gataaaactta	taatccttgc	tcacaatact	717720
ttttctttcc	gggttagcgg	agaaactggt	ttttataatc	cataattctc	tcgaggaaat	717780
atagaaaacc	gagagccacg	aggggggacta	gtccgggtcca	aggaatttca	ccccctgccg	717840
tgacccctag	taaaataata	aattgaacta	ctgtaaaagat	cttgccccaa	aataaagagc	717900
cataatcata	gcctttccaa	ccttttaacta	aagaaaaggta	gaacacaaag	gtnataaggga	717960
ataagtctcg	agcgcaaatg	aaaaagaggt	gtgctattga	taaggatcct	tccatataga	718020
ggaccgtgat	acaaacgaac	acaaagactt	tatctgtaat	agggctctagg	attgaaccga	718080
gacgacttgt	cgcttttatag	cgctcgagcaa	gatagccatc	taagacatcg	cttagcatag	718140
ctccaacaat	agcaagtaag	cggatatgca	atttttcttg	gcagaagtat	agcgctagcc	718200
acaaacgtga	tagagaaaagt	aggttgcaaaa	attgtctcat	aattttgggt	aactagtacg	718260
atccttttag	gaaccttata	attcggcccc	attatagagc	atgctaaatc	tacaaacaag	718320
catagagttc	gctcaaacgg	tttctcatct	tgcaactggt	cggctctaca	ttgacatata	718380
ttaggctttc	tttaaaaaaga	atacgaaaaa	gggtgcgaac	tacaactagc	ttgcgttanc	718440
aaggtagagg	ttattcggaa	agagagggat	tcgaaccctc	ggtacccttt	aggggtacgc	718500
gtccttagca	gggacgtact	ttcgaccact	cagtcactct	tccttattta	ttcatcacag	718560
cctaacaatg	aattttgatc	tcactgttat	tgtaggata	ggttaactat	caaaatgaaa	718620
aatgtcaact	tgtgcaaac	tgacaagaaa	aaaggaaggc	aatctcttaa	aattcacctc	718680
tgaactccct	atagatttgg	aaacttgcaa	taaaagggtc	tgagcagttc	ctcgaaaatc	718740
tctctgagca	actagcactt	gagggatata	tgctagataa	cataacctat	ctagaagtat	718800
cctaaccctc	cacgaattac	gaaagtctgc	ttctaattgga	caaactctact	gggtgacctc	718860
tccctctccc	tcctcattcg	aaagaatcgg	aaatgatagt	tttaggttgc	atgctgacag	718920
gggtacatta	tctaaatctt	gcagccaacc	aactctacga	agaagatttt	tattaccttg	718980
aacataaaat	tatttttctga	gtcctccaag	aatgccttca	agcaagataa	acctatcgat	719040
gttcacttag	ctggagaaag	aactcaaacg	ggcacaacca	gattactgta	attggggggcc	719100
cttcgtatct	aaattacttt	agccgaattt	gcaggtagccg	nagcctatct	tgaagaatac	719160
gtagacatca	tccgatcgaa	gtcgattcta	aggaagatga	tttctacagc	aaaagaaatc	719220
gaaaaaagag	cttttagagca	gccgaaaaat	gttgccgaag	ccttagatga	agctcagaat	719280
tcttttttta	aaatcagcca	atcaacatcg	gttaagtcatg	acactttagt	tgctgacaaa	719340
ttacgcgggt	taacaacaac	tacagataag	ccttaccttg	tacaattaca	agagagacaa	719400
gaattatttt	tacagaatgc	tcaaggagac	aataagtctt	tcttcaactg	cattcccaca	719460
cactttattg	atttagacca	gctgattcac	ggattttctc	cttcaaattt	gatgatctta	719520
gctgcccgcc	ctgccatggg	gaaaacagca	ctcgctttga	atattgcaga	gaatctttgt	719580
tttcaaaaacc	gcctcccat	tggaaatttt	tcttttagaga	tgacagtggg	tcagctgatt	719640
catcgtagat	tttgctctcg	atccgaagtt	gactctaaaa	aaatctctat	agggcgacctt	719700
tccggtagat	actttcaaag	aattgtttcg	gtaatcaatg	acacactttg	acacactttg	719760
ctcattgatg	tacagccagg	gttaaaaagt	tctgatctac	gagctcgggc	tcgtagaatg	719820
aaggaaaagct	atgatattca	atttctcatt	attgattatt	tacaattact	ttccgggtca	719880
gggactttgc	gtgctacaga	aagtcgtcaa	acagaaattt	cagagatttc	ccgaatggtg	719940
aagactcttg	cccgtgagtt	aaacattccg	attctttgtc	tttcacagct	ttctcgaaaa	720000
gttgaggatc	gggcaaatca	tcgtccgatg	atgagtgatc	ttcgggaaag	tggaaagtatt	720060
gagcaagatt	cggatttagt	gatgttctta	cttcgtagag	aatattatga	tcccaatgat	720120
aagcctggca	ctgcagaact	tattatagca	aaaaaccgtc	atggttctat	aggttctgtc	720180
cctctagttt	ttgaaaaaga	actcgcacgt	tttcgcaatt	attcggcttt	tgaatgtatc	720240
agctagttag	ttcgcaatgc	gaatcagagt	caagttagatt	ggacaatccg	atttgtctta	720300
aaaccaaga	atcagtatag	ttgtttgggtc	ggctgaggat	agcaccatat	ttgcaaagaa	720360
atagcgtctg	catcctattg	aaccagagtt	ccgccggaaa	aattcaaact	tcggtttgaa	720420
tatgaagaat	cttcgtcact	tatgacgaag	gggatgtcaa	atcgatacgt	taaccataaa	720480
gatattatgt	catctgttaa	gaagaaacga	agactcaaga	tcgccaagca	caagcgtaaa	720540
aaaagacgtc	gtagagatcg	tcataaaaaac	aagtagtttt	tagtaactta	tgtggactca	720600
cccaattgct	tatgatgtga	ttgtagtggg	agctggacat	gcaggtttgtg	aggcagcata	720660
ttgctctgca	aagatgggtg	tctccgttct	tatgctcacc	tccaatttgg	atactattgc	720720
caagtttagt	tgcaatcctg	ctgctgggtg	tatcgccaaa	gggcacattg	ttcgagagat	720780
cgatgccctt	gggtgtatta	tggcggaagt	gacagatcaa	tctggcatac	aatttcgcat	720840
tctgaaccaa	accaagggac	ctgctgtccg	agcaccacga	gctcaagtag	ataagcaact	720900
ttatcatatt	catatgaaac	gtcttttgga	gaatactccg	ggccttcata	ttatgcaggc	720960
cactgtagag	tctctattag	ataaagaagg	tgtgatttct	ggagtcacta	ctaaagaagg	721020
ctggatgttc	tcaggaaaga	ctgtagttct	ttcttcggga	acttttatgc	gcggcctaact	721080
tcatattggg	gaccgtaatt	tctctggagg	acgttttaggc	gacccttcat	cacaaggttt	721140
atcggaagat	cttaaaaaac	gtggttttcc	tataagcaga	ttgaaaactg	ggacccctcc	721200

cçgtttacta	gcctcttcta	taaatttttc	ctgcatggaa	gagcaacccg	gagatttagg	721260
tggtgggttt	gtacacagaa	cçgagccttt	tcagcctcct	ttaccacaac	tttcttggtt	721320
cattacccac	accatggaaa	aaactaaggc	aatcatttca	gcaaacttac	atcggtcggc	721380
actttatggg	ggctgcattg	aaggggtagg	tcctcgctat	tgctcttcta	tagaagataa	721440
aattgtaaag	ttctcggaca	aagaacgtca	ccacgtcttt	ctagagccag	aagggctgca	721500
tacccaagag	atctatgcta	atgggttata	tacttctatg	ccttttgatg	tacaatacga	721560
tatgatccgt	tctgtactgg	ggttagaaaa	tgcaattatc	actcgaccag	cttatgctat	721620
agaatatgat	tatattcacg	gcaatgtgat	ccaccccaca	ctggagagta	aacttattga	721680
agggtctctc	ttatgtgggc	agattaatgg	caccacaggt	tatgaagaag	cçgcagccca	721740
agggttaatt	gçcggcatta	acgctgtgaa	caagggtttc	aacaggcctc	ctttttattcc	721800
ttcacgccaa	gaatcttaca	tcggcgctcat	gctagacgat	ctcaccacac	agatttttgga	721860
tgaaccttac	cçcatgttta	caggaagagc	agaacaccgg	ctcttattaa	gacaagataa	721920
tgçgtgtgct	cçactatcgc	actatggtta	tgaattaggg	ttactctcag	aggaacgtta	721980
cgaacttgct	aaaaagcaaa	accagctatt	agaagaagaa	aaggttcgcc	tccaaaagac	722040
atthagggcag	tacggccagt	ctgtagtctc	tttagcaaaa	gcactatctc	gtcctgaagt	722100
ttcttatgac	atgcttagag	aagcattccc	aaatgatatc	cgtgatttag	gagcggttct	722160
caatgcctcc	ttagaaatgg	aaatcaaata	ttctggatat	atagatcgcc	agaaaattct	722220
gattcagagt	ttagaaaaag	cçgagagttt	actaattcca	gaagacttag	attataagca	722280
gataacagcc	ttaagcttag	aagctcaaga	gaaattagcg	aaatttacac	ctcgaactct	722340
tggttctgca	tcgagaatat	cçggcatagc	ttctgctgac	attcaagttt	tgatgatagc	722400
tttaaaaaaa	catgcccacc	actaactgta	ttttcctaga	tttacgggga	cactctattc	722460
ttcaccaact	gcaaattgaa	gaggtcttac	taagagtcgc	gaatcaaaa	ttttgcatta	722520
taaattcagg	tgccaaagac	tctatagttt	taggaatttc	tcgaaaacttg	aatcaagacg	722580
ttcatatttc	tagagcacia	gcagaccata	ttcctatcat	acgccgctat	agtggagggg	722640
ggacgggtatt	catagattcc	aataccttga	tggtatcttg	gattatgaac	agttcagaag	722700
cttctgccc	acctcaggaa	ttattagcat	ggacttatgg	catctatagt	ccactacttc	722760
ctaatacctt	ttctattcga	gaaaacgact	atgttcttgg	tcataagaaa	ataggaggta	722820
atgcacaata	tattcaaaga	catcgctggg	tacatcacac	gacatttctg	tgggatatcg	722880
acctagataa	gttgtcctac	tacctgccaa	ttcctcaaca	acaacctacc	taccgtaatc	722940
aacgctctca	cgaagaattt	ttgactacgt	tacgtccttg	gttccctctc	cçcgatgact	723000
tcttggaag	gatcaaggca	tctggtagtt	tgttgtttta	cctgggaaga	atttcttgat	723060
aatgagctag	aagaaattct	tgctcaacct	catcgtaaag	caactacagt	actaaactaa	723120
acgagaggtt	tcgaagcggt	aacaacttct	atcttactga	agaagtaagc	gatttcgaca	723180
gcagcatttt	ctaaagtatc	agatccatga	acagcattca	cçcctataga	ttccccaaac	723240
ttagctcgaa	tggttcctga	agcagcttct	gcaggatttg	tagctcccat	aagttcacga	723300
tttcgggaaa	cçgcatttgc	cccttccaat	actaaaacta	caacagggcc	tgagaccata	723360
aaatcaacaa	gttcttgga	aaaaggacgc	tctctatgca	caaaataaaa	cccttcggct	723420
tcagtttggt	ataggtgcat	cattttcata	gcagctatac	gtaatccaga	ttgttcaaaa	723480
atagataaga	tctctccgat	atgggctttg	ctaacagaat	ctggtttaat	aatggatagc	723540
gtttggtcca	ttgtgtatc	atatctcctt	taaaataaat	cgttttattt	taggaggagt	723600
atagcatgat	cttttaggaa	gtctagtctc	tgttcactcc	tgaaaaattc	tttttcagag	723660
cçataggaag	gatattctgtt	aaagaagatc	cctcagggag	atctttgatt	gcttcggcaa	723720
tcatacgttc	agcagcaatt	tttgaataac	ccaaagctgc	taaagcctga	atgccttctc	723780
ccaagcaaga	agaggtggta	tgtgtttggc	tggtctccac	tctcgagtct	agaggaagta	723840
aatctggtaa	tttttggtta	agctcaacca	tgagtttttc	agcagttttt	ttcccaattc	723900
cçgatacgga	agctaaagca	cgaatatctt	cagatcggac	tacagaacat	agtaccttta	723960
aaggtagcgc	attaagaatc	gcgagggcta	gcttaggtcc	tattccagaa	aaagaaatta	724020
aaatacggaa	acactctcgc	tcttctcgag	aatgaaaccc	atagagcaag	tgttccgttt	724080
cacggaatat	cacatgagtg	aagacgagaa	agtcttgatg	taaagccctg	atgcattcta	724140
ttgcccacag	ttctgtaata	gcaatatggt	agccaatacc	ttggcattct	ataacaattg	724200
caccagtatg	cacataggtc	agtgttccac	gaatatagtc	gtacatctta	tctcactcca	724260
caaagagggc	tacgcgctac	atgagtatga	catatagcaa	gtgcaaaggc	atcagcaata	724320
tcttcattcg	aagggtgcaa	aacttcggga	acatttagaa	tcttgcttac	catcacctgg	724380
acctgtcttt	tacttgcatg	acccttaccg	actactgctt	tcttagcaac	atttggggca	724440
tattcaaaaa	tgaggatatc	acgctgagct	gcagccaata	aaacgattcc	tcgtgcata	724500
gctaatttca	tagtactttg	aggattctta	tttacaattt	gcggtttctag	gaccatagca	724560
ttaggttgçg	tatcatctaa	tactcctgag	agttgctcaa	acaaagtctt	atagcgcata	724620
ggcagtgçga	tgctggaaga	taaacgaatg	gcaccataac	tataaggacg	taattgatag	724680
cçgtgttcca	ctgcaatgat	ggcatatcct	gcgactatcg	ttcctggatc	cacacctata	724740
atcagttctg	acacaatcga	ttcctgaaat	actttgaaat	tattgtcttt	aaaagatgat	724800
cctaacctag	ataatcactt	ctcaagtagt	gaattctcgg	tttctagaaa	aaaatttctc	724860
gctattttaa	acagtcctgt	ttactacgta	ggaatcttaa	ctccctaaag	atthagattc	724920
tgagaatact	acgtctactt	cactctcagg	ttctttgçct	aaaagtcctt	tcaaatgatc	724980
taactttgta	tttgaaggca	tagccatacc	tttctcttta	tgtagatctc	gaagctgaca	725040

atattgatcc	tcaacaatat	cttggagtaa	ggctatggct	ttcttttttt	cagctagatc	725100
ggtttgcacc	tctgttaact	tctcaataga	acaaacctca	gagctagttt	gagctccttc	725160
ttgtcgtgt	aattttttctc	ttaacttagc	aatctctgaa	tgatatgttt	ttatataaat	725220
atctttttct	tggtgcaaat	ctataagact	ttcttccaaa	cggttgatct	ctgcataatgc	725280
ggctgaagat	ttgtcttctt	ctatctctat	agagggggct	ccgtgttgcg	aaacataacg	725340
ctgtagttgt	tcttccagct	gtttaatttt	atgctcatag	cataaacgac	gcccttcaact	725400
aattttctgtt	cgtgttacac	tttgaagcag	ttcttttttt	atctcgtcga	taatatcact	725460
ttgggtgtcga	atttgttgta	atttctcagc	aaggcgattt	tgcaaccagg	tattttcttg	725520
ttgtaacttt	tctaaatctt	gatttttagc	ttcttcacga	cggcgatatt	cttcttccaa	725580
agcagatagc	tggtcccgat	actgtaagt	aatacgttca	tgctcctgat	gacaagagtc	725640
ttgggtttcc	ttctgcaaag	aaaccaactt	tccactcatt	ctgctacaga	ctcctgaaag	725700
aatattgcaa	atctgctgcc	attccataat	atcagcatct	ttccagcgac	aaagcaaatg	725760
aagcatggaa	cgggagcatg	aatgataata	gtgaggggat	aatgaactgg	aagatcgtag	725820
cgagaagaga	tgagcgttaa	gtatagataa	gagccgcaca	gagtacctct	aaaattaacc	725880
taatcattca	tcgtatagca	tacgactgag	ttcttgtcct	aattcgtcat	aagtgacttt	725940
taaaaagaca	ggcaacttat	ttggataact	ctacagatta	aaaaacttag	aaaattgtct	726000
agaacaagac	tcgaacttgc	acgggcctac	gcccaaggga	ttttaagtcc	ctagtgtcta	726060
ccattccacc	atctgagcac	gaaaagacag	tctgttcaga	gaagccttca	attaaaaggc	726120
gtgttcttta	aagatgatct	ttttccataa	ggatagaaaa	ctaaagaaca	tcttatcaca	726180
gttttttttc	tagatcaatg	atttttcaaa	aaagggaaag	gtatgcctta	agttaaagtg	726240
aacttaaacc	atacctttta	aaatagctat	tcttcttctg	tagcagaaga	tgtttcgggg	726300
aagaacattg	cagaagactc	ttcaaaagaa	gctgaggtag	gttctcttct	tgtctcagga	726360
aaatgtatag	catcatctgc	cgatagcaaa	gcattgatga	gatcgtgtgt	ctcacgaacc	726420
aaagcttgta	acgactcgtt	aagatccgca	gaagtaacta	ctggatctac	aacagtttga	726480
gagataaact	cggagatcaa	ctttgctggg	gggtgaagta	aagaaaactt	cttctgttca	726540
acaatctcat	tttcttgaga	ttcttcccaa	agctcttctt	taacagtatc	caagatttct	726600
tgagatgctc	cagttacttc	agcaatctct	ttatgatttc	tacgacggct	gagctttttc	726660
ttttctcttc	acttctcccc	tttaaaggaa	tctttccttg	cctctttctt	ttccttttta	726720
ctaggagatg	taggctcggg	tccttctctt	gggctatcag	ctagaggctt	ctcatcaatc	726780
acaggaagcg	gagtcgattt	ggtcaacttg	attagagctt	ctctaccacc	agcaattttc	726840
actccacgat	ctaaaccgac	agctttcaaa	ttgatttttag	tatcacggac	ttccataacc	726900
tcatatgtct	cggcagggac	taaaaaaggt	ttactatgat	cacagttacg	gaaaaaacaa	726960
atatttccta	aagagatcac	ttctatagct	tcaaccataa	aaggatcttg	tgaaaaatgc	727020
tttgatttcc	ttaccgacaa	cttatacccc	tctcgagagg	taattacagt	ttctatgacg	727080
gggtctcttg	taaaatacac	gtaattataa	ccttttctatt	tagagttttt	ttctacatac	727140
tctaataagt	ctactatacg	cgtggcatat	cctgtttcgt	tatcatacca	cgcaactaac	727200
ttgaagaacc	gatcattcaa	agcgatacca	gctagagcat	cgaatatcga	ggagtactca	727260
gatcctataa	aatctgaaga	aactacctgc	tcactctgat	aatctaaaat	gccttttaaa	727320
tcagtttctg	aagcctgttt	catagctttg	caaattgtcat	cgtatgtcgt	agacttatct	727380
aacctgacgg	tcaagtcaac	tacagacacg	ttctcgatag	gaacccgaaa	agccattcct	727440
gttaattttc	cctttaactc	gggaagacat	agagtttacag	cttttgcagc	tcgggttgag	727500
gcggggaataa	tattttgtaa	acatccacga	cctcctctcc	aatctttctt	agaagggtccg	727560
tcaacaacta	gttgagtagc	agtagcagca	tgaactgttg	tcatcaaacc	ttctgttaatt	727620
ccgaaattat	ctagtaaaac	tttagcaata	ggagctaaac	aattcgtagt	gcaagaagca	727680
ttcgatataa	caaagtcttt	ttctggattg	aaagtcttat	ggttccactcc	cataacgaaa	727740
gtaggaatat	caccttttcc	aggagcagag	attaagactc	gtttcgtctcc	agcttgaata	727800
tgcttctcag	catcttcttt	ttttgtgaac	aatcctgtac	attcaataac	gagatcaacc	727860
cctaaatctt	tccaaggaag	attttgaaca	ttgcgttcag	ataaaaattg	aatttttctc	727920
ttcccaacga	tgaggtgggc	cgcttcacaa	cgtacatcct	caggaaaaacg	tccatgtgta	727980
gagtcgaatt	taaatagata	ggtaagcgca	tccccaggaa	caagatcatt	aatggcgagg	728040
acttctactg	aagagtttct	ctttaagatt	tgtctaaaaa	ctaaacgacc	aattcgcccc	728100
aaaccattaa	ttacaacttt	catcgcttac	cctcagagtt	caataaattg	gaaattgatt	728160
agcttttagct	agctaaaaac	tctataatac	acttttgagc	attatcacca	agttctatct	728220
tgagttttta	gaatacgtgt	gtaaccacct	tttcttttcta	caaaacgatt	ccccaaactca	728280
tcgaataact	tattcacaac	caaacgatcg	acattatata	cagaggtgtc	tccaccttta	728340
gcttgctcag	cttctttgtc	tgtttaattta	ttgtatctga	ccataagccg	tccaatagct	728400
atagctcgtg	ctgctaagga	gttttttttta	gctaagggtaa	tcattttatc	agcatgtcgg	728460
cgtagttctt	tagcttttagg	caaagtagtc	tcaattcttt	cataatgaat	tagagacttt	728520
aacatggttag	ctaacataca	gcgatttatgc	gaggaagtac	gaccaactct	aaattttttt	728580
ctagcgtgtt	gcattactta	ctatcccttt	atatttttag	cccgaatctt	ttcgggcatac	728640
cacttcattt	tttctttttac	gttatctaaa	cctacgccaa	attgcgttag	gtccattcct	728700
aattcaagct	tcattttcttt	caattttattc	ttgatctcac	acagtgattt	ctttccaaaa	728760
tttctgaatt	gtagcaatcg	aggttcaggc	ataataacaa	gttcgccaat	agtcctcaata	728820
tttgcattag	acaaacaatt	tgttgatctg	actgagagtt	ctatttcatt	aattcctaaa	728880

attaacttat	gaagaatata	atctttgttt	tctttctcaa	tagaaatagc	ttcttcaaat	728940
acgattttct	tctcatccat	attttcaaaa	atggaaaaat	gtttagtcaa	aatttgagtt	729000
gaaaaagcca	gagcttcttt	cggagtcact	cttccatctg	tttcaactat	taaaactaaa	729060
cggtcaaaat	ctgtatcctg	accaccccg	gtatcttcta	caaagtagtt	gactaaagtg	729120
actggagaaa	aggctgcac	caaaacgatt	tcataaacac	ccttatcttc	caaaacaatc	729180
ctttcagaag	gtgtatatcc	cctacaaaa	gcaattcgta	gatcgacttc	caactgtatg	729240
ggttgagtaa	cagtaaaaa	gacttgatct	gggttaacgg	cttcaaagtc	cccttcttgc	729300
aatagatctt	gtagagtcac	ttctttttgt	ccattagctg	cggctaaatc	ggaagcatct	729360
atagaaattg	aagcttttaa	gacctgagtg	gttcttctta	aagaactatc	ctgcatgggg	729420
tactttttta	atagggcacc	ttttaaattc	agaatgatgt	tagttacatc	ctcaataacc	729480
ccttcgattg	ccatatattc	atgaagtag	cctgtcatag	caaacgagat	taaatacctg	729540
gagcttctaa	accaataagc	aaagcacgtc	ttagagcatt	tcctaaagtg	tggcccattc	729600
ctctttctag	aggctcagca	atgaagcgag	catgtttgtc	tattggaagc	ccttcaacag	729660
gcaacatttt	aactgcttca	ggcagttcaa	acttatcata	aagtaaattg	tgtgcgttat	729720
ctgacatccc	tttctccttc	cctaaaaacta	cactctgcgc	ctttttcttg	gccggcaacc	729780
attatgagga	acaggagttt	catcacggat	tacagaaact	accaaaccag	cagatatcaa	729840
agcacgaaca	gcagactctc	tcccagctcc	agtacccttc	aaacaaacct	ntanttcctt	729900
taaaccagag	ttcatggcag	ttttagcagc	gtcttgagct	gctacagtgg	cagcaaaggc	729960
tgaagatttt	nttgaaccag	aatatcctac	tttacctgct	gatgcccaag	aatcacatt	730020
accagcagga	tctgttatag	atactattgt	attgtttaaag	gttgctttta	catgcacaac	730080
acctgaagga	atatttttta	gttggtttct	ttttacgctc	ttttttgcct	gcgcttgatt	730140
tttaaccaaa	acacgactcc	taattaaaaa	ttatttcttc	ttacctgcga	ctgttttctt	730200
ttttaccttt	cgagtacgag	aattagtttt	tgtactgtgt	cctcttactg	gtaaagaaag	730260
tctatgtctc	tgacctcgat	aagaatggat	ggcgatcaat	cttttgatat	ccgattgaac	730320
acgacgtcgc	aaatccccct	ctacgggtata	ttctgattgt	agcagagagt	tcagtcgtcc	730380
tactttctct	tcagtttaatt	cagaggctct	tgcttcagga	tctaacttca	actttttaat	730440
gatttcatca	gaacgagctg	atcctattcc	ataaatatat	gtcagactta	tttttaactt	730500
tttctttgca	ggaatatcaa	ttccaatgat	gcgtggcata	cgttgggcct	cccttaaaat	730560
agtataagca	tcttaggtca	aaaattgtta	tttttcaatg	tcttcttttc	gtccgatctg	730620
ttttcagcac	gctatcgtag	cgacgcatta	acaaaaaggc	ttcattgtat	ttcattgtat	730680
ctaaaacgac	ccctacgacg	ataagcattg	cagtaccgcc	taagaaatag	cttacattag	730740
aatccacacg	aagcagacaa	cctaaaagtg	aaggtaatat	cgcgatcgcc	gctaagaaca	730800
acgctcctaa	aagggtcaca	cgattcattg	tatactctaa	gtaatgttgc	gtaggcttgc	730860
cctgacgtat	gccaggaata	aaggcattat	tttttttcat	ttcagaagca	atttgttctg	730920
gatgaaattg	tgtggctgtc	caaaagtatg	taaaaaatat	aatgagcaac	acataacata	730980
tagaataaac	taaactgcct	ggagcaagta	aagctgctat	acgcttcac	caagaagact	731040
ctgacgcaat	aaactgtcct	atagttgctg	ggaacatcag	tagcgaggaa	gcaaaaaatca	731100
caggaatgac	gccagcatag	ttaactttta	aaggaagata	ggaccctcca	ccggggactt	731160
ctcttcttcc	aattaccctt	cgagcatatt	gcacagggat	ttttctcact	ccctcgataa	731220
tcaaaatcgt	agtaatcaga	acaaaaacaa	aaacaagagc	aaggattaaa	attgaaatta	731280
gacccaaatc	agaggagtct	tgagatccta	aattttaactt	attaacaata	gatcccaata	731340
cagaaggaaa	tgaggataga	attccaaggg	cgataattaa	acttatcccg	ttcccaatcc	731400
ccttatcgga	gatctgttca	ccgatccaca	tcaataagag	agttcctgta	gtcatgacta	731460
caactgtagt	gatataaaaa	atccagggga	ctccaaatag	ttttgaagat	aataaagtgg	731520
gcagaacaat	ccccggaata	gttagattca	ttctaagagc	aaacttagca	aataagagag	731580
actgtattac	agctaaagca	acggtaaaaca	aacgtgtgag	tctaccaatc	ctacgtttcc	731640
cttgatcaga	agactccctc	atcttctttt	gcagcgcagg	cataaagact	aggaacagct	731700
gaacgataat	tgaggctgaa	atgtaaggaa	ccacaccag	cgcaattacg	gtcatttggg	731760
caaaagcgcc	tccagaaaaa	atatcagcta	gttgaaataa	attctgacct	gatcccaata	731820
actgcttgaa	gtaagctaca	gctaattcac	cattaattcc	tggaaacagga	ataaatacac	731880
ccactctaca	ggccgtaagc	aaagcaaaaag	tatagaataa	cttttgtcgt	aattcggtta	731940
tcagaaaaaa	ttgtctcaat	gtggctcatat	acggcctaaa	caatcttatt	ttttaagtaa	732000
tgcttagcaa	attttgtact	ccttgcgata	ggactacagc	agtatcttgc	catacaaaag	732060
tcttttccaa	atctcctttg	agaatgactt	tgactcgtag	agcttgtctc	gcaatggcct	732120
tctttgtctt	taatgcattt	aaagtaattg	cttctccttc	ttggaaaaagc	tcggctaaac	732180
gtcctgtagt	aatttcttca	acgcatttat	caaaacgttt	atgagaaaac	cctcttgtag	732240
gaactcttct	atataaagga	actcctcccc	cttcatagcc	aaaacgacgt	ttgtatcccc	732300
aacggctacc	gtctccttta	tgaccacgac	cactgggttt	cccatgaccg	gaagaaggac	732360
cacgacctaa	taattttttt	cttcggtttac	gttcagaaat	atcaaataat	gattctaact	732420
taatcattta	tagccgctcc	tcttcttaac	aaatccttac	gtgggctgag	tcctgtaaga	732480
gctttaaacg	ccgctttcac	ttgggtcata	gggttattag	atccgaaact	tttagtaca	732540
atatctttta	taccagccat	ttctaggatc	aaacgaatac	gagaaccggc	aacaattcca	732600
gttccagggt	tgtcgggttt	taacagcaac	tgtgctccat	cgtgatggac	aagaacttca	732660
tgaggaatag	aaccatcttc	taaagcttct	atcttcatta	aattcttttt	tcgagcttca	732720



ccacctttac	gaatggcatc	tgtgagttca	ttggcttttag	caaaaccata	gccccaaacga	732780
cccttgccat	ctcctactaa	aattaaagca	gaaaaactga	actttcgtcc	tcccttaaca	732840
actttggagc	aacggttaac	aacaagaact	ttctcttcta	attgatcttc	tttatgagaa	732900
ttctttgata	gcgacatctc	ttcctaaacc	ttcattaaaa	ctgtaaacca	ccctctctag	732960
ccccatcagc	taccatagaa	acaattccgt	gatatttgaa	aggaccgcga	tcgaaaacaa	733020
ctcgatcaag	ttgaaggttt	tttcccaatt	cagcaatttg	agttcctaata	actttagcaa	733080
cttcttggtt	tttttttagtc	agaccttgac	tcttatttaa	ttttgataga	gtggaaacgg	733140
gaagccaacg	tcttgccgat	agaatcgctc	atcaactgta	cataaatatg	tttatttggt	733200
ttcactacgg	acaaacgagg	ctttgtaggg	gaacctttaa	tactttacgc	actcgcaaac	733260
ctcttcgtct	tttcattaat	gactttttac	ataacgaact	ttccataacc	ctcgacctat	733320
tttttgccctg	ttttcgcagc	tttaccagct	ttacgacgga	catattcatt	ttcataacga	733380
attcccttac	ctttataagg	ttcaggagga	cgtttgccgc	gaataacttg	agcaaattca	733440
ccaaccaact	gcttatcaag	ccctttcact	gaaatcagag	tatttttttc	aactgatacc	733500
tgaagagtag	atgggatagg	aaatttttgt	agggtgagaa	accccaatgg	agagatccaa	733560
aatgacacct	tgaacagagg	ctctgaaacc	cactccaact	attttctaaac	gtttttctaaa	733620
tcctaaatgg	acacattgaa	ccatatttga	aatgagcgcc	caatataacc	cctgcataca	733680
gctaggtcta	tcgacaacat	ggggagctgc	gtgtacaaat	atactgttat	cttttaagggt	733740
gattttctact	tctttgaccg	atttctgtgt	taaggaccct	ttaggacctt	ttacaataat	733800
tttatcatct	tgaatcgaaa	cttctactcc	ttgaggaagt	agaatagggt	ctcgagcctt	733860
acgagacatg	ctttaccggt	cctatactta	atcctgttac	cacaccaaac	agagcaattc	733920
gcccccaata	ttcttagatc	tggctagaga	accttccata	actccctgag	aagtggagag	733980
gactgaaatt	cccatatttc	caaagacgta	agggattttc	gcagccgata	catagactct	734040
tcgagagggt	tttgataccc	gtttcagttg	gtgtattact	ggtttacgat	catcggaata	734100
ttgtaaaaac	acacgcatag	cgcgtttgcn	gttttcttcc	tnactaaat	aatgagccac	734160
aaaaccttta	tgtttgagga	tttttacaat	agcctctcgc	attttactgt	gctctacgtc	734220
tacatacaga	tgtttcgcca	tcaaagcggt	acgaattcgc	gttaacaaat	ctgctataga	734280
atcacttgct	atgcccataat	agatcctttt	cctctttatt	gagctttctt	aaatcgtaag	734340
cccatacaact	ctaataagagt	ggtgcactca	tcactctgtt	gcgcggtagt	tacccatgtg	734400
atattcaatc	cctgggtgcg	cttcacacga	tctaaattaa	tttctgggaa	aatttggtga	734460
tcgtctaate	ctacagaata	gcaacccctt	ccgtctcctt	tattagaaaa	tccgcggaag	734520
tcgcgaatcc	gtggagaaac	aatattacag	aaacgatcca	taaaatcgta	catacgaatt	734580
ccacgaaggg	taacttttgc	accgattcct	tgaccttctc	gtaattttaa	accggcaata	734640
gaatttcgag	ctttttgttac	taacgggtttt	tgcccagaga	tcattggtcaa	ttctttctaag	734700
tgggcttgga	ataaaattttt	atcttttagcg	gcttcagcaa	gtcccatact	taagacaatt	734760
tttttaagaa	cagggatctg	catttttattt	gcatagccaa	actttttcaa	caaagatttg	734820
cgaattttctt	cagtatagaa	ttttttttaat	ctactcatat	tagcctttct	ttccccctcac	734880
tagacgatac	agctgggatg	ttccgtcagg	gcgtctttgc	cacaactccc	gccccctgttc	734940
agtcactttg	acagagagtt	tggcaggttc	accagctatg	gttaaacgta	cattagaaat	735000
atggatagga	gcctctatac	taatccggtt	accttttagga	ttttgttgac	tacgttttat	735060
atttttttatg	cgaacgttta	caccttcgac	actactttta	tcttcagtaa	gagaaaggac	735120
ttttccttct	tttccctttat	cattaccagc	taatataaat	accttatcac	caacacgaat	735180
gtttttgcttt	ttcataactt	ccttctcctt	aaattacctc	aggagctaaa	gaactaattt	735240
ttataaaaacc	tctatctcga	atttctcgag	ctacggggcc	aaaaatcctt	gttcccttag	735300
gatttccctt	atcatcgata	attacacagc	tatttgatc	aaatttttaa	gtagacccat	735360
cttttcttgt	aatatgccga	cgtgtgcgca	cgatcacagc	tttgataacg	tctccctttt	735420
tttatagaac	tattaggttc	gacatctcta	actgagcata	caatgacatc	tccgacagta	735480
gcataacgct	tacgagaacc	tccaagaacc	ttgaagcatt	ttactttttt	agctccagta	735540
ttatcggcaa	cttttaactg	actttcttgc	tgaatcataa	tctctatcta	cctaattgtt	735600
ctaactttacc	acgccaacat	gttctataac	gcgccatctt	ttaagcttag	acaaagggtcg	735660
tgtttcttga	atttttaactt	tatccccctt	agaaactttt	agttcagtg	gagcgtaata	735720
tttctttgaa	cttctcacta	ctttaagata	ctgaggatga	gaaaatatcc	tttctactcg	735780
aacaacgaca	gtttttttcca	tttttgccga	gacaacaaca	ccaatcttaa	cttttctaga	735840
gcctcttggt	tcactagcca	tggactttac	cttttctttc	ttgttttact	gttagagctc	735900
gagcaatatt	tttcttatgc	gtagaaaaca	tatgaacttt	cacaactttg	ttttgcagta	735960
aattttctgc	tcttaaagca	aacaaagcct	ttttgttttc	atgaacatac	gcattctaaat	736020
cgctgctgct	tttccccctt	aactgggtca	ataaatcctt	tttttagcagc	catgtttata	736080
ccctttccac	tcgcttaaca	aaacgtgttt	ttattcctag	tttggcagca	gctcttcgga	736140
gggcatcttg	agcatcttct	ttagagacat	tcgctacttc	aaacaatata	cgctcctggac	736200
gaactactgc	tacccaatga	tctggggccc	ctttaccttt	acccatacga	gtttctgcag	736260
gcttttttgt	tacacttttg	tctggaaaaa	tacgaatcca	tacttttctt	cgacgtttta	736320
aatatctatt	aatcgcaacc	ctgcaggctt	caatttttacg	actggtgacc	aagccacgct	736380
caagagtttg	cattgcatat	tctccgaagt	ctacaaatgt	agctccctta	cttaactctg	736440
caaactgtcc	tnnttggtgc	ttacgaaagt	ttgttcgttt	aggcattaac	ataataattc	736500
actcatcctt	atttacaact	ttaagcagct	gcagagggtg	ctgccggatt	gttaggagtt	736560



gtagaagagg	agttctctcc	aagattaatc	caaactttta	taccgataat	tccgtaggta	736620
gtttccgcac	aagctgtagc	ataatcaatg	tcagctctta	gcgtatgaag	cggcacacgg	736680
ccatttttat	accattcaga	acgagcaatc	tcggctcctg	ctaacctgcc	tgaaacttga	736740
atttttacac	caacagctcc	agcatccatt	actgattgca	ttgccttttt	catagcccg	736800
ctaaaagaga	ctcgacgttc	aattttgtct	gcaatgttat	cagctactaa	ttttgcat	736860
agttcgggac	gtttaatttc	cgcgatttct	aaccagactt	cttttccggt	aagagctctg	736920
agctcttctt	taagcagatc	aacttcagcg	ccttttttcc	caattaccaa	cccaggacga	736980
gcggtttgga	tggtcacttc	aattttacca	ctcatcacgac	ggacaacaaa	tccagcggca	737040
ccttgacatg	aagggttttt	tcttaaaaaa	tgtegaattc	ttacatcttc	tatgagaaat	737100
ttaccaaat	cttggtttatt	tccgtaccaa	agagaacgcc	atttttttgt	aacctctgt	737160
cgaaatccga	ttggacaacc	ttcttgaccc	atgatccttc	ttccctttta	ccgttctctc	737220
tcaccaacaa	taacagtcaa	gtgactggta	cgtttttaaaa	tgggagagcg	tcctcctcta	737280
ctttttgatt	tagatcgctt	gtagacaggc	ccggcatcta	ctcgaacttc	ggtaacgctt	737340
aaattttcac	gctttatatt	ttcatgcaat	tcagcattag	ctacagcgct	atttaaaacc	737400
tttttttaaac	atcttccagc	tttcaactga	gaaaatccca	gctgttctct	agcctcttgc	737460
acacttagat	ttctcataag	cccagcagct	aatctagctt	tacgaggttg	tacccgaata	737520
tatcgggagg	tcgctttaaa	catgctatgt	ctcctttaga	cttacccttt	cttcacagga	737580
tggtttttta	atctccttgt	gggagaaaat	tctcctaatt	tatgaccac	catagtttct	737640
gaaacaaata	cggttaaaaa	tttcttcccg	ttgtgaactt	caaacgtatg	gccgatcatc	737700
tcaggagtaa	tcattgaacg	acgagaccat	gttttgatag	gagttttttt	ctcctctatg	737760
ttcattgcac	gcactttttt	taggaggttg	tgatcaacaa	acggaccttt	cttaacgat	737820
ctactcataa	tccttatctc	ctacgatctt	taacaattcca	tttattactt	ttgttcttgt	737880
cacgtgtttt	taattccctc	gtaacccttc	cccaagggtg	acgtggaata	taaccattat	737940
ggcgaccctc	tcaccaccgg	tggggatgat	ctacaggggt	cattgcagta	ccacggactg	738000
taggacgaac	tcocatccaa	cgtcttcttc	cagctttgcc	atctacacgt	aggttgatgat	738060
cggcattgga	aacttcacca	atggttagctc	tgcatccctc	atttaacata	cggaaactctc	738120
cagaaggcat	ctttaagta	acgtatcctg	gagacttagc	tataacttga	gcagctaate	738180
cagcagatct	tacaagcttt	ccacctgaag	aaggacgcat	ttcaatatta	tgaactgaca	738240
atcctaaagg	tatgcttttt	aaagtcatac	aacatccagg	cttaaatgga	cttccctcac	738300
ctgaaacaac	aacgtctccc	ctttggatgc	ctttaggggc	gagaatgtaa	cgtttttctc	738360
cgtctctgta	gcttaagaga	gcaatgtatg	cagaacgatt	aggatcgat	tctacagtaa	738420
ctactttcgc	agtaaatcca	tctttattac	gtttgaagtc	aacgacccta	tacaattggt	738480
ttgctcctcc	gccacgatga	cggcaggata	tatggcctaa	attatctctt	ccaccagaac	738540
tcttcttaaa	gaaagagagc	tttttatttg	gtcgaagact	tctttttgac	ttcgtaccgc	738600
gcaactcacc	acgcgttggt	aactcatcaa	aagcgggaag	gaccagctgt	ctagttcctg	738660
gagttactgg	tttaaatttt	ttaaacatgc	tgtttatctc	tctaataaat	tatccgacag	738720
agtgcccttg	atagaaagtt	acaattgctt	tcttaaatcc	tgagggtttt	cctttacggc	738780
gccctcgaaa	catgcggggc	ggttgagggt	ttacatttat	ggtgttcaca	ctctttactt	738840
ttacattttt	atcaacgtaa	attgcctcta	aagcttgggc	gattaatggc	tttggtgcat	738900
catgagagac	tataaaaaa	aatttagggt	ctttacaaaa	gcttcccttt	ttctttccct	738960
ctccagttcc	agcgcttaaa	tgctctaaca	ttttagcttt	ctctgttacg	tagtgacgct	739020
taattacatc	ataaggatct	ttcatatcct	aaaattcctt	cttaatcttt	cgtttcagaa	739080
acaagacgct	caacaagttc	ctgcaaagct	tttttagaaa	taacaatatt	atgagcagaa	739140
gctaagtcac	acccattgat	attgattcca	tagacaaaaa	ccttaactgc	agttaggtta	739200
cgcaaactta	atcttaaat	ttcattcttc	tctacatgat	ctaagtgatc	aataaagaga	739260
atgctacgac	actcaacatt	gcaatctttt	aaaaacctta	acgctgactg	agtttttagga	739320
gctgttaaa	catctacaaa	gaccgtatcg	tcaactacag	tcaatttggt	tgtttgaatt	739380
ttttgcgcca	acaaaagcct	gattgcgggt	tttctttctt	tacggtttat	acgtacgtgt	739440
tgattaaatt	taggcttagg	cccaaaaaca	atcccccccc	cacgaaactg	aggagaagct	739500
aaacatccct	gacgggaatt	acccgtacct	ttttgtttga	aagggtttttt	tgtagaatga	739560
ctcacttcag	aacgatttct	agtgcacgca	gaccactgtc	ttttattcgc	gcgaatagca	739620
acaatataat	ccttgatcaa	ttgaaggcca	tcgccctcat	ctgcaacaa	agagctgtgt	739680
acttcaactt	cgcctatttt	atttcctgaa	aaatcaagat	tttgataata	aaaccattag	739740
gtcctctctg	tctaccctt	gtccgtatcc	taagttctag	aagaatgttt	cactataaca	739800
atagagcctc	gcgtccagg	aatggcacct	ttactaaca	gtactttttt	ttctaaatct	739860
acttttatta	ctttctaaat	ttttacagta	acgttctctg	cgcccatatg	actaggacgc	739920
ttacttccag	ggaaacaacg	accaggagtc	gatcgcatc	ctatagaacc	tgcatgacga	739980
tgaaaccctg	aacctatggc	tcttgaccg	ccacgaaaac	caaatttctt	catgacacct	740040
tgaaaacctt	ttctttttga	aattccacga	acatcaactg	aggaaacatc	ttcaaaaact	740100
tccaatccaa	aagcatctcc	caaagacacc	ccattaagag	cctcttcaga	acctcggact	740160
tctttaagaa	aacgaaaaac	tcgaccacca	gctttacgca	aatgtccgag	tttaggctta	740220
ctaacacggt	ttgtaattgt	atgagcgggg	gcattcattt	cttccgctcc	tatttgcaag	740280
gagaaatata	cgctcgcttc	cttagttttg	atctgggtta	caacggttag	ctcaacgcga	740340
attactgagc	aagcaaccaa	ggatccatct	ttatcaaaga	tgtgaatcat	cccttctttt	740400

t'tccccatca	cactaatatg	agaccgcata	aacttatcca	ttacaataa	tgatttgctt	740460
tcctcttgga	ggaacaaaga	aacaaatctg	cttagtattt	tacttatcga	attctctaaa	740520
aagaaaagga	aattttccct	taagaaaata	aaggacagg	ttatcagagg	gggaagattt	740580
ttacaatagg	aaaagtactc	taggtactaa	gaactcaaag	ataaaagatt	cttggaanaat	740640
tcctatttat	agaaatagaa	agtcgcttcc	aaaaaatttt	ttagaagcga	cttcttttaa	740700
ataaagataa	aactagctta	tttgccagac	tttgttttct	gccatatgct	atataagcca	740760
attcctgagg	atgctgccgt	caaggctcca	gaaattgcag	cggagcaagc	cactgtaatc	740820
ggtaaaggaa	tgagtttgac	tccatccact	accaactcta	aagctttttc	aagaagagtt	740880
aaaacatttc	tttttagagt	agcaacgtgt	tctttacgta	atgccctttc	cgcgcttaga	740940
atcacgtccc	cactcaactg	agattgttgg	ttttctaagg	cacatctctc	attgtatagg	741000
gattccttcg	cacgtttgaa	cagcttttgt	tctaattgca	ttccgccaac	agcaccagca	741060
actcctgcca	tatgattaat	ggtcataatt	ccagcaacag	ccgtgccaaa	attgcctaca	741120
gtcgtcttgt	ctaagaatgg	ttttgctgtg	agtttattga	ttaacattaa	cggacgtaaa	741180
acaccgaatg	tcgctgagta	agtcgttgca	ccgactgccg	tacaagcttc	cctggaagct	741240
gccaataggt	aatcacctcg	agtttaattg	attttactat	actccccagg	cgtttttctt	741300
tcttttgtct	tgcttcctaa	ctcgaaggct	tgacgtgtgt	attggtaaca	cctctgagtc	741360
gagtttaacga	tagatggaac	agctccattg	agcacattag	ctaaggcaac	aacttctcga	741420
gttggttttta	acataccctg	ggcgttttct	gaggaggtca	atgcgtcccc	tgtgcatccc	741480
gcctcttcca	gcgacccctac	gacacagtca	gaaaccgcct	tacttagctt	aaagcattta	741540
tctaaacttt	ttgttgcccc	tacaaacttt	gctaacttat	ttccagggtt	tgtaaaaaaa	741600
ttgttggaata	caataaatcc	ctttctgagc	aaaggagctg	acagccgctg	gttctttggc	741660
aactggcagc	agcatcttac	ttgctgcact	tcctgcccag	ctaattgctg	tagtcgccat	741720
ttttacctcc	ttacaaggct	ttttaaaaaa	aaattagagc	ctataataac	ataaaacgac	741780
ttaatattagt	ttaaattgcc	tataataaaaa	acacgttgta	aagttaatta	tttaaagtaa	741840
aaactatttt	taatttcttt	gctggatagc	cgtttaaaaa	ggattttgag	ttcgtagaac	741900
ccttgccctc	tacctgcact	tcgtgcaagc	aatggctcc	ctcagaacag	gcaatagcaa	741960
gctcttgcc	atctgttaca	acaacagtc	cgggggctcc	atatcttccc	gcctctgcta	742020
aaagagaggc	cttacggatc	atcaagcggt	ttggcgcttt	ttcagaaaaa	gagaataggg	742080
tccacgctcc	tggagctggc	gtgactcctc	gtatatgagc	ataagcctct	ttagcaggtt	742140
tatcccaagg	aacctgtcct	tcttcccttag	acaatttttg	cgctattgtc	gccaaagcag	742200
cgtcttgact	gacgagttgc	agttgacctg	actcaatttg	ttgtaaaagt	tttttagaga	742260
cttctgcgcc	ctgcgatgca	agagcatccg	ccaattctcc	tgaagtcata	tcaggaccta	742320
tggggacacg	cgtaaatatt	gccatgtcgc	ctgtatccat	acctgcatcc	atacggatga	742380
cagtattttc	agattctgta	gtccttccca	taatacagcg	ttgtatggga	gctgcgcctc	742440
ggtaggctgg	caagagccct	gcatgcagat	tgtaacaacc	ataacgagga	atatcgagga	742500
ctatctgacg	aagaatcgct	ccataggcaa	ccacaataaa	aacatcagca	ttaaaagccc	742560
gaagttcttc	aataaattgg	gggtctgacg	ctttactagg	ttggagtaaa	ggtagaccgt	742620
gagttagagc	tatagttttt	actggagaag	gaatgagttg	tgccgatctt	ttttggggt	742680
tatcaactcg	ggtaacaaca	gctgtaattt	ggattttgtg	atgcaacaaa	tcttgcaaaa	742740
cggtggctgc	aaatgtgggt	gtgccgaaat	agacaacctt	aagattcaat	caaaactcct	742800
tctttgtctg	cgctttcttc	ttcaagggtc	tgcttatcta	tgcttcgttc	gatgccgcgc	742860
ttacttgggc	tttgacaaaa	ctcaatgaag	ttttttactt	ctggaatgtc	tccatattct	742920
tctagagttt	cttctagaga	ttcaaaaaaa	catccgtcag	cacgataaat	cttttttaaa	742980
gccttaatga	gggctaattc	cgtagcaaaa	ggaacctgcc	tacgtttag	tcctacttta	743040
ttaataccag	cgagttggta	agggtttcca	cttccaatgg	tatagggagg	aacatcacga	743100
cgaatccccc	tgagggtccc	taccatagca	tgcgctccga	tgcaacaaaa	ctggtgcact	743160
ccaaccatcc	ccaagaat	agcgtaatca	ccgacttgaa	catgtcctgc	aagttgtgca	743220
tggttactta	gaacgcacatt	atttccaata	gtacagttat	gggcaacatg	agcccagggc	743280
ataatcaaac	aattattccc	gatagagact	gttgtaacct	cgaatgttga	agacgtgatg	743340
atagcgaact	ctcgaatttc	gcaattttca	ccaatagtca	cataggtttt	ttccccttga	743400
tactttaaat	cttgggggtt	attaccgatc	attgcagagg	gccatattgt	tgcccccttg	743460
cctatgggtg	tattgccatc	gatatatgcg	taggacttaa	caacaacgtt	gtcacaaaagg	743520
gttaccgtag	cttttataac	aacgtacgg	tcaataacaa	catcctttcc	aatttttagct	743580
cctggctcga	taattgcagt	tgggtgaatg	ctcgccatgt	ttctccgtga	ttatatggat	743640
tccctatcta	ccagagcaaa	gctcagctct	gcttcagtga	ctagctgtga	atctacacgc	743700
gcctgtgccc	aagctttacc	tcctttcgat	gatattaaag	aaaaatctgc	ttgcagggtg	743760
agtacatctc	cagggcgaac	agcttgacga	aacttagctt	tctgtatccc	taaaaataat	743820
gcgatacgct	tattcctatc	attttctaga	actaagccta	tcaatacacc	agcagcttgg	743880
gccaaagctt	ctaatatcaa	gactccaggc	ataataggcg	cgttaggaaa	atgccccata	743940
aaaaaaggct	catttattgt	gacatttttt	tgtgcccgtg	tactgagagc	ctcgatgtca	744000
taagataaaa	ctttatccac	taataaaaaa	ggatatctgt	gggggagtaa	atctaataat	744060
tcgcgtaatt	tgatgacaga	gggttgatc	atttattctt	tctttatagt	tctaattgctt	744120
ccaaaatttt	tttaccaaaa	gcaatattgg	aggagtggcc	ggagccgaca	gctaatacat	744180
gcgcaacaaa	aggcctgcc	actaaggaaa	gatctccaat	cagatccagt	attttatgtc	744240

gtactgggttc	atcgggcaaat	cttaattgtc	ctctactaat	aataccatcg	tccttaaaaa	744300
ctacagcatt	atccaaacat	ccccctccaa	ttagccctt	ttccattaag	aaacatagct	744360
cattgtatag	agcaaatgtt	ctacaaggag	caatttcctg	gcgaaaagac	tcttcattaa	744420
tcaccaaaga	tttgtattga	gtccctattg	ttgaactttg	aggataatgc	aacgtatagg	744480
aaatcttcag	ctcatcagag	ggaaaagctg	ctaaaaaaat	gtcctgatgt	tgataatata	744540
caggacgtgt	tagtctcgca	atggaaaccn	atatcttctt	gttcacaaat	acctgcttga	744600
tcgattaact	caacaaagac	atcttgagctt	ccatccccta	tggggatttc	ctctccacta	744660
cattggataa	ttagattatc	tatatgttta	gatcgcaatg	ctgccataag	atgttcgaca	744720
gtggcgatta	cagcactacc	cctagataat	gttgacttct	ttcctgtagt	gtagacatga	744780
tctagtaaag	cagggacatt	ttcgtagtta	cctgaggcag	actgtctttg	aaaaacaata	744840
cctgtattttg	tttgtgcagg	ttgcaaattg	agagttgagg	acttccctaa	gtgaattccc	744900
actccagaat	agcgaacctc	tcgctttaac	gttcttttgag	ttcgtttctaa	catgtaaaaa	744960
cctgacaacg	agtctccgta	tattatcgaa	tttctttttt	agcaagcaag	cgatatccta	745020
agaatcctcc	tcctagataa	ctgactgcac	agaaagctat	caaaatcata	gggtaactct	745080
cacaataccc	ataaagcggt	ttataattaa	atagaggcaa	agagggtttc	aatacccctg	745140
agggggcttt	agtttctcta	gtatcataag	gaagaatttt	gagtattcga	cctagagaat	745200
ccacagttgc	tgtaacacca	gtttggcaag	ctcgcacgca	aggcatccca	aactcttgat	745260
ttctcaacat	cccatggagg	aaatggactt	tagggagtcg	tgattcagga	taccatccgt	745320
catttgttaa	gttaacaagg	agttcggctc	cttgtctctt	gtaggattgc	aaccgatagc	745380
cgaaagtttc	ttcgtagcaa	atggtgatcc	cgatacgagg	taaacctcgg	acctgcacaa	745440
ctccagaacg	tctacctgga	agtctcttgc	atcctagagc	atatttagga	aatagtgttc	745500
tacaaattag	ggatccgaat	ttccctctgt	gtatatattc	gccaccaggc	acaaggatag	745560
gcttatcgta	tcctacggaa	attcctttgt	gtgatattac	ctcagcagag	ttataccaat	745620
acaaaacgtt	ctcttttttc	acccaccgtt	ctaagccaat	aattactgga	cactgaaagt	745680
gttgtgacag	agctgtggca	caatcactat	tcgatagaaa	tgccctacct	tcgggaagtg	745740
gagcaaaaga	agacaataaa	tgtgcgaggg	attcataggg	atagacttgc	ctatgcttac	745800
caaaaggcac	gactacttct	gggaaaatca	gcaaatctat	gggttggtgt	attggggata	745860
cgagttggag	gagttgttcc	cagacgacta	ttggggactt	aagtttcggt	cgtatggggg	745920
gatgcgcggg	ttgaacaaca	gcgacacgca	gcgctctctt	atcttggtga	aacgcgtgtt	745980
taagatactc	ataatgaatt	gctccaaaag	tatagggcaa	aagaagagtg	agcaccata	746040
acattttagc	atagggtttt	ttcagtagta	gacaataaaa	gctcatattt	acagctatga	746100
cagcgaagct	ctgacctgcc	caccccaaaa	atccgccaaa	ctgccgtcca	taagcagagg	746160
ctgtcatagg	ccaaccaaga	taatcgaagg	acatcccaga	aaagatccca	taaaatcgaa	746220
gcattctcgat	agcgacccat	acgccaggaa	ggctccataa	aaaagctgtg	cgtttctgac	746280
gtacgattgc	aactagaagg	caagaaaatc	ctgaaaatag	aacggacaaa	atcgtgatta	746340
atgtaagcca	taccaaatag	atgagtttgc	ctatatattg	atccgagagc	atccaagaaa	746400
aatgaatccc	ctctattgtg	aagatccaga	aaaaacagga	tacaaaaaga	gtccttagag	746460
gtaattgagg	tttttttaag	ggttctagac	tataccaaaa	gaatccataa	ccacaggcgg	746520
ctcctaatat	ggaaacgaat	ccacttaaat	ctggttgagc	aaaagctata	aggcaccaag	746580
aaataacaaa	gcaaaagatt	cgtagcacag	gctctcctta	tttcagttca	agccttgctt	746640
gacgtcgctg	atctgcttca	ttataccgac	gtttttcttc	tggagtttct	ggaacaatct	746700
gatggacagg	aatgggctgg	ttgtcttcgt	tgacagcaac	aaatgtaaag	tatgcggagg	746760
taatatgacg	tcgttctctg	ttataaaatat	tttctgccc	cactttaacc	ccgacttcta	746820
gggaagtagc	ccatgttctg	tttactgcag	ctttacaaat	cagattttcc	cccataatg	746880
caggagcata	gaagcggagg	gcatcaacaa	aagcagtaac	acagacggat	tctgtgtgct	746940
gttctgcgac	cactaaggct	aaacgatcga	gcaaatcat	taataatccc	ccgaagacag	747000
tattattagc	attaagatca	ttagggaata	ttttataaat	atgtccgtca	atacagctaa	747060
acgagacggg	ttttttctta	agcattgttg	actctaccga	aaggattttt	atagggtatt	747120
cttggttgcg	atagtatcgg	tcaactgaaa	gaaaatctat	gattttctnt	cataagttac	747180
tgaaattttt	gattattttt	tagaaaatcga	agtgtttaca	attccataaa	gggattgtta	747240
acttgtgaaa	atccgggtccc	cttttgctta	tgcttgattt	catgacggat	agaaaaaaga	747300
aggtctgaat	cgaaatccat	ttttgatgcc	cattgaagat	aggcaagagg	aatttctgaa	747360
aaacatcgct	ccttggtgtt	ccctaggggc	atatatttca	ttttgctaac	747420	
acctgtttca	gttgttctaa	cgctcggaac	cgtttacaaa	gatgtttaaa	aatattgata	747480
tttaatttcta	catccttcat	ggcacgatga	ttcccatcat	agggaaacatt	aaagtgtacg	747540
gctaaggatt	ctagagaatt	attaggacta	tctccatatt	cttttgctaa	tcggagggta	747600
tcaataatgg	tatactttga	gaggaaggct	tctccgattc	tttccatctc	ttgagcgaga	747660
acctgcaaat	caaaaccgac	gctatgtcct	acgatatagt	cgccttcttt	aaaaaatgct	747720
ttgatttgag	gaaaaacttc	ggcgattttc	ggctgatctc	tcaacatagc	gttgagagata	747780
tggtggactc	tctgggactc	cgagatatac	acgcgttctg	gattgattaa	aaattctatc	747840
gaactaatta	cactatcgaa	agtaaaagcga	acagcgcgaa	tttcaataat	acgatctttt	747900
ttacatctta	gacctgtcat	ttcacaatct	aggcaagtaa	aaaccgtatc	ttttaataaa	747960
ctcataattt	ccttctactt	cctctatctt	tggttgatat	ccttctgact	gtagaaggat	748020
ttctgtgttt	aactttatat	tttgcactctg	tgacagagaat	gccttgcgaa	cagaaaaggg	748080

ttccagggaa	cctatactat	tattacatcg	cggtcactc	ttctttatgc	ctatcagtat	748140
gcaaggatac	tatggagaat	aaagactagc	gcttctctat	aataatttct	ctttccatgt	748200
ttgtttgcat	ggtaatgtag	atattttattg	tatcacaaaa	tcgtggctta	ggcaagcgat	748260
ccgcccattc	aatacaaaagg	acatcgtctt	cttctgcatac	ttgaaaaatg	tattcctgat	748320
ttttctgatac	aatccggtaa	agatcatagt	ggcacaaccg	cttaggttca	ttaccataaa	748380
catgtaatat	agagaacgag	ggactagcaa	cttcttccgc	gatagtatct	ccgagatatac	748440
cagagactat	gccacgtaca	aattctgtct	taccagcccc	ataatcacca	aataagagca	748500
atacagctcc	tggaacaagg	acttgctcta	actcagttcc	tagtaatagg	gtttcttgag	748560
aagaatggct	tactcttctg	tatctaccca	ttggctaata	tacacatgaa	aggctgtatc	748620
gtctgctaaa	ctttctataa	atgctgcgat	cttatcttct	accagcgcat	cttgcaatag	748680
agaaaggaag	gaactttcca	attgaaactt	agtttgattt	tgacttctt	ccagggtcat	748740
aggacgcaag	tagctagaga	taaaatcctc	taaaagaggg	ggtaaactat	ggaacaattt	748800
acctgtaatt	gccgaagcaa	acactgtttt	tataataggt	tcttttggtg	ggactgcgta	748860
ttcttttatc	acatcaggat	cttctgatac	gaggaaacgc	ttgattcgca	ccccacctg	748920
tttttccata	ttttgagggc	aagaagacag	ccagtcataa	attgcgtctt	gagggtttgc	748980
atagacgttg	tcagcaaaga	ccttaccggt	aaatgggcaa	atatagatac	gcttcgtatt	749040
ttcgtttacc	tgtggctttt	cagaagaaat	ttggatttct	gtttctctcc	aaatcttttt	749100
atcctgttcg	agaatacggg	ccgcatactc	nnggagtttt	gaaaattatc	ttgtcgcgaa	749160
caaacaccac	aggacgaagg	cttagagcct	gttccagata	gaaaagatac	gttgccaaca	749220
attctgggtt	tttttggttt	cccaaaaact	gcaaaagt	ctgtttgact	gctccagaaa	749280
tatccatgcc	tacccttttt	cagctaata	cttaacgttc	ttaagcaaac	ttcccataaa	749340
aggaatataa	ccacatatgg	gttgtcttac	ctcacgttaa	atcagaaata	ctatcagagc	749400
cgagaattat	gttgaacata	aaggatcac	aacaaggttc	atccaaaaaa	attctgtgtt	749460
tttcttataa	aagtttctta	attgtgtttt	ttattatcta	tagtctacaa	ttttacgaaa	749520
cgcagctatg	gcgaaatcgg	tagacgcgct	agattcaggt	tctagttagc	ttatgtctcat	749580
ggaagttaa	gtcttcttag	ctgcaagaaa	ataacaggga	cagtaattcg	atttttcgag	749640
aagggaaact	tatggtaaag	atcatatcaa	gtgaaaattt	tgactctttt	attgcacggg	749700
ggctcgttct	cgttgatctt	tttgcaaat	gggtgtggcc	ctgtcggatg	ctcactccta	749760
tcttagaaaa	tcttgctgcg	gaacttctc	atgtcactat	tggaaaaatc	aatatagatg	749820
agaacagcaa	gcctgcagaa	acgtacgaag	tcagctctat	tcctacgctt	attcttttta	749880
aggatgggaa	cgaggtggct	cgggtcgtag	gtcttaagg	ttaaagaattc	ctaaccaatc	749940
ttatcaataa	gcacgcttaa	aaagacgctg	caatatttaa	ccgtaggatt	cttttgcaat	750000
gctacgggtt	tctgccttac	cacttcatat	aaaacgatcc	ctacactggg	agctaaattt	750060
agagaacgga	tgtcttgttg	catgggaatg	cgcaggcaat	ttttataata	tttttttaag	750120
atctcttttg	gaagaccttt	ggattcagat	ccaaagacgt	aggtgcctga	agatggcaag	750180
gaaaattcag	tataagatgc	tgaacctttg	gtacaaagac	aaaaaatctg	atcttcaggg	750240
acatcatgta	gtgcttcttc	tatagaatcc	actactgtca	attggagttt	gtcccagtag	750300
tccatccctg	cacgtttgac	aaatttatcg	gctaagaaaa	agcccaaggg	ccgaaccaaa	750360
atgagttcgg	cgcctagggc	tacacaagtt	ctacctatat	ttccagttat	ctgtggcaata	750420
tcaggacaat	gcagaactac	tctcattcac	cttgatttcc	ttcttggggg	acagcagcaa	750480
cttcatctgc	tgaagcctga	atcaagttaa	tttcaaaaat	taataaagag	tttgagggaa	750540
gttgctctgc	ggttccgtaa	gcaagatcag	gatggatgta	gagaactcga	gtttctcctt	750600
ctttcatgcc	ctgcatacct	aaagcaaaac	caggaattgt	ttggcctaga	ggaagcaaga	750660
taggctcatt	gttgccctct	gaactgctaa	atacttggcc	attgatgaag	gaacccttgt	750720
agtgaatag	agctgaagg	ttacctgaaa	ttgctttccc	tgacacctct	ttaataattt	750780
tgtattgcaa	tttacttggt	tgcacttcaa	caacaccagc	gttcttgcta	ttttctttta	750840
agaatttttc	tgccaatgaa	agattttctt	ttgatttttt	ttcaaaaacc	aacttctgtt	750900
cttcagccat	tttttcttca	tactctgttt	ctgttaaagg	agcactttta	caaaccaatt	750960
ccgctgcaa	ccccttagcc	acttctgcaa	tatcaaaaaa	catatcttct	gacttgcgta	751020
attggcggtg	taataaatga	ccaaatgttc	tggataactt	ttgattatcg	gataattcta	751080
tgctattggg	atctttgtta	tctttatatt	ccactaacga	cccctgatcc	ttgtctttat	751140
ccttagaccg	tacgtcacia	gaagcgacgg	agagtgcag	agctactgtt	gctaaaacta	751200
aattccaccg	tctgttcatt	ttccttctcc	tatctttgat	cttaaggcaa	cgactattgt	751260
acatgcccg	agcaattaca	acttatatca	aaaagctacc	ttataactta	gctcttttaa	751320
ttgggaagac	ataatttctg	agggagcatt	catcataaga	ttccgatgctt	tctgtgtttt	751380
aggaaacgcy	atgacctcgc	gaatgctctc	tgtgtgtgtt	aaaaccataa	ccaatcgatc	751440
taaccctaag	gcaatcccta	gatgaggtgg	ggttccaaaa	ctcaaagctt	tgataaagaa	751500
tccaaatttt	tcttgatgc	tctcaggact	tattttttaa	atagtaaata	tttgactttg	751560
caagtctggg	ttatgaattc	tttgagatcc	cgaagcaatt	tcatatccat	ttaaaaccaa	751620
gtcatagctt	gacgaacgca	ctgctagagg	atctgtttct	aacagaggaa	tatcctcttc	751680
caaaggtgct	gtaaacggat	gggtgtccgc	cacaattttt	ccatcttcta	aagagaaaag	751740
agggaaatct	gtaattccaa	caaagtata	ttgattgtcg	ctatacaatt	cgcgctcttt	751800
tgcgatcaat	ctacgcagat	gatcgagaga	ctgattcgct	actgattcag	gagctgctat	751860
caagagcaaa	atatactgat	ctttggcctc	aaaataagca	aagagtctgt	ggaaaacctc	751920

ttcatccata	aatttagcaa	tattggaagc	aactttcccc	tcttgatttt	taatccagac	751980
aagccccata	gccccataac	gctttacaaa	ctcgggtataa	ccatcgagtt	gcttgcggga	752040
catagtagcc	ccacctggaa	cacaaaaacc	tttgatcgta	cctccgtgag	ccaactgatc	752100
taagaaaata	gagaatgagg	aacgttttgc	atagtctcga	caatctttta	atttaagatc	752160
gaatcttaaa	tctggtttat	ctgtaccata	ggaatcctta	gcttcttgat	aggtcatttt	752220
agccaaaggc	aaaggaatct	ctataccttg	cgtagcaaac	agtgttgcca	ccaattgttc	752280
tataatggga	agtaggtcct	gggtatcccc	aaagctcatt	tcaatatcta	tttgagcaaa	752340
ttcaggttga	cgatctgctc	gcaaattcttc	gtctctaaag	cacgtggcga	tttggaataa	752400
acgatccaag	cctccaacca	ttaaaagctg	cttaaaaagt	tgtggtgatt	gcggtagagc	752460
ataaaatttt	ccaggataga	ttctagaggg	aacaagataa	tctctagcac	cttcaggagt	752520
ggattttcct	aatacagggg	tcacgatttc	tgtgaatcct	tgagcatcca	taaagtgtcg	752580
gcaagcaagc	atgacctgat	gacgacaaag	caacttctca	ataatatccc	cgcgacgat	752640
atctagataa	cgatactcta	aacgcagctc	ctcattcaca	ttgatgtggt	catcggaat	752700
ggaaaaaggg	agattttgcg	acttggtatg	cacttcaaag	cttgcaactt	caacttcaat	752760
atgtcctggt	gctaagttag	gattttccat	tcctgcaaga	cgtggacata	ctttccctcg	752820
tacagaaaaga	accatttcaga	aacgcacagc	atccaaacgt	tggtgcagtt	ctggttgctc	752880
atcttcacgg	cacacaattt	gagtaatacc	aaaacgatct	cgcaaatnta	tgaagacaac	752940
accccatga	ttacgataac	ggtgcaccca	tcctgccaat	tgaacattct	cacctatatg	753000
attacttggt	agttcattac	aacggtgtgt	tctgtatttc	atataacaac	ctttgctcta	753060
cttcttcttt	tgttccaaag	aattctttac	gcagagacat	atttttaata	actaactggt	753120
gagaaattaa	ctctcgctca	ccgattaagc	aaacgaaaga	aacctgttct	gtactcgctg	753180
cttttagagc	tccttttact	tttttatgag	accaatcgac	ttccgtaggg	attcctaacc	753240
gtcgcaaatg	ttgcgacct	tcctaaacaaa	actgatccgc	atctggttcc	attggaatca	753300
aacgcagttt	atgagggaa	tgtggctcaa	tacgcttttg	agctaataac	gtttgaatcg	753360
ctctttcaag	gccaacaccg	aaaccacagg	caggaagaga	agctcctcca	aaagctgaaa	753420
tcaagccgtc	atagcgcccg	cctcccccta	aggcataaga	gacctcttgg	aatgtggtag	753480
tcgcttcaaa	gactaagtct	gaataataat	ccaaaccacg	cactaaacga	ggattgatag	753540
catatgggat	ttctaaaact	ctcaaagcgt	ctaaaatttc	attaaaatac	ttaagatctt	753600
catcagaaac	atagtctaga	atcgggggcg	cttgacggat	aatttcttga	tcttcagggt	753660
cctttgaatc	caaaatacgc	aaaacattcg	ttgaaaatct	ctgctggctt	aatgccgata	753720
attctcccat	ggactctttc	aaataagcgc	gtagaacctt	atcgatatga	aatcttgtct	753780
cacttccctc	taagaaattg	agttgaattt	gcatatgttg	caaaccgaca	cgagagtaga	753840
aatcccaaag	caaagcgaga	acttctgcat	ctcttagagg	gtgacgcaca	ccaatagcct	753900
caacaccgaa	ctgatgggtg	tgacgatatc	taccgcgttg	ctgacgttcg	tagcgaaaca	753960
tggaagaat	ataatagaac	ttattatcac	ttcgatgaga	ggccccgtgt	tcaagaaaag	754020
aacgggacaac	agcgggcagtc	ccttcggggac	gcaaagtcat	ggaacgacct	tttctatcta	754080
aaaacgaata	gacttctttt	ttaacaacat	cactttcttc	ccctacatgt	aaaaacactt	754140
ctgatttttc	aaaaatagga	gtacgaattt	cacaaaatcc	ataaagcatg	caaacgggat	754200
gaattgcctt	ctcaaacacta	tgccaaagtg	aagtgtgacg	ccacaattgt	ttagcatctg	754260
caagataagg	aaatatatca	aagacccctt	tggggagagt	tacagtcacg	tgatgtcttc	754320
gctcaaaatg	attacttttt	tagataatgg	aatatctgga	gcttagtgac	tcctgcctaa	754380
gcctaagtca	tattcacact	cgaatctacc	ctctttttta	tgaagggcat	ttcgacagac	754440
cttgctagag	ataatccagg	agcgcgctac	gcgcacgacc	ataattatat	gctagcttat	754500
ggttttttgta	actaagtatt	ggagaaaaac	cgcgccctat	gaatgctata	aactattctt	754560
aaaattcttt	attaagaagc	atgttttacag	acgaaaacaa	aagataattt	tgcttttttc	754620
tagatcggtta	taacctggaa	cttggttatag	tttaccatccc	ttcattcaac	aatcaaaccc	754680
acccttcata	atgtaccagg	caatcggggag	aaataggctc	gataaacttcg	tgtacaggga	754740
aaacatcctg	aacaaagaac	aaattatact	ttgctctggc	cgctttttaa	acagtcgcgt	754800
gagcgctcgt	ttccttattg	gtatttcctt	ttattggaac	aagaaatata	cctatcaaag	754860
caatcaattt	tttcattgca	tgcgccctccc	aaagttaatt	atgtcacgat	gagactttca	754920
aatctggagc	agtaaaaaata	cgtgttttta	gtatttctta	tttaattaaa	aataaccaag	754980
aaaaacactc	tactaatgca	tctttactct	cgcaacctga	aacgattccc	tccttgtttt	755040
ttcatccttg	atatggtaaa	gtaggctttt	cttcgcattt	catctcagtg	aaaaagattt	755100
tacacatgga	aattgaaaga	tgaacgtttg	gactaaaattt	ttccaacctc	caaagcacat	755160
taaagaaatt	gaagaccaag	aagtggtcaa	gaaaaaatac	aaatactggc	gtatttcgtat	755220
tttctatagc	atgttcacg	gctacatttt	ctattatttc	acaagaaaaa	gctttacctt	755280
tgcatgccc	acgctaattg	ctgatttggtg	ttttgataaa	gcgcaattag	ggatcatagg	755340
aagtacctta	tatttttctt	atggaatcag	taagtttggt	agcggagtc	tgtccgacca	755400
atccaatcct	agatatttca	tggttatagg	attgatgatt	acagggtc	ctaactctt	755460
tttcgggatg	tcacctctta	ttgtattatt	tgctctttgg	tggggactaa	acggatgggt	755520
ccaaggggtg	ggctggcctc	catgtgctcg	tctactcacc	cactgggtatg	cgaaatcaga	755580
acggggcact	tggtggagtg	tgtggagtag	ctcccacaat	attggggggag	cacttatctc	755640
tattctcaca	ggatttcatta	ttgattatag	tggtatggcg	ggagccatgt	atgttccagg	755700
cattctttgt	attggaatgg	gttttagttt	aattaatcgt	ttacgagaca	cgcctcagtc	755760

cttagggcta	cctcctatat	agaagtacaa	gcgtgatccc	catcacgcac	atcacgaggg	755820
caaatacagcc	tcagaaggaa	ctgaggaaat	cgaacgcgag	ctatccacta	gagaaattct	755880
ttttacctat	gtccttacaa	atcagtggtt	ttgggttttta	gctgctgcct	cggtcttttat	755940
ttatatagta	cgaatggcag	tcaacgattg	gagcgcgttta	ttccttattg	agacaaaaca	756000
ttatgctgga	gtgaaagcca	atttttgcgt	atctctatctt	gagattgggtg	gtttatttcgg	756060
catgctagtt	gctgggttgg	tatctgataa	gatttctaaag	ggcaatcgtg	ggcctatgaa	756120
acgtcctctt	ctcttttaggt	ttgctgtttg	ctatttttagg	catgtgggttt	tcacgtagtc	756180
ataatcagtg	gtgggtggac	ggaaccttac	ttttcgttat	tgggttttttc	ttatacggcc	756240
ctcaaatgat	gatcgggtcta	gcagcagcag	aactctctca	taaaaaagct	gctgggtactg	756300
ctagcggatt	tactggatgg	ttcgcttatt	ttggagctac	ctttgcaggg	tatccttttag	756360
gaaagggttac	tgatgttttg	gggtggaaag	gggtttttcat	tgctctctta	gcctgtgcat	756420
ccatagcttt	attgctcttt	ttaccaactt	ggaacgctac	ggagaaaaaac	actcgtagta	756480
aagcctagcc	gttcttgagg	attttttttg	acctggatac	cccttcaactg	tcattctcaa	756540
tactctgttc	ttgatgcaat	gagctccatc	aaagatttcg	ttgcgaaagg	tcaggaattt	756600
ggaattcccg	ctctggctct	aacagaccat	gggaatcttt	atggagctgt	tgatttctat	756660
aaagaatgca	ctcaaaaagg	gatccaaccc	atcattgggt	gcgagtgtta	tattgtctca	756720
ggatcacggt	tcgataagaa	aaaagagaag	cgtagtcgtg	cagcacacca	tctcatttta	756780
ttatgtaaaa	atgaacaagg	gtaccgcaac	ctttgtatctt	taacctccct	agcatttact	756840
gaggggtttct	attactttcc	tcggatagac	aaggatcttt	tgagacagta	ctctgaaggc	756900
ttaatctgtt	tatctgggtt	tttatctagt	tctgtttcag	atgctgcctt	aaaatctccg	756960
gaagctctgc	ttcttgaaat	gcaatgggtt	caagacctat	tcaaagatga	ttatttcaca	757020
gaagtacaac	tacacaagat	gtccgaagag	agcattgcag	gcttttaaaga	ggaattggta	757080
aagcaagaat	attactctct	cattgaaaaa	cagatcaaa	tcaatactgc	agtgttagaa	757140
gcaagtaagc	gcttaggcat	tcctactgta	gcacgaatg	acatccatta	catcaatgca	757200
aacgattggc	aagctcatga	aatcctgttg	aatgtccaat	ctggggagac	tgtgcggatt	757260
gcgaaacaga	atactcatat	ccccaatcct	aaacgaaagg	tctatcgcag	tcgcgagtag	757320
tattttaaat	cccctgcgca	aatggcagag	ttatttaaag	atattcctga	ggtcattttcc	757380
aacacattag	aagttgccaa	acggtgtgat	tttacttttg	atttttccaa	gaaacactac	757440
cctatctatg	tcctgaatc	tttaaaaacc	ttaaacagct	acacggagga	agaccgttat	757500
caagcttctg	cagtcttctt	aaaacagcta	gctgaagaag	ctttgcctaa	gaaatactct	757560
tctgaagttc	ttgctcatat	tgctaagaaa	tttccacatc	gggaccctat	cgattattgtc	757620
aaagaaagga	ttgacattgga	gatggccatc	atcattccta	aaggaatgtg	tgactatctt	757680
ttgattgttt	gggacattat	tcattgggccc	aaagcaaatg	gcattcctgt	aggccctgga	757740
agaggttcag	gagctggatc	cgtattacta	tttttggttag	ggatcacaga	aatcgagccc	757800
atacgatttg	atttattctt	tgagagattt	atcaatcctg	agcgtttgtc	ttaccagat	757860
attgacatcg	atatttgcat	ggcaggacgt	gaacgtgtca	ttaattatgc	aattgagcgt	757920
catggcaaa	ataatgtagc	tcaaatcatt	acttttggaa	ctatgaaagc	caaaatggct	757980
gtcaaaagat	tggaagaagc	tttagacatg	gccttatcta	aagtgaacca	cattgcgaaa	758040
catattccag	atttaaatac	tacgttgtct	aaagctttag	aaacagatcc	tgacctacat	758100
cagctctata	ttaacgatgc	cgaatctgca	caagtgtattg	atatggcgct	ttgcttagaa	758160
ggctccatac	ggaatacagg	ggttcatgct	gctgggtgtga	ttatctgtgg	agaccagctg	758220
accaatcaca	ttccgatttg	tatttctaaa	gactccacaa	tgattacaac	acaatactct	758280
atgaaacccg	tggaagatgt	tggaatgctt	aaagtcgact	tattaggggt	caagacttta	758340
accagtatca	atattgcaat	gtctgcaatt	gaaaagaaaa	caggacaatc	gctagctatg	758400
gcgacactgc	ctttggatga	tgccaccaca	ttttctcttt	tacatcaggg	aaagactatg	758460
gggatatttc	aaatggaatc	caaggggagc	caagaattag	caaaaaacct	acgcctgac	758520
ctctttgagg	aaatcattgc	tatgggtgct	ttataccgcc	caggccctat	ggatattgatt	758580
ccttctttta	tttaaccgca	gcatggcaaa	gaaattatag	aatacgacca	tccccttatg	758640
gaatccattc	ttaaggaaac	ctatggaatt	atggtctacc	aagagcaagt	catgcagatt	758700
gctgggtgcat	tagctagtta	ttctcttgga	gaaggtgatg	tattacgacg	tgccatgggg	758760
aagaaagact	tccaacagat	ggagcaggag	cgcgaaaagt	tctgtaaaacg	cgcctgcaat	758820
aacggcatag	atcctgagtt	agcgaactgtc	atctttgata	agatggaaaa	atttgctgcc	758880
tacggcttta	acaaatctca	tgctgctgcc	tatggcttga	ttacttatac	aacggcgat	758940
ctcaaagcaa	attatcctaa	agagtggctt	gcggccttac	ttacctgtga	ttctgacgat	759000
attgagaaga	taggaaaaact	gattcgagaa	gctcagagta	tgggcattcc	gattcttctc	759060
cctcatatca	atgtctctag	caatcacttt	gtagctactg	atgaaggcat	acgctttgcg	759120
atgggagcta	ttaaagggat	tgggcggtgtt	tttaattgaga	gcattgtaga	agagagagat	759180
catcatggtc	cttatgagag	catccgcgac	tttatccaga	ggctctgattt	aaaaaaagtt	759240
tcgaaaaaaa	gtatagaaag	tttaatcgat	gcgggtgtgtt	ttgattgctt	tgattctaac	759300
cgagattttgc	tgtagcctc	tgtagagccc	ctctatgaag	ctattgccaa	agacaagaaa	759360
gaggctgcat	ctggtgtgat	gacgttctct	actttaggag	ctatggatcg	aaaaaatgaa	759420
gtccccattt	gtcttcctaa	agacattccc	actcgtctca	agaaagaact	tttaaaaaaa	759480
gaaaaagagc	ttctagggat	ttaccttaca	gagcacccta	tgatatacgt	gcgagatcat	759540
ctttctcgtc	tttctgtagt	tcttgctgga	gaatttgaaa	atctcccgca	tggttctgta	759600

gtccgcaccg	tgttttattat	tgataaaagta	acgactaaaa	tttcatcaaa	agcgcaaaaag	759660
aagtttgctg	tccttcgtgt	tagtgatggc	atcgattcctt	atgaactgcc	gatctggcca	759720
gatatgtatg	aagaacaaca	agaacttcta	gaagaagatc	gtcttatcta	tgctattcctt	759780
gttttagata	agcgagtg	ttctctacgt	atttcttgct	gctggatgaa	agatctttct	759840
attgttaatg	aaaacatcat	ttatgagtg	gatcaagctt	ttgatagaat	aaaaaatcag	759900
gtgcaaaaaa	tgctatttac	aatgtcaacc	tctggcaaa	aaactaaagc	taaaggggaat	759960
aagcctaag	agaatgggca	tacacaagct	ttagctcctg	tgactctatc	tttagatctc	760020
aatgaactcc	gtcatagtca	tctatgtatc	ttaaagaaga	ttgtgcaaaa	gcaccctggc	760080
tcacggacat	tagttttagt	ttttactcaa	gataacgaaa	gagttgcctc	gatgtctcct	760140
gacgacgct	atttcgtttg	tgaagatatt	gaagaactcc	gtcaagaact	tgtagactgca	760200
gaccttcctg	tgctgttaat	tactgtttga	gattttctag	acgctagggt	gcatgcttga	760260
agttctcaaa	gacatgaggg	catgcctatc	tatctataga	tcttgaaaag	attttcccgt	760320
gactgcgttg	atgtattcaa	cacggacact	attatctgca	gaaactaggg	agatcttata	760380
gacaggtaca	tagaccatcg	agctacgtac	aattaaaaaa	ttatctccaa	agatcatctt	760440
cactaaatga	cgcacacgat	cttcggaata	ctgcgcaggg	aacacggctg	cgtgacgtgg	760500
tttttgcaac	cacacaggat	tgttattgag	tgttgttgta	cacctcgga	taggctggaa	760560
ctgttggaag	tgcttcccta	tttgattccc	ggaggcaaa	atcagttttt	tcttctgaca	760620
ttccttaatt	actcgtctctg	cacggatatt	ctttagggct	aaggcttggg	ctaaggattc	760680
ccgggatgtg	gttcccccta	aggtagctag	cgtttgatc	acccgcatat	cttgcttacc	760740
agcgtgcaaa	aggaggcact	ctcgaaatcc	cttagagcat	gtccaagtcc	ctgtatgcaa	760800
taccatctca	ccattaacta	agctccaaag	gatttctccc	tcttggtctga	taatatgctt	760860
tttgacaggt	tcttcttttag	agaagcgtac	gtgcataaag	gtatgtggga	tgaaggcgag	760920
ctctacaaaa	gacttgccat	cacgatattc	tgggaacaat	gccaacgcct	gttctggaga	760980
gacgtgacgt	tcaaaaaactt	gtaactcttc	aaatcctgag	attttctgta	caaagcggca	761040
gctcttagaa	aatacttctg	agctatggtc	agcagcaagc	cgcataattt	tttgtgcaca	761100
aggaactcga	tcccacaaaa	aaacaccaca	aaaaagagaa	gcaacaaaag	cagcaaaaata	761160
tagaattaac	ttcttcataa	agtacctttt	ttgtatttta	cacaataaag	aaatgtttta	761220
tcaataaaaa	aaaataacaa	gttataaata	aaacaaaaac	aaggcatttg	acaaattctg	761280
tttttctttt	ttatgatggc	gttttgttgt	tgtaaagccc	cgtctaatta	tgaattttct	761340
attatacggt	ccacttcttc	ttgttctcgt	attctacggg	tgcgatgcaa	aaacctgttc	761400
ttttgagccc	ttttcaggaa	agctttccac	ccagcgtttt	gagcctcagc	actctgctga	761460
agaatatattt	tctcaggga	aggaattctt	aaaaaaagga	aatttcagaa	aagctttact	761520
atgctttgga	atcattacgc	atcacttccc	tagggacatc	ttgcgtaatc	aagcacagta	761580
tcttatagga	gtctgttact	tcacgcagga	tcacccagat	ttagcagaca	aggcatattgc	761640
atcttactta	caacttcctg	atgcggagta	ctctgaagag	ttgttccaga	tgaatatatgc	761700
gattgctcaa	agatttgctc	aaggggaagcg	taaacggatt	tgctcgattag	agggtctccc	761760
aaaactaatg	aatgctgatg	aagatgcgta	cgcatttatg	acgagattct	aacagcgttt	761820
cctagtaaa	acttaggagc	tcaggccctc	tatagtaaa	ctgcgttact	tattgtaaaa	761880
aacgatctta	cagaagccac	caaaacctta	aaaaaactca	cgttacaatt	tcctctacat	761940
attttatctt	cagaggcctt	tgtacgttta	tcggaaatct	atttacagca	agctaagaaa	762000
gagcctcaca	atcttcaata	tcttcatatt	gcaaagctta	atgaagaggc	aatgaaaaag	762060
cagcatccta	accatcctct	gaatgaggtt	gtttctgcta	atggtggagc	tatgcgggaa	762120
cattatgctc	gaggtttgta	tgccacaggt	cgtttctatg	agaagaagaa	aaaagccgag	762180
gctgcgaata	tctattaccg	cactgcgatt	acaaactacc	cagacacttt	attagtggct	762240
aaatgtcaaa	agcgtctaga	tagaataatc	aagcatactt	cctaagatag	aaatcaatat	762300
gagattgttt	tctttaggca	cgatttatct	tttttttctt	ctagcacttt	cgtcatgctg	762360
tggttactct	attttaaaca	gcccgtatca	cttatcgtct	ttaggttaagt	ctttattaca	762420
ggaaagaatt	ttcattgctc	ccataaaaga	agatcctcat	ggtcagctct	gctcagctct	762480
aacttatgag	cttagtaagc	gttcttttgc	tatctctgga	aggagtctct	gcgcaggcta	762540
tactcttaaa	gtagagcttc	tgaatgggtat	tgacaagaat	ataggtttta	cgtatgcccc	762600
aaataaaactc	ggagataaga	ctcacaggca	ttttatagtc	tctaatagaag	gcagactatc	762660
actatctgca	aaagtacagc	ttatcaataa	tgacactcaa	gaagtcctta	tagaccaatg	762720
tggtgtctga	gagctctgag	actttgactt	tgagcctgac	ttaggaacag	caaacgctca	762780
tgaatttgct	tagggccaat	ttgaaatgca	tagtgaagcc	ataaaaaagt	ctcgcctgat	762840
actatctata	cgcctagccg	agacgattgc	tcaacaggta	tactatgacc	ttttttgaag	762900
gagaaaccgt	ttttcctgca	gtacttagtg	aacttcatag	catgttgagc	ttaatcaaac	762960
gtgcaggaaa	acaatctaag	tgcccccaag	agaagttgtt	aaagctcgag	cttgcttgtg	763020
aggagcttct	cgtcaatatc	atttcttatg	cttatcaggg	cgaaaattct	ccaggaacga	763080
ttgcgatttc	ttgcatctcc	catagaggag	acttagaagt	tgtagattaaa	gaccattggac	763140
cttctttcaa	tctctttgct	gtttcaatca	acattcagga	agatcttccc	ttagaacagc	763200
gtaaactcgg	gggcttaggg	atttttctgg	ctaaaagttc	tgtaggacgag	tttctttatg	763260
ctcgtgaaga	tcattgcaat	attgtgcatt	taaaaatgct	caatggccaa	cattcctaaa	763320
cctagtgtac	gttatttaaag	cggaaagaac	gcagagcatt	ttcagtatct	ttaatatcct	763380
taagatataa	ctgcagggct	tcgagaatca	gcgacgactg	attgtattgt	ccagaggctt	763440



cgaaagccat	ttctggttca	tagtttcctt	ctccttgga	aaccgcaata	tatccccgag	763500
tgactgcctg	tccttgaaca	agctcaggaa	cgagccaaat	agcaaaatca	gcgttaaata	763560
atgtgagttt	atcttttagat	tctgcaataa	taaaatcggt	gtcagactgg	ctacagagaa	763620
agtcagtggt	agcatcagtg	caatgaggat	aagagagtat	ttctgcaata	tttaagtatc	763680
cttcggggaa	ggacgtccct	gtattgagta	ttgactgatg	atagaactcc	tcgaaaaaat	763740
ctaaactcat	agtatatttc	ctctgattta	tggaatttct	ttattttcag	agccgtcaag	763800
tcctttctat	tctgttgaat	ttcctaataa	cgtaagtaat	aaacaatcaa	aagtcgcgat	763860
atgaaaagac	ctttttttac	ctatctatgc	atcatcttct	acggatcttg	tgcacgttta	763920
tcctttacatg	caggactctc	tttcccagaa	gtacgtggag	ctacggctgc	tgttggtccat	763980
gccgactctg	ggaaggtatt	ctatgataaa	gacatagatg	ctgtaatcta	tcctgccagc	764040
atgacgaaaa	tcgcaactgc	cctcttttatc	ctaaagcact	atcccacagt	cctcgatact	764100
ctcatcaaag	tcaaacaaga	tgcgatcgct	tccatcactc	cgcaagcaaa	aaaacaatca	764160
ggatatcgta	gtcctcccca	ctgggttagaa	actgatggat	ctacaataca	gctccatctt	764220
cgagaagagc	ttttaggggtg	ggacctgttc	cacgccttac	tggtctgttc	tgctaagtat	764280
gctgcgaatg	tcttagctat	ggcatgttgc	ggatctgtag	agaagtttat	ggataagctg	764340
aacttcttct	taaaagaaga	aatcggtcgc	actcataccc	attttaataa	tccccatggg	764400
ttacatcatc	cgaatcacta	tactacaacc	cgtgatctta	ttagcatcat	gcgttgcgct	764460
ctgaaagaac	ctccatttcg	aggggtcatc	tccacgacaa	gctataaaat	aggggctaca	764520
aacctgcatg	gcgaacggat	cctatcccca	acaaacaaat	tgcttcttcc	tgggtctacc	764580
taccactatc	ccccagcttt	aggagggaaa	acagggacca	ccaagactgc	agggaaaaat	764640
ctaattatgg	ctgctgaaaa	aaataaccgc	ctcttggtaa	cgatcgcaac	gggctattcg	764700
ggtcctgtga	gtgatctcta	ccaagatgtc	attgctctat	gtgaaacggt	atttaacgag	764760
ccgctattaa	gaaaagagct	cgcccccccc	tcogactgtc	tccaattaga	aatagcgaat	764820
cttggggaagc	tcttctggcc	tcttcttgag	ggactctact	atgacttcta	tgcttccgaa	764880
gatcgcgaac	ctctttctgt	atcttttatt	gcacatgcgg	acgccttccc	tattgaacaa	764940
ggagatcttc	ttggtcattg	ggttttttat	gacgatgaag	gcaagaaaaat	ttcttcccag	765000
cctttctatg	ccccttgctg	ttttgagcgc	actatcaagc	cttggaact	ctatatgaaa	765060
cgtgtcttca	catcgtatag	aacctatatg	tctataacca	tgctgctcat	gtattttcgc	765120
atccgcaagc	accgcaagta	taaaaattta	aaacactatt	ctaaaaatcta	actttttctt	765180
ttaattttata	aaaaacccaa	ggtttatgta	agattttgcgc	ttttcaatcc	aacaagaatc	765240
ccttgctgcg	acattacttt	gctgtttact	tgtcttctact	tgacttctct	caagttatgc	765300
tcagatatcc	tttcttaaaa	aggattctct	cctctctttt	ttattgtctt	ggaactctta	765360
gggaaaatct	acagaaggaa	aagcatacca	ctgtttcctt	aagcaagtgt	ctattgcctt	765420
aaaccgagaa	gaagtttggg	ataatcccca	tcacttaatg	tttatcttaa	tgcaattcca	765480
acaattttca	ggggaacagg	atcgttttgg	aagtttctta	gaagcaacca	tcctgtgatcg	765540
ggtctctttt	ttagtcttac	aagaaaagat	tgccacttta	aagtagcagt	ttaaaactct	765600
gcataccaaa	gatagagctt	cttatcgtta	ctttagggaa	cggtaatggt	tgattttctt	765660
tgaaagattc	gggcgctcta	cagcgcctct	attctagatt	ttttgaaaaat	gagaagtaaa	765720
aaatgcgtcg	cccttacctta	cttgtaaggg	aagcgttttt	ctgtggactt	ctttccaacc	765780
taaagatgic	atgtaggcaa	catgagcctc	attttcttct	tttaaaagag	aacaggtaat	765840
gtagacaagt	cgccccgag	gtcccacata	agcacttgct	tgttttaaga	tgctcttttg	765900
cactcgcaca	tagttcaaca	acaatttctt	agaaaattgc	cacttatggt	cgggatgtcg	765960
tcggaaaact	cccgttccag	aacaaggagc	gtctacgata	actacagaaa	aggatcctaa	766020
acgtaattga	tccgctaaag	aaaaattcct	agctccagca	cgtaataaac	gatgctttgc	766080
agtttgcaaa	atagctttac	gactgtcatt	gatcacaaca	tgttttgctt	tctgcgcaaa	766140
gataaggctt	ttcccgcctg	ctcctgcaca	aaaatccaag	acgatatctt	tatctgttag	766200
ggaaatgccc	tgagaaattc	tctgagagtt	ttcatcttgg	atttcgaaaa	acccacgacg	766260
aaatgcttct	gtagattgta	agggatgacg	tttggaagag	tgcaatgcct	caggaagctc	766320
tccaggagaa	cttgatatt	ctaacttctc	ttggagttct	ttgacggaga	ttttatctgt	766380
attcacacga	atcgtaatcg	gagcttccgt	taaccaaatc	ttggcgatct	cctcggcctg	766440
ttcttctcca	taatcttgaa	ctaagaagtg	cgcaagatca	tcagatatag	agtaacgcac	766500
aggccagggg	atagcgctgt	aactgtccaa	gttctctaga	accccttcgt	ttactttcgc	766560
aacgagagct	tctggagtta	cttggttctc	cgaatcaaga	attaaagttt	caagaagacg	766620
gcgatgacgc	aaaatattaa	aaataatatt	ttgaatccac	tgacgatcct	tagaccctaa	766680
agaacgggtt	tgtttaaaat	agtacgaaac	tctatctgct	tctgaaattg	cagacgtgtg	766740
tagctgtttt	aacagctgat	aagcatgatg	ctgacgaaaa	ggaaccatag	tgacatagag	766800
tatacctcgt	catcacctat	tttgcttgga	aaatcttaca	gaagacaaaa	taaagagagc	766860
catcagtata	gtaaaaaata	tgcattacgg	acgacgttgc	cataatctca	agaattgtct	766920
ccaaaaagaa	ggatgcggat	tatagtattc	cgtgtctttt	cttaaggcta	taccgatatc	766980
tctatcatag	tctaacaacc	aacgcataag	taacatggta	atcattttat	cccacagggc	767040
gggatttttg	tctcgaatac	tataaatatt	ccccacctcc	tcaggagtgg	tattgtcgga	767100
cttagatata	tggagtttct	tttctacgat	gactttccgc	aatacttctg	caagaaagcc	767160
cagggctaata	ttggaatcct	caggggaggc	tagggcagtc	tcttgccata	gacctacaaa	767220
agtcttccca	tgaaatgtta	aaggctgggt	cccaataaga	gagtttgcca	atacctcaga	767280



tagagaatct	gagataatac	tcataataat	cgtttgga	tcctcggcac	tcaaagaaaa	767340
aagctggatc	agctcgcgta	acaatacgt	gctcttttct	gataatgttt	ttaggggttg	767400
cgctttttct	cctataaaact	ggttgagcaa	ttctaaactt	aaggggaagat	acgccgtatg	767460
cccttcaagt	aatgtgggta	acgcttctat	gatcatttgt	agagaggcat	ctgctgccaa	767520
tcttctttgc	acctctccag	ccagaggcgt	ctgaacttct	gataccgtaa	cctcatgagt	767580
aaaatcttcc	catgaggaaa	aattactttt	ccctttagag	aacaccttat	ttgcagcttg	767640
cacaatttta	tcgacaggac	gcttggactc	aaaaagaatc	aaagacttaa	acatacatag	767700
tttgtctaca	atggcttttt	tgatgtgata	cttggagggg	aagaacagcc	ggtagagcca	767760
tcttggttgg	ggtttttctt	catgcaaacg	caattcaata	attgctaaaa	gtcgactcga	767820
tatcgaataa	gaaattgctg	accaggaaaa	gagctcgtga	attacctgac	gaatcgtgga	767880
tacgcttgta	tcatagttgg	taggtaaggg	gtcattgacc	ggccatgcat	ctaagagaag	767940
tcgttttctg	tcatatgcga	gtatgcgcgt	gccatcccta	attgctagtt	caagaacccg	768000
taaataatat	cctatagaaa	attgaaaatc	taaaatcata	gatagtggta	cttagagctt	768060
ttctatgttt	tattcttcag	gagaaatatt	atttcatcat	atttatttcc	tgaagtact	768120
ataggcaatc	gttaacaatg	agaactttta	ttaaaaagtc	ctgaatacta	gtctttgggc	768180
tctattgatg	tcagacgctc	gctacagaaa	aactgacaga	tcacatagtt	taatntcttc	768240
tgatatgcta	gggatgcga	gcgatagtct	tcttctaaga	tagggagatt	tacttctaag	768300
atagcgagaa	cgacatcnta	gtttacttct	gaggcgtgct	cttctgacca	catcattaaa	768360
aagtcctcga	gctctttgct	acgatcttga	cgtactaaat	agaggatgtc	tttcataacg	768420
agagcttcgt	tctctccttt	atcggaacac	tcatcaattt	gggaggcaca	ggcaagtacc	768480
tgagtatagt	tacgaccaag	atcatatgtt	tttaggttgt	caacaacgct	gacgcattgc	768540
ccagctccta	aataaggaga	ggtaaattaa	tcttagtaat	cccacggacg	ttagctaacc	768600
catcaatacg	tttgtctgag	tataatagtt	cggagagcct	tttggagact	tcttctactg	768660
ttgttgtagc	ttctaaagaa	aacgcattat	acattcctgc	ctcttctgatg	acttctaaag	768720
cgagtccttc	ttgaactgcg	tccgtagcta	cccacttgca	gcaagaacgt	aagattaaag	768780
caaatgcaac	tgacgttctt	ggacttatag	gatctgtacc	acaaagggtct	aaaggagcct	768840
ctgggtgttg	acgacgtaaa	agagtgaata	gccttaaaaa	tacatgaaag	aaaaagcttc	768900
ggcatgaagc	tagtgctgtt	tctaaagcat	aaaagtatgg	agggtccgca	gtttcttttag	768960
ggagtgcgct	tgctttgaga	agatcacaa	ggatgtcccc	caaggaacgc	actccctgtt	769020
cttttggtatg	gcgttttgtt	ttaacatgca	tccaaatctg	cgatactgct	ttacgaatcc	769080
gcgcaagcat	cgtagttaac	aggcttccgc	gagcttcata	tctactcta	tctacaaggt	769140
cgctatttaa	atcactattc	gtacctcag	atggagtgtc	ttctgggatc	cccgtatccg	769200
ctatggtttc	tatcacttgg	gtagcacttt	ccgataccgc	atcctctaaa	tctgaatccc	769260
cctcttctgc	ggcactttct	tctaaaggat	ctgatatcgt	attacgggtca	ccatcattgc	769320
cagatatagg	agttcccatc	gattaactac	tccacaacaa	tgcttctgcc	ttttttatct	769380
aaaaagatcc	ccgattaaaa	ctgtcattgt	attcgcccaa	gctccgaccg	ataacacttt	769440
cataccttga	agtagtctac	tcgactcatt	ggccattcgc	acaacgtcac	gagtgtgatt	769500
ctttcctgca	tttgcgattc	ggacggaagt	agcatgagag	tgtacagccg	caccgagttc	769560
tcgtgcta	gctatccata	ttctaggcat	ctcatagga	tgattttcgc	gtacccgatac	769620
taaagctgac	cctaactcgag	ctatatcact	tgtataactc	atgtcgctat	catctccacc	769680
gaaatccgaa	accctagtgt	ctaaaaagtt	ttggatagat	tctcctgggt	ctaagttagg	769740
tccctcgata	cctaagctta	taaccacttg	catgagtaca	ccatcaggat	cattacctgg	769800
cttaggattt	tctaaattct	taattgcgcc	tctaactgtc	tgagttacag	catccttagc	769860
tacagtcact	gcttgcgga	ctggtcctgt	agatgaagtc	ccttcgataa	gcatagattg	769920
ttctgtgtat	gtttgctgca	aagctcgagc	aatgacacga	taaccatgca	aaagatagtc	769980
tggaccccta	ttattttccc	aatccgtcca	ctttgtttgt	agctcttgag	ataccttttt	770040
aagtactttt	tgagactccg	catgactatg	gactgcacat	tttaattcac	tcacaagttt	770100
agcgacttca	gaactcatgg	cagtaggttg	ctctgatcct	gaagaagacc	ccgccgtagg	770160
agggtgaggt	gctcgacctt	tcccatgcgt	tgccgggacgt	ttcgcattag	ccccaccctg	770220
tgtaggaggt	ggaggtgccc	gacgcgtagg	ccgtattgta	ggctcctgaag	gactttgcat	770280
tgcaggtccc	gaagcaccct	gagaagaatc	gggtgatttc	ttccctaaaa	agaactccct	770340
taccgtctgc	cataactgct	ttgctttaga	agcaacttgc	ggctgtgagg	ttgatgtagt	770400
tacgttgtga	gcaccaagat	ttgagtttgt	agctcctgta	ccttgggtac	tggagctatc	770460
gccttgagct	cctctaacc	atacatcacc	tggtgatcta	ttaccggaag	gattgatctc	770520
cattgcaatt	ctctatttat	ttttcttttt	taaatttaaa	taatttttaa	aagaaaaataa	770580
ttatgtataa	acttttttaa	attaattaat	aattaactat	tacaaaaacc	actaaactat	770640
aaagatcgct	tactaagacg	tagaatgtgc	gtactacctc	tgtaagttcc	gtaataccca	770700
agcccaatag	agagaaaagca	ccccgccaat	ctcttagaga	gacaggcctg	agtggttctc	770760
ttgttcaccg	cctttttaaag	gaaaacctta	gtggctacat	ttaatcttcg	tcagaccagc	770820
tgacacgctt	ctttcctgaa	gtcccagact	gcccaggctg	tttcaaaaatg	cccttaggag	770880
gttgaggtgc	tggacctttc	ccatgcgttg	ctgcgcgctt	agcattgggtc	ccacctgttt	770940
taggaggctg	gggtgctgga	cccttcccgt	gcgttgccgg	acgttttgca	ttagttccac	771000
ccgttttagg	agggtggggg	gccggacgcg	taggcttttag	tgtcgtgcta	cctgatgaac	771060
gttgggcccc	tcctccagga	acctgtggga	tagtgacttt	catccctggg	tggtaaccct	771120

ttttaattaa	gttcctacca	gtccctcgg	tagcgcgagc	atccccctccc	ggcaacggggc	771180
tacgtacagt	atctgcagat	ggagcagagg	gttggttggt	acctcttgga	gtcccgatc	771240
tgaagaagct	catccgacta	aaaaacccgg	ttactgcttc	tttgattcgt	gctaataacc	771300
cttggcgctc	tcctgaggca	gtcactctat	gacttcctag	gttagcactt	gtaaccccg	771360
attctttaac	atcgggatgc	tgatcatgag	ctcccgtaat	ccagagatcg	ttcttggaat	771420
ttcctgatgg	attaacagac	attataat	tctatTTTTA	TTTTTcttta	ttacttaatt	771480
ttaagaatta	aattaattta	tctataaaca	TTTTaaataa	aattaattcg	caattagaaa	771540
atataactat	tctatttcta	agagaaaaaa	gacgtTTTTA	taataaaaaa	catctaaagt	771600
tcaggggagtt	atctccagag	gagtcctctg	gtgaaaattt	gaaaaatcgg	aatgtattaa	771660
ggtttggaga	attacaacct	aaagatagac	caaagcctgg	gggaaagagt	tacccacaca	771720
tagacaagca	ccgcagctct	ccatgttaag	agagaagaag	agcgcgatgc	atcgtgttta	771780
cctaaacgac	aacaagatac	atctcttaac	acgaattctt	aagtatgttg	atttaagagt	771840
acttttagctt	ttggatggag	ataaaacttc	tgtacctggg	aggaagccct	gctctagaaa	771900
ctctaaagaa	gccccctctc	cagtagaaac	atgggaaact	tttgtagagc	agcctgccaa	771960
agcaaccaca	gctgccgcat	ctcctccacc	cacgacagta	acagctgaag	ggtgattgcc	772020
taaggcattc	gctatagcaa	tagatccaga	gtcaaaagga	gggacctcat	aaacaccac	772080
aggaccattc	caaaacacag	tcgctgattg	gtttataata	cggataaatt	cttcggttgt	772140
tctaggtcca	atatcaaagc	cttgaagatg	cggaggaatg	ccttgatcta	tagaaatcac	772200
agaatattcc	ttagattgga	gattttcggc	tgctttcaca	tcgctaggca	aaactatggt	772260
aacattacga	cttttagcaa	ttttcaatac	atttctagca	agatccaagg	cagattttctc	772320
cacaagagag	ttccctaggg	attttcccaa	ggcttgtagg	aaagtaaatac	ccatacctcc	772380
agctaataag	aggtagtcta	cttgattcag	tagagcctct	ataactccaa	ttttagaaga	772440
aatcttagct	cctccaagga	tggcagtgaa	aggcctctta	ggggaggtca	atagatgtct	772500
tcctaaaaat	tccaattctt	ttcccataag	caggcctgct	gcggctctac	ctgggaaagc	772560
ctgcggcact	acatagactg	aagcatgttt	tctatgcgaa	gttccgaaag	catcggtgac	772620
atagaaatcc	ccgtaggaag	agagtctctg	ggcgaaacgtc	gggtcttttt	ctggatgttc	772680
ttctcctata	tggaaacgca	agttctcaag	aagcaaaacg	cgaccaggag	aaagctgagc	772740
tacagcttga	cgtgcaacct	caccacacaca	atctggagct	agaggcacat	gatgtcctaa	772800
gtatccttcg	agaacatcca	caacgggttg	cagagaatat	tcctcttgga	accctgtcc	772860
tttaggtcgc	cctaaatgac	tcattaaaat	cactgcagca	tgtttcttaa	gtagatagtt	772920
gattgtaggc	atcgactgc	gaatacgaat	gtcatcgagt	atcttgccat	cttgcatggg	772980
gacattgaaa	tctacacgta	cgaggacttt	tttttcttct	ggagaaagat	cttgactgtg	773040
tagcttatcc	atatatcctc	aagaacctac	tatttgattt	ttcttatttt	taatggaaca	773100
aagctcttaa	agcaaaagaa	aagagtatgg	ataataaagc	tcctgcagga	agcgtaataa	773160
accaggagag	tacaatatct	ttgataatgt	ttaagttaat	ggcacggatc	cctcggtgcta	773220
aacctattcc	taaaacagct	ccaacaacaa	catgtgtcgt	agatatagga	agtcctaaaa	773280
tagaagctaa	agcaattggt	aatgctgagc	ccatccccac	ggaaaaccct	cgagacgggg	773340
ttaactcggt	aatttttacag	cctacagttt	ctataacacg	ccatccccaa	atcgcaaggc	773400
ctatgaccaa	gcctatgcct	ccaaatgcca	tgagccta	taagtatac	gacgtatagg	773460
aagcaggata	tgcctgacgc	aagactccag	ctacaggagc	aatggcatta	gcaacatcat	773520
tagatccgtg	atgcaaacg	ataaagcaag	ctacgataat	ctgtaggtag	gcaaaagattc	773580
tttctacaac	aagatacttt	cttcataat	ttccgctcgc	ttctttcaaa	cgataggtaa	773640
gactgccttt	ttttggtgta	tctgaaatgt	aggaacagtg	cttggtatgg	acgtagtaaa	773700
acgtaatgat	ataacttaga	agtccacaaa	ccagaacccc	actaactgcc	cagggagttg	773760
aagaaacctt	aaggatcacg	ccccagaga	tcatcacggt	tcctaaagtc	atgatcacca	773820
aagctgctaa	aaacggagca	acacgaacca	tagcaagaac	aggatcattc	ttataaaaaa	773880
tatggcgccg	aatgaaagaa	aagatcaggt	aagcaacaca	cccaccata	aaaggggaga	773940
gaatccagct	aattaaaata	atgcctacgg	aattccagta	aatgattggt	cccttaccaa	774000
ggaccaatcc	aaagccaatc	acagctccaa	ctatagaatg	cgttgttgag	acggggccaac	774060
caaaaaaaga	ggccagctgc	aaccacacgc	ctgttgctag	taaggctgcc	gtcatgccgt	774120
acatatagtc	cccagaggca	atcataggat	tggtcacaga	aacgatacta	ctttctatag	774180
tccttgcaac	acgatctcca	agaaggagag	cacaaaaaaa	ctcaaagata	gcagcgatga	774240
ccacggcttg	tcgcaatgtc	aataccccag	atcctacact	agggcctaca	gcattagcga	774300
catcattagc	tcctatatct	caagaagtat	aaaagccaca	tagaaggaca	aaaatgatta	774360
atggaagcat	ggagtattac	ttttcttcta	gggtcatatt	aatcttatgt	gcgagctttt	774420
cagaactatc	tgaatcccc	gcagtcgctc	gaattacttg	taaccaaaga	taaaactctt	774480
tttcaggaa	tataaaatca	tcagaaaaaa	atatttgcat	aagttctcgt	tgcaaaacat	774540
ccgattcatg	ttcagattta	gccacacgcc	ctacaagcaa	gcgtgcttta	tctgccttcc	774600
tcccccaaaa	tgaactttca	agcaattggt	tgaattcatg	tagcaatgtc	atagttaact	774660
caaaagcttc	tagatttttt	tccaaaaatc	ggaaaaaaag	cgtttccata	gatggataaa	774720
agtttaaatcg	tctgatgggt	aataagatag	caacatcttc	agcagtatcc	gcgatgctat	774780
cttgtataga	aataattttct	agaatccccg	ctcgagatat	cggcatgaat	aatcctgcag	774840
gaagatgatt	cctcatatca	ttttttatac	aatctgcttg	atactcttta	tcagaaacaa	774900
gttttgccat	ttctaataat	tcttcatatc	ttccatctcg	gagagcagtg	aatataggaa	774960

gcatgtattc	cacacaagag	accaccattt	ccagatgagc	ttgtaaagga	gcaaatggag	775020
attggccaaa	tagacgagca	aggggtttgca	taagaatagc	ctttttcgca	ataataactt	775080
gcctaaacga	tcttgtaaac	gacttatggc	ttctaattccc	attttacaga	tagaggatct	775140
atccataacc	ttggcaaaac	aacgccaaaca	gtaccccatc	gtccaatctt	tatcgtttac	775200
tatcaatgaa	ggacaaacct	tagcaatcat	tggagaatca	ggatcaggaa	aatctgtctc	775260
tgcgcatgca	atccttcgat	tacttccttg	ccccccattt	tctgtttctg	gccagggtcaa	775320
cttccaaggc	cacaacttac	ttacggcttc	gcgctctata	caaaaaaaga	ttatagggac	775380
agaaattttt	atgatctttc	aaaacccgca	agcatctcta	aaccccggtg	ttactattga	775440
acagcagttt	cgagaaatta	ttcataccca	cctagcctta	actgcagaag	ttgctaaaga	775500
aaagatgtta	tacgctcttg	aagaaacagg	gtttcatgat	cccagggtgt	gcttgaatct	775560
ctaccccccac	caactctctg	gagggatgct	tcaaagaatt	tgcattgcca	tggcgctcct	775620
ctgttctcct	aaacttctta	ttgctgatga	acctacgact	gcttttagatg	tttctgttca	775680
gtatcagatt	ctacaattac	taaaaacact	acagaaaaaa	acgggaatga	gccttcttat	775740
tattacccat	aatatgggag	tcggtgcaga	aactgctgat	gacgtgctcg	tgctctatgc	775800
aggacgcatg	gtagaatgtg	ccccgcggt	tcaaattgttc	cataatcctt	ctcatcccta	775860
tacccgagat	cttttagcat	ccagaccctc	tctacaaccg	gttccctcaa	gttccctcaa	775920
ccccattcca	ggacagcccc	cacactacac	ggcctttccc	tggggatgtc	gctatcaccc	775980
tagatgctca	aaaattttta	atcgatgttc	tgcggaagct	ccagaaatct	atccgggtacg	776040
cgaaggtcac	aaagtaagggt	gttggtctga	tgacgactaa	ttttccccc	cctttaattc	776100
aagcaacctc	attaacaaag	cactattaca	agcggttcctt	ttgggtttcag	ggaagacaa	776160
ttgccagtcg	tctgttgac	gacgtctctt	tttcaactata	ctccagacgt	gctgtcggac	776220
ttattggaga	atctggatca	gggaaaagta	ccctggcggt	agctctcgca	ggtctcctac	776280
ctctcacctc	tgggttctta	acttttaacg	gcaccccaat	caagttgcat	tctaaacacg	776340
gacgccatca	attacgatct	caagtacggt	tgggtcttca	aaatccacaa	gcttcattaa	776400
acccgcgaaa	aactatccta	gatagtttag	gccactctct	gctttaccat	aaactcgtcc	776460
caaaagaaaa	agtactagca	acggtaagggt	aatattttaga	attggtagggt	ttatctgagg	776520
agtattttta	tcggtatcct	caccagcttt	ctggaggaca	acaacaacga	gtctctatag	776580
cgagagccct	attaggagtc	cctcagttaa	ttatttgtga	cgaaattgtt	tctgtcttag	776640
atztatctat	tcaagcacia	attctgaata	tgcttgccga	gctgcaaaaa	aaactcagcc	776700
tcacatatct	cttcattttcg	catgatcttg	ccgttgtagc	ctcgttctgc	acagagggtat	776760
tcattatgta	taagggggcaa	attgtagaaa	aaggaaatac	aaaacgcatt	ttttctgata	776820
cacaacatcc	ttatacgcg	atggtgttaa	atgcccaact	tccagagact	cctgatcaaa	776880
ggcaatctaa	acctatattc	caagaatattc	acaaagattc	tgaagaatct	tgctctacag	776940
gatgctactt	ttacaatcgt	tgtccacaaa	aacaagaagc	ttgcaagtca	gagatcatcc	777000
caaatcaagg	agacgcgcac	catacatacc	gttgatcca	ttgattcgtc	ctctacgcta	777060
ttcttaagct	accattaagg	aatcccaagg	gagagggtctg	ctctatatat	cctgagtgat	777120
gtttgacttt	atgttagcta	gagcattccg	agctgcaaac	acaattgtaa	atacaaaaaca	777180
aaagccattc	catatccatg	gaatggctac	tttaagacct	aacgcaacat	ccattcttaa	777240
tataaaaagaa	gacgctctta	gcctaggcac	cggtgggatct	ttcgcaagta	ccgctagtat	777300
taagatagac	tctcactgag	tgtcccatgg	ctggaaaagcc	aagcttccaa	cttttgaaga	777360
tcttgagtat	tttgcaaatg	aaaagagact	gtagcctttg	atccccgggt	ttttatctgg	777420
accttatacc	cacaaagatc	actgagacgt	tggttgaatt	cttcatgctg	ctttgacgac	777480
tctgccatgt	ctaaaggagt	gggcttcaac	tctatcgaag	agccctcttc	acttataagc	777540
tgttcgctat	cagttccgct	tcacgtactg	ccaaatgctc	ttgtatgatg	atctcattca	777600
gcttttccct	aagtatagga	tcttccagag	tcaagatgac	tttagcatgg	ccgagagtaa	777660
tctgaccctg	caacaagctt	tcttgatcgc	tcttagaaaag	agcaagtaac	cgcaataaat	777720
ttgctactgt	agaacgtttt	ttccctactt	tataagcaac	tntgtcctga	gtgagtcctaa	777780
agacatgaat	taatctttta	aaggcctcag	ccatttctat	agggttttaa	tttacccttt	777840
ggatgttctc	aatcaatgta	gcttctgcag	cagtaccatc	agcaatgaca	tgcttgagaa	777900
tcacagggtat	cgtagttgct	cctgcgagct	gcattggccc	ccagcgggct	cgccagcaat	777960
aagctcataa	tataacaccc	gatctccagt	gcaaatttca	cgcactacag	gaggatgaat	778020
caaacctaca	gctttttatcg	acgctattaa	ttcttgagc	tcctcattag	agaataactcg	778080
acgaggctga	aaaggactca	cacgaatatc	atctatagct	acttctataa	ttgtatcctt	778140
actgatttcc	tcagtcacaa	tatctcctga	tttttccctaa	tagaattttg	gatttgcaag	778200
catttgaaat	cctggacgta	cagggaaatgc	ttacagatca	acgtaagcat	atccaaatgc	778260
tgcataaaca	taacagcatt	gaaatttttc	tatcaaacat	ggttgtagaa	gtgaagctct	778320
tttttaaaac	ctttaagtaa	aaatctgggc	ttttctatcg	ggaagtttag	gtgctgtaac	778380
gacgggtaga	gcttctctagg	tcttctttgc	tcgcagacat	aaacagacga	aaagaaaaat	778440
aactcttgat	aaacacgaaa	caacctcccc	ccacgcacat	tcgagtcctt	agcttatgtt	778500
ctggaaaaga	gaaaaaaatt	gaatgcgaat	gctaaaattgc	gataacataa	agtgaagct	778560
tcaaatcaaa	atagggtttta	gccataaaac	tccaaacgga	agagcaciaa	ctctagttag	778620
aggaagatcc	ataaaaaatct	tcggcatgct	tatagatttt	caacgccaaa	ctgtcgtttc	778680
tttatgcaaa	agctagtcca	taatatttgg	aaaaaatttt	attctttttc	ttcggcaatt	778740
gccatttgta	tcgttcttgc	gtccttccta	tcctaaaga	ttgtttctaa	cacgtataaa	778800

cattcccaag	ccaaacgtaa	tagcattctt	ctacttacga	gagcagctga	agtcgctggt	778860
tctcaaggat	tccttccatc	taaatctgcc	ttgtcgtcat	tggaacaagc	ctatcatctt	778920
ggaggagaat	ccatgaagcc	ctatgcaggg	tttttagctt	cgtgcttcta	tattcataat	778980
gagcctttac	gtggagccta	ctacgcagga	ctcgtttata	acaatagtca	agcactgcag	779040
ctgccccacc	ccattcaaaa	actcctcaag	gaaatttcag	aagcacaagc	tgatcaattg	779100
tatgatgttg	ctttaagtaa	atcctatcag	ctcttacaaa	ctgctaacag	ctctcctgaa	779160
tatcctactc	tatctttttt	aaccctacta	cgtgtgatcg	aactcaaaga	actcctccac	779220
caagatgtaa	gtcaagactt	tgcagcattg	aaaagctccc	ccctatttca	ccaatttgaa	779280
cgcattgtata	gcgatggaga	atggacatta	agcaaacggt	ttggcaaaaa	aggataaaac	779340
tcttaaggac	ctctatgtca	gaatctctag	aaatcccggg	acttactgaa	gtgctttctg	779400
agcagccgtc	tctttctact	cccgaactctc	cccctaaagt	aatcacaggg	accttaaccc	779460
tatactttcca	agaagatatt	gacctgctt	cttaaagcct	tatgctcata	gttcttgctt	779520
tccgacaggt	ctttttttcc	cactctcgtt	cccagttaga	ccgtctaaaa	aattacctac	779580
ggctcctaaa	acaaaacttt	gctattaccc	tccccaaaga	acgaacctca	aaaggacatt	779640
cgctaattgt	cacttttgac	ttcgctcctt	ttgacttcta	tacaaatatc	tttcccttcc	779700
ttgaggaaca	aaagattcct	gctgttgtag	gggtagcttc	ccgatatatt	ccatcaaatg	779760
ctgctcaaga	ctctaccctt	tcacatcggt	taaaaccctc	tgaactcta	gcattccaag	779820
acgagatctt	ctctaactac	atgccctttt	gttgccaaaa	tgaactgata	gaaatggcaa	779880
agtctcccta	tatccaatta	gcacctcag	gattcgcaat	tcggaatctc	atgaataatc	779940
ctccgtatct	cactacagaa	attttacttt	cgcgacatca	catagaaaca	ataacaggag	780000
ccaagccctt	ggcattcctc	ttccccttcg	ggaagtcaga	tcctacaagc	cggaagcttg	780060
ctgcagatca	ctacccttat	tctttcctgt	tagggaatac	cattaacaga	aaattaaana	780120
ctcataacat	ctaccgctta	gacataaaa	ctatgcagta	cgtctgccc	agtttatctt	780180
agagctctag	gtattttaaaa	aactggatta	aagagaaaa	taaacagctg	tatctcaaaa	780240
aacaacttcc	aaaaagataa	ccttaccacg	tccaaaaaaa	tagaagatcc	tatcgagac	780300
gggtcatcta	cgaatcttat	ctaaagaatc	ctgcaaaa	aggatgaatt	gatcgatctc	780360
atcctcatca	ttatagattc	ctaaggacac	tctcaacaca	tgaccacat	tccatcgctc	780420
catagcaggt	tgggcacatt	gatgaccgt	ccgcacagca	attcctctaa	gatctaataa	780480
aaaacctaga	tccaaaggat	gggtccatc	gattgtcatg	cctataagag	ctcccctggg	780540
ttcctctata	gaagggtccga	gaatctctac	acctggaatc	tcaagcagct	ctttatgtaa	780600
atatgtagtt	agggcaatct	ctttgtcgta	gataaaactta	gctgacaagc	catcgagata	780660
atctaaagca	gcccctaagc	ctaaaactcc	agcaatatctt	ggagtccag	cttcaaatctt	780720
cataggtgca	ggaagatatt	caggattctg	atgatcgtag	atagcaacca	tatcaccacc	780780
tccttctact	ggaggcaact	gatctaatag	atcttttttc	ccatataaga	ctcctatgcc	780840
cgtgggtcca	taaatcttat	gtgacgaaaa	cacatagaaa	tctacatccc	aaagctgaac	780900
gtctatagga	agatgaggag	ctccctgagc	accatcaaca	gcaaggtaag	cgtcatagcg	780960
gtggacaagc	tcagcaactt	gttgagagg	ttggacacaa	cccgtaacat	tactcacatg	781020
aggaatgctt	acaaattgag	caccttcatt	tagaagcttt	tccaaatcat	caagatctat	781080
aagccctgaa	tcatgaactc	tgatcttttt	tactaaagaa	cctcgccgcc	gacaggaatc	781140
tcccaagata	aaacattcgc	atggtgttct	gcctcagaaa	ccagaacaac	acccccctta	781200
gggatccaga	ggtcattaac	agaaatggct	aataaaattta	accttgagct	tgtcccacgg	781260
gtgaatacga	tttactatc	agaggctgag	gatacccaact	tacgcacttt	ttcgcaaca	781320
gctgcgtatg	cttccgtgac	gttccctagag	gagctataaa	tcgcacgatt	tacagttgca	781380
tatgaagaag	tataaaagtt	agcaacggca	tctatcacct	gttgaggttt	ctgagtcggt	781440
gcagctgaat	ctaaataaat	aaaaggctcg	ttctcttttg	cttttagcagc	aaaaatcgga	781500
aaatcttctt	ttaaattctt	cactgatcat	ccccccctt	aaatcctaaa	cctaggaggt	781560
ttgatttagc	tgaaaagaag	atcccaaaaa	cgtatcgga	actaatcctt	gttttaggaa	781620
cccattgtatg	agtttttctt	gagcctctgc	ctctgtcatg	cctcgagaac	gcatgtaaaa	781680
gatctgctga	ggatctaaag	gtcctactgt	agcgccgtgg	gatgccttca	cctcgtctgt	781740
ttctatctct	aaacgtggaa	atgtagatac	acgagcttct	gaacttaata	acaacgtatc	781800
atgcttttga	ttcgcatccg	acaagtctcc	ttgagaagaa	atagaaattg	tcccttcaaa	781860
tagaaaatgc	cctgaatata	aaatcgattt	aatattctga	cgcgataccg	tctcttcagc	781920
atcgtgagac	attaaattat	tgacccaagt	ttttcttggc	gattggacta	acactagaga	781980
ttctgcgtgt	cccttcttcc	cgactatgta	gctcgtattg	tcaaaccatc	cgaacacctg	782040
acaactttca	agcaaattct	gagtcactct	gcagatagca	tctttctcaa	ccgtcgcaat	782100
agtggaccac	ctcaaggat	cctcttcaga	atatcctgga	accataaaca	ctgtaagatc	782160
cgcccttctt	ccaacgaaga	gctcggtaac	cccatgact	atagttttac	tagaaccac	782220
catctctaaa	tcaacatcat	gtgatatttg	tatttgagcg	gacgcccgtt	gtcctaaaat	782280
aacgacgac	ctaggagaga	aaatcacatc	atgatccgaa	actgtaggaa	aactaatatg	782340
acgtacaaaa	ataggatcgc	tcgtctgcat	ctcttcagga	atgtaaatca	ctacaccccg	782400
atcttcagaa	caaacagcat	ttaaaaaatgc	taagggatgc	ttattttacat	caaacccttg	782460
catgaatgaa	gacaatgatc	ccctagcttc	gtctatacca	cagacaatca	ccccctcagg	782520
caactgggat	aacgaaggtt	cgtatttttc	attaattaaa	atacactcaa	aggctaaaga	782580
atggttattg	tgtagccaat	gttgcttaat	tagttctgaa	gctccagtcg	caagattatt	782640

agcgatcagg	aaaaagagaa	agctcctgaa	tccaagaaaa	gctactaagc	acctcttttg	782700
aagaaggctg	cttgctatat	tgagtgtagc	aagcttccgc	agctttttgc	acaggagaac	782760
ccgaagcaat	agaagaaaat	gtctctattg	aaactaacac	cttatctcca	cgcaacacgc	782820
ttagtcacct	cttggttagct	ttttgcttct	aattcatgca	tcaaagaaac	gtctcctgaa	782880
agcgctactc	gaccatctaa	taaaagatga	acaacatcag	ggcgaatgag	gtttcctaata	782940
ttgggggtgt	gagtcacaaat	gcataaggaa	ctggtaggat	gtaactctcg	gtatttctcc	783000
aagactctac	aaatcaaacg	taatgcatct	acatccaaac	cagaatcagg	ttcatctaagt	783060
aagaccattt	cgggttctaa	aactagcatc	tggaatcat	cattgcgctt	tctttctcct	783120
ccagaaaaac	cctcggtgac	attcctatct	aaaaatagat	ctgtagtcgc	gttatactca	783180
tatgtctcta	atacagtcga	aagcagagta	ttaaactcat	caatagaaat	atctccctct	783240
tgattcgcac	gacggcgggc	attataggcg	tctcgcaaaa	acatcttggt	attgactcca	783300
ggaatctctg	gaggcatttg	aaaaccaaca	aatagccctg	ctcgggaacg	ctcttctggc	783360
aacatagaaa	gcaaattttg	ctcctgtaat	gcaatctcac	ccgaagatac	caagacactc	783420
tcactctccg	ctaaaatttt	agcaagagtc	gattttcctg	ccccattagg	ccccattagg	783480
acatgcatag	ntccagggtg	gatattcaaa	ttgaaatcat	ccgaatcctt	cacatcatta	783540
cagctagcat	gtaagtgcct	tatttttaac	attgaacctt	acccacgcta	ttttctaatt	783600
taattaacaa	taacttcgat	gcttcctgag	caaattctaa	aggtaattgt	tctataattt	783660
cccgacaaaa	accatggatc	actaagctga	ctgcttcctc	aggactcagt	ccacgactac	783720
gtaaatacaa	taactgatcc	tcacgtaatt	ttgaggctcg	ggcttcatgc	tcaattgaag	783780
atgttggaatt	ttctactaca	atcttcggat	ccgtataggc	tccggaagcc	ttgcctatca	783840
acatggagtc	gcattgcgta	tagttactac	tatgttcagc	ctttttccct	aaggagacca	783900
aactttctaa	cgtgttctta	gactcgtcag	aagaaattcc	cttagagatc	accgtggatg	783960
tggtgcggtt	ccctacgtgt	agcatttttg	tgctgtgtgc	ggcctgcatt	ttcccactag	784020
taagagctac	agaataaaat	tctccaacac	tctcgtcgcc	ctttaaaata	caactagggt	784080
atttccatgt	aattgcagca	ccaacctcaa	cctgtgacca	ggagatctta	gaacgatagc	784140
ctgcgcacag	acctcggttt	gttacaaaat	tataaatgcc	gcctttccct	gttttcttat	784200
caccagcata	ccaattttgc	accgtggaat	accttatgac	cgcatgctca	tgagccacca	784260
attcaacaac	cgcagcatgt	agctgattag	aagagtatgc	cggcgccgta	cacccctcaa	784320
gataactcgc	atagccgcca	tctccacaa	caatgagagt	acgctcaaat	tgaccgcgtt	784380
ccttgttatt	aatccgaaaa	taggtagaaa	tatccatagg	acatttcacc	cttttaggaa	784440
cataaacaac	agagccgtca	ctaaaaacag	ccgcattcaa	agcagcaaac	aaattatccc	784500
gatgcgaaac	aacggagcct	aaatatTTTT	ttaccaaatt	cggatgttct	tgaatcgctt	784560
cgcccaaaaga	acagaaaata	actccggcct	tttccaacgc	ttctttaaat	gtggttccaa	784620
tagagaccga	gtcaaaaact	aaatctacag	caacattctc	gacatttagt	aagcgcttct	784680
gctcatctaa	aggatatacct	aattttttga	acgtatctaa	aattttctgga	tccgcatctt	784740
ctaaacgtcc	aagagggttt	ttctgcttag	gagatgaaaa	atagactata	tcacataggt	784800
ctataggacc	ataatgcagg	cgtgcccagg	ctgggtcatg	caactgcttc	caataacggt	784860
atgcttgtaa	acgaaaatct	ataataaact	gaggttcat	acgtagagca	cgatttctct	784920
cgattgtctc	ttcactaagt	cctcgcgtca	atccttgaga	ctctatagga	gtcacaaaaac	784980
cgtaaggata	gtcctcacgc	tcttctaaaa	aaacctttac	tgattcgccc	ataaccttta	785040
atcccgctcg	gcaaaactct	tgaatttatc	gtattaaatt	acacgaggac	aaagctaaga	785100
tagcacacag	attatttttt	cagtataaca	aagaaggctt	gaaagacgaa	cctaccctct	785160
tcaagcccag	aagaaaagag	aaagaatttt	ctaaaaatcc	taactccctt	ggagatcaca	785220
ccatcagcat	ggaatacact	aaggcgctta	catgcaaacg	cattctaggg	aaataaaaaa	785280
ttttgtctct	ctaattttcaa	ttgaaaacac	tatttcccta	gtttattgct	gtgacgtttt	785340
ttctacttaa	catgccttaa	gaaatagtat	ctaaacgcct	ttcaaattgc	attgaggagg	785400
gatctgacac	cacagtcttc	tgcaataagg	gagcaaacgt	agaatccctt	ttttgcaaaa	785460
ataaaaagctc	ttttgttgcc	ttatcggtct	ctccttgcat	atgatgcaaa	tagcccagaa	785520
gatagtgagc	gcgctcatgt	tctaaattaa	tagacaacgc	gctattaaaa	gcctcatacg	785580
cttcccgcct	ttgcttaaga	tccaagttag	caagtccgac	ataaaaaatgt	gcacagcat	785640
cttcagcatt	gagaaacaac	gcttcttgaa	aagccttcaa	agctaactga	gttttatcta	785700
aagttagata	acataaacct	aaattgtaat	gaccatcaga	caaatcaggt	cgcagctgaa	785760
caacacgttc	ataagcctca	gtagccttgt	cccatcggtt	gcttcgagaa	agcaaaaaac	785820
ctaactttac	ccaagctttc	caatataagg	gattcttcgc	tacagcaact	tcaagcaaac	785880
gaatggactc	cgttccatcg	tccatttcag	aaaggatcac	tgctttatta	tataaacttt	785940
gtggattcca	aggatcaagt	gcaaggatct	tatcaaaaaca	atctaaagcc	tcttgaagtc	786000
tcttcaaacg	atgatataca	cttccaagac	taaaccagca	ctcaacatca	tccgggatgca	786060
aagcaacata	cgcactatac	tgttcgatag	ctgcttcata	ttgattcccc	cgggtctaacg	786120
ctacaccata	acaataacgg	agatagctgt	ctcccggctc	ggatgctaaa	cctttagaac	786180
accagttcaa	agcctcggag	actcttccag	tctctaaagc	aataatccct	aaataacaat	786240
aagcgagtgc	tgctgtagag	tctaattcta	aggtttcttt	cagctttttt	tccgcttgct	786300
catattcacc	gtcctaaaaa	aggtttaattc	ctgaacacag	aaattctttt	gccaaagtgt	786360
tcgcagcttc	ttccatggat	atttctccca	gcacatgatt	cggtgatctc	aactaaatga	786420
ggagcgaaaa	ccatgccaaa	agaaaactat	ccccttaaaa	aagattctct	ttgttgaatt	786480

ttttcccaca	tatcaatcat	ttttaccgcc	ataggagccg	catctcgacc	aaattctcct	786540
aagcgtaaat	agactatgac	tacgatcgta	ggaagagata	aatcttgatc	agaaaaaccc	786600
accgcagcaa	accagatgtc	tttcattttc	atgggtaccat	attcccgatc	cagtcaccaca	786660
cgcataatgg	actctgctgt	acttgctctt	ccaataatac	gagacaaaag	ttgtggaggga	786720
aattgacttt	gtattgctcg	agctgttccg	tattgacccc	agataacatt	gcgcattgcca	786780
gtcttaagca	cctctactac	agcatcaggc	atgaaaatcg	ttcgcttctt	tttagaagag	786840
agataagaaa	catgctcccc	ctcccattct	ccaagcaata	acttggggac	ataaaccaca	786900
ccgccattaa	ctaaagaagc	taacatcact	gctgtctgca	aaggagttac	aacaagagta	786960
tcgtgtccaa	tcgctgttgc	gtataaacgc	gaacggttat	acgccaaatc	atgaggcacc	787020
ctaccgcgat	actctcctgg	caatcctaaa	cctgttttct	cgccaaaacc	aaataaagaa	787080
gccgcgtctg	ctaaatcttc	aggatcccca	agaccttccc	ctaccaataa	tgaaaagtac	787140
gggttgctag	acatctctaa	tgctgagact	aaatcaataa	agcctcttcc	catgaaatca	787200
tttcccggca	aactcccccc	acggaaaaac	gtgggaatcg	gtgtgccatc	tttaaaaaag	787260
cccacgtgag	gcttagaact	cctatagcca	aaggaatttt	tatcaataat	gaccaaggga	787320
ttcgcaggct	cctcattatg	tcccataag	atcctctgag	ataacacaga	atatgcagat	787380
actaatctaa	aaatagaacc	taaggtagct	gcttgcccgt	aggcatgagg	acgtagggtat	787440
ccgtatccat	atactggata	aaaagaagca	gctaaatctt	gttctgtctg	cctcttattt	787500
ctcacaatcg	agatgggata	tttgccaat	agaggacgtt	gcaattcatt	gaattcacga	787560
aatgtagaaa	aaagtgcagg	gagatgttct	gaaagatgcg	acacacgttc	ttttagaaaa	787620
agataatggt	cgttccaaga	taacgctcta	tgcgctccat	tatctaattc	atztatccat	787680
aaatctaaaa	tatcatagta	aggctctaag	ccttctttat	aaggggtttt	agaaaaataaa	787740
tacgcaagaa	atgtatccaa	atgttcttgg	cagaacattt	tatatgtcct	tgttttttct	787800
tcctctaagt	aatctacata	aggtgtagga	tacctctgtt	tccttaatgc	ttcctcttga	787860
cgtttcgcag	caagatatgt	aagaaattca	ctcttacgcc	acgacttaaa	atgcacctca	787920
ataaaagcat	cttctaaaaat	agtagagaat	gcagagcgaa	gcaccacata	acgtccttga	787980
agctctgtaa	attcagataa	cgagagccta	tgaacctctg	aaggaagtac	aggagaaaaa	788040
cgctctggat	ctacaatcag	cctaaggata	tcggtataca	agattttatc	gtaattcgca	788100
ggaagctcat	taaaaacttg	gtctaattgt	tccttaagct	cttcaatatc	tgctttatgc	788160
tgattcagac	attccatgat	ccatttttgt	tcctgaagag	aaatgacttc	ttggattaag	788220
atatgcccct	cttcattagg	gaaaactgca	tcaaaaatag	cggacaacagg	acacgtcccc	788280
tcttcataag	gaaataaaga	aagcaaacga	gtcaccaagt	tttgaacctc	tatcgcttgt	788340
cctacaaagc	tgtttctttt	taactgcaat	ttaatcacag	agttttcagg	gaaaagaaaa	788400
tcaaggaagc	aatcaaaggt	taatggcaaa	atctcttcat	aacataatcc	agtaagagga	788460
ttccttcttt	cccgaattag	agggactttc	ctatcataaa	tttctgcaat	atgctcttta	788520
ttttctaacc	atccagataa	atagacgata	ttaccgcttt	agaatcttcc	gcaaccttcg	788580
cattcacaaa	atcattgtta	cgataacggg	gagaagaagc	catggctaaa	atctctccgt	788640
tattaggatc	taacgcaata	atggctcctc	ctttaatcca	agggaacaaa	ggaggaagct	788700
tctctcgttt	cttcaatgac	ttagcactac	gaaacgtctc	cgttttttca	tattctaaaa	788760
gtaacgcac	cgcatacgct	tgtagctcag	cagacaaagt	caactgcaat	ttagttccag	788820
gagcttcagg	aacagcaccc	tccatttctt	gaatgaagtt	cccacgacga	tctactaaaa	788880
tcggtttttt	tcgcatctta	cctcgtaatt	ttgagtccca	acagtgcctc	aacacccatt	788940
tttcctacta	aagcatttaa	actataagcg	ttgctctcca	cagactctaa	taaagcacgc	789000
acctgatcta	tacttgctaa	tccttcaggc	aacttaggat	cttcaccctc	ttcataagca	789060
cgcacacact	cacgcaattg	actcagctcc	tgagtgactc	tcttatactc	ttgaagactg	789120
ataggctcta	cataacctaa	aatatctgaa	gccacgcttt	cttgaggata	atgacgacga	789180
actacagcct	ctacatgcaa	tccaggccaa	tcttttagata	acattttgag	tttcaaatag	789240
gtgcgctcag	aaacattagc	agccactaaa	taagggaccg	aacctaatat	agaagctttt	789300
gcatgaattg	catcttcgat	cgccctcgca	tctaaatgca	attcctgaga	taaaagctca	789360
gacaaacaca	ttatataatg	cttacgcaca	ggaatgagct	gtttatgcc	atgctcatcg	789420
acacgccaa	cccgagtagg	caaatacaga	atggcccat	aagcaacgct	cacatcatat	789480
tgcaactgat	tcacagccaa	tgtctttcca	aaacgatcac	aaatcgttgc	tctttccaca	789540
tattgaggaa	gcactcgaat	ctgtggcttg	tatgcctctt	ctaacttttg	ttcatgttca	789600
acaacagcaa	gataaccataa	acgcaatgca	atcacagcaa	atgcaataac	aatcccagac	789660
aacagtctgt	tggtcttttg	agcaatggaa	agataaatag	gaaatttttt	cggtcgtttc	789720
atgctatgga	tattatgagc	ttcactctcg	cttgaaaatt	acagagaact	atgctctcac	789780
attattttca	atcatagtct	gctaaatata	ataataaaaa	gaagcacgat	atttaagaag	789840
aatagtcaat	ctaatacgaa	aaaatctaga	gaagatacag	ttcgcaaaat	acaactaatt	789900
ttagtccaat	caaaacatat	taaaacccaa	aatcatgttc	taaataataa	aaataaacia	789960
aaaaatttct	caagagaaaa	agacttgaga	aggtagttag	gagccatttt	taaggggaac	790020
taaattatat	atataatgaa	agaatatata	aaaaaagcta	tagctttcct	atagctcata	790080
acagaagttc	ttggttgaaa	tatgctggta	aaaacactta	atcttcttat	cgtctttact	790140
ataataagaa	aagtgttgata	tgttttcgac	tatgagctgt	tatgttcata	tttaaggccg	790200
tttttcaatg	ataagagctt	cctaaatttg	cctgcaggat	atcttgtctg	gctttaattt	790260
ggacgtcgtg	tcgccaaaaat	atgagtaata	gcgagcacat	aaataaaaaga	tactaagcat	790320

aatcttttaga	ggtgagtatg	aaaaaactct	taaagtcggc	gttattatcc	gccgcatttg	790380
ctggttctgt	cggctcctta	caagccttgc	ctgtaggga	cccttctgat	ccaagcttat	790440
taattgatgg	tacaatatgg	gaaggtgctg	caggagatcc	ttgcgatcct	tgcgctactt	790500
ggtgcgacgc	tattagctta	cgtgctggat	tttacggaga	ctatgttttc	gaccgtatct	790560
taaaagtaga	tgcacctaaa	acatttttcta	tgggagccaa	gcctactgga	tccgctgctg	790620
caaactatac	tactgccgta	gatagaccta	acccggccta	caataagcat	ttacacgatg	790680
cagagtgggt	cactaatgca	ggcttcattg	ccttaaacad	ttgggatcgc	tttgatgttt	790740
tctgtacttt	aggagcttct	aatgggttaca	ttagaggaaa	ctnntacagg	ttcaatctcg	790800
ttggttttatt	cggagttaaa	ggtactactg	taaatgcaaa	tgnactacca	aacgtttctt	790860
taagtaacgg	agttgttgaa	ctttacacag	acacctcttt	ctcttggagc	gtaggcgctc	790920
gtggagcctt	atgggaatgc	ggttgtgcaa	ctttgggagc	tgaattccaa	tatgcacagt	790980
ccaaacctaa	agttgaagaa	cttaatgtga	tctgtaacgt	atcgcaattc	tctgtaaaca	791040
aacccaaggg	ctataaaggc	gttgctttcc	ccttgccaac	agacgctggc	gtagcaacag	791100
ctactggaac	aaagtctgcg	accatcaatt	atcatgaatg	gcaagtagga	gcctctctat	791160
cttcacagact	aaactcttta	gtgccataca	ttggagtaca	atgggtctcg	gcaacttttg	791220
atgctgataa	catccgcatt	gctcagccaa	aactacctac	agctgtttta	aacttaactg	791280
catggaaccc	ttctttacta	ggaaatgcc	cagcattgtc	tactactgat	tcgttctcag	791340
acttcatgca	aattgtttcc	tgtcagatca	acaagtttaa	atctagaaaa	gcttgtggag	791400
ttactgtagg	agctacttta	gttgatgctg	ataaatgggtc	acttactgca	gaagctcggt	791460
taattaacga	gagagctgct	cacgtatctg	gtcagttcag	attctaaaga	tttgcttaga	791520
atctctctct	accttggttat	cagagtctac	atggttaggtc	ctgatttatg	ctcagagctt	791580
cttaattttct	gagcaattttt	tattcccccc	ctacttcaca	tcacatcaag	acaaatgaat	791640
tatttactta	tgctatttttc	taatagcttc	ctgtagatta	cacgcttgcg	ttaaaagcat	791700
tattacacta	ctataccctt	taatccagtt	tgcgcccgta	gctcaatggg	agagctgtag	791760
ccttccaagc	taccgggtgtc	agttcgattc	tgatcgggcg	ctttctttac	acaaccaaga	791820
ctgaaattct	ggctttttatg	tcagaatgcc	gttggttaacg	tattctaatt	ttgaaataga	791880
ggtacaaagc	ttggaatccc	aatcctgcaa	acttacaatt	aaagacctta	tgagtgcgcg	791940
tgctcatttt	ggacaccaaa	ctcgaagatg	gaacccaaag	atgaaacttt	acatctttga	792000
ggagaaaaaac	ggtcttttaca	tcacatcaat	agcaaaaaact	ttacagcaat	tacgcaatgc	792060
tcttccccac	attcgcaaaag	taattcaaga	caataaaaact	gtcctattcg	taggaacaaa	792120
aaaacaagca	aagtgtgtca	ttcgagaagc	tgcaaatagaa	gctggcgaaat	tttttattgc	792180
tgaacgttgg	ctaggcgga	tgtaaccaaa	catgacgact	atccgaaatt	ccattaaaac	792240
gtagagacaaa	attgaaaaag	atcttatctag	aaatcaggcc	tatcttacta	agaaagaagc	792300
agctctttta	gctaaacgtc	atcaaaaaatt	attgcgaaac	cttgaaggga	ttcgttacat	792360
gaagaaggct	cctggtcttc	tagttgttgt	tgaccctagc	tatgaaaaaa	ttgctgttgc	792420
agaagcaaaa	aaactcggaa	ttcctgttct	tgctctctgc	gatactaact	gcgactctac	792480
tcctatcgac	catgtgatcc	cctgtaatga	tgactctctt	aaaagcattc	gattaatcat	792540
caatgtgatt	aaagaaaata	ttatcgagcg	caaacaataag	cttggatatag	aaattgtttc	792600
tccagtga	tctttagaag	tgcccgatct	ctcagctttc	gaatctagcc	aagatgacga	792660
atctgacgaa	gagaatcgag	aagaagatct	attagcaaaa	aaatttgatg	gcgaggcaaa	792720
ctaattgagcg	acttttctat	ggagacccta	aaaacattaa	gacaacaaac	tggtgtaggg	792780
ttaacaaagt	gtaaggaagc	tttagaagct	tgcgggtggt	acctagaaga	agctgtgtgc	792840
tatttacgta	agttgggatt	ggcatctgct	gggaaaaaag	aacacagaga	aactaaagaa	792900
ggcatcatag	cagctaaaac	tgacgccaac	ggcactgcat	taattgaagt	gaacgtagag	792960
acagattttg	ttgcaaaaca	cgcagctctt	agagaatttg	tttccaatct	acttaatgac	793020
atcttcaaat	acaaagtaga	taccgttgaa	ggcctatcgc	aagcagcctc	gtcccaagat	793080
ccctctcttt	ctgtgacga	actcagagca	gtgactatgc	agactgtagg	agaaaacatc	793140
cgtattagta	gagtggtcata	ctttcctaag	gctacaaaat	ctactgtagg	aatttatctc	793200
catggcaacg	gcaagacagt	agctctgact	atgctttcag	gctcctctac	tgctgacagc	793260
ttagcaaaag	acattgcaat	gcatgttgtt	gctgctcaac	ctcaattcct	cagtaaaaga	793320
agcgttctctg	ctgaagctat	tgctaaagaa	aaagaagtga	ttgcttctca	aattcaagga	793380
aaacctcaag	aagttattga	gaagatcggt	acaggaaaaat	taaacacatt	cttccaagaa	793440
gcctgtttat	tagaacaacc	atcttattaag	aacgcccagc	tttctattca	aagtttaata	793500
gatgatttct	ccaaaacctc	tgggaagctct	gttgcaatag	aacagttcat	tttatggaaa	793560
ataggagcct	aataaaaaaca	tggctaagca	aactagacga	gtcttgttta	aaatttctgg	793620
ggaagcatta	tctaaagatt	ctagcaatag	aattgatgaa	atgctgtttat	cccgaactgg	793680
atcagagcta	agagcagttc	gtaataatga	tatagaaatc	gcccttgtaa	tcggcggtgg	793740
caatatttta	agaggactcg	ctgagcaaaa	ggaacttcaa	attaatcgtg	tatcggcaga	793800
tcaaatggga	atgctggcta	ccttgatcaa	tggtatggca	gtagcagatg	ctttaaaagc	793860
tgaggatata	ccttgtcttt	tgacatctac	cctatcgtgc	ccacagttag	ctgatcttta	793920
tactccacaa	aatcaaatag	aagcttttag	ccagggaag	attcttatct	gcaccactgg	793980
agctgggttct	ccttatctga	ctacagatac	tggagctgct	ttacgagctt	gtgagcttaa	794040
tggtgacggt	ttaatacaag	cgactatgca	tgtagacggt	gtctatgata	aagatcctag	794100
gctctttcca	gatgctgtaa	aatatgattt	tgtttcttat	aaggattttt	tgagcaatca	794160



actaggggta	atggatgcat	cagcaatttc	cctatgtatg	gattctcata	ttccaattcg	794220
tgtcttttagc	tttttacagc	actctctaga	aaaggctcta	tttgacccta	cgattggaac	794280
attagtttagc	gaggatgtaa	accatgtctg	ttctccaaga	cactgagaaa	aaaatggctg	794340
cggcttttaga	tttttttcat	aaagaagtaa	agtccttttag	aacaggaaaa	gctcatccag	794400
cattagtaga	aactgtttgta	gtcgatgttt	atggcactac	aatgcgtttg	tctgatatcg	794460
cttcgattttc	tgttgagat	cttcggcaat	tggttatttc	tccctatgac	gggaacaatg	794520
cttctgccat	tgcaaaaagga	attattgcag	cgaattttaa	cttacagcct	gaagtccaag	794580
ggctctattat	tcgtattaag	gtccctgagc	ctactgctga	ttaccgacaa	gagatgatta	794640
agcaacttcg	ccgcaagtgt	gaagaagcta	agatcaacgt	tagaaatata	cgcagagaag	794700
ctaatagacaa	gttgaaaaaa	gactcggctc	ttacagaaga	tgttgtaaaa	ggtaacgaga	794760
aaaaaattca	ggagttaact	gacaagtttt	gcaagcagct	tgatgagtta	acaaagcaaa	794820
aagaagctga	aatagcttca	atataagtat	acttaggggt	tttcttttcc	ctctgacttt	794880
tttagtcata	gagagggaaa	aagattgctc	taaagagaga	aaattagtaa	catttattcg	794940
tcttggtcccc	atcgtctagc	ctggcccagg	acatcggatt	ttcattccgg	taacaggggt	795000
tcgaatcccc	ttgggggtcaa	agtataaaat	taacaagata	tttcgggtct	ttagctcagc	795060
ggtagagca	cctcactttt	aatgaggggg	tcgaagggtc	aaatccttca	agaccatttt	795120
aatgattctt	gttaacttta	tctttttctaa	aaaaaatctt	tttcccccta	gttctatttt	795180
tgctatgtac	tgagtaccga	gcttaatgga	acttaactca	tggttcactc	acctacccac	795240
caatgttatc	attgtcaaca	gcctgccacc	atatgctata	cagaaataga	taaggataag	795300
gttatacgct	cttatgtatg	cgcaacatgt	ccttgctcta	gccattacta	taataatgag	795360
cacctgagtc	tatctaaagg	ggttgggggt	ctcacttttag	agtgcggcaa	ctgtaaaacc	795420
gtatggcatt	caaagcaaga	cgacgaacaa	ctgtaggct	gccaccaatg	ttatacaaat	795480
ttcaaaaatc	agattaccag	caaactcaaa	agtgagagag	tggtatcttc	atcctttact	795540
atggagaaa	gccaaggctc	tcttcatata	ggtcgagccc	ctggggaagc	ttccaataca	795600
aatcctcttt	taaaacttat	agcattaaat	gaagctttac	aagatacctt	agaacgagag	795660
gactacgagc	aagcagcagt	aatccgagat	cagattaatc	atttaaaaac	caaaaatcca	795720
gatgaccctt	cctaattgatt	tactagagac	cttagtaaag	agaaaagaaa	gtccacaggc	795780
aaacaaagtg	tggcctgtaa	ctacattttc	tttagctaga	aatctctctg	tatctaagtt	795840
ccttccctgt	ttatctaaag	aacagaaaat	agagattctc	caatttatca	cctctcattt	795900
taatcatatt	gaaggctttg	gggaatttat	agtgccttct	ctaaaagaca	ctccccatg	795960
gcagaaagag	tttctacttg	agcatttttt	actcccttat	gatttggtgg	ggaacccaga	796020
aggtgaggca	ttagtagtta	gcagatctgg	agacttctta	gcagctataa	attttcaaga	796080
tcactctgtt	ttacatggaa	ttgatttcca	aggaaatgtt	gagaaaactc	ttgatcaact	796140
tgtacaattg	gatagttatc	tccatagcaa	gttatctttt	gctttttctt	cagaatttgg	796200
attttttaaca	accaatccta	agaactgtgg	gacgggggta	aaaagccaat	gttttctgca	796260
tattcctgcg	cttctatatt	ctaaagaatt	taccaatctt	attgatgaag	aggtggagat	796320
aattacttct	agttttattac	taggggttac	aggatttctt	ggcaatattg	tggtattatc	796380
gaatcgttgt	tcttttagggc	tactgaaga	actgttctt	tcttctttaa	ggattactgc	796440
ttccaagctc	agtgttgctg	aggttgagc	aaaaaaaagg	cttcttgagg	agaattctgg	796500
cgatttaaag	aatcttatcc	ttcgttctct	aggcttactt	acccattcct	gccaacttga	796560
gctgaaagag	actctagatg	ccttgagctg	gatacaactg	ggatatagatt	taggcttgat	796620
taaagtaacc	gaaaatcatc	ccctatggaa	tccattattt	tggcaaatac	gtcgagcaca	796680
tcttgccctg	caaaaacaag	ctgaaaactc	ccgggatctg	caaaaagata	cgatttcaca	796740
tttaagagct	agcgtattga	aggagttaac	taaaggatta	tctcctgaga	gtttctgata	796800
aaattctgaa	gatataattt	taaagagaga	tgcccaaagc	cgggatcgaa	ccgacgacct	796860
acacgttacg	aatgtgttgc	tctaccaact	gagntattta	ggcatgtcgt	aggaagttagg	796920
gaacaaaaaa	gccaagaaaa	cataaagtta	tacggccgac	tcttacatct	tcttggcttt	796980
ccccctgaat	gcaacagagt	cagaagctat	tccacggcgg	agaatatcat	cttctctttt	797040
tatataccac	tactgagctt	ctatttctat	tatttttaaag	tcactttcag	cctgtaaaga	797100
aggaggtcct	tggcattcag	gagcatggcg	agggggcact	tgcattggatc	cttcatcagc	797160
ttcccaattg	tatctgtatc	cttccctatt	ggtaacacga	gtgccttctt	caaagctact	797220
aatcacctta	ggcttaataa	acatcatgat	attgcgtttt	tgccttttgg	cgatggtacg	797280
gctaaataaa	ccacgaatta	atggatgga	gttttagcaaa	ggcactcctg	aaaccacttt	797340
tgtagtttta	tctctgatat	gcccactcat	aactaagaaa	caaccgtcgg	gaatttgtaa	797400
gcgtgtggct	gcataagttt	tatctgtgac	aggtgttagt	gatccagacg	cggaatgtaa	797460
tcttgagatc	gtctgttcga	tttgtagtgt	aactacattg	ttgggagcaa	ctgtagaggt	797520
aacgacaagg	ttcactccaa	tatcttcata	atcgatatatt	tgcgttacag	ttcctgtttc	797580
ttggataata	gtattttgtag	tttggttaagg	gaccgtttgc	cctacaaaaa	acgaagcttg	797640
ttgcgtatcc	tgagccatga	ttctaggatt	caagacaatg	acagtatctc	catcttgatc	797700
taaggcactt	aataagcctc	ccaaagtaag	gaaagacttc	cctttatgac	ttaggacatt	797760
tccgatgatt	cctagaccga	atgctgacga	agagttcagc	atatctgaga	accctgtcaa	797820
ttgtcctggc	gtaggaagag	ggatcgaaac	aggatttgcc	gtgccgggag	ggacagttgc	797880
ttttgtaggt	gtggctatgc	cagtattatt	caatagtcca	gaagcataag	ctactttact	797940
ttgttcacat	cctagggcta	cccatgtcac	tccaaaagtc	caggatttct	ctaagctggg	798000



atctagaatt	aaaacttcga	tgtaaacctg	tttaggaggt	aaatctaaac	cgtttaagag	798060
gccaataact	ctgtcgacat	tcccttggtt	tccgataata	actatggagt	tattgacctc	798120
taaccactgg	atactattga	gagtgttaat	gaaatcttcg	tccatagctg	tggttacata	798180
tagattgtaa	ccgatatctt	ggagggcatt	agcaatcact	tctccatttt	gatacttcag	798240
cttgtagata	aagaaccgca	aactcttagg	gctcgtgggt	cctgttcctc	ccaaagccaa	798300
ggcagtaact	gcaggatcat	ctagggtatg	tgccatttct	gggacatcta	aggacttcag	798360
gagctgctct	gccttatttg	caagacgtgg	tgaagagacg	acgaaaattt	tggtcgttcc	798420
aggttggatg	aacatttgga	aagcatcatc	ttcggccaga	gtaccaagaa	catcttggca	798480
gtagcttaaca	agagctgctg	gattggcata	tttaacttcg	tattcagtcg	tggtccacaga	798540
tgtgcctggg	caatctagag	ctgctagcaa	atcactgact	ttatcgacat	taccagcaat	798600
atccgagatg	ataacatgac	gagtagcttc	tgaagcacta	acgatagcat	catgggaaag	798660
taaagggttg	ataatattta	ctgctgcaga	gggctgacgc	tgtaaagacg	gaacactcgg	798720
gtaaccacaa	cagcttcaca	cgtttctttt	aaggagctgt	ctgtgactac	tggtgtagtc	798780
ttagaaagat	gaggattacg	atagataagg	acgttattgc	cttgttcaac	aaccttcaag	798840
tcatgcattt	ttaagacttg	tagtaagatt	gtagataaat	catctacaga	agtaggatcg	798900
tgggaaacga	tcgtgacatt	gaattgcaaa	tcgttgctat	caaagacaaa	gttcgttcca	798960
gaaattttac	ttacgaactg	caacaactct	aaaatagaaa	tgtcttcaaa	attgacagta	799020
tagccgttat	ctttaagggtc	ttcacaggta	agttcccgtc	ttgtcaatcg	ctctttaact	799080
ttttcttctt	cagatttggtc	ttgaggtaca	gccactgttg	ttgtctgttt	ctcgattcct	799140
ggcatagagg	tcgaaggact	tgcaacgttt	ttcttcgaag	cggtgtggtg	tgcttgtgtt	799200
ttaggttgga	cgctcttctc	tgtaactgtg	gaggtttgct	cttcgagttg	tttttttata	799260
ctcagattga	tagcatttac	ggctctgcga	gcataatttt	gtttttcttc	ccaaacctgt	799320
atactactta	attgttcttt	agaggcggca	ggtagcggct	cttcgacttc	ttgtgttggt	799380
aagaagcgtg	gggatctttt	tacatcggca	gtagttctac	gctctgggtc	agggtttttt	799440
ctctcttcca	gttctttcag	ggtggttaggt	tttgctggga	atgcggatcc	tgaagtcttt	799500
tggaaagttt	tatcttgggt	tgctgcgaat	ttagagaaga	ctttactggg	gatagaacct	799560
ggagtgggtt	tcttggtatg	acttttcttt	gctgaaagtg	aggctgctga	attttttagga	799620
caagcagcta	acttttcatc	tctaagattg	tgttttacat	ttgccgaggt	ctctgtaggc	799680
ctctgggnac	ttacaccaag	taaaactaaa	tctaaaaaaa	agagaccact	naaaatcccg	799740
atcttttttt	tctntttttt	gatgccttgc	aagatttttc	ttccaatggt	caatatcaca	799800
gttttcaccg	gattcttttt	aagctaattga	cggttgaggg	agagttactt	ccgtgctgac	799860
gactttgtat	tccaccatgt	atgctctcta	tgggacagaa	tatagctttt	tgcttcttat	799920
cttgcaactc	tgcgagtgat	agggttttta	aggatgcaac	agattcttct	aattccagcg	799980
tacacactac	agcttcatca	cctatttccc	atgcaacctt	ggtttctcga	atttgtaaaag	800040
aagtaatttt	ccctaattcct	ggggaaaagc	tctcaaagtc	ttggacaacc	cttccctgtc	800100
tttttatcca	gaaaacgggt	ttcccacaag	ctatccaaga	gagttcctta	ttttcttttcg	800160
aaatttcgag	gcagagtata	gagataccca	tttcatctat	gggtattttc	atgcgaatca	800220
agcactcatt	gatttcgcat	actctatcta	aaagaggtcg	ctgtagatct	tggtggcaga	800280
ctaaactttt	tacaacagac	aaagctatag	ttgcattact	tataggactg	taacctaac	800340
acagattaaa	aacatctcct	tcaagcaacg	tatcatatgc	atgaggatac	aagggatatc	800400
cttgatgata	gagaactccg	gatataaaat	ctggaaacct	cagagtttct	ggggctaacc	800460
aaaatcggtg	tgtttgcagc	tgttcataga	gagctaccgt	gtgatcttta	atacgtagat	800520
cttcttgcat	gtctccagac	atgcgatagt	gatgtatatc	ctggataaac	tctcgggtcg	800580
agctgtagcg	attattagga	gaaggctgta	acgcttttgc	taaaatttta	cttattcttt	800640
cgggcactaa	tgaagaaaag	acgcgtccta	aagaaaggtg	ccctaagatc	aactcataag	800700
ctaacaaccc	taaagcataa	atatccgaag	cgggagaatg	agactcccct	tggtgtgtgt	800760
ctggactcat	ataataagga	gttccgataa	cgttaggatg	tgctctctgt	atttccgtat	800820
cccaatcagc	gagtcgaaa	tctatgagtt	tgattttacc	ctgaggagtg	atgagaatat	800880
tttcaggctt	gatatcttta	tgtagaatat	tccgactatg	gaggtgctcc	aaagcttgag	800940
caatatcaaa	gataatatct	atggcttggtg	gcaaagagat	aaattgcgcg	aggatatact	801000
ctcttaaaga	gatcccttct	atatactcca	tagcaatgta	gaggcaatct	tgccatttgc	801060
catagcgatg	gaacttaaca	atattaggat	gagtaatttg	atggaggctc	tggtgttctc	801120
taagaaaatt	atagacagag	cgactcgtga	acgaggggga	aggagaaaaa	actttttatga	801180
tcttagaattg	gcgtgtttca	ggatgtagac	catgaacaac	tctacttctt	aattttttac	801240
tcgaattttt	tttaacatga	tatccgccaa	tcacctgagg	ttcaggaaga	gggatgccac	801300
cacgacaatc	cataaatcca	atctttcttt	atacctctaa	aacgcgaata	cctaaaacat	801360
ctcctagagc	gataatttct	cccctaccga	ccttagctcc	atctaaaatg	atatccacac	801420
cgtatgctgg	atggtttccc	aagctcaata	tacttcccaa	gttcaatttt	ataaattcac	801480
tgactgctaa	ggaatatctt	gcaacttcga	ctacgagtct	actgtatcca	gggaggggag	801540
ctgcggaagc	ttgtggattt	tcaggaagag	gaggggtctc	atgagttagg	ttagggtaac	801600
tggtaatttt	aaatttctca	gaggaggcgg	ttaagaaaac	gccaccaaaa	aactgatgtt	801660
tttgactgtg	gagtaaagcg	cggttttctt	cggtttcagg	atcataaaga	cagctatcta	801720
acataatgaa	tgatccctggg	actacctgat	gccattcttc	ttgagttagc	tgagaatacc	801780
cgacttctac	agaaagagag	atctgctgcg	tttgatctat	attatgaaga	tccgactcat	801840

catggagacc	tgagaaaaac	ttctgacaac	tttgggaaggt	atcttctggc	aataacagac	801900
gacatcgaac	atTTTTtcca	tctaggcgca	gagaaatata	tacgacttgg	aaagagcctt	801960
gcagacttgt	agctgtaaat	atagcatccc	ctccgacttt	ggcagacaaa	gagggcaccc	802020
actggagctc	ttcaaataat	ttacaggcct	cggcgacaaa	ataataatgg	aaccctagga	802080
gcttatcttt	ttcatagaaa	tatgaagcaa	ggctggcatc	atcaaatact	gtaccatga	802140
gctcctgaag	gtcttcttct	gatgttagga	acaacagatt	ttctacttcc	caagggttga	802200
ctaccatagg	ttgtattaga	agatgcacgc	cgaattcttt	cgtagcttct	acagcagtta	802260
tagatccacg	aaactttata	gaaacctgga	catcttcaag	tcgaaatttc	tctctaattt	802320
tatgttggca	cagttcctta	ggaaactcag	gagcagcaac	ctgctcctca	gtcttcccta	802380
gggaacttaa	aaaattattc	cgagatttta	gccaacttgc	actagaatcg	gctgctactg	802440
ccataaagta	cctttataaa	cgtgcttctt	cgattttata	agaatcttgt	tctttatcgt	802500
cttggttttg	tttttgattc	tgatctcttt	gatctttctc	ttctctatga	cggatcgtag	802560
atgcaatcat	atgtagagga	gtttgtacct	cttcaatttt	aggaagctgt	actaaaagat	802620
ttccaactga	gaattctttt	aatgtgagtt	gatgaccttt	taaagcactt	accaatgaag	802680
aaagttggct	agggttattc	gttacaaggt	ctgcagcttc	tgccatttgt	gtagcatcta	802740
caaaaactga	gaacttaacg	gaaagatcct	gtccagattg	cactaatgta	agattagctc	802800
caacaaaggc	ttcaggcaca	ctagaactag	catctaatac	caactctaca	agttgctcac	802860
cgttgatttc	tgaaatcacc	atagattcta	cagtagaaag	tatgatattt	tctatccact	802920
gtgtatcgat	actactaaca	gctatgggag	cgacttctac	aacagcttct	gctgatccag	802980
ctgctgcat	atctataaga	gacatacctg	caaaggcggt	ctcagcaagg	caaaattctt	803040
gagattcttg	ctcttcctct	ttggatccta	cttcagcaat	ctcatcatca	actcgcttct	803100
cttcatcagc	aaattttcta	gattctgtac	gtgtatttcc	tttacttgag	gttgtttctt	803160
cttgctggtg	ttgctttcct	tccaaagaaa	atacttttct	atcacgacta	tctctaggtt	803220
caggagagtt	ctgggtatata	gtgtgattgt	ctgttttagc	gctatataat	gattctgctg	803280
ttttctttaa	ttccatgaac	tagcttcccc	ctgattcacg	tttttttttc	tggcgcagtt	803340
ggaaaagcag	ctgccccatc	tcgtcttgtt	ctttttcttc	agcgcgactt	cttctttgag	803400
agcttctttc	atccattctt	ctttatggag	tcgtgttttc	tcttcttctt	ttctacgctt	803460
cgctaaattt	acttctgctt	tttcgagttc	tttagaagca	gcaagcacaa	cttctttttg	803520
tttgttgact	ttctcttctt	cttccgaaag	ctgtactgca	accactttta	tgtacgattt	803580
tatctgtaag	acggcgctgc	ttgttgtaac	ttcgtccaac	aaatcgcgga	gttggttggat	803640
tttttgcata	tagtgatttt	taactttatc	gcgttcagct	tctttctctc	gtaatttctc	803700
ttgttctatt	ttcaaaagac	gtcgtttttc	tttaacaact	tttctgctc	tatctacacg	803760
atccttttta	atcgctaaaa	caggctctag	tggatatttt	gccacagcat	actactcttt	803820
atttaccgga	aaatggcgcg	cagttgttgt	gctgcttctc	catagtttgt	cttttctgtg	803880
atatcttgct	ttaaaaaccg	gttcaatttg	tcaatatggt	cgatagcaaa	atctatctca	803940
cgatcagaac	ctcgtcggtg	ttctccaata	cggatcaaca	tctcgttggc	tttatattta	804000
gctaaaactt	ctcttgcttt	ccctatgatc	cgtcgttgtt	cttcaggaac	aatagcagtc	804060
aggagtggc	taatcgaagc	aagtacgtca	attgcaggat	aatgggatgc	ttgagctagt	804120
gcattggaga	gaacaatatg	cccgtaaga	atcgatttga	cttcgtcagc	aacaggctcg	804180
ttcatatcat	ctcctgctac	caagacggtg	taaaatgctg	taatgggtcc	tttatcggag	804240
gctcctgata	tttccaatag	acggggtaga	gtggaaaaaa	ccgatggagt	gtatcctgct	804300
ctagcaggag	gctctccagc	ggctaacccc	acttcccgcg	atgcacgagc	aaatcgtgtc	804360
acggaatcca	tcataagtac	gacagttttc	ccttgatcac	gaaaatactc	tgcaattgca	804420
gtccctacat	aggcggtcatt	aagtcgcaat	tgcgacgatt	ggtcagaagt	agaaacgaca	804480
attacggaac	gtttcattcc	ttcttctccc	aaatccccct	ctataaaactc	acgtacttca	804540
cgcccccttt	ctccaataag	cgcgattaca	ttaacgtcgg	cttcttcagc	gtttcttgcg	804600
atcataccta	agagcgaaga	ttttcccact	ccagcaccag	caaaaattcc	aatcagctgc	804660
cccctagcga	ccgtgagcat	accgtctata	caacgcacac	ccgtagacag	gatctgtcgt	804720
aatctcgccc	tatgcagggg	atctgggggt	gcacgaaaaa	taggaaatgt	ttgatccaca	804780
ttttgtaatg	gacctttagt	ttctacatct	atgggttctc	ccaaccatt	gagaacacga	804840
cctaagaggc	cgtttcctgc	tcgaatgtgt	aaggggagtc	ctgtagggat	gacttcggaa	804900
gaaggactca	ctcctgataa	ctctcctaaa	ggagagagaa	aggcaaaact	ctgggtaaaa	804960
ccaacgactt	ctgttacgag	aggttccatg	ccgttacgtt	tcactaagca	tacttctcca	805020
acacgcacat	taggaactac	ggctttgatt	aacatgccga	ccacttctgt	aatcgggcct	805080
actacagtgc	taagattcac	atcaccaagt	tgtgacatga	gagtgtcgaa	atccgttgtt	805140
aactgatcca	tggttaacct	attgcgttgt	cataatcggt	ttcacgctac	ttacagaggt	805200
accgacaata	ctcgcaaaac	gttctgctct	ttgtgtagct	cgctgcacag	catattgtac	805260
tttaaggaag	tttgctaaac	tctcacgatt	cccatctcta	tcagagaagt	agagcaacgc	805320
acgattgagg	acctcttctc	cggaggagac	ccaatcaatg	atcttctctag	ttaccgaacc	805380
ctcttcttta	tcttctttcc	gagcatcttg	ttgtgtgtgc	tcagcaatcg	tattcaagtc	805440
ttcgttaatt	aaatctatga	tgactcctac	agcttggaaa	tgctcgtctg	caaactgtgc	805500
tgttgtctga	ctatcttcga	aagttgagcg	gaaatcccg	aggcgccctt	tcaagttgtt	805560
aatttgctct	tggagctctt	ctgattccaa	ggcctcttgc	aactcaggat	cgattaaatt	805620
agaattttga	tcctgcatca	ttgcatcgg	atcttggtta	aatccttgaa	caagggtcgt	805680

atcttttagga	gcagcataag	atcccaaagc	aaatggagaa	atatcttttt	ttaattcact	805740
tgctaagggg	gtgccagaat	tctgagttat	agattgcgct	tctgcatctc	catcaagggt	805800
ggggaaacat	tctacaggg	ctatcataaa	gcaaaaaaac	cgttttactg	ttttaaaagc	805860
ctagcccaaa	ggacctgcac	tttttgccac	taaagtgtca	tgccaatcta	agacagattg	805920
agcaagagct	cttgtggact	ctatttttaca	atgtgtatc	acttgatcag	caaatttttag	805980
gcaactttct	agactctctc	tgcgcacttc	aaaagaactt	ccttgatgca	agacgatgag	806040
catatgggta	agagataaaa	atgcttttat	actccaatta	tcttcattgc	cttttatcag	806100
cgcactgagg	cggtcttcag	catcgaaaag	atccatttta	tgcaaagaaa	tcaatgcgag	806160
tcttagatca	tgaccataat	gattagggtt	tagaatatgg	agagattgaa	ataactttct	806220
tgcgctatct	tcactctccct	gtttaatggc	caaaaggcct	gcttcaaata	acaaagcaaa	806280
gtctgcttga	aatactttcca	aatctgccat	gatctctctc	ttatattatt	aacttccttt	806340
aactgctcta	gccattgtga	tcactctctgt	gttcacagcg	gttaggatgt	tggacaccga	806400
ttccatatac	tgtgataaga	tctgcatacg	gaattgcaaa	ttaaacatgg	ttcccaaate	806460
gacagtgcct	tgtgttgatg	tctctaactc	agttaaatac	tgttgaaacac	ccttcacgta	806520
agtacatacg	ccgtctagca	tcttatttaa	atcgaatgct	gtgcaacttt	tatttgtagc	806580
catagatttc	tctcctctgg	acctttatat	catcttgcgg	ttgatccgac	ccagaacttt	806640
ctgtagagct	acatagcctg	ctaacaacga	ctgttgttgc	ccaaaagatt	ctttgtcaga	806700
accttctcga	agcagcgcat	gtaacttatg	aacttttatc	tgcacactag	ctttaagttc	806760
ttgagctctg	tcattgatctt	gcatactctg	ttctaaatct	aacagcggtt	gagaattttt	806820
ttcttctttc	gctgtatttt	ccatattaaa	catagaatat	ctacctaaat	ataaataatt	806880
aataaaccct	aatacttggg	tattttattgt	agtctatttt	atattttcaac	ccntccttct	806940
ctaaaaagat	cgcggttaggt	tgtatacttg	ttactgtcat	accatcaatc	acgtcccctc	807000
ttgtgaggat	tctgccattg	acaactacat	tgatacttat	ttctccgtat	ctagaattgc	807060
ctgtaacacg	atagcgattg	gggtaacgta	ggtttaaatc	tatgattccc	tcttcagctg	807120
ggagtaagac	agcaaaattc	ttgaccaacc	tcacaccagg	aatccccgac	agctcttgca	807180
ctacagcacg	gaacttctct	gcacatcgt	tattgacgta	accagtaagg	ataacttcac	807240
cgttcacaaa	ggccacatgg	atgtttgcaa	aacctccttg	aagaagatgg	cctgcaattg	807300
cttttaacat	ntgggttttna	acaacaactt	tattctctag	taacgagagg	gaattaaaaat	807360
gtatattttaa	ataatcaacg	aggcaagctg	cttgctcctc	agtcttgaca	tagcctgtga	807420
tgatgaattt	cccagggttct	ggggaatgca	tgctgatgcc	tttaaaactcg	ggtcgctttg	807480
ataacaggat	gttcatctcc	tgccaaacag	cttcacatc	aataacatta	tcacttacgg	807540
atttcacaaa	ggaaagggcg	tctactttat	acagcagctc	gcttttgtcc	gtactatttt	807600
tgacatgtcc	gattaagaaa	agttggctgt	tcgttttatt	aaacgtataa	cgcaccgtag	807660
ggaactgatt	gataacctgg	gcaagatctt	cttgataatc	aatattttct	aaaggaacca	807720
cttcttttgg	atggaaaaga	gaagctgttc	ctataccaaa	gagaatagcc	aatcctccaa	807780
caaacagggg	aagaatgaaa	gatcctgcgg	gtagtgtagc	gcgtttttgt	ttttcttctt	807840
cttcttgggc	ctcttgtctt	tctaaggctt	cggcgtcttg	ctgtctccca	aacaaactgt	807900
aatcgtctgg	ggatagagaa	gcaactatag	tatcagcggg	ggcatgatga	tctataagta	807960
aaaataatgt	cgttcctaaa	gccacaactt	caatcgagct	gtcttatcaa	gtcttatcaa	808020
tttttctgct	ttcaacaatg	acaccgtttt	tactatcgag	atcctcgata	agaatgcccc	808080
cgtcattacc	gacagtaatt	ttagcatggt	gatgagaaac	acttaagtca	ttaaataacta	808140
tgtcacaagt	tgtaggatcc	gtacctaaaa	tatagggttt	tcttgagtct	aaatggaact	808200
ctgctccaaa	tattagctcc	ggctaaaact	ttgagtaaaa	aacgagaagg	ctgcgtcaag	808260
tctacagaga	tatttttttt	cgcaatatca	tcaatctctg	ctggaaaaat	tgtttgatcg	808320
aatcgaaata	agtcttgaac	atgaaatggg	gatagaactg	cgctcttttc	gttctcgact	808380
tttttaggag	tttctttgtt	atcctctgca	gtatggtcac	ttgccgtgtc	gtcatttgca	808440
tcagcggcac	tgtcagaate	ttctttatta	tcttcctgta	ggttctcttc	ttcttcttgt	808500
acaaagggtt	cttctgcttc	cttatcctcg	gattcttttt	gtgaatccaa	aggtgttgct	808560
tctatttttag	agccttccct	tttagaacct	tcctcagggt	gatctttttt	ttctggagaa	808620
tccggtgttg	ctttcttatt	agccttctct	tctacagggt	tattttcttt	caagggagtc	808680
tcactccctg	ctgtgttttt	aagagagggt	tctgctgact	ttgggtgcgg	atcttgccta	808740
ggcgaagtcc	gttatcttcc	ataatggcgt	tctgggggtt	gttgggtctt	tcctctcctt	808800
tcggagaatc	ctttgcattt	tgttcctttg	gattcaaaga	ctcgtttgaa	gattctttta	808860
aaccttctct	agcaactttg	gctcttgggt	gatttttttc	cgcttttgct	gatgttaaaa	808920
aagcatcagc	aagctcctga	tccccacttg	taattggatc	gctacttccc	tgtatcttgg	808980
tcagcttttc	cttaggcttc	gggtgaatgat	ttgtttccga	agtttgccga	ggctcaagat	809040
cttttccctg	ttcattacta	tcggacaaat	cccctgaatc	attagaaaaa	ttttcttcgg	809100
gaatatcaaa	atcataaaca	agatcttgag	gatcaaattc	atctgataag	aaagaatact	809160
gattgcttcc	taataagata	gtatcttcat	tttttaactg	tgtagtctct	tggatcgcta	809220
cgccattttac	aacaatagga	attgtatcat	ctaaatttgt	gatgtagtag	cttccgctag	809280
tcttattgat	aatggcttgc	gatgcaccga	gtttaggatc	ttcaatagga	atgtcattag	809340
cactagagtc	gcgtcctata	gaccagctta	tcccactctc	cagaacaaaa	attacaccag	809400
acaaggggccc	ttcatcaaca	attaatcgta	tccgcattta	ttccaccttg	ttactgttta	809460
cctaggccaa	gatctgacag	ccatgtctct	gaaaaattca	taaaactctc	aacatgtcgt	809520

a'caaaatcat	catatgtagt	atccccagaa	aatctgcgga	ccatgacaac	attgccctcg	809580
gaatccaaac	ctaaagcact	gcctcctggt	tctctaccga	ataaattgcc	aatcatcatt	809640
tgcaagtata	atthttgctgt	atcagcagat	ggaggcaaag	ctcctaacga	agcacttaaa	809700
acaatttcgt	tatcagcatt	ttgctgagca	cgcactttta	ctacctcact	tataggcagg	809760
acataggctc	cgtcagcatc	taactcgaga	gttgacgtta	tacccatata	cgtggcaaaa	809820
ttttttatta	atthtttccaa	catactcgtg	ttttccaacg	cagcaatggt	tgtctttggt	809880
ccctgaggaa	tggaaacaat	ctcattttcta	aaacctgctt	tttcttcctt	taaactcgagt	809940
tatgccaaata	cgaactttta	aaataaaaac	gatttcttat	ttgcagaaac	agcattgagc	810000
gcttttcttt	gctcatcttt	ttcattataa	agaacaagag	gccacaagaa	aaatcgagct	810060
gaatccataa	caagaataat	tataatctat	caattaaccc	gagcacgccc	attccctcac	810120
agacatcaga	ggatattcgt	acttctaattg	aaagcttaga	gtattttcga	aagctgtata	810180
tgtcaagcga	tgaattaggc	attaaagcat	caatagctta	gaacggaagg	aatacgtggg	810240
gatgaaattt	gcctctgggt	tatatgtgag	ctcttttttt	cataaatttc	ccattgtttt	810300
ttcgcggcac	aagttaacaa	aagttttgct	ttattttactc	cttctttggt	gcattgagct	810360
cttttttgca	cgcattcact	gatgaaatct	atatctaaat	aaacaaaacc	tgtagggggt	810420
tctttccata	aaaaggttcg	tggcacgtta	aaatcaaaga	caatacgttt	gggaatgcta	810480
gcaagactct	cacaggaaag	atcggaataa	tgtgaagctg	attctgaaga	gccaaagaaa	810540
atcacatcat	agggttgctg	aaatgagagc	gtttctcgag	acaaggttct	atagggggcc	810600
gtgacttggt	gtctagagca	aaaggtaatc	ctatgatacc	catgttgata	taagtaggca	810660
gcgactttcc	tattgatata	cgagtatcct	acgaataaaa	aattcgtata	tatcgacttg	810720
tcgtagctga	gtagaatttc	ttgaacgaca	gattctatgg	tcacttgatg	atcgggaaac	810780
ccgatgcgtg	agcgatactc	cttcccttcc	tttagagctt	tttgaaataa	aaaatgaaga	810840
tcaaaaggca	actctctctc	tttgcttctc	tttaaatagg	ctcgttttac	ctgctcttga	810900
atthtccgth	ccccaaagat	caaactatct	ataccactgg	tgacctgaaa	cagatgagta	810960
aaacaagaca	aacctctatg	acggtaagga	cgtattccct	gggatgtcaa	ttctgaaagt	811020
aaggcggtct	gagcaatttc	aggactttct	gaataataat	aaagttcggc	tcgatgacaa	811080
gtaagtaacg	ggataaacgc	tctctctttg	cctaaaaaac	gctgtgcaag	gaaaagattt	811140
ttttcaaaag	attgcagata	ttgaatcgca	cgctctcttt	ctttcaaagc	ggcttcacga	811200
taactgattc	caacaactcc	taacaccata	agcacgattc	gataatttca	gaacagtatg	811260
aaggaaactt	atactaaatt	tataaatgaa	aagtaactta	gctgtataga	cgaagagaaa	811320
attagaagcc	atcaaataat	ctattttctc	tgctcattgc	gttttgaagg	cggttgcccta	811380
tcccatatag	cagaggatct	ttacgtttgct	ttaaaaattg	aaaggtaatt	ttgactacga	811440
tctctaggag	aaatcaatga	agaaggcagg	cctatgtttt	gcagttcccc	tgthttgttc	811500
ttccttgatt	aggaaaaaga	ggttcgggta	agatgcgttt	tgagctcctc	ggggagttcc	811560
aaggattctg	tcctttaaag	ataagacttt	agcggatgga	tatgcagttt	aaagctgagt	811620
tcattgtaata	gcgatacatt	cccaagacta	agatccataa	gtttcgtctt	agtacgaaac	811680
ttatatgttg	agcttggtcc	ttttcttggt	gcaaaataga	taagcaatca	aaagattgtc	811740
ctatccgctc	ttcttaaaaa	ttcaacaaaa	tatcacacat	ggcggcatac	acagaagcaa	811800
gcattctttc	tttggtcctc	cttgatcaca	ttcgtcttcg	ggcggggatg	taacttgcaa	811860
ggcttggaac	tggtttctca	aaagaggatg	ggatttacac	tcctttttaa	gaagtggttg	811920
ataatgggat	tgtatgaattt	atcatgggtc	atggtaaatc	tttaaaaaat	tctgtagtgt	811980
acaagcagat	ctccattcaa	gatcaagggtc	gtggcattcc	tttaggtaaa	cttatagatt	812040
gtgtttctaa	aatcaatacg	ggagctaaat	atacccaaga	tgthttccat	ttctctgtag	812100
ggctgaatgg	cgtgggactc	aaagctgtga	atgcactttc	agaaatattt	tctgtacgtt	812160
ctgtaagaaa	gaaaaaatac	caccttgcca	ccttccatcg	aggagttctg	caagagtcta	812220
agcaagggtc	taccaaagat	cctgatggaa	cttttgthtc	ctttactcct	gatcctagta	812280
tcttccctga	gtttactttt	aaccacgact	tcctaaaaga	taaaatccgc	caatacacct	812340
acctacattc	gggattagag	atccgattta	atgatagggt	gttcatatct	cacaacgggtc	812400
tcaaagatct	tttcgatgca	gagatcactg	agcccccttt	atactctcct	cttttttttc	812460
aaaatgagga	tttaactttt	atcttttctc	accttgaagg	aaatacggag	cgthattttt	812520
cttttgthcaa	tggacaagag	actcttgacg	gaggaaacaca	cctgactgcc	tttaagggaag	812580
ccatagtaaa	aggggtcaac	gagthttttg	gaaaaacatt	tgthttccaat	gacattcgag	812640
aaggcattgt	gggctgcata	gcaataaaaa	tagcctcgcc	aatttttgaa	tcgcaaacga	812700
aaaataagct	tgggaatata	cagattcgggt	cttctttaa	taaagatgta	aagggaagcga	812760
ttgtacaggg	cctacgtaaa	gataaagtgg	ctcctgagct	cttttttagaa	aaaataaaat	812820
tcaatgagaa	aactcgaaag	aatatccaat	ttataaaaca	agatcttaag	agcaaacaga	812880
agaaagtcca	ttataaaaat	cccaaaacttc	gggactgtaa	attccattat	aacgatcgct	812940
ctctgtatgg	tgaggcctct	tcgatttttc	ttaccgaagg	gagctctgct	ccgcatcaat	813000
tcttgcttca	agaaatcccc	tcacacaagc	tgtcttttca	cttcgaggaa	agcctatgaa	813060
tgtcttttcc	ttagaagaaa	ccaaaatgta	taaaaatgat	gagthatttt	atttagcaac	813120
tgctctaggc	atcacgcaaa	acgagattca	gcattttacgt	tataacaaag	tcactcctggc	813180
tactgatgcg	gatgtagacg	gtatgcata	tcgtaattct	ttgattactt	tcttcccttaa	813240
aacactcttg	cctcttgtag	aaaataatca	cctctttatc	ttagaaacc	ctttgtttaa	813300
agthtagaaac	aaaacgacta	cgctctacta	ctattctgag	caagaaaaga	tgcaaggcgtt	813360

acagcaattt	gggaaaaagg	actcctcttt	agaaatcaca	aggtttaaag	gtttaggaga	813420
aatttctcct	aaggaatttg	ctgcgtttat	aggctctgag	atccgcctca	ccccagttac	813480
gattacctct	ttagagagca	tttcttcgat	cttacaattc	tatatgggga	aaaatacaaa	813540
agagagaaaa	caattttatta	tggataacct	tattactgat	ttttaattta	tgcgtgacgt	813600
ttcagagctt	tttcgaacac	attttatgca	ttacgcgtct	tacgtaattt	tagagagagc	813660
gattcctcat	attcttgatg	gcttaaaacc	ggtgcagcgt	cgacttctat	ggactttatt	813720
ccttatggac	gacgggaaaa	tgcataaagt	tgccaatatt	gcaggaagaa	ctatggctct	813780
ccatcccat	ggcgatgccc	ctattgttga	agctcttggt	gtcttagcaa	ataaaggcta	813840
cctcatcgac	acgcaaggaa	acttcggaaa	tccccttacg	ggagatcctc	acgctgctgc	813900
ccgttatata	gaagcacgac	tcagtccttt	agctcgagaa	acgctcttta	ataccgactt	813960
gatagctttt	catgactctt	atgatggaag	agaaaaagaa	cctgatattt	tacctgcaaa	814020
gctccccgtg	cttttacttc	atgggtgtgga	cgggattgct	gtggggatga	ccacgaaaat	814080
tttccctcac	aatttttgag	aacttttgaa	agcgcaaat	gcaattttta	atgataaaaa	814140
attcactgtg	tttcctgact	ttccttcggg	aggattgatg	gatccctcgg	agtatcaaga	814200
tggattggga	tcgattacac	tgcgtgcac	tatagacatt	attaatgata	aaacgcttgt	814260
agtgaacaa	atttgtcctc	aatctacgac	tgagactttg	atccgttcta	tagagaacgc	814320
agcaaaacgt	ggcacaatta	aaatcgatac	catccaagac	ttctctacag	atgtccctca	814380
cattgaaatt	aagctgccaa	aaggctctcg	agccaaagag	atgcttcctc	tgttattcga	814440
gcatactgaa	tgccagggtga	ttctctattc	taagcccaca	gtcattttacg	agaataagcc	814500
tgtagaatgt	tcgatatccg	agattctcaa	actgcatact	acagctctac	aggggtatct	814560
tgaaaaagaa	cttttggttg	tccaagaaca	acttactttg	gaccattatc	ataaaacctt	814620
agaatacatc	tttattaaac	ataagctcta	tgattctgtc	cgagaagtc	tagccataaa	814680
caagaaaatt	tctgctgatg	acctacatca	agcagtgtct	catgctctgg	agccctggct	814740
tcattgagctt	gcaactcccg	ttacaaaaca	agacacctct	caacttgctt	cactaacgat	814800
taagaaaatc	ctttgcttta	atgaagaggc	atgcactaag	gaactgctag	ccatagaaaa	814860
aaaacaagca	gcgatacaaa	aagatcttgg	aagaataaaa	gaagtcaccg	tcaagtacct	814920
caaaggactt	ttagaacgcc	atggacactt	aggagagaga	aaaacacaga	tcacaaactt	814980
taagacggca	aagacatcta	tcttgaaaca	acaaacctta	atttaaaaaa	ctaagtttat	815040
ctaaaaaact	tctgattaat	aagagatggg	aaaatatttt	ctttttaaat	tagaattaaa	815100
tttatagaca	ctataaccat	tgtagtacgt	atggaaccac	gtcacattta	tataagaaaa	815160
ccagagactc	caaaaagctcc	tgacgtagaa	aagcctgggt	tacctgagta	catgacgatg	815220
gcaaacactc	ctaccttcga	gggtcctgta	aaaactcttg	atcactacgc	cgagctctta	815280
tcgagcaacg	aggagctgag	gaagggcaaa	aaatgtatga	taatttcatt	cagtctatct	815340
taatttcaac	atttgggctt	gtacataagg	atatggaccg	agcacaaaaa	gcttctaagc	815400
gtatgagatc	tgtctataaa	gagcagtaat	gtcgtttacc	tatttcctag	cgcttcccgt	815460
agataggctt	atgcaagaac	ggttcctctg	ttctcccaaa	cgttgggctc	cttttatcaa	815520
ttcgccttta	taccttactc	tcattgctga	ccacgatact	ccttatttgg	ctaagaatct	815580
tgataagttt	cccttacctg	tagagcaatg	ggaaaaaacg	gtcctgcacg	tctctagcct	815640
attgaagtct	atatttttat	gttcagacct	ttcctcttta	aggttgctgg	cctgtacaaa	815700
attcgaaatc	ttgactttga	acgaccttta	ttgcgcccaa	aatatctaaa	aaattgcttt	815760
acaaagacac	tcgcatcttt	cccttgacta	aaaattttgc	ttgtcaaaact	gccatcgaag	815820
tttgtcatga	tgatgtttga	gctacatagg	ttagcctcag	ttgattccag	cattttatct	815880
taattcaacg	catttctatc	tttttagact	cattaaatta	tttttgaaaa	attctaagtg	815940
tctaagattc	aaaaagagac	tctttctttc	aataaaatcg	ctagatcctt	aactgattcg	816000
atattaaact	agtaaagaaa	gttatcaaga	tttcaatgaa	aactgtgact	tcctttactg	816060
tatgtaaaga	aaactcgggg	cgtttagaca	agtacctgac	tgaggtgcac	cccaaatatt	816120
ctcgagcttt	ctaccaagaa	catatcttaa	gtggctttgt	ccaaatcaat	gggcaataaa	816180
acaccagggt	ggcaacgcgc	ttaaattgtg	gtgatatagt	cactatagat	atccaagaaa	816240
aggaagaact	tcttgagctc	ctacccgaag	ccatccctct	agataagggt	tatgaggatg	816300
gaatgatctt	agtgatcaat	aaacctcggg	atatgggtgg	ccatccagca	cctggctcatt	816360
tccatggaac	cctgggttcat	gctcttctcc	atgaaatagg	agagagactg	aaggaagaat	816420
tccctgagga	accttgagga	cctggaatcg	tacatcgact	tgataaagat	acctcgggat	816480
tgattattac	tgcaaaaaacg	cggcaggcca	agaaggtttt	cagcgagctt	ttttcaacca	816540
agcgggttaa	gaaaagctac	ttagcagttt	gtatagggaa	acctaggagt	actacgatcc	816600
atacacatat	aagccggcat	caaaacaaac	gtaaagaaat	gactgtaagc	tctcaaggaa	816660
aagaagccgt	taccactcgc	caagtccttg	cttttaaatg	aaaactgagt	tttggtgcct	816720
tgtctccaga	gacaggaagg	acccaccagc	ttaggggttca	tatgaaacat	ttagggactc	816780
ctattcttgg	ggatcctgtg	tatggaatcc	cctctatgaa	ttcgagttac	ggctcttgata	816840
aacaacaatt	gcatgcctat	agcgttgatt	tcactcatcc	agaaacccgg	caattttgtt	816900
cattaaaggc	gggttttacc	gaggatatgc	gttcctctct	aataaaagaa	ttccgcaatg	816960
aaacaactat	attaaataaa	aatttatttg	aatcgatttt	aaaagaacaa	taattcatta	817020
aaaagttcat	ttatttttag	aaacgcatta	aaattgaatt	aaatttttta	tcatttttta	817080
acatctcttt	ttaaagacaa	cgcaatttag	ttaaggatta	ctatgaaaga	attttttagcc	817140
tatatcatta	agaatctagt	ggaccgcctt	gaagaagtcc	gtattaaaga	agttcagggg	817200

actcacacga	ttattttatga	actaagtgtg	gctaaacctg	atatcgggaa	gatcattggc	817260
aaagaaggcc	gtacgatcaa	agcgattcgt	actcttctgg	tttctgtagc	aagcaggaac	817320
aatgtaaggg	tcagtttaga	aattatggaa	gaaaagtagc	cttaagccta	gcttaagtag	817380
ttctcattga	aattgctagc	ctaagggaaa	ccgaaggcta	ccacttcaat	aaaaaataat	817440
tgcacgcata	aagataaact	cggaccgagc	aggactcgaa	cctgcgacca	ttcgccttaga	817500
aggcgaatgc	tctatccact	gagctatcgg	tccctattct	tgtacaacct	tgggggtattg	817560
agcacgaaag	cgagcaaagg	aaatccctca	atcagtatag	gtctaccaag	aaaaaagtca	817620
attctgacac	aagattttct	tgttccctaa	agaacttctt	tcaaagctat	ataaaaagcg	817680
aattccacct	ccttacctgt	aattttatag	gtaaaattaa	ggagcaactt	ggattgtatt	817740
ctccgatctt	ataacctgga	aagttagaac	caaaagttgc	tttattctaa	aaaaggatgg	817800
tcatgttcaa	taacaaaatg	atcctaattg	ctggcccttg	tgttattgag	ggggaagata	817860
ttacattgga	aatcgcaggg	aaattacagt	ccatactcgc	cccttattcg	gatcggatcc	817920
aatgggtttt	taaaagcagt	tacgacaaag	caaatecgctc	ttccctaaac	tcatttcgag	817980
ggcctgggtt	gacagagggg	ttgcgcatac	ttgccaaagt	caaagaaaact	tttggcgtgg	818040
gcattctttac	agatgtccat	acgcctcaag	acgcttacgc	ggctgccgaa	gtctgcaata	818100
tccttcaggt	acctgcgttc	ctctgcanac	aaaccgacct	cctcgttgca	actgcaaaa	818160
ctggcgctat	agtaaattta	aaaaaagggc	agtttctctc	cccttgggat	atggaaggcc	818220
caataaataa	agtactctct	acaggaaata	acaaaatctt	acttacagaa	agagggtgta	818280
gcttcgggtta	caataacctt	gtttctgata	tgcgtctgat	tcctgtttta	tcccgttcag	818340
gatttctctgt	aattttttgat	gccacgcact	ccgtgcagct	ccctggagct	ctatctacag	818400
aaagcgggtgg	tctgacagaa	ttcgttccta	ctctttcacg	agctgcttta	gctgcaggag	818460
ctcatggcct	ttttatagag	accataacca	atccaaaaat	cgctaaaagt	gatgcagctt	818520
ctatgttgag	cttagaagaa	ttcgcagctc	tcctccccac	ctgggatcaa	ttattttactt	818580
gcgtcagttc	ctttgatatg	gtctcagcat	gacaaaaattt	ctatactgcg	ggctctttta	818640
ttctctagga	ctacttgtct	tggtctttgg	gactatggta	gccattattc	aagtggacca	818700
gatttgcgat	gtttcctgta	tgaacaagca	cttccaagaa	tccccccctt	ttttaaaaat	818760
aaaaaagggtg	aatgtctcca	aacaaatttg	ctctcctgaa	gaacgattct	tccattgtaa	818820
aattgataaa	tcgtgtatgg	aactgcattt	tcctcagctc	agttattcct	gtaaagaata	818880
cctcaccggg	atctcagggc	atattctaac	acaaaatttt	gaaaagcaaa	tgcaattccg	818940
aggaaactca	ggattactaa	attaccaaga	tggttcctta	catgtgtatg	actgccgttt	819000
ccaagtagat	cctgtacctg	ggtatgggtc	tccagataag	gaggacagtt	cttcaggagg	819060
tatgaaaacc	ctctattttat	ctttattcag	gaattaaagc	tctatgccta	tactttctgt	819120
gtgtaattctc	gtaagaagtg	ataacaagaa	gcccgtagca	aatgatgtgt	ctttccaaat	819180
caaccccggg	gagattgtcg	gcctactcgg	ccctaaccgga	gcaggaaaaa	caacagcatt	819240
ttatcttact	gtaggcttaa	ttcgccctga	ctctgggaag	attatcttta	aaaatgtcga	819300
tgtcacccaaa	aaaactatgg	accatcggtc	acgactggga	atcggttatc	ttgctcaaga	819360
accacaattt	tttaagaagc	tcacagttca	agataaacctg	atttgcattt	tagagatcat	819420
ttacaaagcg	cgtaaacac	aatcccatct	tttaaacacc	ctgggtgatg	atttgcaact	819480
aggttcctgc	ctccataaaa	aggcaggaac	cctatctgga	ggggaacgac	gaagattgga	819540
gatcgccgtg	gtatttagctt	taaatcccg	cgtattgttg	ttagatgagc	cttttgcgaa	819600
tgtagatcct	ctcgtcattc	aaaacgtcaa	gtaccttaatt	aaaattctag	caggacgtgg	819660
aatcggcatt	ctaattacag	atcacaatgc	taaagagctc	ctttctattg	ctgatagggtg	819720
ttattttgatt	attgatggga	agatcttctt	tgaagggtct	tcaagccaaa	tgatcagtaa	819780
ccctatggta	aagcaacatt	acctgggaga	ctcgttctca	tactaatgga	tctcacaaaa	819840
gtctctaggg	aaaggagcgc	tactgtattc	tgtaagaatc	cttgctaata	cctcaaagcc	819900
atcttcttct	aggatagtg	ctcctgggtt	gactcctcgc	tcagctaatt	taaatgcctt	819960
aaatgtattg	caaatacgtc	ctgtgagctc	gatgccacac	ccctttaagt	tcattacgga	820020
ggcataatct	ccaaacattt	ttaaggaaag	ttcacagaca	gtaactgcaa	agagaatttg	820080
atatccaggg	tagcgctttt	ttaaagtgtg	taaatgtttt	cgatatctta	taaatgtagg	820140
gatgatcaca	gtagtgtatc	tacgagcatt	cagccgcctc	atgggtcccta	tagaacatga	820200
ggcacatgta	ggatgtgaag	gatcataccg	acaagcatca	ttgaaacgcc	cttcaggaca	820260
tgcccttaggc	ttttgacaat	aagaaaatcc	taacaaaagg	attctatgag	gacgacgcat	820320
ctcctctaaa	atatactcaa	tattactaca	gccataaaaa	aatagggttg	cctcctgtaa	820380
ggcctcctta	ggagctatca	aagccttagc	taaccgagct	aaagaaccag	gatcttttcag	820440
aaaatcatag	gcaagctgtc	tagcatcttt	taaagaggcc	agataagcaa	gcgtcttcat	820500
acgcagaccc	cgtcttgtag	ctttagtaat	ataaggaata	ttagggttgt	gctctggtct	820560
agacataaat	acggaatcat	aacaattagc	aacggccgca	cactgccacg	aagcacaggg	820620
gcagtcacac	aaaaacccta	gaagcatttt	ccatagctca	gggaatggca	atatttttaga	820680
tagtatacag	cctgaacgat	aatctaatct	agtagagggt	cgtcatcaga	gaggacttcc	820740
tctgcgattg	ccttgattgt	agtgcagcct	tcagggaaac	ctaaactaca	taataattca	820800
tttacatgtt	ctaactctgt	agtcagctgg	tcgttgataa	actccaagcg	agcgagttgc	820860
tgttgcatat	gagatgttgg	atgcataaga	cccctccgta	acgattcata	aagaagagga	820920
gcgaaaaaca	tgccaacatc	tccgcaagat	taaaattttt	ttaagattta	gaaatccaag	820980
tttagaaatt	gaagaactat	cctgtcaggc	ttcgtgctaa	acttaagtac	atttgattta	821040

aaagctgtag	agaagtcgcg	actacagtec	actcctgctg	catagaagtc	aggtgcatct	821100
gcaaatctaa	ctggaagttc	tgtcccatat	ccgcaaaaga	ttgctggctc	gactgtattg	821160
tagattgcag	tgggaacata	ccccatttaa	tcatatttcc	tactaaccgc	gacactaaag	821220
cttcttcaag	aatctgcaat	cgcgcttgcc	attgctcttg	cccctcttta	acttcaaaaag	821280
ttcctgctac	agaacctcca	gctatagaca	aaggctgtaa	gtaattttgc	aataacacta	821340
aagaacctga	gatagaattg	atgtttgtcct	cgtagttcct	taaggaatct	aaaatcgtgg	821400
agcgctgctc	attcgtgatt	ttatcatctt	taagcactct	agctctttgt	tcttcaataa	821460
ctgtaagagc	tccccgtggt	tcttgagat	acaaagcagc	ttgctttcgc	tcttgatcca	821520
actttgctcg	agcgctttct	tgagatcctg	ggaaggcatt	cgctcccca	gcacctactg	821580
ccggctggtg	tcccacataa	ctagcaaaat	tgaatacgt	agctccattg	acatattgag	821640
aaatcgcatc	aataatggaa	tttccgacag	aagatcctaa	gttgctataa	tatagcttct	821700
tatagatttc	atthagataa	tgcacctctt	taggcatata	acgatcgatc	aacacagagg	821760
cgactgccga	aagtaggggg	agagcccgta	attcactagc	ctgtgataac	aattgcccat	821820
caaacagttc	tgttttcata	ttggtgaatt	gttgcaattg	actctgaaga	tcttcgattt	821880
tgttctgtac	attttctgat	tctacagcag	caagagcctt	aaaccgaaaa	taacttcgtg	821940
ccgtagattc	ggcgtttgg	tttgctagtt	tctgaatttc	tggcaaaaat	cctgtagatc	822000
cataatttaa	caggatttga	ttaatctcaa	ctttgccgtt	tttctcagaa	tatatagtat	822060
attgtaaggt	acttgagttc	accgttacgg	aaaaggaacc	gcttgaattt	acaattgaag	822120
tcacgcgga	ttttatagat	gatgctaact	gaaactaga	gttatcta	tctttagctt	822180
cttcaaggat	agcagcttta	acgtgggtcca	tgggtgcagt	aggggtttaa	gcaactacag	822240
tagatgctgt	aaaataagcc	cagatagcac	caaggtgctc	accacactta	aaggtaacca	822300
aagatttata	cactcattaa	tcagtttctg	ttgctcagca	gttaactcat	tgaacgaga	822360
atttaacctt	cgggctgttt	gtagagctcc	agctaaagcc	gcactactaa	tatcaccttg	822420
agaggaactc	agatcaattg	gagcaaaagt	tccaattaaa	gagccaacaa	agctagacaa	822480
attggaaaac	atcgcttctt	gatgctgggt	aacatagata	cttgcatcaa	gtaccgtatc	822540
aaaggatcct	aaagccgcaa	cttgatctga	gtataagtct	gttatatgtt	gacagaacat	822600
aattttatca	tttctagtca	ggtcagaaga	attaatgact	gcgcgaggtt	tttctccagc	822660
atcctcaatc	cgttgtaatc	ctgcttcac	aaaattacct	acatgatctg	ctaaagcctg	822720
cagctctgtc	gcaatctcag	caaagatagt	aaactgctct	ggtgtaagga	ctccttgtag	822780
cgctgtaagg	atgtctttga	acccttcgac	tctaccgtct	gcaaacggtt	gagttaaagt	822840
agcttgattt	ccatatttgc	ctgccaactg	gttcgtaaag	tctgttttca	ttccccag	822900
aaacgtatct	gctcggttga	ttgcagtgaa	gatctcctct	gggaaattgt	agagagctctg	822960
aaaattctct	tctgtttaa	tattccccgc	agcgactaaa	gcctgaagtt	cagtatttaa	823020
tttatcaaag	acatctttat	ttgcaggatt	cttactatta	actgaggcca	tgatagtgg	823080
cataaccgta	ttaagctcaa	cgataagatc	ttgcgcccac	ttctgtttta	ctgcgttata	823140
ataggccccg	actccagatc	ctgtagctgc	tggcgctact	gctgtaacct	gaacagatgc	823200
atgtgtagag	gaaagaggtt	tctcatgaat	ggctgccaca	ggaatagact	tcgctactgt	823260
cgcacgctcc	acttcatatt	tgtgtagctt	ctcgacggca	gagcggtagc	gctcgctcgc	823320
cctctgateg	aaaacttcga	tcaaccgttt	tagtatgtca	cgctccgctg	tagtcttctc	823380
ataatttcgc	atatgttcta	aagattccct	gtgtctttgt	gcaaaagaat	gcattgaaga	823440
cactagagag	agttttttat	aaaatgttga	aatagaagtg	ctataaatca	tatcaatgtc	823500
tgcttagata	agaacagtgt	tattttta	taacattaac	attaataaat	tattttttta	823560
attcaaaaaa	ttcgtcaa	gtttaaaaag	aaaactatca	atattataga	aaacaaatta	823620
ttttttat	gaaaagcttc	atagaaaaaa	acaaaacaaa	gtacgaaaat	aaaataaaaa	823680
tattatttat	tttctatgtc	taccttttct	atccaaaatc	gactaagaac	catttcaggt	823740
gaaagtactc	gaatcatcaa	gctggaccat	aagtactctg	gttttgatcc	cagatcagtg	823800
cctgcgataa	atttagaaga	gttaaattca	gggatttatg	ctctaaggca	tttaatgaac	823860
gccctgcaat	cagaaaatac	caatgttgct	gctttattaa	acccaaacaa	tacgatcttc	823920
cccacaacat	cttggaacaga	ttacaagcat	tcgctccgc	aagctagctc	tccaagagca	823980
ccctcatcac	aaactcccac	agatatcgta	tcagcagcag	ctcttgcttt	agttcttggt	824040
attgacggag	gtctagcgga	attagtggcc	tccgttacag	aaattgatct	cggagcttta	824100
tccactatat	ccacagttcg	tcagttaatg	gcgagctacc	tcgggttgac	aactctaaca	824160
gctgaacaag	aaaaggttgt	attttccagc	tcctatgttc	cttcagaaaa	aaatctcctt	824220
gaacatgtaa	aacaagaaaa	agctgctgaa	atccaagcta	agcaagaaga	aataaaagca	824280
gtattagaag	ctaaaggagt	ctctactgaa	gagatcgaag	cgatacttaa	ggaatattct	824340
gatattctatg	cagcagattt	cttcaaagag	tttatagaag	agcctttaca	tacatatcgt	824400
gcaaaagtcg	gtgcaccgat	ccaagagatg	aatgagaacg	cgattcagct	gcttcctaca	824460
cctcctgcga	tactcctga	caatgtcaat	gaagtcaacg	gaatgaacac	cctcagcact	824520
attttacaag	ctatagatga	tgctattaaa	caagctcctg	cacttggtgg	ggatcaggaa	824580
atcattacta	tactacaaac	tttgggtccc	ctagtcgata	agaccacgtt	tacaaaagct	824640
gaattcgatc	ttattttacg	agcaacacaa	cttcctaata	cagcatcttt	aaaactctac	824700
cttacggata	gacaaattgc	tgagtataca	gggaaaaatca	cgaaagtata	tcaaaattct	824760
atccaaaaatc	tctctgagac	aaaacgtgta	gttgaaaaaca	accgaagcat	gctagaaaca	824820
caactctcca	tgttccaaca	agcacaaaat	tgctttgtta	cttggttag	tcaagccaat	824880



gcacttaaca	tagccatcac	taataaatat	atctctgctg	tacttacgac	ttctatggag	824940
atgtacggag	gtctcctttg	cctttcttat	atgtacgaaa	ggtagccga	tgatgaaaaa	825000
gcaatttttg	acaaaagtgt	gaatgagtat	ttaccgattc	acatcgttgt	tggtgggttca	825060
tgggtaaaatg	gctggatagc	aaaaatggca	gcctatcaag	aactcgcgga	atactcttta	825120
ggaaccgcag	ttacaagtca	agatcaaate	aaagcttatt	tacaaacacg	aggggaatgag	825180
tttaaagcta	cgcgtcattt	tttccataat	attggggatc	aaatgtacca	atttgctaatt	825240
gagactgtct	ttggaaattg	tcttacaaca	gcaaattggtg	cgatacagcc	cgatttaggt	825300
ggttttatca	gagaagcaat	gacgaatggt	ggaactgttg	aagccgatta	tgtaagcaat	825360
gctcagagga	tcctaaatga	atttaatacg	gctgcaactg	cgcattgtttt	acaattacaa	825420
ttacaaatag	ctgagttaca	aaagaaagca	gatgacttag	acccaggaaa	agcctctttc	825480
actgagaacc	gtaaatttgc	tggtgcccgt	ttggatcaca	tcggagagct	taggagatgc	825540
tttaattttct	atgatttttna	actctcagct	accaaagcaa	gagggttttt	taaaaccttt	825600
gatcgaagaa	attaacttca	ataacctcgc	agcgaatgcc	ttaaacagct	tgctacagat	825660
taccaatgaa	ttttctacga	cttctgtcta	ctatagcctc	tcttcctatt	tagttcagag	825720
taaaactgga	caaaacctgt	ttgctgggtg	ttactatgaa	acacttctag	ctgcagctag	825780
agaacgggag	tatattttatc	gcgacactgc	gagatgtaaa	caagcgatta	atctagtcaa	825840
tggaacttctc	caaaaaatta	actctcttcc	aggggctacc	tcagcacaaa	aacaagaaat	825900
gcttaacgca	actacctatt	atcaatacag	cttatcagtc	actttaaacc	aacttactgt	825960
attagaatct	ttactcgcgg	gtctcaaaat	gactcttcag	acaactagta	ataacaaata	826020
cgacaaaagt	gtgttttaaaa	ttgaaagtgt	tgatgactgg	attccaactc	tagctgcttt	826080
ggaaagtgtt	ctaactagt	gattccctaa	tatcagtgcg	acaggaggcc	taggtccttt	826140
atttaccag	gtgcaatccg	atcagcaaac	gtatacttct	caaggccaga	cacagcagtt	826200
gaacctacaa	aaccaaata	ccactatcca	acaggagtgg	acattagtgt	ccacatccat	826260
gcaagtatta	aacggtattt	tatcacagct	tgctgggtgcc	atctattcca	actaattgca	826320
tccttaggag	tttttagagc	tcctaaagga	tcttttcttc	tcctttacc	tatacttttt	826380
ctttatccat	ctgcagctta	gaaagaacat	ctcctaagct	gctgatcaat	taacaagatt	826440
ggaatcaatc	atggaagaga	aactctaaaa	aagtatagag	gaccttgcaa	accattctct	826500
aaaatcaaat	aaaagcttag	aaaagaagtt	taaaactggt	gtcttttatt	tattgaagat	826560
cgttctagt	tggttggttaag	gcctcaacaa	aggccttacc	aaagcacata	ataatctctc	826620
caaacgaaca	cttaggtgtt	gttattggag	ataaccagaa	tatagagagc	cgatattgac	826680
cagcacctgc	tgaataaaca	aggagtctgt	ttcaaaggaa	agtgtcttta	tttcagctgc	826740
tgctctagat	tcctcagcaa	acaaactttc	taatttagct	atgaacttct	gtgtagagtc	826800
attagaaagt	tgacacataag	gatagccaaa	ctgtggaggc	tttgtcactg	ccgatgtaag	826860
cttttgtctg	atctcctcat	tattcgcttg	aggattcgac	tggtatgatct	gcattacaga	826920
ttgtagtgcc	gaaacttgac	tatagacatc	tccaagagtt	ctgctattgc	cagaaatcac	826980
cctagcgagg	gcttgatctg	ttttttctgg	tcctcgagct	tctgttcgtg	ctctaggaac	827040
ggatcgtgtg	agagcggggg	tacttacatt	gtttatcaca	tcacgagtcg	catcatttcg	827100
tgccctacca	taggcatcat	tgatggattt	gtaagcatca	taacctgctg	atatctgtgt	827160
tttataatca	gaacctgtag	attttgaggt	cttgtaagc	tggtttacag	atgacctat	827220
agaacttgct	gcagcgggag	gaactcctgc	gctcacaaac	agcagcagaa	gcgatctgtc	827280
ctaaagcatt	gagtatgccc	tggtgttgcc	cagctttacc	tagagccgct	tctaaagctt	827340
tctgagcatc	tgccagcgtc	gcagcagcac	tgctcatctc	agcggcttcc	gctgctctag	827400
cttgtgctgc	gagctcctgt	tgggcagctt	gagaatcagg	attttccgta	ttgaacatgt	827460
gaatcatctg	acgaaaccca	gacatcaaaa	tggaagcggg	ctcattttca	gcacatctca	827520
acagcatgga	aacacgaata	ctaccaatac	tacttccttg	ttgcttgagg	cctccaactg	827580
tagttcctgg	atttggaaaca	tcagaacctat	ctgcaggttt	gatattttta	agatttttct	827640
cagcctgtat	taccatttgt	tcgccttctt	gaagaattgg	agagtcgggg	aactttttct	827700
gagcttcagc	tatttgtgtc	ttagcagtag	cgattgctgc	tttagctgaa	tctatgttgc	827760
ttatactgtt	attagattta	gcatttttcta	cagctccact	agcgttctgt	cctgcaaaat	827820
atgcatccct	aatcgcatth	ccatctttct	ctatctgtgt	cgctgtagca	tctgtctgat	827880
caactaaaga	ttgagcaatt	gcaggcgttt	tccttgggac	tactgggtta	tcttgcatct	827940
ctttaagaag	ctcagctgct	ttgttattgt	ttgctacaga	ttggagaaga	gcagcctgta	828000
agaggctcga	ggaagtcaat	ttacctaaag	agtcaagaat	cgcttggtta	tccgaagcat	828060
atttcgctaa	ttctgtaatt	tgccgcgcaa	ctttaactgc	atcggcattc	ttagtttccc	828120
actccgcagc	gattgcgggt	tcctctcag	tagccgctgt	atcctttata	ttagtgcag	828180
catcctggag	gctcacaaa	gcagcctgta	tgctcagctag	tgatgttgag	gtaaagatag	828240
tatcgtaaag	tggttgccgt	tgagctctat	aatcatcaaa	cggtgggtgga	ggaggcgtag	828300
gtgcgggtgc	tgctcggtgag	tcacagctctg	cagatctgct	agtagaagac	gagctgttac	828360
tagaagcaat	acccagctta	tctgccagac	tcatgagagc	attcactgca	gaacgcaaga	828420
tgctccatcg	ctctacagaa	tcgggtcttag	attcttttagg	cttagcttcc	gcacctgcta	828480
ttcttttgagc	ttccgcactc	ttatttgctg	cactcgcttc	caatccttga	gcagaagaat	828540
tgccggggagg	tggtgcgttct	gtttcgtcta	taggacctgg	accaatagga	ttaccataaa	828600
aaactcaaaa	aataataaaa	atcttttagt	tttattataa	aaaataaaaa	aaaagctctc	828660
actaataatt	aatgcgagcc	tggtttttaa	gattttatta	aaatttgact	taaaacgctg	828720



aaattataacc	tagatcaaac	tttcggaag	taaaatcact	gccgagttta	tcgtttgctg	828780
gtttggagta	agccccataa	gctctgaatg	atagagaatc	tgtgatgcca	tacatatata	828840
gagcggaaaa	tcctttataa	tttgtaaaac	cattagcctc	tttaggatca	tagtttagcag	828900
caattgcttg	ggcgaaccaa	aactttaata	aattaccacg	gccaatccct	gaaacatcta	828960
tttctggaac	cgacaaggct	tcgacatact	cataacgtac	tgtggcagac	cagtctccag	829020
cttttctgag	ttccccctaaa	gttcctccaa	taaaccaagc	taggttttct	tttccattta	829080
acgtagtctt	cgtagccttt	gctaaagggt	tcattaagaa	agctccataa	agatatagag	829140
gctttttctg	tccattgatc	caaggaacct	gactatgctt	tccgacgagc	cactgccaaa	829200
cacagtattt	gtattttcata	gcgtttgtag	cagctttttc	tgtagtggag	gtttctgaag	829260
gaacgaatgt	gttccagtcg	acaacactac	atttcacaaa	aaactgttta	ggcaaacgat	829320
tgagaatccc	ttctacaacc	caagcataat	gtttttttgt	catgttcacg	acgaaaggac	829380
ctccatgaac	aatcacttga	taaggatagt	ccttagaaag	ttctcgagtc	caatatatat	829440
gtagtccgtc	aaaattactt	tgggaattgga	cttctgactc	aaagagatct	cctaaaccag	829500
aacgtccgat	ttccataaag	aaatctgtac	gtgtttcggg	attcttataa	aaacgatatac	829560
ctagaaatgc	tctgttgata	tcaacaccag	ctgcagtggt	ttccccctct	gcaattgctg	829620
ttcaattcat	ctttgaagac	agccagttcc	tctcagcgcg	ataatcaata	tagagataaa	829680
attcactacg	ataacgattt	actggttaagg	gattgtattt	atctttatct	gaggggtttt	829740
tgatatcttc	tctgaaatac	aaccaccggg	ctctaacatc	tcctgctatt	cttaaaacgc	829800
catcttgctt	tcgcgtttct	acaaaacccc	gtttacttaa	gtagtctttg	acttcgtcta	829860
aaagttgtata	agtgtgactt	tttacttttt	gttccgagag	aggaagttca	gcgtatcctg	829920
aaattgtcag	cgctaaaaga	accacactcg	ctaaccattg	atatacctgt	tttttcatag	829980
tatccttagt	atcaatatta	agtgtagaaa	cagaagacca	agcaggctat	caaaacctaa	830040
agctaaaaga	aagcgactga	gctacaagaa	acaaaacatg	attaattttg	agtgtcttgc	830100
atcacgtggt	gtctttgcaa	aagaccccg	tgcccacgcc	agtattcaaa	agaagccaaa	830160
tttaataagat	cttctactcg	aagcagtttt	gcaaaaacca	acaaaaaagc	caagaaaatg	830220
cagctctcag	ataaaaaagc	aattgcttga	gccgttatgg	aggataaggg	ccaagcaagt	830280
ggtgtgaggg	ggtttaagaa	aattacatat	gtagtttgcg	taaggatatt	taagcctaga	830340
gtaatcatac	aagcaagcat	agtggttccc	ataactttta	tggaaacgcc	gatgctctcc	830400
caaagtaact	tagagtacat	agggagtctt	ttcgaagaat	aataccagag	gaaatataac	830460
tgcacccaag	cagttatgga	tgtagcatag	gaaatgcccg	agacgtcttt	taaaacccaa	830520
cgacctagaa	ccaagcttaa	aacaatatgt	gccaagccg	taccgattcc	tataaagagc	830580
ggaacagcat	actgccgctg	tgcatataaaa	agaacagaga	ctaaaggagc	caaggccata	830640
gggataatac	tggcaccata	acctcgcaat	acacgaacaa	tagcgtagac	agcactctga	830700
gggaaaagtc	cgtgttcata	aaggacacgg	actccaggta	aagctaagag	caatagccct	830760
gctgtcataa	tgatcattac	ggacatgggt	aggggtgagaa	cgaacttcat	aagtttcaat	830820
cccctctcat	gatcttctcg	ctgtacacaa	cgagaaattg	ctgggaggag	aacggtaaac	830880
acaccaaagc	caaagagatg	tatggggagc	tgataaatct	ttaaggagta	cataagatat	830940
agagggccta	tttcatgtac	atagcgagcc	aagcagatat	cagaaagaag	gttcagctgg	831000
aagatgcttg	aagttaaaaa	acccaaagat	aagggaagcta	ataaagctca	aacactatcg	831060
tggtcttgag	gtgggctctt	cgcttcta	agaaatttcc	atactccagg	aaccgtgatt	831120
aaccattcga	agaaaaaccc	gataactaga	gccacggata	aaccgataat	acgctctcta	831180
ggatctgaat	gacgagccgc	tataacaaag	aaaatccaaa	tgatatttac	aactacggga	831240
gctaattcca	ccccgaaaaa	cttattttca	cagtgaagca	aagcgccgtt	tacattgtac	831300
atcattaaga	aaatgccaca	gggcaagagt	atcatagtaa	ggagaatcat	atcgtaaagtc	831360
ccctcttcaa	cgtattgaag	aactaccac	aatactgctt	caataagcag	agtgaatata	831420
atagtgtgc	ctttaatcaa	tctagaaaaa	cgctcgaaaa	aaaacgccgc	acgatcgaga	831480
ctttgagc	ggagaaattc	aaaatgaggg	atgaaggctt	gttctagaat	gagccctcct	831540
aaaatttttc	tttaagaaaaa	aacagtagcg	aaacctaacc	agaaagcagc	tacaattgga	831600
tcagctccaa	aataggttgc	cattgcaatt	tctcgaaata	tcctgtaat	acgactacag	831660
aaagttccgg	ataatatatt	aaaaattgaa	cgagctaagg	aaacctcatt	gtcttttctg	831720
ctcattaaac	cgttttcccc	tcctccttta	aaacaagact	atctcttcga	catttcccc	831780
tatacttctt	cagaaatcac	aattggagga	agctatttca	agctaaataa	agcatcttta	831840
cagagctcta	cattgcgttt	gagaagcata	agtatcattt	cataatctct	atgatattcga	831900
catagaaaga	agcctttgtt	tcataacacc	gtaaacgata	ccgtgtcagca	gcttttttct	831960
atataaaact	gatgctttct	tcttataaaa	agagcttttt	atggatgatt	ctttaaaaata	832020
tattttttct	gtattattgc	gatactgcgc	attcggtttt	gttcaaaact	caagaatatg	832080
aaattctgtg	ggggaagaca	tacgaaagtt	attattaaaa	tttttgaaaa	attgaaaaag	832140
cctcaagaaa	tgagcagctc	aatcaaagga	cctaggtttc	ctctgaaact	gggtagttaa	832200
gaaaagacct	tgaaatttta	tgaaagtact	tcctctctcc	tccattccct	tactaggggc	832260
tcacacttca	actgctgggtg	gactcaaaaa	tgcgatttat	gaaggccggg	atataggggc	832320
ttctacagtt	cagattttta	cagcaaacca	aaggcagtg	caaagacggg	ctctaaaaga	832380
agaagtgtat	gaagatttca	aagcagcgct	caaagaaact	gacctttctt	atattatgag	832440
tcattgcagga	tacttgatta	atccaggagc	ccctgatccg	gtaatttttag	aaaaaagtcg	832500
gattggcatt	tatcaagaaa	ttctggactg	catcacttta	ggcattttct	ttgttaattt	832560

tcaccctgga	gcagctctca	aaagctctaa	agaagactgc	atgaataaaa	ttgtcagcag	832620
ttttagccaa	tcgccccctt	tatttgatag	ttctcctcct	cttgttggtt	tactggaaac	832680
cacagcgggt	cagggaaact	taattgggag	taactttgaa	gaattggggt	acctcggtca	832740
gaatttgaaa	aatcaaattc	ccattggcgt	gtgtgtagat	acttgtcata	tttttgctgc	832800
ggggtacgac	attacctctc	cacaggggtg	ggaagatggt	cttaatgaat	ttgacgagta	832860
tgtcggttta	tcttatctac	gagcctttca	tctcaatgat	tctatgtttc	cattaggagc	832920
gaacaaagac	cgccatgcgc	cccttggaga	gggctatata	ggtaaggaat	cttttaaatt	832980
tttaattgaca	gatgaacgaa	ctagaaaaat	tcctaagtat	ttagaaaccc	ctgggtgggccc	833040
tgaaaattgg	caaaaagaaa	ttgggggaact	tttgaagttt	tcaaaaaaca	gagatagtta	833100
ggaagttttt	taagtgtctt	tagatcccgga	agcaatccag	tagatcttct	gaaatcaaaa	833160
aaaacgccat	actgatatac	agttggcggt	ttctagaaaa	gattctaaat	caactacact	833220
tatgttctat	gagataggaa	ctcacaaaaca	acagaaatgt	tgataggtag	aggcaattga	833280
gcctcgattt	gatcttgctc	aggagatata	agtaattccc	ctttaaagcc	tgtcttatct	833340
aaagaaatgt	aagaaggcag	agaactttcg	tctttgcttt	ctagggcatc	ttttacagac	833400
tgaagtcggt	tagatttttc	cttttaagag	aaatctgcac	tccaggacgt	aaaaagaaag	833460
agcgtctatc	gactcttcgc	ccattaacta	agatatgtcc	gtgagcaaca	agctgctgag	833520
cagcaaaaaa	tgtttttgca	aagcccatatc	ggatataccat	gttatcaaga	cgacactcaa	833580
atctttcaag	gaacatttga	gcaacatttc	cctgcttatg	tataacttct	ttgaaagcct	833640
taaccagctg	cttttccata	atcatgccgt	agcaagcttt	aagcttctgt	ttctcttcca	833700
gttgaggccc	atagtcagac	tttttctttc	tctgcatacc	atgttgacct	ggaggatgag	833760
gcttctttaa	caaaggattt	cggcttctgc	caaagatggt	cgcacaaaaa	cgccttgcca	833820
ctctattttt	agggccacaa	tatcgagcca	tgtatttcag	tccttatatt	taatccttgg	833880
aaatcatcta	tgccccctga	ttttcatcct	agggcaattt	tggcactatt	ttacaaaagt	833940
caaggtgcgg	agtaaaaata	aaataaaaacg	cacactcata	acttgacaaa	ataccaaaga	834000
gcatttttagt	tctaattggca	attttctaca	attgcaattat	ttccaagatt	atgttagagt	834060
atttatcatg	gaaaaaaaat	attatgcact	agcctattat	tatattactc	gtgtggataa	834120
tccacatgaa	gaaatcgctt	tacacaaaaa	gttcttagaa	gacctcgatg	tctcttgctg	834180
tatttacatt	tcagagcagg	gtatcaatgg	acaattcagt	ggttatgagc	cccatgctga	834240
gctctatatg	caatggctta	aagagcgctc	taatttttct	aagattaagt	ttaaaatcca	834300
tcataattaag	gaaaaatatct	ttcctaggat	cacagtaaaag	tatcgaaaag	aacttgctgc	834360
cttaggatgt	gaggtagatc	tttccaaaca	ggcaaagcac	atttctcctc	aagaatggca	834420
cgaaaaactc	caagaaaatc	gttgcccttat	cttagatgtc	cgaaataact	atgagtggaa	834480
aatgtgtcac	tttgataatg	cgactctacc	tgatattcaa	actttcagag	agtttccaga	834540
gtatgctgag	aagcttgctc	aagaatgtga	tcccgaacc	actcccgtta	tgatgtactg	834600
tacggggggga	attcgtttgtg	agctttactc	tccagtttta	ttagaaaaag	gctttaaaga	834660
agtcctatcaa	cttgatgggtg	gtgtcattgc	ttatggacaa	caagtaggca	ccggcaagtg	834720
gttaggaaag	ctctttgttt	ttgatgatcg	cctagctatt	cccattgatg	agagtgaccc	834780
tgatgtggcc	cctatagcag	aatgtttgtca	ttgtcaaact	cctagtgcag	cttattacaa	834840
ttgtgcgaac	acagattgca	atgctctatt	tctttgctgt	gatgaatgta	ttcatcaaca	834900
tcaaggatgt	ttgggtgaag	agtgcctcta	aagccctaga	gttcgtaaat	ttgatagttc	834960
acgaggaaat	aagccttttc	gacgtgctca	tttgtgtgag	atcagcgaaa	acagtgaatc	835020
agcaagttgt	tgtttgattt	aatacctatt	ctggtttctt	catctgggag	ttgtaaaact	835080
tagaaaagtg	aagaaaccag	aacacatgtc	tcttaaaaaa	aaattactta	gagttgacca	835140
tataatacgt	ctcatcgctt	tccagggcat	tctctaaatg	atttttaatt	ttctgtgaca	835200
aaatatttgt	tactacgttt	tgtcggtaat	ttccatgtac	aatgatataca	gcataatttc	835260
gagtcggctc	tataaaatttc	tcatgcatag	gctttaccat	agaaagataa	cgagacatga	835320
tgcagtccac	gctatctcct	tgttcttgaa	catctcgaaac	catacggcgt	agtatccttt	835380
catcagcatc	ggtgtctaca	aagatcctaa	tatccataag	atctctaagt	tcttgatttt	835440
caaagaccag	aataccttca	acaagaataa	cttttagatgg	atagatcggt	tctatctccg	835500
tttttagatcg	attacctaaa	acaaaatcaa	aaactggggc	ttggacaatc	tcattatttt	835560
ttagacgttt	tatgtctgaa	attaataagt	cattatcaaa	ggcgtccgga	tgatcccaaa	835620
ttaaattggc	acgttcttca	ggagtataat	gagatctatc	tttgtaataa	ttatcttggc	835680
agataacact	cacatcctca	ccgaaaattt	ctttaatggt	ttgggttagg	gtgggttttc	835740
cagctccaga	acctcctgta	attccaataa	tcatacataag	catcatcaac	ataaaatttt	835800
ctccttagta	cttctcttgt	aatcagcaca	caacaaaatg	cgggtccttt	gagaatttat	835860
tgatttataa	ggagacaaaa	gaaaaagctt	cgtgatcaga	aattgaaatc	tttagatata	835920
gtcattttct	gatcacgaag	tttaggatag	aattctatcc	aaaaaaatat	ttcatccccc	835980
aataaacaag	ggatgttata	caaaacccca	attcacgtat	agatagattt	aaaaaagcaa	836040
aaacactgtc	agaatgcctt	ataagaacga	tttacggtat	cttagatggt	tcctaaagga	836100
gtacaagact	ccttatgcat	gaggaaacac	tagagtataa	atcactcttt	ttttcccttc	836160
tttctgaaca	agttgtatcg	gatgcaagtc	gataccttgt	tcttgtagta	tggtatgtaa	836220
tctctctaca	ttcttgggta	gtcccaaaca	tacaacactg	acatcaggaa	attttttcaa	836280
agatgttttc	aggtgatttg	cttgtagaac	agcccaggca	ctttgggcct	cagaatcggt	836340
atctctaaca	ctagagacaa	ctgtgggaac	acaccaagac	aataaccacg	ctctccatcc	836400

tggcactaat	ttttgggtcga	gaatgatgac	tctgcttctc	actgttttgg	ttagagcagc	836460
taaaacacgt	cggattttccc	tataactttg	tacggcaaca	aaataacatt	tcgggctcga	836520
agactggtgg	atttttaaat	agtaacctag	ctgccgtctt	aatatgatac	ccaacaacag	836580
gcgatagacg	tgttctctcc	atatccataa	tgtccagata	gagacagcga	gcacaaacca	836640
accgatatag	aaaaaacttg	tttcaggaga	caagcctaag	ttacttccca	aaactcggat	836700
cactcctgca	gcgactaaca	ctccaaagaa	atctaaaaag	ttattggcag	ccaaaatttg	836760
ccctctctta	tgttccgggc	ttgcatattg	tacataagca	tggagaggca	cttgatacac	836820
cccaccaaga	aatcccagtg	cgagtaaaaa	aaacaacacg	aatagtatcg	aacaagcaaa	836880
ggcatacagc	cccataaata	cgagagctag	gccgatagcg	gccaaaggga	cgtatcctat	836940
tttgatatct	tttcctgaga	ttttcccggg	gatgtacgac	cccgtgccta	cacctaacgc	837000
cactatagga	aacaagtaag	cgccataatg	cttaggatat	tttaaaataa	attctacaaa	837060
agggatgata	tctagctgag	tataagcacc	tatcaataag	aagaaagatc	ccaaaaaaat	837120
cgatacagtc	aaataatgaa	tcatccgggt	atctttcaaa	actttccata	aatctttgaa	837180
actcaccaag	gtgattttct	gtttcacatt	tttcacattg	ctaggtcgga	tacagagaga	837240
aataagagta	ctgataatag	aaacaataac	ttcacattag	gtaggccaga	catagctatt	837300
tacacctaag	cgatagtgta	catcgacaag	aagaggagca	aggcaagaac	ctaaaatact	837360
tccgtgatat	gtggctgctg	tcataatccc	gttggcttgg	gagagctgtt	ctgagggtag	837420
catttccggga	agaatcccga	gctttgctgg	cccaaagatt	gtgggtgtgac	atgccattaa	837480
aattaagact	acataccccc	caactacaga	ttggataaag	aaaaagtagc	ttccgagaat	837540
tgtacataaaa	atctctataa	atctgggtgc	taagataata	ttccggttct	gaaagcgatc	837600
tgctaaactt	ccagctagcc	ggagctagta	aaagaaaggg	aaggggcaaaa	aagaaactta	837660
cacaggagag	aatctttgca	ttctctgtta	gagttttgcc	ttccaatagg	aaaaacgcta	837720
aaagaaattt	atataaatta	tcgtttataa	tcgtcaggaa	atgtgtagtt	actagtgcct	837780
taaacgattt	ttttttaacc	gaaacagtca	tgaatgccac	caaacattgt	cgagcaagct	837840
tcagtaactc	gccccgtcac	ctcctagctc	agcttgccga	ggatattacg	tcacacatc	837900
aaaaaccttt	taccaaagg	tggattcttg	ttgcaaagtc	tactacaggg	cactggataa	837960
aaaaccaact	tgtacatgtc	ttgtcagacc	acatctttat	gggatcaact	attttcactg	838020
cttcggattc	cattgtcaaa	cacttattct	tgggttcggg	ttgctcgcag	cccaatatcc	838080
cggactacct	tacccttccc	ttgttaataa	ataatatttt	agaagaaatc	tcgaaggctt	838140
ccaaatttga	aaatggaagg	gagtttttat	ctccaccac	atacggnaca	acaaaaaaac	838200
ttgctgctgc	tttaagcag	ttccatacgt	tttcacaacg	cccgaacaaa	aacgcctccc	838260
attaccaaga	attatttcaa	atcttggaag	gccatttttc	ttcttatgaa	gagatgttca	838320
ccactatttt	aaataatcga	acgcaagagg	aggactgtct	ccttcatatt	tttgggtatg	838380
ctcatcttcc	caaacatctt	gcggaatttt	ttattaattt	aagtacgtat	ttccctgtat	838440
atttctattg	tttttctccc	tgtcgagaat	attttgggtga	tttactttcc	gatagagcta	838500
ttgatttctt	ttggaatcaa	cttcccagct	ccccataaaa	aaatgcctgg	gaacactatg	838560
tattatcaga	caggcaagca	cttcttgcaa	acttagctca	taaatctcag	tcgtcgcaaa	838620
attttttcct	agatagggaa	atagactatc	aagagatgtt	ttcccttcca	aaacacgata	838680
gttcttttag	ggtaatacag	aactctattt	tagacctcaa	gcccacgtct	cctcaagatt	838740
tctctcaaac	aaagcagacc	atttgtattt	atagagctct	aaatattccc	agagaagtcc	838800
aggaggtatt	ttgtaaagtt	acagaacttc	tgcacgcggg	agtgacacct	gaggagattt	838860
ttattctctc	ttctcacata	gagagctaca	aggtacatct	aaacgctatt	ttcaatcctc	838920
atgtgcctat	atactttact	gatgaagtag	atccacgggc	tgaagatctc	agaaataaaa	838980
atcctcctac	tttcttctat	tttacaacaa	caagggggatt	tacattacat	tcttcaactc	839040
cttacgcacc	cacaactaca	acaacctata	gatcaaaaaca	aggttcccta	tctgattaaa	839100
aagcttttct	cagaatgggg	aaaaatttct	tcaaaaagaac	gagcttcggg	tcaacaaatg	839160
aaagctctag	gtgatctgat	attagaagaa	taccatttcc	atcaagaggg	tgggcgtgtg	839220
agccaaagtag	aagtttgagg	aacaacagta	cctttaattt	atttcattca	agagcgtatc	839280
aacctttatc	tttccagctc	ccaacatagc	tatgaagatc	tatttcaaaa	cgtgttttct	839340
tgttttagaaa	agatttttgt	tttatctccc	gaagagacct	ctttcattac	aacgttaagg	839400
aactctcttt	tcccaacctt	tgtacatctt	tcctgttctc	ttcttttttt	cactgatttc	839460
tgttttagact	ttttgcttca	tttccataaa	cccagtcctc	tgtatgacaa	gccaggacct	839520
tacataggta	gtttgagtag	cctcagctta	attcctaaag	gctatgtctt	tatttttagga	839580
gctaataaaa	caacatcgct	tgacattttt	gatcttttaa	ataggacaac	aacacatgaa	839640
gagcttgcata	tttcttctac	agaagacgag	gaaaatttcc	acttcctaca	aatttttagtc	839700
tctacaaaac	atgaacttca	tattagttat	atatcatcgg	cagcgcaatt	caaccttctt	839760
agtccctttc	taaaccatat	taaagacacc	ttagacctgc	ctgtagaaac	gttacctaca	839820
caaccttacc	tctctgcttt	cttcaagaat	aaagcttggt	tacacacctc	tcaagaatac	839880
aactactctc	ttgctcatgc	tttctattct	aaaaaagctc	tcctcccttc	cttgttttatt	839940
ccaactgtaa	agcagggtaaa	tcttctctca	catctctctc	tcaatgaaat	tatcaaagga	840000
atcttttctc	cttttagacct	cttttttaaaa	accaattata	atctcagaat	ttctactcca	840060
gaacacctta	aaaaacaaca	gaaactcttt	ccaacaaaac	atcaaatcga	agacttttgg	840120
aatgaatggt	ttgtagacaa	agagcatgac	ctgatcccta	gtatctctcc	tcatgctgaa	840180
gagcttttta	cttactatag	ggaaaagaca	atcctattgc	gtaatggatt	ggacaaagat	840240

ccgaaacatt	caccttatac	agtcacattc	tcttctctcaa	ttttcgaaga	gagaccctat	840300
catgaaagtt	accttttccc	gcctctttct	ttatctttcc	aaggaaatcc	ggtccaaatc	840360
catggaacaa	ttcatggggt	atgcaatgag	ggactttatt	tatgttctat	agatcctaga	840420
gattccctaa	aaaaaacaac	cagaacccta	gggagtctcc	cagaaacctc	ttctgaacaa	840480
aaacagctct	tagaaagata	tgtagcggtg	gcgggtgtac	aatgtgtctca	gcacctctct	840540
tcagattcgg	ctttaataaaa	gcttacatcg	ttcaatacta	aagaaaacca	ccatcctcct	840600
ttttcggatc	ctgaagggtta	tctccgtaaa	gttttagaag	tctatcacct	gatgtcttcg	840660
caaccattc	cctactatc	tccattatgt	tggaaaacct	tagacgatga	agaaaaatct	840720
catcaggcag	tactttctgc	tataagtga	gaagctaaaa	atccttctct	tcctattttc	840780
tggcagtttc	acaatcgtaa	tatcgaggag	atcttaaate	acgtgggtgc	atccgaacgt	840840
ttgaaaattt	tatctctttt	cagagggtccc	tgtgaagccg	tttaatatct	ttgactcaaa	840900
ctcttcgatt	cagggaaaaat	ttttcctaga	agcctctgca	ggcacaggaa	aaacattttac	840960
tatagaacag	atcggtgttg	gagccttgat	tgaaggctcg	ctaacacatg	tagaacatgc	841020
cttagcaatt	acattttacga	atgcttctac	caatgagctt	aagggttcgca	tcaaagacaa	841080
tcttgctcaa	actttaagag	aattaaaagc	ggttctaaac	tctcagccgg	cttctttacc	841140
cacatatcta	gatacaatt	gcaatgtaaa	gcagatttac	atgcaagttc	gcaatgctct	841200
tgctactcta	gatcagatgt	ctttgtttac	gattcatggc	ttttgcaact	ttgttctaga	841260
acaatatctt	cctaagaccc	gtcttattca	caaaaacctt	gctctgacct	actctcaatt	841320
agttcttcat	cacatcacta	actatttaaa	acaagacctc	tggaaaaatg	tactttttca	841380
agaacagttt	catctattag	cagttcgcta	caatgtaacc	tcgaagcata	catcttctct	841440
ggtggataag	ctacttgcca	gctataacca	accaatctcc	tcctactttt	cctcacgtgt	841500
tgaagagact	gagcaaatct	ctctttggca	tcaacaaata	tacaactctc	ttttagaaat	841560
tccaaaacag	gttttttctag	atcagctaac	tgccacatc	tcaggattta	aaaagcagcc	841620
cttttccatt	cttgatgatc	tccatcattt	tgtggatctc	ctttacactt	cggagaccca	841680
tagctcttta	ttttcattct	ttaaaattgc	agaaacattc	aacttcaaac	accgtcttgc	841740
acgttacaag	ccttgtgctg	cctttactgt	tttagaaaac	atgtcttggg	tagagcgtac	841800
tttagagttt	tgttaacttg	atcgaatctt	caatactttg	ttagtcgatc	tccaagagta	841860
tcttaaacaa	aattataccc	cttggtcttc	tcccgatgaa	agcgtctttg	ccctcgagaa	841920
actactctct	tcatctgaag	ctcaacctgt	agttcaagct	cttagagagc	aataaccagct	841980
cgtattaatt	gatgaatttc	aagatacaga	caagcaacaa	tggagcatct	tttcgaatct	842040
ctttattttct	ccgaaattta	caggatcggt	atttcttata	ggagacccca	agcaatctat	842100
ttatgaatgg	agaagtgcgg	atcttctctac	ctttcttaca	gccaaatctt	cgttttcaga	842160
agacaagcaa	ctacagcttg	tcaattaatt	accgtctctac	acccaaactc	atggaagcca	842220
tcaaccaaat	attcgggaaa	atctctccat	ttttagagat	ccctggctac	ctacctatag	842280
aataccatgc	gctaaatcct	cagagtagtg	agacatttga	aaatcccccc	cacgtcctta	842340
ttcattttct	cttttatgaa	actattaaag	accaggcatt	atggatattc	tcagaagcgc	842400
taagactaca	aaaagaacaa	aagattcccc	tagggaatat	ggttgtcctg	gtctcagact	842460
caaatcaagc	ttttgagtta	atttctctatg	cgactattcc	tgtttccttt	tctaaaaaca	842520
aatctatatt	tcatcttaca	gaaactcaca	tactgactac	agctctacta	gaagccattc	842580
ttcacccgga	gaattatgaa	aaaatcagca	agatattggt	ctcatctctt	tttggacttt	842640
ctttagacga	agtnacaaca	aaaaaagaag	actttacgat	ttattttcaa	tcactacata	842700
gctacatctc	acatcatgga	cttctggcta	cattttaccg	agtgatgact	acgcaaggaa	842760
acgtattgtt	ctcatctcct	agaggggatac	ttatttttca	ggaaatggag	aaactttgtg	842820
gttacctaga	tacaattttct	tcttatccct	accaccaact	tcttcacctg	aaaaactttt	842880
ctgaaacagg	acggtgggaa	gaagaactcg	ctatatcttc	ttattctgag	gacttggaaa	842940
ctttaaaaat	cactaccatt	cactcttcta	aagggtctga	atacgatata	gtcttttgtc	843000
caggaattga	gaaaagtaaa	aaaaataaaa	gctcttcaga	attactaaga	gaaatgtacg	843060
ttgcttgac	gagagcaaaa	aaacagctgt	acctacctat	aagcacgcaa	ccgccttctc	843120
ttcagagaag	ctccgcatta	acaaattacg	tgaatttaga	aggtacgcag	agttcggcct	843180
atgacttagc	tatccaccta	catcaagaac	atcctgattt	attttcgtat	tcgctacctt	843240
aggaccatgg	acatgctacc	acagtgttga	atctgccact	tttagagacg	ttcgctctaa	843300
aagtgcaccc	cccgaaaact	attttttccct	tctcatctac	aaaatttcta	ttggacactc	843360
acaaagactc	gcaatcgatc	ccatattcca	actccccgatt	tcaaaaacaac	agcttctctct	843420
gggagaaaaa	acaggaattc	ttatacacaa	aatttttagaa	tctattcaat	tttctctatt	843480
acaagacact	gagtacttga	tgtctacgat	catgcgtttc	ataaaacaca	ctcatcttga	843540
aggatttcgag	ttaaactgatt	ttaaactact	tagtaagacg	tttttttctc	ctttaacatt	843600
ttcatcgcag	acatttttctc	tatctcaagt	tctaccgaat	aagatatttc	gagagacttc	843660
tttttttatt	ttagagaacc	aagagctgtg	gcaaggggtg	attgatcttt	tttttgagca	843720
tgaaggaaaag	tactacatta	ttgactggaa	aacatcgttt	ttaggagaga	caaactccga	843780
ttactcaaaa	agcaacctat	ctatctacat	aaaacaagaa	aaattagatt	accaaggcag	843840
gatctacgtc	aaagctgtca	ggaagttttt	aaatcaattt	gaaattgatg	atgatgtaga	843900
gttggaggtt	atcttttatcc	gtggcatatt	cacccaagga	aatgggtttt	tcgctttaaa	843960
tagcagcgaa	gacattccta	acttcaatcc	caaagcaatc	caaaaatgtc	aggcctatca	844020
ttaggatttaa	attctagggg	aggtaaaaata	aagagctgat	ccagctccat	aagcttttct	844080

tc	caaagact	gagcttctat	cttgaaagta	caggctccat	cacgaggagc	ttttaccttg	844140
gt	gactctag	ccaccaacag	tcctggggga	aataccccat	ctaactcctgt	tgtcactaag	844200
at	atctccag	gtagcagagt	ttttccctcg	ctaaagtaga	atccttctcc	ctctaaacat	844260
aa	agaccctt	ctttccataa	agccccaccc	actccagaaa	gtattcctct	taggagagct	844320
tg	gtttttctc	cttctccctg	tattaaagaa	tctaactctt	gtagctgaga	gattttttca	844380
tact	tatcct	tttcaaggat	ataggcgtgt	gaaatctgct	ctacttgct	gattagttct	844440
cta	agactgt	gttttatcca	ccaagactga	atatcaccgc	gcatagcaac	tacagagggc	844500
ttc	attccta	catctgtgat	taatcgtata	cggttggt	gttctccaac	ataatcgaca	844560
agt	cctacta	gaacatttcc	agaaagcacc	ggagaatttt	tcttgattcc	atgagttttt	844620
cct	acattca	cccaacaaga	actagaccaa	tgtgtgtaat	ctcgatagac	aacctttccc	844680
tct	accaact	tatgaaaata	gggagttaag	atctctggaa	ataaaggagg	agtgtgatta	844740
gag	acctcat	aaagtttgag	tttctcttct	aaagaagcca	ccctctcctt	aagaacgagg	844800
ttct	tctaatt	ctaaattagc	aagatgagaa	gaaggagctt	gtttaatttt	agggaaaaat	844860
ttg	acgtgta	gagagacaaa	actgcttctg	atcttatcat	agacctcttg	agggatgctt	844920
cg	aaagaga	gaatccctaa	agcaataata	atagagacgc	agatttttgt	ttttttattg	844980
cgt	aggctat	agctcataag	cttgaataaa	actttgcact	acatgatcta	tatttttttc	845040
cgt	aattcca	tttaatttca	ttcttctctc	cgctgttgta	taaacagcgt	gttggtctct	845100
t	aaaaagagc	acctgtttat	cggaaaaccc	agggatgca	aagaatccat	gttgggacaa	845160
t	aaaaagtca	aatgtatgac	cggcaacctt	acgcaaagct	tgaacaaatc	ttgttctcat	845220
ttt	accctaaa	gactctctta	taaaattgag	ttctgattgc	cattcttctt	tcaaatatgg	845280
att	actctaaa	attgtagaaa	caattttctac	accccaacgt	tgtggtgaag	agtattcccc	845340
tcg	aattttt	tcttctaaga	aactgtgaat	tttaaccaac	tcacagtaa	aagtactgtg	845400
aac	agcaaaa	tatctacac	gctcaccata	aagagcaaa	tttttgcttg	atgaagcagc	845460
gac	agaaccc	gtatttccct	ctgatataaa	aattttctata	ggttttctat	ccaactctat	845520
gcc	gtgagca	aaaccttggt	atgcggtatc	aaaaaatgga	attaactctc	tttctttcat	845580
ta	agatggcg	agttctttcc	acatatcttc	agtaaaatct	acacctgtag	ggttgtgaca	845640
aca	accatgc	aataagataa	cggaattctt	ttctacttcc	ttcaaaaatg	cgatcagggg	845700
ttc	aaataac	agctgttttt	gttcttttgc	ataataagga	tatcggatta	cctcaagacc	845760
ctc	ttgagag	aaaatgcgta	tatgattgct	ccaagtctgc	tcgggaacat	aaaccttacc	845820
agat	cctttt	gccacggaaa	gaagccgggc	tcccaagtgt	agcgctcctg	tacctcctaa	845880
agact	gaaac	ccgactatag	cactcggatc	tacagcacca	aaaaccagct	cacgcactctc	845940
atc	taaaaat	atttgcaacc	ctgaaatagg	aagataactc	ttattttgtt	cttcttccaa	846000
a	atgacagtt	tgtgccttac	gtatacaaga	caagccgcgc	taacgctttt	gcggatgctc	846060
ata	aacacca	atcacaaggt	taaccttttc	gggacgctta	tctgcaaaga	aaacgttctg	846120
caa	acctaaa	atagcatccg	gagaaaatgt	tggtatgtga	ttaaaaaac	tcatatatga	846180
ctac	acctaa	ttataacaaa	gattgattct	aaaccttgga	acatgatact	tttttgatc	846240
tttt	ggggta	ttagctcagt	tggtagagcg	caacaatggc	attgttgagg	tcagcggttc	846300
gacc	ccgcta	tgctccatgt	tcttcccaaa	tggtattgat	ccgagaaaatc	ttatactcct	846360
ttc	cttgag	tattaccacg	tcattcaact	tcttccctaa	catgttctgc	gcaagcttgg	846420
att	gtaaaaga	aagtatacaa	ctatctggat	cggcatccca	aggtcctaaa	attgtatact	846480
cc	acaacctc	tccagcatcc	cctttttaaag	taactttaca	gccaacacca	actttatctg	846540
t	aaagacaag	gtcttttgta	agaattctcg	cccgattaat	ttcttccgat	agcacgcgaa	846600
ttt	cttcttg	taagcgagct	ctcttctcta	aagcaaactt	gtactcagaa	ttttcccgca	846660
a	atcccttaa	agaacgagca	tcttcaattt	ccttagcatt	atcaaccatc	tccttgccaa	846720
ca	agagattg	tagcttggt	ttcattcttg	aaaaactctc	agaagtcgac	cataaaacat	846780
ttt	cttcttc	tactatagac	ttgtgctttt	ttagcgttgg	ctgaacaact	tcagcaaggc	846840
ttt	gtaaaac	gttcaaatca	gaagaagaaa	actgcgggca	tttgggtggat	agtaatatga	846900
att	ctttttta	aaagggaagg	gatgcgcctt	ctatcatctg	acgcacagcg	agataccttt	846960
g	ccccacca	gtagtgggtg	aacttttttc	ccagttcttt	atgaggtgta	gangctactt	847020
g	atacataaa	attcaaagct	gactctaaga	acaatcttaa	gacttccttg	tcttcaggat	847080
caa	agagacc	atcttcatgg	ttcccaagct	tcaagaaaaa	ccaaacaaac	agctcagggg	847140
ac	atcattgg	ttgatgggca	ctatctagaa	gtcttttctt	taaaacctct	acgcttgatg	847200
ga	tcgttttt	aatggtttta	tatacaaaa	ccctcatggt	tgagagaggtg	gtataaagaa	847260
ga	atttgcat	aaaaacttgt	tgccagaagg	agaagtactt	tcttaccaaa	gacaaaaagg	847320
act	tttgcaa	agcaacaata	ggcatgtttt	ccaaaagacg	actggtatca	tcttctgata	847380
agg	atgttat	atactctttg	tctatgctcg	catccttaat	tcccaaatac	tcagaaagaa	847440
gc	agttctct	ctgcaaaatt	aaagacttat	taccttctct	aacatcaaga	tcttgcaaaag	847500
ctt	taactag	actcttgcca	atctctatat	ttttcaattc	actatgcaaa	tctctaataa	847560
a	atgatagat	cagagagatc	ttttctgcgc	tattgagact	caatcccaac	ttacgctcca	847620
act	gtcccat	atgagaacac	cctgcacacg	ataaaacata	gggctcttta	ggattgtctg	847680
ggg	atataat	tctagtctcc	tttttaactc	tagtcttagc	tgattggccac	caccgattcc	847740
a	atctgcctc	aggaatcaca	agatcaacta	actcgtcttt	gatttccttt	gcgggtctttg	847800
gtc	caagatc	tctaaggaga	atctcaacaa	cttcaatagg	gttttctctta	gcaaaagcct	847860
caa	accctac	gggatctcca	aaccgtcgtg	aaaggagtg	atcgccgctc	aaaggagtta	847920

aactttttaa	tgccgtctcg	aaagaaatat	ccttggcact	cataattcct	tcaaactcta	847980
tcaacacctt	ctgctgaaga	aacgagaccc	ccataacctc	gccaacaccc	caacccctt	848040
gatggaagac	aaagtttccc	ttatgcatat	gcatcaaaaa	atcaaaacgg	ctgaggctaa	848100
actgaaaatc	acgaccatca	cgaagcccaa	caacacgcaa	agcctcgtta	aagttttctt	848160
ctccactgta	ctttttatct	acatattcag	tggtctatct	aaaaaacatc	tggtctgttag	848220
atgtttgcaa	atctaaaatt	aattgaagaa	ctcgatcttt	atcctttccc	tcgggtattt	848280
tttcccaaag	aggaacgacg	gtatccacaa	tctttccaaa	taaagatgct	aaagaggaag	848340
actttacttt	ttctaggatc	tcaacaagct	cccgcccccg	cactacatcg	ttaaaacaat	848400
actcctccca	aaggctttaa	aagttcgcag	attggccttc	ttctattaag	acttgcaact	848460
tttctaaata	gtccacgatg	tctccagttt	ttaacctaaa	aatatactct	tacgtatgaa	848520
aaagagcaat	atcacaatac	aaaataatca	aacttatttt	ataataaact	aaaatgatgg	848580
tgattgttat	gaatagtaaa	tctgcgcaaa	aaataataga	ttctataaaa	caaatectaa	848640
ctatttataa	tatagacttc	gatccctcct	ttggatcctc	gttatcttca	gattctgatg	848700
cagattacga	atatctaate	acaaaaactc	aagaaaaaat	ccaagagcta	gacaaaagag	848760
ctcaagagat	tctaacacag	acaggaatgt	caaagaaca	gatggaagtc	tttgcaata	848820
atccagataa	cttctctcca	gaagagtggc	tggtcttaga	aaaagtccgt	tcttcttgcg	848880
atgagtatcg	aaaagagaca	gaaaatttaa	tcaacgaaat	taccctagat	ttacatccca	848940
caaaaagaatc	aaaacgcccc	aaacaaaaat	tgctcatctac	caaaaaaaat	aagaaaaaaa	849000
actggattcc	tctataaaat	cacttataat	cccgtattgaa	tgaaacaccc	aaggacagag	849060
tccaagggac	ttccctttta	aatttttatg	aaaattacag	tcaatcgggg	tttagattta	849120
tccttacaag	ggctctccca	agaatctggt	ttctataaca	aaatcgatcc	agaattcgta	849180
tctatagact	taaggccatt	ccaaccttta	tctcttaaac	ttaaggtaga	gcaaggagat	849240
gcggtctgtt	caggagctcc	tatagcagaa	tacaagcact	ttcctaacac	ctacattacc	849300
tctcacgttt	caggagttagt	taccgctata	cgactggaa	ataaacgttc	tcttttagat	849360
gtcatcatta	agaaaactcc	tggtcctaca	tctacagaat	atacgtatga	tctccaaact	849420
ctctcacgtt	cagatctttc	cgaaatcttt	aaggaaaatg	ggctctttgc	attaatcaaa	849480
caacgtcctt	ttgatattcc	cgcaattcca	acacaaactc	cgagagatgt	tttcatcaat	849540
ttagctgaca	atcgctcctt	tactccaagc	ccagaaaaac	atctggctct	cttttcctct	849600
agagaagaag	gatttttatgt	atttgtggta	ggagtctcag	ctatagctaa	acttttttga	849660
ctccgtcctc	atatagtttt	cagagatcgt	ttaactctac	ctacgcaaga	actaaagaca	849720
attgtctacc	ttcataccgt	ttcgggacca	ttccctctcg	gatctccatc	gatacatatt	849780
cacagcgtag	ccctatttac	caatgagaaa	gaagtggat	tcacactgtc	atttcaagat	849840
gtccttacta	ttggccatct	tttcttaaag	ggaagaattc	tgacagagca	agtcacagca	849900
cttgctggta	ctgcactaaa	aagtctctta	agacgtatg	tgattactac	aaaaggagct	849960
agcttctcta	gtttaatcaa	tcttaatgac	atctcggata	acgatacatt	aattagcgga	850020
gatcccttaa	caggaaggct	atgcaaaaag	gaagaggaac	ccttttttagg	atttcgagac	850080
cattcaattt	cagtcttaca	caacccaaca	aaacgggagt	tgtttagctt	tttaagaatt	850140
gggttttaaca	aaccgacatt	tacaaaaacc	tatctctcag	gattttttcaa	gaaaaagcgt	850200
acctatagca	atccagatac	taacctccac	ggagaaaactc	ggcggattat	tgatactgac	850260
atctatagca	aagttatgcc	gatgagaatt	cctgtagtcc	ctctgattaa	agctgtaatt	850320
actaaaaatt	ttgatttagc	taatgaacta	gggttttttag	aggtttgtgg	tgaagatttc	850380
gccttaccga	ctcttataga	tccatctaaa	acagaaatgc	ttaccatagt	caaggaatcc	850440
ttaatagagt	atgccaagga	atcagggtac	ctaactcccc	atcaagattg	attttttgtt	850500
cttcaaagaa	cttaaaattc	aaatccctga	tgcatgaatt	ccaaaataaa	aggagcggag	850560
taactaataa	tcatatctgc	gccagtctct	tgattgctat	caaagactca	tgaaatagtg	850620
tttctttatc	taaccaacct	tggtgaaagg	ctgataagat	catagcgtat	tccccactga	850680
cctgatacgc	agctagaggc	aaacaggtat	tttgtcgaat	ccgatagatc	acatcaagat	850740
agagtcctgc	aggcttcacc	attaagatat	ctgtccctc	ctcctcgtct	aaagaagatt	850800
caagcaatgc	ctctaatacg	tttttagggg	tcactctgata	ctgtttttta	tctcctgaag	850860
ttacgtgaga	actcagcgca	tcacgaaaag	gagaatacaa	acaagaagcg	tactttacac	850920
tataagacat	tatagaggtc	tttgagttagc	cagactggtc	taacttagag	cgaatgtagc	850980
caatccttcc	atccatcata	tactcggag	ctacgatatc	cgctcccat	tcagcatgta	851040
aagttgcaat	atttccaaaa	attctaacac	tttcatcatt	aaggacctct	ccattaagga	851100
aaatcccatc	atgaccgtgt	gtcgtataag	gatctaaagc	tatatcacta	atcagacata	851160
gggtgaggaaa	tgcggttttt	atttcatgaa	tgctatgaca	taagatgttt	ttaggatttg	851220
aggagtaaga	accgtaagca	tctttaagat	catcaggaat	aatgggaaac	agcattacag	851280
ctcgtaaccc	gtaggtacac	aaacgctcta	tttcccttaa	tagcaaatcc	aaactccatc	851340
ggaacactcc	aggaagactc	gggatctctt	ccttttatgtt	atttccatac	ttcacaagaa	851400
atggtgctat	gagatctttt	gggcttaagt	gagtttcggc	caacaaatct	cttatagctg	851460
ctgtctttcg	gtttcttcta	ggacgtctac	ttagtgttaa	agaactcatt	tctcagatcc	851520
tttcaacagt	ttccacagg	cctaaatata	tattgttata	tttatacata	atattctctt	851580
cttcttttagg	gggtgtggaa	actgttttaa	actttgtttt	tcgagggag	tttatgtggg	851640
tttgtgttcc	aaaactttgt	taaaactattg	ttcattttgt	tgataagtga	ggattttgca	851700
tgtttataaa	cacaagatca	accctttttc	tacatcaatt	tttcaaagaa	aaataggatg	851760

aggggaattttt	tgttagttgt	gtagaaactg	tgatctttttg	gcttttgattt	ggataaaaaa	851820
tttctgtttt	ctctctgttt	tttgtatgca	ataggttgta	gaattacaaa	aatttctctt	851880
gtgatttcgg	aggtttgagg	tgaaattttt	tcaccgatac	ttgggtacaa	aaaccataag	851940
ctaaagtatg	cttgggggtca	taagcgacgt	tatacgtcgt	gctcccctgt	agggatgagg	852000
cgcgcgaatc	gtcgaagcag	gaatccactt	aagcaagttt	atattatccg	agtatatagg	852060
tagttttcgg	gaagatgtcc	gttcagtttt	gaggttttca	tgttgggcaa	agaagaagag	852120
tttacgtgta	aacaaaagca	gtgtttgtca	cattttgtta	ccaatctgac	gtccgatgta	852180
tttgctttta	aaaatcttcc	agaagtcgtt	aagggagctt	tattttctaa	atactcccgt	852240
tcagtttttag	gtttgcgagc	acttttggtta	aaagaatttc	tatctaata	agaggatgga	852300
gatgttttg	acgaagccta	tgacttcgaa	accgatgtac	agaaagctgc	ggacttttac	852360
caaaggggttc	ttgataattt	tggggatgat	tctgtaggag	agcttggcgg	agcacctggc	852420
tatggaaaat	gtctctattt	tggctgctaa	agtttttagag	gatgtctgaa	ttggcgggac	852480
cccgttagaa	aagtccacaa	gatacgtcta	tttcgatcaa	aaggtacggg	gggagtattt	852540
atattaccga	gaccctattt	tgatgacttc	ggccttttaa	gacatgtttt	tgggtatttg	852600
tgattttttta	ttcgataacct	attctgcttt	aatccctcaa	gttcgtgcct	attttgaaaa	852660
actgtatcct	aaagattcta	aaacaccgcg	atctgcctat	gccacatcat	tacgagctaa	852720
agtttttagat	tgtatacggg	gacttcttcc	tgcggcaact	ttgacaaatc	taggattttt	852780
cggtaacggg	aggtttttggc	aaaatctgat	tcacaagtta	caaggtcata	accttgcgaga	852840
gttgcgacgt	ttaggagatg	aatccctaac	agagcttatg	aaagttattc	cttcatttgt	852900
aagtagagcc	gagcctcatc	atcaccatca	tcaagctatg	atgcaatatc	gaagagcttt	852960
aaaagagcag	ctcaagggac	ttgctgaaca	agcaacattt	agtgaggaga	tgtcttcttc	853020
accgagtgtt	cagttgggtat	acggagaccc	tgatggcatt	tataaagtag	ctgtgggatt	853080
tcttttttct	tattcaaate	gttctcttca	agatctcata	gactattgta	aaaaaatgcc	853140
tcagtgaagt	cttgtacaga	ttttagagag	cagtgtttct	gcaagagaaa	accgccggca	853200
taagtctcct	cgtgtgttag	aatgcgtaga	atttggcttt	gatatacttg	ctgatttcgg	853260
tgcataccgc	gatttgcaac	gacatcggac	gctgactcaa	gaacgacagt	tactctctac	853320
acatcatgga	tacaattttc	ctgtggagct	tctagatact	cctatggaaa	aatcttatcg	853380
agaagctatg	gagagggcga	atgaaacccta	taatgagatt	gttcaggagt	tccctgagga	853440
agctcagtat	atgggttccca	tggcttacaa	tatacgttgg	tttttccatg	taaatgctcg	853500
ggctttgcaa	tggatttgtg	agttacgctc	acagcctcaa	ggctatcaaa	attaccgcac	853560
tatagttaca	ggttttagtgc	gagaggttgt	caagttcaat	cctatgtacg	aattattttt	853620
caaatttgta	gattattctg	acatagattt	aggacgggta	aatcaggaaa	tgcgaaaaga	853680
accaacgacc	taagtctcta	gatctgtaat	tttagatatt	gtaaaaacat	aatctttgca	853740
tttacaggaa	cattctctac	tgggtattttt	attctttttt	catgaagaga	tcataaaatg	853800
aaagatctta	tatataataa	cttgggttagg	tttaaaaaaca	tttctaaaac	caaaaacttca	853860
aggtaaagg	tgtcaaaggga	ggagcctcat	ttacagcttc	tatagctgta	gatatagact	853920
ctgcggattt	atcttcccgag	gattctatgg	agggtattat	agaaaaatgt	gctcagattg	853980
gcgttgctga	attccaaaaa	tgcgaattcc	aaatttgagg	tattacctgt	ttgtagaaat	854040
ctagtttctc	gggtgtagcg	cacctggtag	cgcacttgga	tgggggtgcaa	ggggggcggag	854100
gttcaaatcc	tctcatccag	atctctctcg	gggatgaaga	ttttatcttc	atcccttttt	854160
tataagaaat	tttgttagta	aagatagaag	ccaaggtggc	tgtaaagtta	aaatagcacc	854220
ttagaatatc	cttgaagatt	taaaaagatc	ctaaactcga	gataatcggt	tcgaattcag	854280
aactattctt	taatccacca	gcactgagac	gatccaagag	ctctaagcaa	ttgttttgag	854340
atcttgctaa	tagctctaga	gcggcctttt	ctccaaatag	taaagcataa	tttagcccaa	854400
tttgttgagg	gtctttttgt	aaatctgaaa	aatcatcttt	tatttgaaaa	agtaagccaa	854460
aattatttga	gaaacttgta	attatagggt	caaattgtgt	gtctccgcca	ccaaataaac	854520
aaccagaaat	acatgcaatc	tcaaataagag	aaccctgttt	tttgatcata	atagattgta	854580
cgtgttcttg	acctcggtta	gaaaagaaca	tatcatcata	ctgcccctct	aataccccag	854640
aacatccaat	atttttgtct	gtaatatctc	cgataatggt	gtaagcgata	tctattttct	854700
taggatcaca	gccctgttct	tttaacttct	ttgcgtttta	gcgaagggtg	gagtaagcag	854760
caggaattag	ggcgtaagat	gcgagtaagg	cgggttgcttc	atcgaaagct	ttatgtaccg	854820
tcgggctgct	cctacgctca	tcgtcggtgt	ccatgcaagg	aagatcgctc	gcaattaggg	854880
tggaaagtgt	gacaaaactc	acagctaaag	ctgagtcctt	aacgtcatga	tttaagccca	854940
aaccttgagc	catcatgcag	actaaaccag	gtcttaaacg	ctttccaccg	ccctgttaaag	855000
cgtattctac	aggagagcga	atcgggtgac	ctataggacc	aaatccttcc	aaagcctttt	855060
ctatagcact	ttctatagaa	ggtcgatacg	tatctaaagc	atgtaacaca	agagtcacct	855120
attttttaa	gacttgacca	ggacgaattc	tagtatgagg	gagaatatgt	tggcctggat	855180
tgatgacaac	attgcatact	atagcaaccc	cttttctctaa	aaaggcacca	agtttacgac	855240
gccctgtatc	gatttttttt	gatttatctg	aggtagaacg	aacatagatg	ttccttccat	855300
ctagacggaa	attagcacia	cgactccag	cacctagatt	gacttctgaa	cttaacacag	855360
aatctccgag	gtaagcaaa	tgagcggctt	tcgtatgatg	acctaaatag	ctattcttga	855420
tttcagtaca	gtgaccccaa	acacagcgac	tgccctgtgt	gacattgcct	cgcagatagg	855480
ccccatgacg	aacttctgtt	tgtgagccaa	gaatgcatgg	tcctacaatg	taagccccag	855540
actctacgta	ggcatcttca	gcaatctcaa	tcttttctat	atttttttaa	gttacaccag	855600



actctacagt	accatgaatc	ccagaaaaca	cgtgggttttc	cagcatctga	tccattaaat	855660
caagaatatc	ccaggtatag	tgagcttttg	agattatctc	aggatagaga	aagtcctcag	855720
gagaaaatat	agacgaggct	agataagtca	tatagcatat	tcaagctatt	tgccctcagta	855780
ttttcatact	ctgaagattt	acttacaaga	tataaagaac	ttactttact	cttcgatttg	855840
atgcgctgta	ttgtcatgat	tctggagagg	aatactgtca	gcattctgaaa	atagatagcc	855900
tacaccacga	atcggtacaa	tttttagatcc	gtagggacct	aatttttttc	ttaaagaagc	855960
aatatggaca	tccacgttgc	gagcaatgat	ttcttagta	tttcttttaa	tctctgctaa	856020
aagattcttt	cggagacata	ggtgtccacg	gttgataagg	agttttttta	gaatacctgc	856080
ttcagaaggg	gtaaggata	cgttctcttc	tggagattct	atcacgagat	tcaagactcg	856140
gaatgtatga	tctccaaaag	tcattgtatc	tggaaatgcta	tgctctagaa	cttcgtgttg	856200
gcgtaggaaa	gctctgatca	cggcatctaa	tactttcgct	gtaataggac	ggagaagata	856260
ccctgttgct	ccttgattta	acacctttgt	gatcgccctct	tcttgaaatg	tatcgaatag	856320
aacaattaaa	tcttcttctg	gaaagatccc	aggagagaaa	atttgctcag	gtagcaatag	856380
gtattcacaa	aatatagcaa	cagattcaaa	agatgtcggg	aacaccggag	atacgagtat	856440
ttggtaatca	gatctttgtg	atgccaaagt	ttttaattgc	gaagataaac	tgagatcctc	856500
agtaacaaac	aatatgattt	tatcacccgat	catatgaaaa	caaaatagat	tatatgaatg	856560
aatacgtaat	ataaaatcag	ttatttttca	aaggtcactt	acactttttt	acttttttct	856620
tttttgaaaa	atagttttgc	ataaacacaa	cactatatat	ataattttaa	attaataatt	856680
tagaagcgac	atagtttttt	aacttctttg	aaggccgttc	aggacgtaaa	tgtttcgttg	856740
catattgttt	ggtattttcc	tactcacgtg	tttttcttct	ggcgggggtg	tatattactt	856800
attctgttcc	catgattttt	ctatagggcc	taaggaaaaa	tcacgatccg	tggtggattga	856860
ggaagaaaaa	gagttcacgg	attccgtatt	acatcatctg	ccatcgcaac	atcagcattt	856920
gcatattctt	tgtttccaag	ggtttttact	acagaagcaa	caaaagtttt	ctcaagcaga	856980
aaagattttt	tctaaagttt	acgacgagcg	tcaggacggt	ccttttcttt	ttaaggagga	857040
aatttttagga	tcccgcagtga	tcaacagttt	tttttttagaa	aaaacagacg	tcatggagac	857100
cattctttgt	cttctgaatc	agcgctgtcc	caactcccc	tactaccact	tatttaaggc	857160
tctagtatgc	tataagcaaa	agctataccg	tgaggtcata	gagcaactag	cctactggca	857220
agaagagaaa	actcgagcgc	ttgctccttt	attgaatata	agtattgaac	agctgctaac	857280
agattttctg	ttagattata	tttctgcgca	ttctctgata	gaacagaaaa	tgttccccga	857340
aggcagagta	attcttaatc	gcaatatcaa	taggttatta	aaacacgaat	gtgagtggaa	857400
tgcaagaca	tacgatcgta	ttgcgattct	tcttagccgg	agttattttt	tagagttggg	857460
agaatctaa	tttgcagata	tttattttga	ttattatgag	atgggtgctt	tctatctcaa	857520
aaagatctat	atttttagagc	agtgtcctta	tgcagaactt	ctccccgagg	aagagcttgt	857580
ttccttgatt	atggaacacg	tgttttatcct	tcctaaagat	aaatttatat	ctttaattca	857640
gctcctagag	atgtggcaga	agcattatgt	tcacccaaat	agttcttttag	tagtttcagat	857700
attggttagac	cgtttttcta	cacatatgga	aggggctatt	cggttttgtg	aggcttttagt	857760
ttctttctct	ggatttgaag	aattacatca	gcaaattatt	accacttttg	aagagctgct	857820
ttcaaaataa	gtacagcaga	taaaaactga	agaggctaaa	caatgtgttg	cctactttca	857880
tatttttgat	ccttctattt	ccattagtga	aaaattatag	ctttcttcgg	atacattaca	857940
aaatagagtt	tctggggacg	acgagcagca	tacaaaactc	cgcaattacc	tagatctttg	858000
ggaagccata	cagtcttatg	atattgatcg	ccaacagctc	gttcatcact	tagttttatgg	858060
tgcaaaagat	cttttgaaaa	aaggaggatc	tgatgaaaag	gcattgaacc	ttcttcagct	858120
ggtcttgagg	tttacaagct	acgatataga	atgcgaaaagt	ggtgtgtttc	tttttataaa	858180
acaggcgat	aagcaagcac	tgtcttccca	tgccattgct	cgtcttttaa	agtttagaaaa	858240
atztatatcg	gaagcgaata	ttccctctat	agtgattagt	gaggctgaga	aggccaattt	858300
cttagcagat	gctgaatatc	tttttgctca	tgaagactat	gacaaatgct	atttgtatag	858360
catgtgggtg	actaaggtgg	ccccctcccc	tcaatcctat	cgttagcgat	ggttatgcct	858420
gatggaaaa	aagcgttacg	acgaagcttt	agaattttct	tgtatgctct	cacccaatga	858480
tagtatcaac	gactataaga	cgcagaaggc	attagcattt	tgccaaaaac	atcaatctaa	858540
ggaccgagct	gcctcttagc	attctcccc	catcttttca	ctcttaaagt	aaagagtttt	858600
tgtgtagtaa	attttttata	gttttgctta	ggaactatct	tccgagtgtt	taggaaaaga	858660
ttttcgaatc	ttcatgcatt	catgttatgt	tagactctat	aacggaaatca	aagtagggat	858720
gggcattgca	cacagaattt	gctccttttt	tagaagaact	agtacatcag	caggtgatat	858780
cccctttaga	catcgctttt	gcttctaagc	acatctcttc	ggactttgaa	gagctttttg	858840
tttttctcgc	ggtctcctca	gcgctttggc	gttatgggtca	tccctttctt	tcccttgagg	858900
aaaatcgcac	tagaccttct	ctaggaggga	tctcagaaac	agattttgtat	cggggatttc	858960
ataaccttcc	taaggaagtt	cgagataaat	tatttgtcgt	tgtttcagga	cgtttgcatt	859020
tacggtctct	gtatacgata	cgatcgaaac	tcttagacaa	gctttcgttg	ctttgttcag	859080
caaccccgaa	ttatttttct	ccttctatag	attcttcgat	cctttcagaa	gagcaaaact	859140
ttatttttaa	taaaataact	caaggatggt	tttctatagt	ttctggaggc	ccaggaacag	859200
gaaaaacttt	tttagctgca	caactcatcc	tctcttttag	gaagcagcaa	cctaagttac	859260
gtattgctat	agtatctcct	acaggaaagg	ccacgtctca	tattcgtcag	attcttatga	859320
aatataatat	atgtgacgac	atggtgttga	tgcagacggg	gcaccacttt	cttcaggagt	859380
atgcgtaccg	tcgctataac	tctatagatg	tccttttagt	agatgaaggc	tctatggtaa	859440



cttttgactt	gttggtatagt	ttgggtacaaa	ccctacaggg	atatgagaaa	gacaaaaaac	859500
tttatacctc	gagtttaatt	attctcggag	ataccaatca	attgcctcct	attggcattg	859560
gggttgga	tccccttcaa	gatctcatag	gataattccc	atgaaaatac	gtttttcctg	859620
aagacatcgc	atagggcaaa	gactggaggt	gtggatcagc	tgactcaatc	tgtattgcgt	859680
ggcgaaatga	tttctttttc	tctctcccca	tcgatatacct	cagctataga	agtcttgaaa	859740
aatcgttttg	taaagtcggt	acgtcaatca	gaagcacgtt	tgtgtgtatt	gactcctatg	859800
cgccatggcc	cttggggggg	tctgaactta	aacacaatga	tacatcaaag	attggcgaga	859860
agcgatcctg	atttacgtat	tcttattatg	gtgacgagtc	gttatgaaac	ttggggacta	859920
tttaattggag	acacaggatt	actgtgttta	aaaactcaga	aattgcattt	ccctcaacat	859980
gaaccatag	attctagggc	tctatcacaa	tacgtctaca	attacgttat	gtctgtacac	860040
aagagccagg	ggagtgaata	cgatgaggtt	attgttaatta	ttcccaaggg	aagcgaagtg	860100
tttgggggtg	ctattctcta	tactgcaatt	acccgagcta	aatatagagt	ttcagtttgg	860160
agagatcccc	agacgttaca	taaaacaatt	aagaagtcta	attactagat	tcttatcaaa	860220
ataaaaaaac	cctcaaagaa	tactctaaga	gggttttttt	gctgcgaatg	tcgttaaaaa	860280
ctatcctatt	ttagcataat	ctttaacaaa	gtttatgaca	cagctaatac	atccagaagt	860340
agccataatt	agaacagcat	ggactccaag	aatagcagga	aggaatagag	aaagagtgcc	860400
aagagcatca	caaactaaat	caactacatc	tccaagccat	gcaatgaagg	cgtttcttat	860460
agctttggaa	cgtgctgcga	attcggcaga	aggcttggtt	ctgttttcgg	ggcgggagat	860520
tgtttcaggc	ctggtgctta	aaattctgta	aagtgaattt	gaactctcag	ttaaagagca	860580
tctgttagcc	actaagttta	ggcaggaagt	caccttacat	ccaattttgt	ttgcattggc	860640
tctaaggaa	accacgtcca	tttcatgtaa	gaatgtagct	gttccaagag	tctttgatgc	860700
taaacgagca	acttttctctg	tgatagttag	ggctgatcgt	cgttgtagtt	tttgagtcac	860760
acaaccctca	gcactctgctt	cgttgcaacg	tctgagttct	cctgtttcct	catcagtttc	860820
gaagatcata	gaaccattaa	gtagtgggcc	ccacaacata	gctcctgcca	ctgcagtgtt	860880
cactccgtca	gcggcaccca	gaaacccttc	agttttctgc	aaagcagcat	gtgcataatg	860940
ggagcttcct	aaagcatgtc	tagagattgc	tgtggaattt	ttaattgctc	cgacgatgtc	861000
gccggcaaac	aaaacgttat	tgtgtagaga	cattgattgc	tgtctgaata	aattgcctga	861060
agctctgatt	gccggagtc	aagatcttaa	atgcagaagt	gcttgtctac	caagatgtgc	861120
tgttgccata	atctacctaa	ttattagatt	gttttaaggt	cacgatgtct	tcgcgttaac	861180
ttttaagggt	gcttttagatt	taatgcgtgc	tgccttatta	tctttgaaga	tacctcgctt	861240
tacagcctta	tctacaacac	tgtagacgga	ttgtaagtgt	ctaagagtgg	cttgagtgtc	861300
gtcaggtttt	aaagatgctt	caaacttttt	gactattggt	ttcactttag	atttgaagct	861360
gtgattgatt	aactctcttt	tttgagcagt	tagaatgcgt	ttttcagcag	aagtcttctt	861420
tgtataacgt	tttttttatt	cggtttttta	gggtgccata	tatctccaga	caagacaaga	861480
actttaagat	ttaaaataaa	ctgctattaa	ttgcagatca	attgagagag	aaaggaaagc	861540
tttttcttat	tttcgatata	catattaaga	aaaaagagaa	tttatgagaa	ataaaaaaag	861600
ttttatgcca	acataacaat	aagaatgggt	ttaaaaaaat	acttttctaa	tcaaatagaa	861660
cttatggcta	tgaagagcaa	tttattctta	tttttgttga	tataaggatt	tattttttat	861720
gttattggta	aggaatgggt	tgcatacttg	tttcaaatat	tggattttact	ttcttccggt	861780
ggtaacgcta	cttcttcccc	tagtgtgtta	cccttttctg	tcgattagtc	aaaaaattta	861840
tggatacttt	gtttttacta	caatttcttc	tttaggctgg	ttttttgcat	tgagacgtag	861900
ggaaaatcaa	ttaaaaacag	cagctgttca	gcttcttcaa	acaaaaatta	gaaaattaac	861960
agaaaataat	gaaggggttaa	gacaaattcg	agaatctctt	aaagaacatc	agcaagagag	862020
tgctcaactg	caaattcaaa	gtcagaagct	taaaaaatagc	ctatttcatc	ttcagggttt	862080
acttgtgaaa	actaaggggag	agggggcaaaa	attagaaact	ttgttacttc	atagaacaga	862140
agagaatcga	tgtttgaaaa	tgcaagttag	ttctttaatt	caggaatacg	gagaaaaaac	862200
agaggaagta	caaactttta	atcgagagtt	ggctgagact	ttagcctacc	agcaagcttt	862260
aaatgacgag	tatcaagcga	ccttctctga	gcaacgcaat	atgctggata	agcggcagat	862320
ctacattgga	aagctggaaa	acaagggttca	ggatttaatg	tatgagatcc	gtaacttgct	862380
tcagttagag	tcagacatag	cagagaatat	tcttcttcaa	gaatcgaatg	ctgttacggg	862440
aaatatttct	ttacaattgt	ctagttaggt	aaaaaaaaatt	gcttttaagg	ctgaaaacat	862500
agaggcagcc	tcttctttta	cagcatcacg	ttaccttcat	acagatacga	gtgtgcataa	862560
ctactcttta	gagtgtcgcc	agttatttga	tagcttaaga	gaagaaaatc	tcgggatgct	862620
ttttgtctac	gctcgtcaat	cccaacgtgc	ggtttttgct	aatgcgttat	ttaaaacgtg	862680
gacgggggtat	tgtgcagaag	attttttaaa	atttggtagt	gacatagtga	tttctggggg	862740
caaacagtgg	atggaggatc	ttcatctctc	tagagaagaa	tgctctggta	gattagtgat	862800
taaaacgaaa	tcacgaggtc	atcttctctt	ccgttattgt	ttaatggctt	tgaataaagg	862860
ccctctttgc	tatcatgttt	tgggggttct	ttatctcttc	cataaagaag	tgcttcagag	862920
ttgatactat	ttcttcttct	atgaggaaaag	ttgtatcaaa	ttgttggtaa	gatattgatt	862980
ttcgtcagcg	tataagataa	aaatccctag	atttcttctc	ttcctttgac	taaactgtcc	863040
tctaaggcta	gaaatccctt	tgtttttatc	caagtaagaa	agttgttcat	gaatacacag	863100
aatagccaag	ctacagaagt	ttcatcagaa	gaagaatctc	aaaagaagtt	agaagagctt	863160
gttgctcttg	ctaaggaaaca	gggtttcttc	acatacgaag	aaatcaatga	aattcttctt	863220
atgtccttcg	acactccgga	gcaaatttgac	caagtgttga	ttttcttaac	tggaaatggac	863280

attcaagttt	tgaatcaaat	tgatgttgaa	aggcagaaa	agaagaaaa	agaagctaaa	863340
gagcttgagg	gttttagctag	gaggactgaa	gggactcctg	acgatcctgt	tcggatgtat	863400
ttgaaagaaa	tggttacagt	acctctcctt	actaggggaag	aagaggtaga	aatttctaa	863460
agaatagaaa	aagctcaagt	acagattgaa	agaatcattt	tacgcttccg	ttattctgct	863520
aaagaagcga	tttctatagc	ccactatttg	attagcggca	aggaacgttt	tgataagatt	863580
atttccgaga	agaagtaga	ggataagact	cactttctta	agttacttcc	caagctaatt	863640
accttgctta	aggaagaaga	tacgtattta	gaaaacttat	tattgtcttt	aaaacagcct	863700
gatttatcca	agcaagaagc	agctaaatta	aatgacagtt	tagagaagt	tcgtattcgg	863760
acgcaagcct	acttgcggtg	tttccattgt	cgtcataatg	tcactgaaga	ttttggcgaa	863820
gttggttttca	aggcttatga	ttctttctta	cacttagaac	agcaaattaa	tgatttgaaa	863880
gttcgtgcag	aaagaaataa	gtttgctgct	gcaaagttgg	cagcagctaa	gcgtaagttg	863940
tataaaagag	aagttgctgc	tggaaggact	ttagaagagt	tcaagaaaga	tgtacgtatg	864000
ttacagcggg	ggatggataa	gagccaagaa	gccaaaaaag	aaatgggtgga	gtccaattta	864060
cgtctagtga	tttctatagc	caaaaagtat	accaaccgtg	ggctttcctt	cttagattta	864120
attcaagaag	ggaatatggg	cttgatgaag	gctgtcgaga	agtttgagta	tcgccgtggg	864180
tataagttct	cgacgtatgc	cacctggtgg	attcgtcaag	ctgtgactcg	tgctattgcg	864240
gatcaggcaa	gaacgatccg	tattccagtc	catatgattg	aaaccatcaa	taaagtctt	864300
cgtggagcga	agaaattaat	gatggaaaca	ggaaaagagc	ccactcctga	agagttagca	864360
gaagagttag	gattaactcc	tgaccgtggt	cgggaaattt	ataagattgc	tcagcaccct	864420
atctctctac	aagccgaggt	tgagaggggt	agtgaagatt	cctttgggga	tttcttgagg	864480
gatactgccg	tagagtctcc	cgcagaggct	acgggggtatt	ctatgcttaa	agacaagatg	864540
aaagagggtct	taaagacgct	tacggatcgt	gagcgatttg	ttttgatcca	tcggtttggc	864600
cttcttgatg	gcaaacctaa	gactttagaa	gaagtgggtt	tgctctttaa	tgttactcgt	864660
gagcgtattc	gtcagattga	agccaaagct	ttaagggaaga	tgctcatcc	tattcgatcg	864720
aaacaattga	gagcattctt	agacttatta	gaggaagaaa	aaaccggaac	tagcaaagtt	864780
aagagtttga	aatccaaata	gtctttgagt	aaaagggttcg	ttttttatag	ccttgataaa	864840
aaaatatattg	tctggtgatt	gctatagaac	gttatcagtt	aattatatcc	aagtttcgta	864900
tgtggttggt	tttaggggtg	tctggtgaag	agcgtcattt	taagcagcct	gttcttattt	864960
cagtgacttt	ttcttataac	gaagtcctcg	ctgcttggtt	atccgacaag	ctttcagatg	865020
cttggttggt	tctagagggt	acctctctta	ttgaagagat	tgcgaaataca	aagccttatg	865080
ctttaataga	gcacctggct	aacgagctat	ttgatagctt	atgatatctt	tttgagata	865140
aagcctccaa	gatagatcta	gaggtagaaa	aagaacggcc	acctgttccc	aacctattaa	865200
atcctataaa	atttacaatt	agtaaagagc	tatgtccgag	ccccgttttg	tctgcttaag	865260
tttaggatca	aatttaggaa	atcgttttaa	aaatctacag	attgctcgta	ctttattagg	865320
cgaacaagct	gttttaggtc	tacgtagtcc	ggtaattcta	gaaacagaag	ccttggtatt	865380
accgggatct	cctccagagt	gggaccttcc	ttattttaat	tcgggtactg	taggggaaac	865440
caccctatct	ttgcgagaac	tactggttac	tatcaaacag	atagagaagg	tggtaggtag	865500
agcagaggag	tcgcccccat	ggtctcctcg	aacctatagat	gtagatattt	tgctttatgg	865560
tgacgagctt	ttttggtgtg	atcacaccga	gataacgatt	cctttgtcca	atttggtatc	865620
acgtcctttt	ttgattgctt	taatagcatc	tctttgtcct	tatcgctcgat	tttgactca	865680
aggttctcct	tatcacaact	ttacatttgg	agagttggcg	catcaccttc	cctcacctcc	865740
agggatgatt	cgtaggagtt	tatctccaga	tacgatgttg	atgggggtgg	taaatgtgac	865800
taacgactct	atgtctgatg	ggggcatggt	tttagatcca	gaaaaagcag	tggtctcaagc	865860
tgagaagtta	tttacagagg	gcgctgcagt	tatagatttt	ggagctcaag	caacaaaccc	865920
taaagtaaag	cagtttttat	ctgtagatca	agaatgggag	cgtctggagc	ctgttttaag	865980
gttgttaaaa	gagacttggg	ccaatagaaa	acaatatcca	atcatctctt	tagatacgtt	866040
ttatcctgaa	attattctta	gggctatgga	tatttatccg	atccagtgga	ttaatgatgt	866100
ctctggggga	tcacagtcct	tggtcgaggt	cgctagggtg	tgtgagctat	ccttggttat	866160
gaatcactcg	tcttcgcttc	ctgtggatcc	taaaaatatc	ttgtcgtttt	ctgtccctat	866220
tggaagagcaa	ctgttgagct	ggggtgagaa	gcaacttaag	atgttttctg	atgttggtct	866280
gaacgcaaat	caggtgattt	ttgatcccg	tataggtttt	gggaaagggg	ctgcgcaatc	866340
tttggttact	ttgtatgaga	ttgcgaaatt	taagcgtttg	ggatgcccta	tccttatttg	866400
acattctcga	aaatcgttct	tatctttatt	tggtaatcat	gatcccaagg	atcgtgattg	866460
ggaaaccgta	ggtctatcta	tactcttaca	acaacaaggt	gtggactact	tgcgagtcca	866520
taatgttgct	gctcatcaaa	aagctttatc	agtagctgct	tgtgaagcct	gtgaccccat	866580
ctaattttga	aaatcctcta	ggtgtcgaga	tgtgtaaaaa	tagaggggtc	cgcggtatcg	866640
tggtttgtga	tcctagaggg	gtgataggtt	tagaaggaaa	gcttccttgg	cattaccctg	866700
aagatctcca	atttttttct	gaaaccatac	aaaaatttcc	tattgttatg	ggaagaaaga	866760
cttgggaaac	acttccctag	aagtattttg	ttgatagagc	agtcgtcgtg	ttttctcatg	866820
aaaaacgaca	gggagtgac	ggggagatct	gggttaactc	tttagaagaa	ttcctgctct	866880
tagatctttc	ttcgccgaca	tttttaatcg	gtggtgggtga	gctttattct	cttttcttag	866940
aaaatcaaat	tggtcgagat	ttttttattt	ctcatatcaa	aaaagaatat	gctgggtgata	867000
catttttccc	tttgtccttg	ctagagacat	ggaccaaacc	tgtgcttaga	gatacccaaa	867060
agatcacaa	gtgttactat	gaaaatcacc	acagtcaaaa	caccaaata	atatacctat	867120

gâtgaacctat	attctattct	agagtcttca	ttgcctaagt	taaacgaacg	ctctattgtt	867180
gtgattacgt	ctaagatagt	ctctttatgt	gaagggtgctg	ttgtagaact	tgagaagggtt	867240
tctaaagatg	aattaataaa	gcaagaagca	gatgcctatg	ttttttaga	gaaatacggc	867300
atataatctaa	ctaagaagtg	ggggatactc	attccttcag	cggggattga	cgagtcacat	867360
gttgaagggtt	attttgtgtt	gtatcctagg	gatgttttgc	tttccgtgaa	tactctaggg	867420
gattgggttaa	ggaattttcta	tcatctcgag	cattgcggaa	tcattatata	ggatagtcac	867480
acgactccgt	tgcgtcgggg	aactatgggt	ttaggcttat	gttggaaatg	tttttccct	867540
ttatataatt	atgtaggaaa	accagattgt	tttggtcgtg	ctttgaagat	gacttatagc	867600
aattttattag	atggttttatc	ggcagctgcg	gttctttgtat	tgggagaggg	agacgagcag	867660
actcccatg	ctattataga	ggaagctccc	aagattacct	tccattcttc	tccaactaca	867720
ttacaagata	tgagcacttt	agcaatcgct	gaggatgaag	atttatatgg	tcctctgcta	867780
caatctatgg	catgggaaac	tcccgcacca	acctcctgag	gtattatgac	atcctggata	867840
gaattacttg	ataagcaaat	tgaagatcaa	catatgttaa	agcacgaatt	ttatcagcgt	867900
tgggtctgaag	gaaagttaga	aaaacaacaa	cttcaagctt	atgccaaaga	ttactattta	867960
catattaaag	catttccttg	ttacctttca	gcgctgcatg	ctcgtgtgta	tgacttgacg	868020
attcgtagac	aaattcttga	gaatctcatg	gatgaagaag	ctggaaatcc	taatcacata	868080
gatttatgga	gacagtttgc	tttatctctt	ggagtttctg	aagaggagct	tgccaatcat	868140
gaattcagtc	aggctgctca	agatatggta	gcgacatttc	gccgcttatg	cgacatgcca	868200
caacttgccg	tgggttttagg	cgctctctat	acttatgaga	ttcagattcc	tcaagtctgt	868260
gtagagaaaa	tccgtggttt	gaaagaatat	tttggagttt	ctgctcgagg	ctatgcatac	868320
tttactgtac	atcaagaagc	tgatattaaa	catgccagcg	aagagaaaga	aatgctacaa	868380
acttttggtag	gcagagagaa	tcctgatgct	gttttgcaag	gatacacaaga	agtttttagat	868440
actctatgga	acttttttag	ctcttttatt	aattcaacgg	agccttggtc	ttgtaagtag	868500
tatcttgga	ggtctagaat	ttttggatct	tattagctta	aaaaatagga	tcatgcatct	868560
gtaaacagaa	tccccctcc	taaagtatta	gaagggggga	ttctttgtct	caaggtaatt	868620
tgtagaatct	ctatgttttc	tatttagaaa	ttacaattta	agcttctact	gtttgagcag	868680
gaacttcctg	agggtgttca	ttagcatgaa	cagagggagt	tttattcgct	gcaattacat	868740
cgtagatgcg	cttctcaatt	tcctcaaaaa	gctttctatt	acgtttaagt	tcttcacgaa	868800
caaattctct	tcctgtcct	aacttcttct	cttgatagtt	gaaccaagaa	ccttttttct	868860
caataatatt	atattcgaca	gcaagatcta	ggatacaacc	tgcagaagaa	atcccttcat	868920
tgaataggat	gtcaaatct	gcgattctga	atggaggagc	aagtttattt	ttagctacct	868980
tcactttaat	tcgatttccg	atgtcagagt	tatcactgcc	ttttattgaa	cctatacggc	869040
gaatatctaa	tcgtattgaa	gagtagaatt	ttaaggcacg	tcctcccgta	gtagtttctg	869100
ggtttccgaa	gctaacaccg	attttctctc	ggatttggtt	aatgaacact	gcacagggtt	869160
ggctacgtga	tagggtagcg	gtgagcttgc	gtaatgcttg	agacatcata	cgagcttgta	869220
ggcctacgtg	tacatcaccg	atgtctcctt	cgagttcgct	tttaggaact	aaagcggcta	869280
cagagtcaat	aacgataaca	tcgacagctc	ctgaacgcgc	gagcaattct	gctatgctta	869340
atgcatcttc	accacagtcg	ggttgagaaa	tcataagatc	atcgatattg	acgccaataa	869400
gagatgcata	ataaggatct	aaagcatggt	cagcatctat	ataggcagca	acaccgcca	869460
ttttttgagc	attcgcgaca	atatgggtag	ctagtgtcgt	tttccctgag	gattcaggac	869520
caaagatttc	gatcacccgt	cctttgggga	ccccatgaat	tccaagagct	aagtctaaag	869580
ataaagctcc	tgttttgatg	gtggagattt	catgtgtggc	agagtgtctt	cctaaactca	869640
tgatggaccc	agcgccgaat	tgcttttcaa	tataagcaac	agcagcttct	agagcctttt	869700
ttctatcagg	taaattcatg	taaatgctcc	tcttggtttc	catattcccc	agagaatagt	869760
tctgtttctc	tgagaatcga	gagaaataga	gaagttcttc	tcatagttag	ttgagagatt	869820
tgggggtgga	agggttttaga	tgatgtgtat	cattctgtat	tgttttgctc	tctatgcata	869880
cttgaatttg	ccatggcagt	caaggcaaaa	agtaacttca	agatggcttg	ttattttctca	869940
ataaatttaa	gaaaagcact	agaatacaag	gaccttagtt	tcagatagta	tatctaaatt	870000
atgaaactga	aaaaatagat	ctattggatg	ccgagattcc	tttaacaagg	gaaactattt	870060
tcaaaaaatc	aaaagaactt	cttcttattt	ctaacataaa	tagatttggg	aaagggggat	870120
gtcatgactt	tcttggggaa	gtctatcgat	tttttggtcg	cagtagccga	tgccgatggg	870180
tcgtatagag	ggatagggat	gttgtgctaa	ccagcgatcg	tagaaaccgt	gaccataacc	870240
aagccgatag	ccctgctgat	caaaggcaag	gcccgggaacg	agcacgtggg	taatcttatc	870300
actcgagatc	gggtgtttgtt	tcgagaaggg	atctttggga	tgcacaacgg	aaataagatc	870360
gtctatcgag	gggataagaa	caggatagag	gttttcttga	tcaatcttgg	gaagagctag	870420
ggtacatttc	tggataagta	tgcgatttgc	ttcttgcgatg	tctatttctg	gattgaaaga	870480
gacaaaagag	agaacgacgc	tctctttaga	aaagctgcga	acgaaagagg	ccactgcaga	870540
agaggcctca	tgcttgcggt	cttcagagag	atccctgcgt	atagagataa	atagtttacg	870600
tagtgcggtg	ttctctattt	taggatcagt	cataggggaag	ttctagttag	gcaaagggtt	870660
gccgtcctga	taggggattt	tttttagtaat	agttccccgc	gacgagaaaa	atactgcagt	870720
cccacaacca	cgatctattt	tagagtaggg	atgacgggtc	ccagggcgga	agtactctcc	870780
tttaattaga	agatcattat	catactcttc	ggtcgccatg	atctgtcctt	cagggtagta	870840
aatggctcag	aacccggatt	ttttgttatt	tacgagttct	ttacaacttt	ctaagggtcc	870900
tccgggatac	caagttttta	ctatcccat	taaaattcct	tcatgccaat	taagaaagca	870960

gcttgggttt	ccctgtctca	ggataaaaga	aaattcttct	ccgtgcttcg	cgcttgcaa	871020
aangttatatac	gtttggacaa	tctgtgttcc	ggagttgtcg	aatctggtaa	ctttccata	871080
aggttccct	cggtaaaatg	ccctagtttc	tataacggca	tacttgccgt	agattgcttg	871140
aatgccgttc	ccttcgtgta	tagtcgcata	gatttcgtga	gtttgaggat	ctaagtactc	871200
tgcttttagg	agtcgtccct	catgatattc	ttcccaggct	aaaacatctt	cttcggaatc	871260
ttcgctgtag	cgaatcgaaa	gaccgtgtct	tttgcttctg	tggttaattct	gttctttgag	871320
cagtttcccc	gaagatgtgt	atgtcaggaa	tttaccttga	ggaactccct	tatgataggg	871380
acactctttc	caaataattcc	cattagtatg	gtaatacacc	gaagatcctt	cgagcagccc	871440
tttttcatag	acgatagcgg	cttctaagat	accttcatca	ttataggcaa	atgtagtttg	871500
atcaaatagc	cagccagact	ctgctgaggg	atgaagatcc	gcaatacctc	cgataacctc	871560
agcttggtatt	ttgatattcc	cgttgacgtg	ccattcacga	tatcttccat	aagcacgatt	871620
attgagacac	tccagggtact	gcttaatttg	cccgttagtg	tgataggctg	ttaaacaaga	871680
aacgttatct	ccgcgtttgt	ttttatacat	cctcatgacc	ttttgatagg	gctggggagc	871740
aagaaagtct	accttgggtg	atttcttttag	cttctcttta	gagcaaatag	tttctgacag	871800
gccgtttcta	tcaatgatata	tgatccctgt	aaggggtgag	ttctcatagt	cacctgtttt	871860
cccataaatg	ggactcatgg	caattagaga	agaacataga	aataagcaaa	agagtttttt	871920
tatatccatc	gacttatagc	ctcagcatgt	gttaaccaga	cctcattttc	tagaggcgta	871980
gtttgttttg	tcattttcca	acaggtgaag	aaaactaggg	gcgcgacagg	gttctctggg	872040
ttgaaaagag	aaaacaagga	ctcgatatct	tcattatcca	tttcagtagc	ttgctctaga	872100
cgacacaaaat	gcaaagtcat	tgtgcatttg	ttcgcagttc	cagacgagct	ggtgatttga	872160
tttttctaga	gcacgctttc	tttcccaaac	ttctttactt	tgtgctagca	aagaatttga	872220
gtttaatttg	tttaaactgt	cgcttctttt	ggatagaggg	cgtaattgct	tgcaagaggg	872280
atttaaactt	tctattgaga	ggttattgct	atccttagaa	atgctgagcat	tgtgtttgat	872340
cacctgatct	tcagtatctc	ttataacttt	cagtgtgaga	atctgagaat	ttagatcaga	872400
ccaacgctga	gagatcttca	cgtgattttt	ggtaatcgct	aggacgggaa	gtataactca	872460
aagagaaaaga	aaaactaagaa	ttaaaataga	aatccatttt	ttcataagac	gtcctaagag	872520
cttaatgtaa	attgtagttt	aaaagatcgt	tgatcttcta	gagactctga	aacatgttgt	872580
agcttggggg	gactcgatat	tttttttaag	aattgagggg	tgtcttcagg	ttgtccttgt	872640
cccttgactt	caactaaggc	actgtagggg	agagaggggt	tatcttttga	gggataactt	872700
gtcatgggtat	aggagaaata	cgagaacttt	attgaggggc	tgcttttccc	aagggcaaga	872760
agaaatttta	atgtttgtct	acttgtggga	attgtaggca	agagtgggta	gttggaagcc	872820
gagttcttct	ttccgattgc	ctttactgtt	ttttctgcgg	cccttaaaga	tcttgggagc	872880
acgccctctt	caggacaagc	gaaagcaaaa	tggttcgaag	ctgaggaaga	aagagattta	872940
agttttaaca	cggatcccag	acttacgact	accgtagcca	tgagggcata	cttccctatc	873000
aacagagagg	agcgtagcag	ccaatgtttt	tgggctgctg	gggaaactga	ggtagcgtca	873060
tagggaaaag	ttagaggctg	tcttgaggcc	ccatgggtgg	cagcagcaat	agtatctcca	873120
taaatttccc	aatcctcgtc	ttccactcca	taagtcatag	attgacagac	cacaagcggg	873180
agagacagtt	tttgttctaa	aatttnttgt	agattcgggg	atatctgtgc	gacgtgaata	873240
gcaggaagca	cagtttgttg	gaatgtttct	tgatatatac	gcaacgttgc	atggatgtcg	873300
tcgcagcttt	tttctgttga	gtggttgcta	aaagaacgag	ctacagcaat	ggcatgattt	873360
tttacaaaaa	tgtaggtaac	ttcttcagaa	ccgccataga	taagaagata	tgcgggcagg	873420
ctctttaaag	ggctctgttc	tgctagaaaa	aaaatatcgg	cagcacgaca	agagagttta	873480
tcagggaaaa	tctgagcctg	ggacagaaaa	gaaagtctct	ttttgagtgt	atttttttga	873540
gcaatccata	gggtcagagg	agtttctcct	ctatccgctg	gtttgcctag	ttgtggctgt	873600
acaatcagag	attcccaggg	tagggcaaga	cttgcttcta	gatttgtgag	agctactttt	873660
aaaatatttt	ttctattttt	aagggatgag	gaagaacttt	tgactaagat	gtcagagccc	873720
tgagagagaga	aagtcgttgg	tgctgcaaac	tatttttttg	ggagagacca	ggtctttcct	873780
tcgggaattt	gttcacagtg	acagacgac	cattcctttac	atgttttctg	taaaattgct	873840
attttaatag	tattgttttc	agctttgggt	agtccaatat	gataaacagg	cagcttgaaa	873900
ttcatagctc	aagaattctt	aaaatataaa	ggcagctatt	ttaatggata	gagggctctt	873960
tttcaagaaa	aacacatatt	aattataatt	aagagagtaa	aatataatgc	tatcttattt	874020
gttaagaacg	ggctattaat	gtttatagct	ttctaatttt	agcctatata	tttgettctt	874080
gggtccctga	ttgccagtct	gcgcgctggt	accagtgggt	ttccaagtgt	gttgaccatt	874140
ttttgatttc	ttcgctgctt	tgttcctaga	attggattta	tagatcccag	tccttttgtt	874200
ggtctgcttt	gccttggaa	ccttcctttt	gttatattaa	gagtcctacg	ttttattatt	874260
cttaattattt	ttcattctcc	atggctgctc	caatatattt	aaaaaatatt	ttacttcgtt	874320
cctctatagt	ctatgctcct	ctagcgggat	tttcagatta	tcctaccgt	tgcatgtccg	874380
cattgtatca	accagggttg	atgttttctg	aaatggtgaa	agtagaagg	atactctacg	874440
ctcctgagcg	tacttcgaag	cttctagatt	ataatgagaa	catgcgtccc	ataggagcgc	874500
agttgtgcgg	tagtaatcca	gaaactagt	gggaggccgc	taaaatttta	gaaggccttg	874560
gtttcgacct	tatagacctt	aattgtggat	gtcctacaga	taaaatcacc	aaagatggca	874620
gtgggtcagg	tctttttgaa	gacgccagag	cttattggga	ggatttttaga	taaaatcatc	874680
aatagcgttt	ccattcctgt	aacagtaaaa	attcgctcgg	gttgggatata	ggaacatata	874740
aacgtagagg	atacggtacg	tattatacgt	gatgctggag	ctagcgcagt	ttttgttcac	874800

gggagaactc	gtgctcaggg	ataccacggt	cctagcaagc	aagagtatat	ttctagagcc	874860
aaggctgctg	caggaaaaga	attcccagtt	tttggtaacg	gagatatttt	ttctccagaa	874920
gctgcgcaag	caatgctaac	tacaggatgt	gatggtgttc	tggtagctcg	aggaaccttg	874980
ggagccccct	ggattggaaa	acaaatccaa	gactatctca	ctacaggaag	ctatgagaaa	875040
attcccttta	tcaaaaggaa	agctgcgttt	ctggagcata	tgcgccctagt	agaagactat	875100
tatcaaagcg	aaacgaagtt	cctttcagaa	acacgtaaat	tatgtggcca	ctacctaat	875160
tccgcggtta	aggtgcgttt	tcttcgttcg	tctctagcaa	aagcgacatc	ctaccaagaa	875220
gtctaccagc	ttgtgaatga	ttacgaagaa	gccgacgact	cgtcattaga	gacctttgtt	875280
aaatgctgac	ttaggtgttt	cgaaagtgg	aacatatacg	taggattcgg	accaatgatc	875340
gtagctaaat	tggtatcagg	aactaaaagt	tttttatttt	ctggtgcctg	taattgatgt	875400
tccttgatgt	aatcccagat	ttttttggtt	gcttctcccc	gagatacggg	nttcgtttcc	875460
gatcattttt	gctagatctg	gagaggggag	gaataaagga	cctgttttct	ttcttgaaga	875520
ttttttaacc	gagctttttg	cttttccctt	tttagaaggt	gttttggctg	cttttgggtt	875580
ttttgctgaa	gattttttct	tggtcggagt	tttttcttta	tagggaattt	tttctgttcc	875640
ttgagtactt	gtgattacag	catctataga	atttccaatc	acactacatt	caggatactc	875700
tgaacaggaa	tagaaaatct	tggtgtaacg	ggagcgtttt	ttgaaaattt	tcccattaca	875760
gcctattgca	gggcagggga	taggctcttc	ctgttcgatt	tcctctccct	ttttatggat	875820
tgatatagt	ccacggcatt	caggatactt	ctcacaccct	aaaaatgttc	catagcggcc	875880
gtgacgtact	ttcataacgc	ctccacaaaag	aggacaagga	ctgtcccagg	gggtgtcttc	875940
agcatagtct	tctttgttga	aagcgagctc	ttcttcagaa	gtgcggtaat	cgcatccagg	876000
atattctgag	cagccataga	aataactggt	tttagaccag	atttttacta	gttttccctt	876060
atggcactta	gaacattcta	tatttgtgag	aattctagga	atgacagctt	ctttttctgc	876120
tgtaatcact	acaggaagga	atgtagtcca	gaattcttga	agtaagagtt	tccaagggtt	876180
tttattatct	gcaatgagtt	caagctcgtc	ttccatgaga	gctgtgaacc	cgatatccat	876240
aattcttgga	aagtttgttt	ctaagaactg	tgagataatc	tttcctaatt	ctgtaggacg	876300
taaccgttga	ttttcttttag	tcgtatatcc	acgactttga	attttgttca	ttatcgtggc	876360
atacgttgaa	ggacggccga	tcccagattt	ttctaactct	ttgactagag	aagcttctgt	876420
gaatctagga	aggggttttg	taaatgcctg	ttcttgggat	acttctctct	tgattaaagg	876480
atcttgggca	tgtagggggg	ggagaggatg	gtcttcttct	tgatcatttt	catcatcttg	876540
cttctcttca	tagacagcga	gaaacccttt	aaatttttagt	aaggatcctg	aagctcggag	876600
gtctatttct	gatatccgtag	taatttgaac	agctaaagta	tcataaattg	caggggtaat	876660
ctgtgaggct	acgaagcgtt	tccagattaa	gttgataact	ttaaattgat	catcagaaag	876720
cttattcttt	aatttgtcag	gagtcagatt	aatatcagtg	ggacgtatgg	cttcgtgagc	876780
atcttgcgtc	atcttttttg	tagtatatac	gtttgctttc	tcagggagat	attctttacc	876840
gaaagtctgt	tggatgtact	ctctaactgt	agttaatgct	tcgggatcta	cacgtacgga	876900
atccgtacgc	atgtaggtaa	tcaaaccctgt	agaatcttca	ctatctaaat	cgacgccctc	876960
atagagggtt	tgcgctatag	acatgggttc	agaagcagaa	aaacgaaaat	gccggcttgc	877020
ttcctgctgg	agagtggatg	taatgaaagg	aggaggagca	aaacgtcgtt	ttgccttagc	877080
ttctacacga	gtgattgtat	acgaggattt	ctctaacagc	tcggcatagt	gacgggcttt	877140
ctcttcagag	ttaataagaa	ggacatcatt	ttcgggtttc	ccttcaggga	tttctttctc	877200
ccactttttt	ccttgacacg	cgtataaatg	cgcccaaaac	gtttttgtcg	ttttgggatc	877260
ttgcattaaa	acgcgtaaat	tccagtattc	aacaggaaca	aaagcatcaa	tagccttttc	877320
tcgatctacg	acaagcttca	aagctacaga	ttgcacacgc	cctgcagata	tccttgagcg	877380
ttgttgtaac	tttcgactta	ggataggaga	aattttatat	cccacaatgc	ggtcagaag	877440
tctccgcgtc	tggtgtgcgt	tgactaaagc	catatcgatg	gttcgagggt	gttttaaggc	877500
ctctgtaacc	gcatttttgg	taatggcatt	aaacgatacc	ctctggatca	gaggagagtc	877560
aggaagctga	ttcgcgatgt	gccaggcaat	tgccctctct	tctctatcag	ggtcagggga	877620
aagatagact	ttttcacact	tcgcggctag	cttgccgatg	tgattgatga	cctcttgttt	877680
atcggaagc	acttggtatt	gtgggttcgaa	atcatgatcc	acatcaatgc	caaattcctt	877740
agcagggaga	tctacaatat	gtcctataga	tgaggcaaaa	acaaattcac	tccttaataa	877800
tttttgtagc	gttttaattt	ttgcagggtga	ttctactata	attaaggact	ttttcattaa	877860
tctaattgcg	tgaggacctt	ggatacttta	ccgagagaaa	acgcgactcc	cttttattaa	877920
tttaattttc	taatttcctaa	aactttgttt	tcagtcaaat	atatgttatt	tattttcaagg	877980
tttcgctgaa	ataataacac	gcatgccaat	agcaaagctc	attaacagtt	acaataagtc	878040
actctagcag	cttttcatga	gtcgggtgctc	ttagtttctc	gatcatggaa	aaataatcaa	878100
ctggatcgtc	caacctatac	tggtgcgttt	tcatacgcta	aataacagga	acgctgggtc	878160
atatgaaggc	tagcatagag	aattcttgat	atgtccctat	ggttatttag	taagaagcaa	878220
attcttttca	aggggaataat	atgatagaaa	ctatttaggt	ttcatcttga	acctgcaact	878280
gtcattcttt	tctgattagt	aaaaagtttt	aaaataaac	aacattaaaa	gagacgagat	878340
ttcttaattg	caagatgcta	aaaccttttc	aattttnttt	gttaacgatt	gtaattttct	878400
tttaataatt	gaaaaaagg	ttgaaaaaga	gccgagcata	gatagaaacc	taggacacga	878460
aacgtggaaa	aacttgagtt	tgaccaccagc	ctttcttctc	ctgatgatga	tttgattact	878520
ttcaataaac	agggattgat	tgacggccca	gaagaagaaa	aggtagcgtt	tcttgtacgt	878580
agcaatgcta	tgctagatgc	aggaccgaa	accccgcgct	cgtttctctg	atctttaagg	878640

gaacaattcg	atattttccc	tgagtatgtt	gaagtgtctt	actctaata	aggattagat	878700
gtctgggaag	caggatgtac	gtggattcta	aataatgaag	tgaccatcca	actgcgtaaa	878760
catcaccgga	aagcttcgag	atggctagga	atgtattcca	gagatgaggt	actcgcacac	878820
gaagccgtgc	atgctgtgag	aatgaaatct	catgagcctg	tctttgaaga	ggtgttagct	878880
tatcaaactt	ctcgttgggg	ttggagaagg	tttttcgggtc	ctctatttcg	ctctccagga	878940
gagagctact	tgctattatt	cttcaccatt	ttaggttttag	gaatctcctt	atggtatcct	879000
gccggtatac	tgattatgct	ggttttacct	atgtattttt	tgatgcgatt	gtgcatggcg	879060
cagagctatt	tgatcgggc	catgaaaaag	attcgtaaaa	tgctcggagt	acctccctta	879120
tgggtgctgc	taaggctgac	ggataaggaa	ataaaaaatgt	ttgctaaaga	gcctattcct	879180
gttttggaac	actatgctag	aaaacgaaag	cttgaaaatg	tccgttggaa	gcaaatttat	879240
caatcctact	ttgtttaact	ttaactagaa	ctgcctatct	ctaaaatgac	tgtttgatga	879300
tcttatgtaa	aacagctttt	ttcttttatt	agcaggcagg	atcttttagtt	gtgcacggta	879360
ttttgctact	gtacgtcggg	cacaaggaat	cccttttgca	gtgattctgt	cactgatcac	879420
actatcagat	agaggagttt	gttccgttgc	gatccattgg	cggatccatt	gtagaacatt	879480
ctctttagaa	tgcgaggaat	cttgatggat	tcctcggggg	aagagggtgct	ttagagggaa	879540
aatccctata	ggagctgcaa	ccgctttgtt	ttcaatggca	cggagatttg	ttgactcatg	879600
aaaagagaga	tcttcagcca	aatctttaat	gcctaaagga	tagggggctg	gaatttttcc	879660
taataaaaaag	tcttcttggt	tgggggagaag	tgctcccatc	acttgaagga	gcggttggtc	879720
tcgttttctg	agatttttga	ttagccactt	tgctgataaa	atgtgttgag	agagggtttt	879780
ctgctcttct	ttaggaaggt	gttcatagaa	gtgaaacgtt	tctttattca	gctttataga	879840
tggcaagcct	cgagtactca	cttcaatttt	ccaagatcct	gaggaataaa	aaagataaat	879900
atcggggaag	ggagttgata	ccatgggctt	cacagtgcac	gctgctgcag	gacaccaagg	879960
tatagatcct	aatgcttttt	ttaaaatatt	tcgaagttcg	gataaagaga	gactgaactt	880020
tttcataata	ggcgcaaaact	cacagttagt	catcaaggga	tagcaatcac	ggacgatgct	880080
ataggcttgt	tggtgggagg	agttgcggag	gagcttcac	caatagcttt	gtagcgaagg	880140
agaggcaatg	ccttcaggac	ttaggttttg	tatagtgtcc	caaactttat	gaattttttc	880200
taagggaagc	tcaagttctt	gagcaaaatc	ctcaggattt	cttagaaaga	gtccttcac	880260
cgagagattc	ccggcaattt	gatgggcaat	gaatcgttct	tctgcagtag	aaaaagcctc	880320
ctcgatttga	ggaaggagac	gagtatataa	agactcttga	ggtccaggag	tctgattcaa	880380
ataggaaaaac	gtagagtttg	taggtcgata	acaaggagac	cattcttctc	cttctagtga	880440
agagagatca	aaaaaaggat	tatcaatgat	ctcttgaact	acatacga	ataactcagt	880500
aagtggcgat	tgcagctctc	gcaggccttg	ttgcatectt	agtgagggtg	gatactttag	880560
agacaacttc	tgctttttgct	gaaacatgtc	taacgcactt	gaatcatata	atcttttgga	880620
atttctctta	aaaatctact	gggcttcac	atccgtacgg	ttccccagag	gctgcgaact	880680
tgtgcggcag	taagatagag	gagatcttga	gctcgagtaa	ttcctacgta	gcataaccgt	880740
cgttcttctt	caatattttc	ataagtgccg	cccagagagt	tcgcatgtgg	aagcaattgt	880800
tcttctagac	ctacaagaaa	tgatacacgg	aactccaacc	cttttccatt	atgaagggtc	880860
atcaaattca	cgcgatccgc	agttaaattt	agatcatcat	cacagccttt	taaggcaaga	880920
tcataagga	aaagtctcaa	atgtgtcttt	ggattttgtt	gttcggattc	caaagcttta	880980
tgatagagtt	cctctaaatt	gcttttccga	tctttgaagg	tatccgcac	ttcttttaag	881040
atctcaaggt	aaccctgtat	cctaactaca	gactctataa	aatctctaag	ggaaagagta	881100
ttgtaggcat	gttcaatttg	agggaaaagt	gcaagatact	cttgaaggcc	ttcttgttgt	881160
tttttagata	atttgacgtc	tttagtatcc	aaggcttggt	ggcatgcttt	gaggataggg	881220
agaccttgag	caattgcata	ttgcgtgagt	gcaaatatcg	ttgttgaacc	gatccctcgt	881280
ttgggtagat	ttacagttct	atcaaaagca	acgatgtcgc	ttttggaaat	aaagatacgg	881340
agaaaggcta	ggatatcttg	gatttccctt	cgtctgtaga	aggagagacc	cccagataatt	881400
tcatagggaa	tgcgctcgag	aagtagagcg	tcttcaaatg	tccgagattg	ggagtctcgt	881460
ctatagaaaa	tacagatgtc	acgtagtttt	atattcccga	ctctatgtaa	ttgaagaatt	881520
tctgcagcga	caaagtctgc	ttcttcgcga	tctgtgcttc	ctaggaaaag	acgaatcttt	881580
tctccaggtc	ctttgacgct	acgcaattct	ttttctaacc	ttgatgcgtt	atttttaatc	881640
agagcattag	cggcattttg	aatattgcc	taactgcggg	agttttcttc	gaggcataag	881700
actttagcat	tagggtaatc	gtttttcaaaa	tttaagatat	tgtgaatatt	tgctcctcgc	881760
caggagtaga	tagactgatc	aggatcccca	acagcaaaga	cattgcgatg	ttgctttgag	881820
aggagctgca	ttaaagtata	ttgtgcattg	ttggtatctt	gatactcatc	gatgagcag	881880
gctttccata	attggttata	taattcctgt	gcttcggggac	ttctcttaag	aagctttacg	881940
gttaaaaaaga	gaagatcatc	gaaatccaga	gcattcgtct	cgataagttt	cttttggtat	882000
tcttggtata	tcgagactac	aggatcgata	tagtcattgg	gatccaagtc	ttcgggaaag	882060
agtaaacggt	tctttgcttg	tgagacgtga	gcttgatatt	tgctcgcaag	attaggtttg	882120
aggttgtgtt	gttgcaaggc	atgcttgatg	agcttttccg	cgtaactttg	atcataaata	882180
gtaaaattat	tttcacgatt	tagcagattt	atagaacgtc	ggagaataaa	aactcctaaa	882240
ctatgaaatg	tacacaccat	cggaaacatca	aattcattag	tggaagcaca	ctgattgaca	882300
atacgttctt	taagttctcg	cgctgcttta	ttcgttaaa	ttacagccag	aatttctcga	882360
ggcgcgatgc	cttggttaat	taggtgttaag	attctatagg	taaccacacg	agttttacct	882420
gctcctgctc	ctgctagaac	gagtacagga	ttgagaggag	ctgttacagc	tttgctgtgt	882480

gcttcggttaa	gttctgagat	acatgtcata	ataagtccta	atcttttagct	ttacacctcg	882540
agactgacaa	tctctgtcga	gctaaaataa	aaagcgagta	tacttttcac	acaattatag	882600
aaaggtgatt	tatgcagaat	gctactatag	atcagctccc	tgtgtcttgg	caagaacagc	882660
ttcctttatg	ttggcgtgag	caacttaagg	aagagtgggc	caaaccctac	atgcagcaac	882720
ttcttatttt	tttaaaacag	gagtataaag	agcatactgt	ttaccctgag	gagaattgcg	882780
tattttctgc	tttgagaagc	acgccccttg	atcaggtgcg	tgttggtatc	ttgggtcaag	882840
atccttatcc	aggaaagggg	caagctcatg	gattgagctt	tagtggtccc	gaaggtcagc	882900
gtttgcccc	ttctttaatt	aatattttcc	gagagttaaa	aacagatttg	gggattgaaa	882960
atcataaggg	gtgtttgcag	tcttggggcaa	accaagggat	cttattattg	aacacagtat	883020
tgacgggtgcg	tgcgggagaa	cccttctctc	atgctggtaa	aggttgggag	ctgtttacag	883080
atgccattgt	gacgaaactg	attcaagaga	gaacccatat	catctttgtt	ttatggggag	883140
ctgctgcaag	aaaaaaatgc	gagcttttat	ttaattcaaa	acatcaacat	gcggttctat	883200
cctctectca	cccctctccg	ttagctgctc	accgtggttt	ttttggttgt	tcacactttt	883260
caaaaattaa	ctatctctct	aataagctga	ataaaccaat	gattaattgg	aagctcccac	883320
gaatgaaggt	atccactctg	tctgttttca	aaaaacacct	cggcttactg	cgaagtccgt	883380
agttagtatg	gagatgctct	taactactca	acagcttcct	tcgcgagaag	ggatgccctc	883440
ggttgctaatt	ttggaagcgg	atttttttacg	agcagaagct	ctgttagcag	aaatgcgaga	883500
aattcgtggg	tgcttggagc	aatctttgcg	aacactagtc	cctagttagt	agggtgtttt	883560
caaataagct	ttgcaggtga	ggggcgaggt	tttgcaatgc	ctttgctctg	tgagaaactt	883620
gattttttcac	atcttctacta	agctcggcaa	atgtttgttt	gtaatcatat	tttacaaga	883680
tagggctcgta	gccgaaccct	gaagaacctt	tttcttgatg	gctgatgtag	ccctcgcata	883740
ttccatacgt	tttaaaaaatc	tcttgattag	gggagactaa	aactacacaa	cactcgaagt	883800
acgcagaacg	gtctactcagg	ctttccaaag	acgacataag	atcaagcagc	ttttttcgat	883860
gatcttttatc	atacgcacct	acaccagcaa	agttcgcaga	taaaggaccc	ggaagaccat	883920
ttaaagcggg	gacgcgtaac	atcgtatcat	ccgcaatgac	ccagcaaccc	aaatgattgg	883980
cagcgtgaat	cccttttagta	agggcggttcg	ccgttataga	atcttctctg	tcttggggaa	884040
gtttatagtc	aggaaaatca	gaaagagaaa	aaatatcgaa	atcacctaaa	cgctttaaaa	884100
aagtcttggt	ttctcgtatt	ttataaccat	gagaactagc	aatcaccaatt	ttcatgaatc	884160
tttcttaatc	ttttgaaatt	ataaagtttt	aacaagatag	agtcagcaag	cgtaatgcgc	884220
aattattagc	cgatgaaaaat	ctttgtagtt	aaagtacaa	atacattgta	tctacgcaat	884280
cgctagtaag	gtagacattc	tagttttattt	ttgttctgaa	gaacttttat	gattgcctgt	884340
tgatgttttt	tcaattttttg	agtttcacaa	tgaagaaaat	tttttactct	tttgtattgt	884400
taagttgtat	tttcccttac	gtaggggtgtg	ctcaagtttt	tgtaggctta	gatcgatttt	884460
tttctgaagg	ggagtataca	cgttgcattc	aaggcaagaa	aatcgctcta	atttctcata	884520
gcgcagctat	caatagtcgt	gggcaggatg	ccctctctgt	attctattct	cgtaagcatg	884580
attgtacegt	ggaaatcctc	tgtacgttgg	aacacgggcta	ttatggagcc	acacctacag	884640
aaacgggtggg	gaatcagcca	tccagatata	caaatttacg	ttctgtatcc	ttgtatggag	884700
tgaaagaggt	tcccaaagag	gttgccgaac	attgtgatgt	atttgtttat	gatgttcagg	884760
atctcggagt	cggttcttat	agctttgtta	ccgtgctgat	gcaaatagta	aaggcttctg	884820
aacgggtacgg	aaaacagctc	attgttttag	atcggccgaa	tcctatggga	ggaaggattg	884880
ttgatggacc	tcttctcta	cccacaactt	caggttcctt	agcgattcct	tattgttatg	884940
gcatgacacc	tggggaatta	gcgttggttt	ttaaaaagac	atacgtcctt	aacgctaattg	885000
ttgtcgtgat	ccctatgaaa	gggtggaatc	gctcgatgac	ctttgatgaa	acaggattga	885060
tttggtatgcc	cacaagtcct	caaatgccag	atccacaatc	accgtttttc	tatgctgcca	885120
cagggattttt	aggtgccttg	tctgtagcaa	gtatcgggtg	aggttatacc	ttacctttca	885180
aagtgtctcg	agctccttgg	atggacgggg	aaaaagttgc	cgacgagctg	aatcgcatga	885240
agcttcccgg	tgttctgttt	cttctttttt	tctatgagcc	ttttttcgga	aaatacaaaa	885300
tggagatggt	ctccgggggtt	cttcttgttc	ttcaagatcc	taagattttc	tatccagtag	885360
aaacacaaatg	tacaatttgg	ggtgtattaa	aagcattata	tcctaaacag	gttgagcaaa	885420
cgttaaaaatc	catagagcgc	attcctgcac	gtcgatcttc	catatgcaat	ttatttgggg	885480
gggatgaatt	tctcagcata	tcgcacaaaag	agcgctatat	tgtatggcca	ttgcgtaggt	885540
tatgtaaaga	gtctcgagag	agctttcatc	aactgcgtag	ttcatgttta	ctctcagagt	885600
atgcagaatc	ctaacaagaa	cacttaagat	cctctacggt	ttgacaggaa	tatttcttgt	885660
ttctaagatg	accttttcat	ggcagaagcc	tttctctgcat	taagaataga	catcagagga	885720
tcgagtgggt	tgggtattta	aaagtcaatt	tgagggactt	tcagcattaa	aacgaggagt	885780
gcatgctctt	actaaagctg	taaccccgag	atgttgacct	cgagggtata	acgtagtcat	885840
caaaaaagga	aaagctccta	ttgtcttaac	gaaaaacgga	attcggattg	ctaaagaaat	885900
catacttcaa	gacgcattcg	aatctcttgg	agtaaagctt	gcaaaggaag	ccttgctaaa	885960
agttgtagaa	caaactggag	atggctcaac	aacagccctt	gttggttatcg	atgctctttt	886020
tactcagggt	ctaaaaggca	ttgctgcagg	tctagatcct	caggagatca	aagcaggcat	886080
tctcttgtca	gtggagatgg	tctaccagca	attacaaagg	caagctatag	agttacagtc	886140
tccaaaagac	gttttgcattg	tcgctatggt	tgcggaacac	catgatgtta	ctttaggtac	886200
cgtggtagca	actgtcatat	cccaagccga	tcttaaaggc	gtcttctcta	gcaaagactc	886260
tggaatttcc	aaaacacgtg	gttttaggaaa	aagagtaaaa	agtggaatac	tttctcccta	886320



ttttgttacg	cgtccagaga	caanggatgt	tgtgtgggaa	gaagcttttag	tgctcatcct	886380
atcccatagc	ctagtgtctt	taagtgaaga	actgattcgg	tatttagaac	tcattctctga	886440
acagaacacc	cacccttag	tgatcatagc	agaagatttt	gatcagaatg	ttttaagaac	886500
tctgattttg	aataagctta	gaaacgggtct	tcctgtttgt	gctgtgaagg	ctccaggatc	886560
tagagaactg	cgacaagtcg	ttttggaaga	tcttgctatt	ttaacgggag	ctacccttat	886620
aggacaagaa	tcagaaaact	gtgaaatacc	agtttcctta	gatgttttgg	ggcgtgtgaa	886680
acaggctcatg	attactaaag	aaacgtttac	cttccttgag	ggagggggag	atgctgagat	886740
catacaagct	aggaaacagg	agctctgttt	agcgatagct	gggagtacct	cagagagtga	886800
gtgtcaggaa	ttagaagaac	ggttagcgat	ctttatagga	agtatccgc	aagtgc aaat	886860
tactgccgat	acggatacag	aacaaaggga	acgacagttc	cagttagaat	ctgccttacg	886920
tgctacaaaa	gctgccatga	aagggtggat	agttcctggg	gggggagtg	ctttcttacg	886980
agcagcacac	gctatcgagg	tgcttgcaaa	cctatcttcg	ggtatgactt	ttgggtttga	887040
gactctccta	caagcgggtac	gaactccctt	gaaggtttta	gctcagaact	gtggtagatc	887100
ttcagaagaa	gtcattcata	ccattctctc	tcacgagaac	cctagatttg	gctataatgg	887160
catgacagat	acattcgagg	atcttgtaga	tgaggggatc	tgcgatcccc	tcattgtaac	887220
aacctcttca	ttaaaatgcg	cagtttcggg	atcatgcctc	ttgctaacga	gttctttttt	887280
tatcagctca	aggacgaaaa	cataatcagt	tgagttctta	ataaggctgc	ctaaaacatg	887340
cggtgttgat	tgaggactct	cttctaaaaa	atccttgatt	tgggatggta	taacggaaat	887400
ttctaagaaa	taaaaatttt	tagtaagatt	agttcattaa	aaatttccac	agcattttct	887460
tatagacaga	gaaaatgttg	atcatttgat	ctttctggga	tacactatgt	tgagcgaaaa	887520
taggcaccag	tagctcagtc	ggatagagta	cctggctacg	aaccagggtg	tcagagggttc	887580
gagtcctctc	tggtgcgga	caataaaaaga	ggtgaagaag	agggttttat	gacactctcc	887640
ctagttggaa	aggaagcccc	tgatttttgt	gcgcaagctg	ttgttaatgg	cgaacgtgt	887700
accgtatctt	taaaagatta	tttaggaaag	tatgttgtgc	tttcttcta	tcctaaagat	887760
tttacttacg	tgtgtcctac	ggaattgcac	gcatttcaag	atgctttagg	agaattccac	887820
acccgaggag	ctgaagtcac	aggctgttcc	gtggatgaca	ttgccaccca	tcaacagtgg	887880
ttagctacta	agaaaaagca	agggtggtatc	gaaggattta	cctatcctct	tctctcagac	887940
gaagataaag	tcattttcaag	aagttatcat	gtgttaaaac	ccgaagaaga	attatctttc	888000
agaggagttt	tcctgattga	taaagggtgaa	atcatccgtc	atcttgtagt	gaatgatctt	888060
cctctaggcc	gttctataga	agaagaactt	agaaccctag	atgctttaat	cttctttgaa	888120
actaatggct	tagtctgtcc	tgcaaaaattg	gcatgaagga	gagcgagcga	tggtcccaa	888180
tgaagaagga	ctgcaaaatn	atttcgggac	tatagactag	anaggctgat	tgaagctcag	888240
caagtcataa	agatcggtat	caaagaacaa	taaaaggcta	ttgtgttttt	ggcataaaga	888300
ccgagaagct	tcaatgatgt	gttgatttcc	aacaccagga	agtccgatag	caatgatgtt	888360
ttttaacgtc	gtttgtgtat	ttaagaaatg	caaaccaaaa	aagtaactat	ctacacagta	888420
gccttcttct	cgaactctga	agtacactac	attataatca	cttaataatg	ttttaatagc	888480
taaagtgatg	cctggactgc	tgacatctcc	aagataatta	tgtagatcta	caagactacg	888540
acagaagtac	gcagtatcgt	aacttctctt	ttctgcttct	caaataaaag	caactgtaaa	888600
tttcatttga	aatatgagat	cgaatcttta	tttctgactg	tacaggactg	tttgtttatt	888660
atctacagag	agaaacttag	ttttgaaaag	atttgcgaat	ctaagatggg	tattattgct	888720
tatttctttg	taaaacaaagt	cggtgcccag	catagatagc	atcggaatct	aatttattaa	888780
ttttcttttaa	ttcagttact	gaaagtttat	atttttttagc	aattttacta	agactatcac	888840
cttcacgtac	tatataaata	ttctcaggaa	caggatccga	gaagtcagca	taggctccag	888900
gagaagagct	gtctactaaa	gcaagtaaag	aacgtcgtac	tagacgcaaa	tcctgagcta	888960
aagctcgggtg	atctttttga	atcttctgtg	gtttactttg	taagttcgtc	tgtaagtctt	889020
taacagaagt	tgtagtagca	gctaattgtt	tcgcaagcgc	cttttgatcg	gactctagct	889080
cgcggttttt	ttgagccagg	gtttctgggt	ttgtgtgtgt	ccatttttgg	aacttagagt	889140
cttgttctac	caagcgctct	gacaacatga	caatctccac	ttcgtgagag	gctaattttg	889200
ccgagatata	ttcgatttct	gcaaggactc	cttgtagaga	aggagacctt	ccagcagcat	889260
gcaaacgact	gcaatctatt	cctgaaaata	acagacttag	aagaataaaa	aagcttagct	889320
tagcgtgcat	gaatcttaaa	ctctgtacgg	cgattttgtt	gccatgctag	ttcgttgtgt	889380
cccgaattta	aaggatgttc	ttttccgtag	gaaatagtag	atagacgatc	tgacagagatt	889440
ccctgctttc	ggagatgctc	tttaatcgca	ttggctcgtc	gtgctcctaa	agcaagggtta	889500
taggatgcag	ctccacgctc	gtcagtatgc	ccttcaatgt	acagtgtagc	tttcgggttt	889560
ttcttcatgt	agtgaaccaa	gttcgtgaga	atcgcaagg	tctcttcacc	tttaattgta	889620
tagctgtctg	tagcaaaagg	gatattacga	aatgctgcaa	cttggcttga	cttgtattgt	889680
ttttcttctt	tggaatcata	ctcaccgaag	gtaaaattag	ggttaaagtc	ctcttcggta	889740
tagagaggaa	caaagccaaa	agaagaaggc	ttttttcgtc	ttgtatgatg	gcatgtatta	889800
caggaatcct	cccagccata	attaggggaa	aggctacatg	ctggcaatgc	aagtaaagcc	889860
aataaagtac	aaagtttcca	taggggaatgt	atattcatag	tgttctcttt	atcgggttgct	889920
gaggggaaagc	acccagggag	gggaaccgtt	tttctcctac	tcctatagca	attttgttag	889980
tttttttggg	gactagactg	attaaatata	actctgattc	ttcagcattc	cccgcactaa	890040
agacaagatg	acggctgtct	atagcccaag	aaggactctc	tttatttggtg	ggagacgtag	890100
tgagttggta	atcctctcca	gaggagagat	cgtaaataca	aatttgctgc	accccttttaa	890160



ttacagagca	gaaggctatt	tttttaccat	ctggagacca	tgcagggcaa	ctgctatttc	890220
tgtatttttt	tgtcagcaag	cgaggtgctt	gggggttcagg	atcgagggac	ataatataaa	890280
gacgcggacg	gccgtctttg	ttcgaataaa	agacaagctg	ggatccttca	gggttgaagg	890340
agggattccc	ttgagtcctg	aaattctcat	taaggaggcg	acgtgggcca	cccataggtc	890400
ctgaagttag	tgagaacggg	tgaataaata	aatcaggatt	tccataccta	tcagcaacga	890460
aagctaaaaa	cttttttctt	ggagaaaacg	taggcatgag	ttgggtgcct	tttaacggaa	890520
ggactttttt	accttcagtg	ttctctaggg	aaccaagaaa	aatttttaggc	acaccatact	890580
tatacgaaac	atagagatag	ggaaaatttg	atcccacacc	caccattttt	ggagttatag	890640
agagcgaaac	ttctgtggtt	aaagggggga	gggtttttccc	atcgtaatct	gtagtccata	890700
attctccttg	cttgagcttt	tgatcttttc	ctaaagaact	tagagcaaaa	acaattttcc	890760
cagcactgat	tccaggaatc	cctgtgaggg	cgtaatgaac	tgtatcagca	gcgtgatgga	890820
ttttttgacg	atctacagaa	agatttttgag	aaatagtaaa	agaacataag	gtttgaggag	890880
tttttgaaga	ctgtaaaaagc	actacagata	gctgaggtac	atgcaaccgt	aaagatattg	890940
ctaaaggaga	tgacgattct	ttagaagccg	ctgtgggttg	tagacaatct	cctaggggcaa	891000
tgtccttgca	aaatatctcc	gttagcgagc	tgagggtattt	ctgtattttt	ggatctttcg	891060
tatcgggtct	gcaagagacc	tcaataggga	gcgtgatatg	ttcgggaacgg	acaacaactt	891120
ctaattcttc	agcatagact	agcgatgcga	agcaaaaagaa	aaaaacttgg	aagcatagtt	891180
gccgtaacat	gccgatatct	cctcacccta	gggatagagc	gttaggattc	attactgacc	891240
agttaatat	gaaaagatta	tattttttcga	gactttgtat	ttttcgagaa	atttttgaaa	891300
tgggagtgca	tgaatcctct	gagtgagcag	ctggttgatca	gcagcactca	cctcagagag	891360
aaaactgcat	tcttgaatct	ctccattcgg	agaaaggact	aatttaatac	gcacataccc	891420
tttagagggg	agagctatgt	gagtgcgaaa	taactcacat	agctcgtctt	cttgagttgc	891480
tttaagttct	gagtgcatgg	tcaattgggg	tgtagatggc	caggagatat	ttttgagaga	891540
agtttcactt	ttctcaattt	tatctacatg	taggggaaagg	gcttgggcaa	cttcggagag	891600
tgttgttagt	ttgggtttttg	ataactgtgt	atttttttta	gttgtagagg	gaggaggttt	891660
ctcagttgcg	gtcgtttttt	ttgctacagt	aggggctggt	gatggtttag	gaggttctgt	891720
ttttataact	tttggaatgg	gtttttgtag	agccttcttg	acgttctctt	gaggagggct	891780
gcatttagct	tgttttttgtg	gctgcgtagt	acagaggggc	gtatcgtttt	agctggatct	891840
acaactactg	agggagtagg	gacaggaggt	ttcgggttga	tagtgacgag	tttttcttga	891900
aaggcttttg	gttgtaaacg	tttttttagga	agaggagaag	caaagacaag	gagaagaatc	891960
cccccatgaa	tacatgccgt	gattgctata	tagggaaatg	acttcatcat	aattcaattc	892020
tgtaggcgta	cgtgaagttc	gtgaaacccc	gcagcttcta	tagcattctt	tacgttttga	892080
tatgtccgaa	aggaggtttc	tccatcttgt	agtaataggg	gggtcttttc	aggataggct	892140
ttatggagga	gggtaaggcg	aacagtgagc	tcttgtagtg	tgatcggatg	ctcgttcaaa	892200
gttaacgaat	gggtccgcaa	tactttaatt	accgctatag	aatcgttttc	gctgctcagc	892260
acttcttgct	cttggtgtgc	aggagcaaga	gctatagaat	ccagttttat	taagggaaca	892320
gcaacgataa	atgccattaa	aatgacaaa	acaatatcaa	tcaacggcgt	taagttcacc	892380
aggggctctt	cttctatttc	ttccgtgaag	cggattttca	taagtttgta	ttcggttatt	892440
tgacttctat	agaattcagt	agtaaatatg	ctgtctgctc	tatctcagaa	atcaattccg	892500
aagaatgtgc	tttaagatag	ttaaaagcga	tcagtggagg	tatagcaaca	aagagtccta	892560
taatcgtcgt	tcccagggtc	gtggcgagtc	cttccataat	ggctgagttt	ccactgcttc	892620
ccgagctaat	gtgggtaaaa	gcgactaaaa	ttccccatac	tgtacctaaa	agtcctagaa	892680
aaggagctaa	gctgatcggt	gtcgccggaa	taaagctggt	tttatgtaaa	agagctttat	892740
atttcggcat	gatggctccc	aggagcgtct	caaagattg	gatattctta	gaagaaagga	892800
tgggacctcg	atctggagcc	gattgccgat	ttttatctaa	gagctccaaa	gttccccggt	892860
ttatagtaaa	atacaagtcc	gcaaaggggc	tgagctctgg	atggatatcc	agagacagag	892920
gtgcgtgacg	gttttttaatt	aagaaatctt	taagagactt	tcctgctttt	aaaaaatttt	892980
tttgaatggc	aagcttttga	tgtagtactg	tccaagtaca	cacagaaaaga	ataagaagac	893040
aaaagaatat	actttttacca	aaaaaatctg	cttccgtgta	ggcctgaatg	atgggggttat	893100
gagagaagtg	taccatggaa	taaaaatctt	tattttacaga	gagtgctctca	aagtaaagat	893160
gatcctaaca	aattttcgtt	atagagccaa	gcgggttttg	taaagaagat	ttataaaaatg	893220
gaatataaaa	attaatgtat	aattagtaac	ttgatttata	aaatcacggg	gttatttttga	893280
ataaattcaa	aacatattta	caaaccgcac	tgatagcacc	tttcttttct	ttcccagcgt	893340
tatctggaag	tttttcctct	atccaggcgg	aagaaattnc	acaacaagtg	aatcatccag	893400
gtgcagaact	cctttctgag	ggtagctaca	tccctggact	acagacattc	cgattggggga	893460
tcaagattta	cagcttccaa	aggagcccat	atctactgga	agaatcccgg	agaaattgga	893520
agtcctctca	aaattttctg	gcagttgccg	aaagggttctg	tgggtgaaga	agagcattgg	893580
cctacccccca	aagtatttga	ggaagagggc	actacatttt	ttggatatga	agattccgct	893640
cttattgtcg	cagatgtccg	tgctcctgaa	ggatacactc	ctgggtcagga	ggtcgaatta	893700
cgagctcagg	tcgaatggct	agcttgtgga	gatagttgct	tgcccgggaa	cgctcgatcta	893760
aaattgacac	tgccctacga	agagaaggag	ccttctcttt	atcctgatac	acacgcagaa	893820
tttactaaaa	cgctgcatgc	gcaacctcgt	gttttagaaa	atgatcactc	tgttcaagtg	893880
gcgcaaggaa	gaagaaatga	gatcatttta	aatatctcta	agaagatcaa	cgctacgaaa	893940
gcatgggttg	tttctgaaaa	agccgataag	cttttttgctt	atgcagagac	ctcttatagc	894000

gggggaacag	gaactgcatg	gagattaaaa	gtaaaaaatc	tctccggagt	tcagaagaat	894060
gagaagcttc	atgggatact	gctgttagcc	gaccacacag	gtcgtcccgt	agaatcactc	894120
accattcata	gtgaagttct	tggcacaaca	ggatctgctg	tagcaggact	gtcacatat	894180
atcacaaattt	tgatcatggc	ctttctcggc	ggggtcttgt	tgaatattat	gccttggtg	894240
cttccttttag	tgaccctgaa	ggtctacggt	ttaataaaat	ctgctggaga	gcaccgctct	894300
tctgtaattg	ccaatggctt	atgggtttact	ttaggggttg	taggatgttt	ctggggattg	894360
gcagggtgtg	cctttatact	taagggttta	ggtcacata	tcggctgggg	cttccaactc	894420
caagagccta	tgtttgttgc	cacattgatc	atagtattct	tcttatttgc	tttaagttct	894480
ctagggcttt	ttgaaatggg	gaccatgttt	gcaaaccctag	gagggaagtt	acaatcttca	894540
gagatgaaga	gctctaataa	taaagctgta	ggggcctttt	ttaatgggtat	tttagctacg	894600
ctagtcacga	ctccttgtac	aggacccttc	ttaggttccg	tattgggatt	agtcagtgtc	894660
ttatctttcc	tgcagcagct	cttgattttt	actgcgatag	gcctggggat	ggcttcacct	894720
tacctagtct	tttctgtatt	tccaaaaatg	ttgtccgtac	ttcctaagcc	tgggggatgg	894780
atgagcacct	tcaaacagct	aacaggattt	atgttggttag	taacggtaac	ttggttggtg	894840
tggatttttg	gttctgaaac	aagtacaact	tctgttggtg	ttctccttgg	aggacttggg	894900
cttgcaggat	taggagcttg	gatttttagga	cgttggggaa	cccccgctct	tcctaaaaaa	894960
caacgtgttt	gtgcttcttt	attgttcttt	gcattcctag	gtggagccat	ctctgtaagt	895020
ggtttagctt	ctcattactt	tgtctgaacct	cagcagacag	tcagtgtgaa	cgaagatagt	895080
ttatggcagc	ctttttcctt	agagaagctt	gcccatttgc	gagcccaagg	tcgtcctgtt	895140
tttgtgaact	tcacgggctaa	gtgggtgcttg	acttgctcaga	tgaacaagcc	tgttttgtat	895200
ggtgatgctg	tgcaaaaagat	gttcgaaact	catggaattg	tgactttaga	ggcagattgg	895260
acccgtaagg	atccagggat	tacagaggag	cttgctcggt	taggtcgcgc	aagtgtccct	895320
tcgtatgtct	actatcctgg	agataactct	gcacctgtct	tacttccaga	naagattaca	895380
caaaactctt	tagaagacgt	cgtaagctga	tttgttaaggt	agctgttaag	tgtgaacca	895440
acacaagcat	tcgtagggtg	aatcatccac	gaggtaacct	aaaaattgtt	agggcagcat	895500
atgctgccct	ttttatttgt	aacaagaata	ccaaagtcca	cctgccttta	aaagcagagc	895560
cgcttcaatc	tttgttagaa	tcttgagtct	ggggagctta	aattttcctt	agtaggacag	895620
agtctcggga	gttcgctgtg	ttttaaggat	tcttcttttag	tgaagatatt	ttcaagagaa	895680
tgtattctat	agggaattct	tgccctgaat	gttctacgac	tttgcttaaa	ctaggagaca	895740
acccgtggat	ttggctgatg	ctcatgtttc	tctttctgat	gatgcttttg	aagaagatat	895800
taacagcgta	ttacagcgcg	ctcaagattc	tgagtgctca	ctagtgtgta	atgtaaccac	895860
aacagaaaag	gaattaaatc	gctcgtttgc	gtatgccgaa	cgttttccta	aaattcgatt	895920
ttgccatgtt	ggagggactc	cccccaaga	tgtagatcag	gatatacgaag	aagactacag	895980
gaattttcat	gctgcagcac	atagtaagaa	actcgccgca	atcggagagg	tcggtttaga	896040
ttattgcttt	gccacggaag	agggaatagc	aaggcagaaa	gagggttctcc	aacgctattt	896100
ggctttatct	ttagaatgcg	aactcccact	tgtagtgcac	tgctcagggtg	cttttaacga	896160
ttttttccgt	atgctagacc	aatactacca	taacgatcca	cgttcacgctc	cagggatgct	896220
gcattgcttt	acaggaacct	tggaagaagc	tcaggaactg	atctctcggg	gatggtttat	896280
ttctataagt	gggactcgtga	cttttaaaaa	tgtccaagat	ttgctgagatc	tggtgttaga	896340
acttctcttt	gagcatcttt	taatagagac	ggatgcgcct	tttctggctc	ctgtacctta	896400
tcggggaaaag	aaaaatgagc	ctgcacatgt	gctccatacg	atcaacgccg	ttgccaatgt	896460
aaaagggatg	ttcccacaag	agcttgcagc	tcttgcttac	aagaacgtct	tacgctttct	896520
gcacgggttaa	tttgatggag	ttcatagAAC	tcataacct	ttctattttg	tcataataagc	896580
ttctgtttct	tatgaaaaat	tactttccat	aattttatct	tagcctctat	cttgagttga	896640
acttaaagtt	tagtaaaaaag	tcttagaatg	tcacgacatg	aaatctgccc	agaagtgtca	896700
cacaagaaag	gcaagtatta	tagcaccttt	atcttccgtt	gtattcactc	cttagcgggt	896760
atagcgttta	cttttttctt	atgtgaacac	ctattttacga	acatgctagc	ttcttcttac	896820
ttttcccagg	ggaagggttt	cgttgctatg	gtcaatgggt	ttcataagat	cccagggtctg	896880
aaaattattg	aagtggcggtg	tttagtcctt	ccttttctct	gtcatgcgat	tatcggcac	896940
gtatatctct	ttcaaggaaa	aagtaattgt	tattctgggtg	acggaagtcg	acctcatttg	897000
cgttatgcta	aaaattatag	ctatacgtgg	caaagggtgga	ctgcctggat	tttactcttt	897060
ggaattgctt	tccacgttgt	gcatttgctg	tttatccgtt	atccagtcca	tgttgatata	897120
catggaacta	cctattatgc	tgtagacatt	caaccttctc	gctatgacgt	gattgttaga	897180
gggactaaag	gcttttttaac	tttgaatctt	cccaatacag	aagcttcgag	tatcgagggtg	897240
tctcgtcatg	atttagggtg	tgctgatgct	gcgttattgt	cggagaggaa	ctctatatta	897300
ttgactccaa	gtgcagggtac	cgcatcttct	tattgtagttc	gtgatgcctt	gggatcacta	897360
ttcatagctc	ttctctatac	tatttttggtc	attgctgcag	catttcatgg	gtttaatggg	897420
ttgtggacct	tttgttgctg	ttggggtgtc	gttgtttctc	tgaggatgca	aggggtattg	897480
aggatagtat	gttacctcgc	tatgattgtt	gtgactttca	tgggagtgag	tgcgggtttg	897540
aattttgtata	gtgtggcata	gcaaatggat	gagaatcgaa	aagtaatcgt	tgttggtggg	897600
ggattggcag	gattatccgc	agctatgcag	ttagccaacc	ctgggattat	tgtagagctc	897660
gtatctctga	ctaaagtcaa	gcgctcccat	tctgtatgtg	ctcaaggggg	aatcaagcgt	897720
gccttaaatc	tgaagcctga	ggaagaggat	tctccctacg	tgcatgccta	tgatacaggt	897780
aaagggtgggg	atttttcttgc	agatcagcct	cctgtcttgg	aaatgtgtct	tgcagcaccc	897840

agaatcatta	aaatgttaga	taacttttgg	tgtcctttta	accgtgggtcc	ttctggaac	897900
ttagatgttc	gtagatttgg	aggtacgtta	taccaccgca	cagtattctg	tggagcttct	897960
acagggcagc	agcttatgta	tacttttagat	gagcaagtgc	gacggcgaga	acatgcgggt	898020
aggggtataa	aacgagaaaa	tcatgaattt	gtacgttttag	ttaccgacca	ttccggacgt	898080
gcttgcgga	ttatattaat	gaacttggtt	aataaccgtc	tggagatttt	acgagggcat	898140
gctgtcatta	tagctacggg	aggccccgga	gtgatcttta	agatgtctac	aaactcgact	898200
ttctgtacgg	gagccgcgaa	cggaagactc	tttttacaag	gcatggccta	tgcaaaccga	898260
gagttctatc	aaattcacc	tacagcaatt	cctggaagg	ataagctacg	attaatttca	898320
gagtcgtg	gtggtaggg	cggtcgtgtg	tgggtgcctg	gggattcttc	aaagcgcata	898380
gtatttccag	atgggtcggg	acgtccttgt	ggagagacag	gagctccttg	gtatttctta	898440
gaagatatgt	atcctgcgta	tgggaatctt	gtcagccgag	atgtaggagc	gcgtgctatt	898500
ttacgtgtat	gtgaagctgg	attaggaatt	gatggacgca	tgggaagcgta	cttagatgtc	898560
actcatcttc	ccgagaaaa	acgtcataag	ttagaagtcg	ttttagatat	ttataagaaa	898620
tttactggcg	aggaccccaa	tacggttcct	atgaggattt	tccctgccgt	gcactattct	898680
atgggaggtg	cttgggtaga	ttggcctgct	gccgatgac	ctgatcgtga	tagtcgcttc	898740
cgtcagatga	cgaatattcc	tggatgtttt	aattgtggag	aatctgattt	ccaatatcat	898800
ggagccaatc	gcttaggtgc	taattcttta	ctttcctgtt	tgtttgcggg	tttggtttct	898860
ggagatgaag	cttctcgttt	tatagaggct	tttggggcat	cacaggcaac	gtctagtgt	898920
tttgatcgtg	ctctacagca	ggaaaaagag	gagaacgcgc	gtcttttatc	tgcatcagga	898980
aaagagaata	tttttgtttt	gcatgaggaa	atcgcaaa	ttatggtgcg	aaatgttacg	899040
gtaaaacgaa	ataatcgtga	tctccaagaa	actatggata	aattgaaaga	atttcgtgag	899100
agattaaaaa	atgtctctgt	attggactct	tcaccatttg	cgaataaatc	cttccatttt	899160
gtacggcaga	tgggacccat	gttagaactc	gcactggcga	ttactaagg	agctcttcta	899220
cgcaatgagt	tctgggggtc	ccattacaaa	ccagaatttc	ctgagagaga	tgacgagcat	899280
tggctgaaga	ctacagtcgc	tgtttatgct	cctgaagaac	ctgagatttc	ctatcttctt	899340
gtggatactc	gccatgtagc	cccgaactct	cgggattaca	caaaatcttc	aacaggaaaa	899400
atagaactca	cgaatattcc	tgataaatat	cgtctaccca	tatagaaaaa	gagagatgat	899460
ggagaatcta	gagactttta	ttttaaaaa	ttacagaggc	gttccaggga	agcaatactg	899520
ggaaagcttt	gaacttcctt	tacatcctgg	ggaaaatgtt	atcagcgctc	ttatggaaat	899580
cgaaaagcga	ccggtaaata	tcttagggga	aaaggtcaat	cctgtagttt	gggagcagg	899640
ttgcttagaa	gaggtctgcg	gatcctgttc	tattctgtg	aatggagtcc	ctcgtcagg	899700
atgtactgct	ctgatccaag	aatatatcga	tgcaacgcaa	tcccagaga	ttgtccttgc	899760
tccctctact	aagtctcccg	taatccgaga	tttaattgta	gatagatcga	ttatgtttga	899820
taatctcgaa	aggattcagg	gttgggttgc	tgccgatatt	gaaggagaga	cgtttggtcc	899880
tcaagtcact	caggaacagc	aagagcttct	ctatgcattg	tcgcagtgtg	tgacgtgtgg	899940
ctgctgtaca	gaagcatgtc	cccaaattga	taataaaaag	gatttcatag	gtcctgcagc	900000
aatttcccaa	gcgcgttatt	ttaatacgtg	tcctggagat	aagcagtcta	agaaaagatg	900060
gcgggctctt	atgggtaaag	gagggattga	gggttgtggt	caagcgcata	actgtctccg	900120
tgtctgccct	aagaaacttc	cccttacctc	gagcatctcg	gccgtgggac	gtgaaatttc	900180
aaagtctctt	ttaagaagt	tattttcagc	tctttttaa	aagaaaaaat	aatctagaaa	900240
aattcttttag	ggaggcggct	gcggtagcct	ggaggcgggt	gcatgccata	atctatagga	900300
tttgcataga	gggtccagg	tcttgacgtt	gcgaacagct	cctggatatt	gtcaagaggc	900360
tgctccttga	gccctgcata	gttaaatatt	caaagatcga	tctctgtggt	tcctggattt	900420
aggatgaatc	caaaataaat	agaaggccag	ttactgtctg	caaagagcaa	aggagcggga	900480
taggcaagat	tatgatgcct	cattgccgtg	gtgaggcgga	ggtacgtatc	ttcttcgggtg	900540
tagatctttt	gataactttg	catgaggaga	cctttataga	tatgcctcag	gtctgctgag	900600
gagagtaagg	tcatttttag	gatggtttcc	tctatcagg	agcggaaatt	ctcataggta	900660
atacgagagg	aaatcccag	atatgaagag	acgttatcta	agacttctgg	aagctgttgt	900720
tctgaaacat	aagggaactc	acggaccata	aggtagagaa	gacggcggtat	atagataaga	900780
gctacggtct	tatcttttgt	gaataaggag	cttagaaaac	gcgatccttt	gtcatagagc	900840
tccggaagag	tcaaggagt	gtcggagcag	aaatcatgaa	agtcatgaac	tacatgttgc	900900
aaagcatatt	tgttacaaaa	attctctatg	aaagcataga	tacttagctg	aggtaatata	900960
gtatcttgaa	ggaaatcttg	gtgttgtttc	acccagacat	cacgaagcca	ggtatagctg	901020
taccaatcat	tatcccaagc	ttcccgaat	aaaggagatc	ctgcgattat	agagaaaacg	901080
tgggtgggtg	atgagctaag	tagagagtgg	gatccttctt	ctagataact	tttaattcct	901140
gtaggagat	ctttaagggc	gtctgcgtag	aaagctgcaa	gctcatgagg	attttcagga	901200
tgcttttctg	taagtgtcag	aggttctgag	ctttcaaaat	aatccaaaag	aagagtgtcc	901260
actgttcttc	cagaaacata	aaccaggga	gtttgtgaca	gctgatctaa	gtggtttaag	901320
atggaggggag	gcacaggaag	ctgataggct	tctaaaattc	ttgtaaggag	agcttcttgg	901380
aaaacatccg	tgtgtagcat	ggcagtgatg	ttgtggacga	gccgagatgt	ttctttctct	901440
aaattgatca	cggcatgttt	ccccagaatg	tctgactctg	tggaggtgaa	gaattcagaa	901500
agaaaacgta	taaatctatt	aatcgaatag	atgggggacc	atgtgttcgg	atgggtgcgt	901560
ccatgcgtga	taagaatacg	gaagccagcg	ggagcattag	catagagatg	agcaaatctt	901620
tgaatgaagg	catcgtaaga	actacgaaag	tataagggaa	tttgctttgt	atagaaagaa	901680

agtaagaatt	caggaagatg	tagaaatttc	tttgcctttt	cttgagcact	atccccactca	901740
taaagagctt	tatttgagttc	ttgacggaag	cgcagtgtgat	ccatcgtcaa	aatctgactg	901800
tcttgattat	ttagtgggtt	gcgcattccgc	ccttcaatat	attctagtgtg	ggagcgtgct	901860
tcgtgatagg	tctgttcaca	ttgttggtact	aaaattccgga	tggtttctac	ttcctcttca	901920
acaaagtgtg	taactagaga	tacaagactg	tgagggtctt	cactttttcca	tcctaaggca	901980
aggcggatat	ggtttgagat	ggtaggttgg	ctagcatccg	caagagtcgc	taaagtatac	902040
tcccaggctt	tcagtaaggg	attttgagtg	tcattggataa	aagcagattt	tgcttcttca	902100
taggcatgta	agtagtggtg	taccggttgt	atttctgaga	gctctctggg	gtgttgcgctc	902160
gagaatgcca	cttgttcttt	gctgaacaac	ccttctttga	agaaaatagc	tcgtacagta	902220
ccttcttgga	gctgatagta	gtgcagaagt	gtcgatttga	taatgtcggt	agcagttaag	902280
gtctcatgga	cattttttag	tttttgcatt	aaatattgat	gcgagagcaa	ctgttggtatt	902340
tgtgcttcag	aatccccaag	agtttcaata	agattggcag	cagaaaaggc	tttttttagt	902400
cctggagatg	aggagagctt	aaccagagga	tcaggataaaa	gatctagaat	ccttaaaggc	902460
ttgaatagct	ctccaatgca	tcccgaagg	tttataggaa	ccgcaatttc	cctttgggtt	902520
acgattctag	agagtttgcc	actgctaatt	agatcattga	gatcctttaag	gaatcgcttc	902580
ggatattctt	ggtgaatgag	aatggcagga	gccgtagcaa	aacaggaacc	tacatcttgc	902640
cgaaggtagg	tgaagagcgc	tgtgagtgtc	gcttgacgca	catgaatcgt	agagagaatt	902700
gtctgtggat	tcaatgctag	tgtatggcga	attaggtttt	ggattgtaga	gtatgaaggg	902760
acaaagagag	ttttgatgct	ttcttttaat	ttaggatttt	ccttttagagc	tttttagcatt	902820
ttaaggaggt	gttcacgac	ttgagcttca	ttatggcgat	gaggccctaa	aggataggta	902880
cattgtgaga	gatgggtgaat	ggcttcgaca	agctttactg	tatcgatttc	cccattgtca	902940
gctaagatat	aattttgcgac	tttacggggc	atatttaggt	tcttagcagc	tagaggggat	903000
tgtagagccg	tagtacggta	ggcttttaaa	aaaactgtgt	cttcagaaca	gaaaatttcc	903060
tcaagaagat	tttgatcctg	gtttgcgac	agagaaatcg	aaacaaaaat	atccaaacgt	903120
gacataggat	gtagaagata	gttatgggat	attcctttgc	tgtaaacacga	atacatgttt	903180
ctgtcactga	tatcctccac	tactattttt	ctagagctcc	gaaggcaagt	ttatgaaaat	903240
gaaaggatgg	tcagagttcc	atctgcagaa	tgctcggttt	cgttggttaa	catcatgggt	903300
agagaatcaa	taagattctc	tgtattttaga	gggttttaaag	gatcttttaa	gagctcttca	903360
ataggaagct	gagaaaagta	cttgaggatg	tcttctcctc	cagtgaggca	gatcaaccga	903420
tctccaggct	gtagagcttg	gtgagtctct	aaggggagac	gtacgaaaga	ttctctcgt	903480
tgtagaaaca	tggttaggagc	tccctcgctt	aacgagagga	gctctagaga	tcgacttttt	903540
tctacatatt	taattgaaagt	catagcaact	acagcctcat	tgcttctgt	tggttttag	903600
aagctgtcgg	cagtatcctt	gctgattttt	tgtaacgaaa	cgtccgagga	agcataggca	903660
agaaaaagac	tccgtgcgga	taaagcatag	agataggaag	gaagaccaat	atcgccagcg	903720
agccctatga	tccctaaaag	ggtatcgcca	ccatcttgaa	ctgtccaacc	attaaaatga	903780
ccggaaagtt	gccttctccg	gagatgttgg	gaactaaagg	taacttttagg	gaacgtaggg	903840
aaatccggac	ttagtaacgc	actttgtagt	gaagataaaa	tccctaattc	tttttghtaat	903900
ttttcgcttg	aatggtaatc	gatatctgct	ttctcaatgg	aattcaataa	gagtaggaga	903960
gtgcaattga	aaatatttcc	tagttcattg	aattcataac	cgttaaggctg	gggttcaaac	904020
ctcacgttat	gggttctctg	ccaggcagct	tccatacaga	aggtcagttc	ttgaagaggc	904080
ttgttaaagtt	tggtgttgat	ccttagagaaa	atccaccaca	tgaggaggaa	agcaagtaca	904140
tagaaaaaac	aaatattgag	aggaaactttc	aaggcggatt	ggatgagatc	agaaactgga	904200
actaaagata	gagtgtaggt	cccttgata	ggaattttat	tcagtaccaa	tcctaggtag	904260
cgtttcttgt	tgatactcac	tgtgattagg	ttctccccac	caagaattcc	agaagctttc	904320
tcaatttcta	tggcagaggg	gcttcttgct	tggaattgctg	gtaaattagg	gagatctaga	904380
gaaaatacaa	aagaagattc	actgtcctga	gcacagaaga	ggacctcgcc	atacttattt	904440
acaaggcaga	tatttccttt	ggtgatgtgt	aaggattgga	ataaatcttt	ctgtataaaa	904500
gacatgggat	agaaaacttac	aagcagtcct	gaagtcgttg	tagaatccca	agatgcgaca	904560
tcttcaacta	gaataagata	atgtaaaagt	ggtttacctg	gaatgggtcaa	taaaaaggct	904620
ttccctacag	ctgcggatag	ctttttcttc	atttcaggat	gctgttttag	atagcgaatg	904680
aaagggtctc	caggattttt	cgctcttaca	gatccatcaa	agggatctat	aaggcataag	904740
gaaaagtctg	tattggagag	tgccatcatc	tcattgtatg	cctgtgcata	gggctctgca	904800
gaaggagatg	cataggattt	taaggctaatt	gtgttggtcaa	gtctatcgag	gaaaagcttg	904860
tgtatcgta	gttttttttc	gaattctata	cttaagttcg	tagcacgggt	atggaggacc	904920
tgtactaaat	ttgcttttagc	ggcagaaaaa	gagaaaaaac	ctacgaccat	aagattgagg	904980
agttagggaa	tgggaatcac	taaaaagaaa	aaaaatagaa	cacgcttggt	aaaggttagt	905040
ttcatgatgc	taataccttt	aatattaata	aggtgatgtc	gtcatgttga	tgggagttcc	905100
cgacaaaagg	ttttacactt	aacatcaacc	tgtggacggc	atcagcagca	cttttccctg	905160
tcaatccttg	aattgcagct	tgtaggcgct	cttctccaaa	catgtcggtt	ttgttattat	905220
gggcttctgt	aataccatca	gaatacaaga	caaagagaga	ccctggctta	ggatgaaata	905280
gctttgaagt	gatgttcgca	acttcgggaa	ggaagcctaa	agccattcca	ggatggaata	905340
gccaaagaagt	ctcgccatca	ggatctaggt	agcaggcagg	aggatgtcca	caagaataat	905400
attccatggt	gttggaagtt	tgatgataac	agtacacaca	tagagtgaca	aacatccctg	905460
agttttttgt	attgttataa	aataagcgtg	aggtttcttg	gattgcctgt	tgaagagacg	905520

aagagcgaga	aaggaatggt	ctgagcatat	tttttagaaa	tagcgaatac	ccacaagcat	905580
taacaccttt	ccctgaggcg	tcagcaacaa	tcaggaatag	gagagccttc	gaaccctctc	905640
ctacaacaaa	aacatcaaag	aaatcaccac	ctacagtaat	ggcagggata	taggcttttg	905700
cgagttctat	atgaggatag	ctggggagag	tattaggaag	aagtcgctgc	tgagcctgct	905760
ctcctaaatg	tagagcggtc	tgtgcatttt	ctttcatctc	aaagttcgtc	ttagcgaggt	905820
gttgctgttt	gtggagattc	tccaccatag	cattaaaaat	atggccaagt	ctggtgatct	905880
caaaccctaa	ggagtcgtca	gtatagaggc	agtttttgtt	tttcctagat	tctatcatcg	905940
cagtggcaag	ttttctgata	ggtaacgaca	atcgcttgc	tacaataaag	gctatgaggc	906000
tccctaagag	aatgcaaaaag	aaataggcag	tgtacatgcg	agctctgcgc	cataaaggcg	906060
caaagctctc	ttctttttta	gcataggaaa	ggactgcaat	atctatactg	ggaacatttt	906120
caatacagcc	ccaaatctca	gtatctttga	ttttaaaaga	atagaaattt	tctccaatat	906180
ccagagggga	gagagttaaa	ggacctaatt	ctgagcttat	agggcaaggga	tcatcattga	906240
gaaaaacttg	gcagaatttt	tctttcgtca	tgtcagggta	gacagtatgg	agatggagag	906300
caggatcaga	agctttttaag	ataacgccgt	atttggaaaag	gacgcagtt	tttcagtgga	906360
gataggattg	cttggtttatc	aggagatctt	tgagtaagct	ctcagcactg	aacgtgggtg	906420
ataagatccc	tggagttctc	tgagtttttg	catcaaaaac	attagcttgc	attacagaaa	906480
agacttcctg	atttttagga	gattgtttta	gggctgctaa	aaatggagtg	ttcttaggga	906540
tgtctatttt	gtgattatag	ttttccccta	agtgttcagg	aatgctagaa	gcaacaacaa	906600
ttttatctcc	atttgggaat	accttgatta	aagagatttc	attatagatc	ccttggaata	906660
ctttctgcat	ttcattgcta	aggagaacgt	tcggagtctc	tgggaatacca	gcatctaaat	906720
ctaagacatc	agaaaataga	gatagaacat	cgacattcaa	agggacaatc	tgagtggagag	906780
tattggcttt	gaaagcagcg	ttttctttca	gtgcagtaga	aatagcagag	actatgggtg	906840
ggtattgatc	taggtttaac	catacgatgt	tgatccctag	aggtgcaatg	atagcaacgg	906900
cgcaacaaac	cacaacgga	accctattgt	tttagtaaaa	gggatcatgg	gtattacggc	906960
gctctattct	taaggcttgt	catccttgag	aaggaacgtc	tttcctctag	tgttttgttt	907020
cttacgcagt	ataaaaaaat	ttccttaagg	agacacctac	tatttctttt	attcttgcta	907080
tatcttagta	aatcaattgc	ttgcaacgaa	gatcttattt	tttcatctcg	atcttctaata	907140
gaatgaaaat	attattctct	aacttctttt	aaatcacatg	gatgttttag	aatatagaca	907200
ataaaaaattg	ttaaagcttt	tgttttttac	tcacaatact	tatgtagaaa	tcttctaatac	907260
acagaagctt	tctactaaaa	aagagcggag	ggaatcaagt	gagtctatat	caaaaatggt	907320
ggaacagtca	gttaaagaag	agcctctgct	attcgactgt	tgctgctcta	ataatttatga	907380
ttccttctca	agaatccttt	gcagatagtc	ttatagattt	aaatttaggt	ttagatcctt	907440
cggctcgaatg	tctgtcagga	gatggtgcat	tttctgttgg	gtattttact	aaggcgggat	907500
cgactcccg	agaatatcag	ccgttttaaat	acgacgtatc	taagaagaca	ttcacaatcc	907560
tttccgtaga	aacggcaaat	cagagcggct	atgcttacgg	aatctcctac	gatggcacga	907620
tcactgtagg	aacgtgtagc	ctaggtgcag	gaaaatataa	cggcgcaaaa	tggagtgcgg	907680
atggcacttt	aacaccctta	actggaatca	cggggggggac	gtcacatacg	gaagcgcgtg	907740
cgattttctaa	ggatactcag	gtgatcgagg	gtttctcata	tgatgcttca	gggcaaccaca	907800
aggctgtgca	gtgggcaagc	ggaggnctac	agtaaacacaa	ttagcagata	tttcaggagg	907860
ctctagaagc	tcttatgcgt	atgctatatc	tgatgatggc	acgattattg	ttgggtctat	907920
ggagagcacg	ataacaagga	aaactacagc	tgtaaaatgg	gtaaataatg	ttcctacgta	907980
tctgggaacc	ttaggaggag	atgcttctac	aggtctttat	atttctggag	acggcaccgt	908040
gattgtaggt	gcggcaaata	cagcaactgt	aaccaatggg	aatcaggaat	cccacgccta	908100
tatgtataaa	gataaccaaa	tgaagatttg	aggaacttta	ggaggggcca	attcttcagc	908160
aactggagtt	tcttcagacg	gttctgtgat	tgttggtcag	gcgcagacag	ccgataaatc	908220
cgtgcatgct	tttcaatact	ataatggtga	gatgaaagat	ttggggactc	ttgggggtac	908280
ctcttctaca	gcaaaaacag	tgtccccaga	tggtaaagtg	atcatgggta	gatcacaaat	908340
tgctgatggc	agttggcacg	catttatgtg	tcatacggat	ttctcctcta	ataatgtact	908400
ctttgatctc	gataatacgt	ataaaactct	aagagaaaat	ggcgcgtcagc	taaattccat	908460
attcaacctta	caaaaatatga	tgttacagag	agcctcagat	catgagttca	cagagtttgg	908520
aaggagtaac	atcgctcttg	gtgccgggct	ttatgtgaat	gccttgcaaga	atctccctag	908580
caanttagca	gcacaatatt	ttggaatcgc	atacaaaaata	cgctcctaaat	atcgtttggg	908640
ggtgtttttg	gaccataatt	tcagctccca	cgtttctctaa	taattttaac	gtaagccaca	908700
atagactctg	gatgggagcc	tttattggat	ggcaggattc	tgatgctcta	ggatctagt	908760
tcaaggtgtc	tttcggatat	ggaaaacaaa	aagccacgat	tacaagagag	caattagaga	908820
atacagaagc	cgggagtggt	gagagccatt	ttgaaggggt	cgctgctcag	atagaagggc	908880
ggtatggtaa	gagcctcgga	ggacatgtca	gggtccagcc	tttcctagga	ctgcagtttg	908940
tccacattac	aaggaaagaa	tataccgaaa	atgcagtgca	atttctctgta	cactatgatc	909000
ctatagacta	ttctacaggt	gtagtgtatt	taggaattgg	atctcatatt	gcactttag	909060
attctttaca	tgtaggcaca	cgcatgggaa	tggagcaaaa	ctttgcagcc	catacggaca	909120
ggttctcagg	atctatagcg	tctattggaa	actttgtgtt	tgaaaagctt	gatgtgactc	909180
acacaagggc	atttgcggaa	atgcgtgtca	actatgagct	tccctatcta	cagctcttga	909240
atcttattct	acgagttaat	caacagcctc	tacaaggggt	tatgggattt	tccagtgatc	909300
ttaggtatgc	cttaggattc	taaagaagaa	aatttaattt	tcttgcgaaac	atttctatcc	909360

atagttgata	gagataaaca	gataaaatat	agctcagaat	ataatctgag	ctatatctct	909420
cttacttgca	gccatgtctg	aatatgagta	tagtcagaaa	ttctgcattg	ccacttccgt	909480
gtttaagcag	atccgaaacc	tttaaaaaag	ttagggtcgca	tatgaaattt	atgaaagtcc	909540
ttactccatg	gatttatcga	aaagatcttt	gggtaacagc	attcttactg	acagcaattc	909600
caggatcttt	tgcacatact	cttgttgata	tagcaggaga	acctcggcat	gctgctcaag	909660
caacaggagt	ttctggagat	ggtaaaattg	ttataggaat	gaaagtcccg	gatgatcctt	909720
ttgctataac	tgtaggattt	caatatattg	atgggcat	gcaaccctta	gaggcagtac	909780
gtcctcaatg	ctctgtatac	cctaattgta	taaccccgga	cggaacggtt	attgtgggta	909840
caaactatgc	catcgggatg	ggtagtggtg	ctgtgaaatg	ggtaaatggc	aagggttctg	909900
aacttcccat	gctccctgac	accctcgatt	ctgtagcatc	ggcagtttct	gcagatggaa	909960
gagtgaattg	agggaataga	aatataaatc	ttggcgcttc	tgttgctgtg	aaatgggagg	910020
acgacgtgat	tacacaactt	ccttctcttc	ctgatgctat	gaatgcttgt	gttaacggaa	910080
tttcttcaga	tgggtctata	attgtaggaa	ccatggtaga	cgtgtcatgg	agaaataaccg	910140
cagtacaatg	gatcggggat	cagctctctg	ttattgggac	tttaggagga	actacttctg	910200
ttgctagtgc	aatctcaaca	gatggcactg	tgattgtagg	agggtctgaa	aatgcagatt	910260
ctcagactca	tgcctatgct	tataaaaacg	gtggtatgag	cgatataggg	accctcggag	910320
gttttttattc	tttagcacat	gcagtatctt	cagatggttc	tgtgattgta	ggagtatcca	910380
cgaactctga	gcatagatat	catgcattcc	aatatgctga	tggacagatg	gtagatttag	910440
gaactttagg	agggcctgaa	tcttatgtct	aagggtgtgc	tggagatgga	aaggtaattg	910500
tgggtagagc	acaagtacca	tctggagatt	ggcatgcgtt	cctatgtcct	ttccaagctc	910560
cgagccctgc	tctgtcccat	gggggaagca	ctgtcgtaac	tagccagaat	ccacgtggaa	910620
tggtagatat	caatgctacg	tactcctctt	tgaaaaatag	ccaacaacaa	ctacaaagat	910680
tgcttatcca	gcatagtgca	aaagttgaaa	gtgtatcctc	aggagcacca	tcttttacaa	910740
gtgtgaaaagg	tgcgatctca	aaacagagcc	ctgcagtgtca	aaatgatgta	cagaaaggga	910800
cgtttttaag	ttaccggttc	caagttcatg	gaaacgtgtca	gaatcagcaa	ttgctcacag	910860
gagcttttat	ggactggaaa	ctcgtctcag	ctcctaaatg	cggttttaaa	gtagctctcc	910920
actatggctc	tcaagatgct	ctcgtagaac	gtgcagctct	tccttacaca	gaacaaggct	910980
taggaagcag	tgtcttgctca	ggttttggag	gacaagttca	aggacgctat	gactttaatt	911040
taggagaaac	tgttggtctg	caacccttta	tgggcattca	agttctccac	ctaagtagag	911100
aagggtattc	tgagaagaat	gttcgatttc	ctgtaagcta	tgattctgta	gcctactcag	911160
cagctactag	ctttatgggt	gcgcatgtat	ttgcctccct	aagccctaaa	atgagtacag	911220
cagcaacttt	agggtgtggag	agagatctga	attcacatat	agatgaattt	aagggtaccg	911280
tctctgctat	gggaaaacttt	gtcttggaat	attctacagt	gagtgtttta	agaccttttg	911340
cttctcttgc	tatgtactat	gacgtaagac	aacagcaact	cgtagcgttg	tcagttagta	911400
tgaatcaaca	acccttaaca	ggcacactaa	gcttagtaag	ccaaagtagc	tataatctta	911460
gcttctaagc	tattgttcaa	taaataatca	gaacatgtgc	agtccatagt	tggaaatgct	911520
gattaagtac	ccaactatgg	actcttcttt	ttagttttta	aaatacacag	atacaacgtg	911580
tagtgccttt	aaaggttcag	agactaataa	aaatattttt	aatttcttct	ggcaattctt	911640
ccgccatata	cttataacta	taagccgttt	aactaagtgt	tgatttttaac	ttggatcaac	911700
gtacttacaa	agtttaggtt	aaatatagat	aagaagataa	aggttctagg	tcatttgacg	911760
ctctgcactc	gttttagagg	agtgtgtgtg	gcagcggccc	tttccaacat	aggatatgag	911820
agtacttctc	aggaatcacc	atatcagaag	tctatagaag	actggaaagg	gtataccttt	911880
acagatcttg	agttactgag	taaggaaggg	tggctctgaag	ctcatgcaat	ttctggaaat	911940
ggcagtagaa	ttgtaggagc	ttcgggagct	ggccaaggta	gtgtgactgc	tgctcatatg	912000
gaaagtcacc	tgataaaaca	tctcggcact	ttagggtggcg	aggcttcata	tgacagaggga	912060
atttcaaacg	atggagaggt	ggctcgttggg	tggctcagata	ctagagaggg	atatactcat	912120
gcctttgtct	tgcacggtag	agatatgaaa	gatctcggta	ctctaggagc	tacctattct	912180
gtagcaaggg	gtgtttcttg	agatggtagt	atcatcgtag	gagtctctgc	aactgtctgt	912240
ggagaggatt	acgggatggc	aagttgggtg	caagtgggaa	aaagggaaaa	tcaaacattt	912300
gaagttggtg	cctcaagggt	tctgggtctg	aggcgaatgc	aatctctgag	gatggtacgg	912360
tgattgtcgg	gagaggggaa	atctctcgca	atcacatcgt	tgtgtgtaaa	tggaaataaaa	912420
atgctgtgta	tagtttgggg	actctcggag	gtagtgtcgc	ttcagcagag	gctatatcgg	912480
caaattgggaa	agtaattgta	ggatgggtcca	cgactaataa	tggtagagact	catgccttta	912540
tgcacaaaaga	tgagacaatg	cacgatctcg	gcactctagg	aggaggtttt	tctgtcggaa	912600
ctggagtttc	tgtctgatggg	agagccatcg	taggattttc	aacagtgaag	accggagaaa	912660
ttcatgcttt	ttactatgca	gaaggagaaa	tggaggattt	aacaactttg	ggaggggaaag	912720
aaagctcgagt	tctcgacata	tctagcgaag	gaaacgatat	cattggctct	ataaaaaactg	912780
acgctggagc	tgaacgcgcc	tatctgttcc	atatacataa	ataaaagcat	cgtagagaaa	912840
agataaacga	agtaaatcgt	aagcttggaa	ttcatgaagt	gattcataat	tccaattttc	912900
atacttggtg	tcttttctct	atgtagataa	agtttaagtgg	tttttgaaat	tatttttggtt	912960
gttagagtc	ctatgaaaaa	gacatgttgc	caaaattaca	gatcgatagg	cggtgtgttc	913020
tctgtgtgtac	ttttcgttct	tacaacacag	acgctgtttg	caggacattt	tattgatatt	913080
ggaacttctg	gattatatct	ttgggctcga	ggtgtatctg	gagatggccg	cggtgtcgta	913140
ggttatgaag	gtggcaatgc	atttaaatat	gttgatgggtg	agaaatttct	gttagaagggt	913200

ttggtccccga	gatccgagggc	cttgggtatttt	aaagcttcttt	atgatgggctc	tgtaattata	913260
ggaatctcgg	atcaagatcc	gtcttgccgc	gctgtgaagt	gggtaaacgg	tgcacttggt	913320
gatcttgga	tattttctga	gggaatgcaa	tcttttgag	aggggtgttc	cagtgatgga	913380
aagacgattg	taggggtgcct	atatagtgat	gatacagaga	caaactttgc	tgtgaagtgg	913440
gatgaaacag	gaatgggtgt	tctccctaac	ttaccagaag	atcgacattc	ttgcgcttgg	913500
gatgcctctg	aagatggctc	tgtgattgta	ggggacgcca	tgggtagcga	ggaaattgcc	913560
aaggcagtg	actggaagga	cgggtgaacaa	catctgcttt	ctaataatccc	aggagctaaa	913620
agatcgtcag	cacatgcagt	ttctaaagat	ggatctttta	tctgtaggcga	gttcatcagt	913680
gaagaaaatg	aagttcatgc	ctttgtttat	cacaacgggtg	ttatcaaaga	tatcgggact	913740
ttagggagag	attactctgt	agcaactgga	gtttctaggg	atggtaagggt	catcgtgggt	913800
cattctacaa	gaacagatgg	tgaataccgt	gcatttaaat	atgtggatgg	aagaatgata	913860
gatttgggga	ctttaggagg	ttcagcatct	tttgcttttg	gtgtttctga	cgatggcaaaa	913920
acaatcgtag	gaaaatttga	aacagagcta	ggagaatgtc	atgcctttat	ctaccttgat	913980
gattaggggt	cttatggaag	tgcgtcctata	ctcagaaaat	tgctaacaca	tcaacgtaga	914040
taaatgtaga	taactgacga	ttcttattct	gattggactc	caacaataat	ttctccatca	914100
atagaaacag	cgtttgaca	ggcttctttc	cgctataact	ctcctaagtc	gatcattctt	914160
ccaccgacat	atttaaaggc	atgcaatttc	ccatttgctg	ttgtggacat	accgacaata	914220
acttttccag	ttgcagagac	tcccttagct	gcagaataag	atcctccgag	gggtgccgagg	914280
tctgacatga	cgccattctt	atgacagaaa	gcattggacct	ctccataata	tgtttcggat	914340
ctccctacaa	tgaccttgcc	attattggat	acagcttttg	caatggcaga	atagcctcct	914400
aaagttccta	gatgtgtaat	agtgttccct	tcccacttta	cagcataaag	aattccagag	914460
gcgtcttgta	cagaccctac	aattatagat	ccattggcag	atacagaatt	cgctacagat	914520
ttgacagccc	agcctactgg	taacacctga	gocctcgtgc	ccgtccactt	cacagcgaaa	914580
gttcgcgacc	aagcatcctt	agcactccct	acaataacag	agccatcaga	agaaattcca	914640
tacgctttag	attgcactgc	ccatgtggaa	gggagcaaat	acatttcatt	gtttttccat	914700
gtgactgcga	aactttgaga	aagctcattc	tgcacaatcc	ccgcgattat	agacccatca	914760
gaggagattc	ctgttgcttt	tgattttttt	acccatgagc	tggtagggag	ttctttgggtc	914820
ccccaataat	tccatcttac	tgcgtatgtt	cgagaccaag	tgtcttttat	aaagccgaca	914880
gttgtagcac	cagttcctga	aacagctttt	gcagaggctt	ttttatttga	taatcttgag	914940
agagttgtct	ttccccaatg	atcccatttt	actgcggatg	aagaatggaa	gtcatcttct	915000
ggtttgtctg	taattacata	gcaataacca	gatagagaat	ataatgaaaa	taggaccatc	915060
cataagctac	tctgagatag	catagaacgt	aaaatttggt	ttatagctgc	catattttcc	915120
tctcgthttc	aaggtttgca	aatgaatttt	tttttaatcc	aagaaactat	accaagatat	915180
caaaagagct	acaagcaaga	tcctaggagc	ggttttttta	tgaaaataga	ataagaaagg	915240
atztatagac	gtgctgatga	agatgtcttg	aaagagggaa	ataaagaaca	cattgcagat	915300
cagaaagata	aggcccatag	atctgcgatg	tattcttgat	ttggagataa	gatagaaata	915360
gagaaaatcc	ctctattcct	cagaatcctc	gtaagaaaat	acattagaat	ctgtgaaaat	915420
tgcttcggat	ccaagctctt	cttcaatttc	catgagtcta	ttgtattttg	caacacgctc	915480
agaacgtgat	aaagagcctg	ttttgatttg	accagcgttg	aaggcaacag	caagactctgc	915540
aatcgtagtg	ctcgtagttt	ctcctgagcg	atgagaaata	attgtagtat	agccagccat	915600
ttgcgcaact	tgatagcata	cactgtttca	gtaagcgtcc	ctatctgatt	tggttttaatc	915660
aacacagagt	tgcgtaatcc	attgctaata	ccctctaata	ttaattccgg	atttgtaaca	915720
aataggtcat	caccacacat	ctgtactttt	tctccaagaa	cttcagttaa	caaggccac	915780
ccgtcatagt	cttcttcagc	aagaccatct	tctatggagt	ctataggata	gcgatcacat	915840
aaattagaaa	ggattgcgat	ttgctcttca	tagtgccctc	catcatacgt	gcctgttttt	915900
acgttataga	atgaggatgc	tgcgcagtct	aaggctagcg	atatactctt	tcctggagta	915960
aagcctgctt	tttcaatagc	cagcaatagg	agctctagag	cttcttcatt	agaagcaaga	916020
ttcggggcga	agcctccttc	gtcaccact	ccagtagata	agcctctttc	atggagtaat	916080
ttttcaaaag	tatgaaaaaac	gtcagcaccc	atgttgacag	cttctttgat	ggaagaggct	916140
ccaataggac	ggatcataaa	ttcttggaac	cccaagccgt	tatcggcag	catgcctcca	916200
ttgatcagat	tcatcatagg	acagggaaga	ctgcaggcaa	aacaccctcc	taaataacga	916260
tacagaggtc	tgcgtagtgt	tgctgctgct	gcatgtgctg	tagctagaga	gactcctaaa	916320
atagcattgg	cccctagagt	ttctttgttc	ggagagccgt	cagaatccat	catcagagaa	916380
tcaattaagg	attgctcata	aacactacat	cccttgacga	ggggaaaaag	aatttctttt	916440
acgtttttta	cagcttgcaa	aacccctttg	ccttgataac	gaggagaatc	tgatatcaga	916500
aactctaagg	cttctttttt	ccctgtggat	gctcctgaag	gaacccgagc	ttctccaaca	916560
gaacctgtgc	tagtggttac	tttaacatgt	aaagtgggat	acccgcgaga	atccaagatt	916620
tccttagcct	ggatatcggc	aatgacagct	tcaaacataa	tttttatctc	ttttctttta	916680
gactttgcta	agagctcaat	agcatgtgaa	cctactgata	ctgctctgct	tcttgaactg	916740
tagatatgta	ttctaaaata	cgtagctacg	gattcacatc	aaactcataa	tgacaaaaat	916800
agataaattt	ggggaggaat	attcttgaat	atcgagatca	gaaattctct	tagaacaat	916860
agagaagctg	ttctttgcaa	gcttgcatgt	catcgcggtg	tttcgagct	tcttggaatc	916920
gaaattcttt	agcagcacgt	tgcatgagag	cttcgtattt	cttaatttgc	tcttcaagat	916980
cttcttttaga	tagggggcggt	tgagattcct	tggggagactc	cgagtcttta	gagggtttgta	917040



gaataggatt	ggcaaaaata	gcttttataa	tgggccttagg	aacaatat	tgctctttat	917100
tgtaatctaa	ctgtatctga	cgccggcggt	cggtctctcg	aagagtctcc	tctatagaac	917160
gggttttttg	atcagcatag	aaaatgactt	taccattgat	attcctagca	gctcttccac	917220
aaaactgaat	cagagatgac	gtgcttctta	aaaagccctc	tttctcagca	tctaagatcg	917280
caactaaaga	gacctcgga	agatcgagtc	cttcacgtag	gagattgact	ccaatcaata	917340
cgtcaataac	gcccagagcg	aggtctgtaa	ggatttgctg	gcgttctgca	gtttctattc	917400
cagaatgcaa	gtatgccgca	gggatctcta	attctgaaag	aaaaccgccc	atatcttcgg	917460
caagtttctt	tggtatagaa	atcactagga	tttttctatg	tttctgagac	agccgcaaac	917520
gaatttcttc	aagaagatca	tccacttgtc	ctgtagcagg	acggatttca	ggcataggat	917580
cggggatccc	cgtcggggcg	atgatttggt	gtacaatatg	acctgagctc	tcttggactt	917640
ccgtatcacc	tggtgttgca	gagacataga	tgactttacg	aaagtacttc	tggtcttctt	917700
caaaagggtta	gcgggcgggt	atcgaaggcc	tgaggggaaa	cggaatccat	attctactaa	917760
agattgcttc	cgagattggt	ctccacgata	catagcacgt	atttgaggta	gtgtttgatg	917820
agactcatcg	ataataagga	gaaagtcctc	aggaaaataa	tctaagaggc	acgtaggcgg	917880
tgctcctggg	ggcgccccctg	taaaatgccg	tgaatagttt	tctatgccct	tgcagaatcc	917940
gatttctctg	atcatctcaa	tgctcatgag	cgtacgatgg	aaaatgcggt	ccttttctat	918000
aggacggctg	tcaaaaaagg	ccatgcgctc	ttctaactcc	tcctgaatgg	ttcggatcgc	918060
ttgctcgcg	attgcctcag	gaatgacgta	atgagatcca	ggatataaag	tagccgaagg	918120
gacacttttc	ttgggaatca	tagtgagggg	atcgctgtat	tctatggagg	taaggggtgc	918180
atttagaaat	tctaactctta	gggcaagttc	actttcgtat	gcagggaaaa	tatcgattac	918240
actcccacgc	tctcgaaatg	cacttctctg	tggtgatggg	gatgcttgat	agtgcatttt	918300
aacaagctga	gctgtcagga	tattcctagg	gtactctttc	cctacctcta	agactaacgc	918360
catggatgta	tagtttttcag	gagaaccaat	accataaatg	caagatactg	aggaaacgat	918420
taaagtgtct	cggcgctcta	aaatagaccg	tggtgctgat	aaacgtaact	tatcgatttc	918480
atcattgata	aggaggcttt	tttctatata	ggtatcacta	cggtgcaaat	aggcctcagg	918540
ttgatagtaa	tcgtagtaag	agatgaaata	ctcaacggca	ttattaggga	aaaattcacg	918600
aaattcttga	tacagctgag	cagctagcgt	ttgtttatgg	gctaaaacca	gggtaggagg	918660
atttacgttg	gcaacaacat	tcgcaatagt	gaatgtcttc	ccagaacctg	tagttccaag	918720
aagtacttgt	gattttacct	gattacgcac	acccgcagac	agccgagcaa	tcgcctctgg	918780
ctggctcgccg	caaggagcaa	aaggagcatg	aagttggaat	gtcatagtaa	aaattattta	918840
agcaatgagc	gccatttatg	gctaaaccca	aatttgcata	gaacttcttc	catagtgaat	918900
ttggctactc	cacgcatttt	atgctgtcca	tcctctaaga	cgttttgtta	tgccagaggc	918960
ttggatagaa	attctgagcg	tctttctttt	atgggtttta	aaaagtgaat	cagctcttca	919020
gcaaggcggtg	cttttacttc	gatgtcttta	atgcaacctt	gacgatagcg	tgctttaaac	919080
tcttcaacct	catctttatg	gggattgaag	atgtcatgat	aaataaagag	gggatttctt	919140
tcaactcgac	ctgggtgtgt	tgctcgaatc	cggttgggat	ccgtgtacat	cttacggact	919200
ttctcagtaa	ttgtagcgtc	gctatcgga	agatagatcg	cgttgttcgc	ggacttactc	919260
attttccctt	gcccgtcaat	tcctacaaga	gaggtaagct	cgcttctgtg	tacctcgggc	919320
tctggaaata	cctgcccata	cagacgggtg	aaatttctag	cgatatcccc	ggtgagctcc	919380
acatgcgctt	cattgtcttt	ccctacaggg	acaaactgtg	ctttcgctag	aagaatatcc	919440
gcacttttga	aaatagggtta	cccaataaga	ccataagaaa	gacttccctc	ctcgattgag	919500
gcatttctggg	ccatatcttt	gaggctggga	atgccatca	ctctattgat	tgagatgagc	919560
atcgaaaata	ggagatgtaa	ctcgtagatc	tcagggatcg	cagattgtag	gtaaattata	919620
gatttctgtg	gatcaatccc	tacacttagc	caatcagcaa	gaacttcata	gatgtgggtta	919680
tctacatcta	aaacctcttc	cttgccgatt	tttgtagtta	gggtgtggag	atcggaata	919740
ataaaaaagc	aatcgctactc	agggctattt	tgaagtctta	atcggttttt	tatagaacca	919800
acccaatgcc	ctaaatggag	tttccctgtg	ggacgatccc	cggttaagtac	gcgctttttt	919860
ttattcatga	cgtccgctat	tgaagtgcct	tagttagctc	atcaaagtga	ttttttaatg	919920
atgtaatttc	ttcttgaatt	tcctgaagat	ttttctctcc	aacaggattc	ttttgtgctt	919980
ctaaaagtct	tgctagttaa	tgacgaatca	agtggcagg	attctgcaca	tcagtcatca	920040
ataagaactc	ttgaccatcg	acacgagcta	atcgatttaa	gaaaatacaa	cgctcttggt	920100
gggtaagcat	atctgaagtg	atgaaattaa	taaattcccc	gcgttcatgg	atgtcttttag	920160
cgacacgaat	aggcatcata	aattcggcaa	ttaaactatg	cgcagcttgc	ttttgctgag	920220
gagcaagttc	ttgtgttaac	ttgccattaa	ttaacatctc	gaaaaagaaa	tttgcaatct	920280
cttgctgacc	attggcacag	ttgaaaacga	cattttgaaa	ttctcgaaa	gttgtgtaac	920340
caataggagt	agcaaaaaatt	cttttttaaat	ttccttcaag	aaggagaaaa	acattgtctt	920400
caagctctaa	gttttttctc	tttgctgcca	taaatcatac	ctttgtatcg	ggaaagaggt	920460
tacttttaac	tttttctagt	ttttttatca	atttttccaa	aatgatctgc	tcatcagaag	920520
agagactcgt	acacttagtt	agtatttgag	agcctttggg	aagcatagca	agagcctgct	920580
ttactgggtga	tgtttttcta	caatctgtct	caactaaggg	gaactctttg	cgaatgcgat	920640
ctaaaagctc	gctttttctt	tccctcgggt	agtttcggat	aatctcttct	tttttttctt	920700
ggggcccttg	acgagatgct	aaagtataga	cagcttgtct	aggcatcttt	tccatctcta	920760
tttttaaagg	ttcaggaaga	agggtaaaga	gttcgtagta	aactaaaaaa	ttataggggg	920820
tttgtctatt	cccataggtt	aagagaagcc	aagaagaaaa	agcaccttca	cgatagcttt	920880



tcagtaaate	acggactttt	gtgatgcgct	ccccatgtaa	aaggacagat	tgatgatgga	920940
tttgcttcac	ttcagcagaa	agagtacaga	gctgggtaag	atcagggttct	tcaatctgtt	921000
ctcgaaagtt	gtagtgtgta	agcagatgac	ggagttgctc	tttttcttta	gaggaaagcg	921060
taggattgga	aaggcgaacg	gcaagaggag	agggatctcc	ttccatgcgt	ttacgggcaa	921120
gcgcttccat	tttagtgga	gtattctttt	tgaagcgact	ttctaagagc	gttttttagat	921180
tccccataga	gctaaatatc	tcttaataaaa	attagcaatt	ctttagttag	gttgaaataa	921240
tcttcagagg	cacgtgcact	gggagatgta	gcaaagacag	gtttgccatg	aatcgtagct	921300
tctgaaacag	tgatgtctct	acgtattttc	gtattcaata	acttcccggg	gaaagttttg	921360
tgaatcagct	cagcaaatgc	ggaattgttt	ttccctctgc	aattccaaaa	ggataaggca	921420
actcctaaaa	tcgttagggg	atgtcgtgct	gaaattcctt	ggatgaaacc	agccagacgt	921480
tctagacctt	tgacactata	aaattctggg	gtagcgcaaa	taagcgcata	atcagcagca	921540
attagggcag	attctgtaag	ccaacaaagt	gaaggaggag	tatcaataat	cacatagtcg	921600
tacttgctct	ggacagaacc	aagtacatat	ttcagttctt	catgagaata	gcgatccgca	921660
gcaagatttc	ctgacacttc	aatacgctct	aaccagggtg	cagcaggaat	taaatccagc	921720
tgagtgtctt	ggatgggtcg	gatgacttct	tgaatttctt	tttcgccttg	taacacaaca	921780
gcaaggctgt	catagcaatc	aggatcctaag	cctaattccag	aggtgagatt	tgcttgagcg	921840
tcaaaataca	taagcaatac	cctggcttga	tggtactggg	caagagccgc	accaagatga	921900
agggttgttg	atgtttttgc	tggtccacct	ttaaagctgt	ttacagcgat	ggctcttcatt	921960
cttgatgcgt	atcctcaaaa	atccttagca	actacaataa	tgtagttaa	cttaaagagt	922020
tcttttcttc	aagtatagtg	tttaagaatc	tctctacaga	gacatcatta	atcactcggt	922080
tatctcgggt	gcgtactgcg	agtacatttt	cattaatttc	atgatctcca	agagtgtatca	922140
tgtaattgac	ctgcatgttt	tgggcattgc	gaatcttttt	acttacagac	tcactagaat	922200
cgtctaagggt	gacgactaag	cctaaacggt	tccacgcttc	ctcgagctct	ttcgctctag	922260
gaatatggcg	atcagcaact	gtgatgatac	gcacttgctc	aggacttaac	cataaggggga	922320
atcttctctt	gaagttctca	atcagaattc	ctaaaaagcg	ttctatagaa	ccaaaaagag	922380
cccgatgtaa	catcacagga	acactcttag	ttccttgagc	tgtgggtgat	tctaattcga	922440
aacgctctgg	aaggaacatg	tctaactgga	tggttccaca	ttgccatgtt	ctttgaaatcg	922500
catctttaac	atggatatca	attttaggac	cgtaaaaagc	accttctcct	ggacgaacaa	922560
tgaagggtgt	cccggactga	actaatgctc	gatttaaggc	atctgttgct	agctcccata	922620
gagaatcatc	cccaatcgta	tctttttctg	gacgtgtgga	gagttccagg	tgatactcta	922680
atccaaatgt	accgtacagt	gtagaaacta	actgaagaat	attcaaagtt	tcctcttcga	922740
cttgctctgg	agtaagaaat	acatgagcat	catcttggtg	gaacgcacgg	acacgcatta	922800
accctgaaag	ggctcccga	gcttcttgac	gatggacatg	accaacttct	gctacacgta	922860
gagggaaactc	cttataacta	tgcaagcggg	ttttataata	gagcatgcat	cctgggcagt	922920
tcatgggctt	aatggcataa	tcttcatcgt	cgatttgtag	tgtgtacatg	tttgcttttat	922980
aattgtccca	gtggcctgaa	acttcccata	actgacgatt	catcaactgt	ggcgttagga	923040
tttccttata	accgcgagct	gtgtgcagct	gcttccaata	acgaatcaat	gcatcccaaa	923100
caatcatacc	gcgaggatgg	aagaagggga	ttccaggaga	actttcttgc	tgagaaaaata	923160
gatctaactt	ggcccccaaa	acacgggtgg	cccgtttttt	tgcttctcca	atttgctcta	923220
aatgtgctcg	aagtttctta	gatgtaggaa	acgaagttcc	gtaaatacgt	actaaagatt	923280
ctcgagaagg	atccctctgc	caataagctg	cagatgtgcg	taagacttta	aacgctttta	923340
catgagctgt	agaggggaagg	tgaggacctc	ggcaaagatc	aaaaaactcc	ccttggctat	923400
aggcagaaat	ttcttcattt	tcaggaagct	cacgaatcaa	ctctgtctta	aatggattct	923460
gtgggaattg	tgctaaagct	tgttgcttat	cgccataagt	aaagcgagaa	atcgcaagct	923520
tttcatcaac	aatttgtttt	actgtatctt	caattaacgg	gaaatcactt	tcgctaattg	923580
aaagattggc	aaaatcatag	taaaagccat	ggctgatgac	agggccgatt	tgaggaattg	923640
catcaggcca	taaacgcaat	acggcttggg	ctagaagatg	ggcagaagta	tgaagaaaaa	923700
tttctcgtct	tcgggatctt	cggaagtcag	aaataactaag	gtgtcgcctt	cgtttaggtg	923760
ggtggaaaga	tctctagggc	gttcgttaat	gagaacacca	atgaattgat	gagaattttt	923820
taattgttta	gcgagttccg	ctgctgtagt	accttcgagt	acttcataat	ttttttgatc	923880
acaagttact	tgaatcatct	tgttccacgc	ctccatgtta	gggggacttt	cgttgttagc	923940
attttagtgt	tttttttgat	caaagcaaga	agcttttttt	tataaaaaaa	cttttatatt	924000
ttaatacaag	ttccaaagcg	ccaggagatt	tagattggaa	ctaataaaaa	catcttttat	924060
actatctgct	taataaacat	tacaaaactgg	tttgcatatg	tcgctttttc	tagtttttct	924120
tacggcattt	atttggctct	cttctctcgc	tcttagcaaa	ctagttatga	atgcttcagc	924180
tccgatattt	gctacaggag	ctcgcatggt	aatcgctggt	gcgatcttgg	ctcttgctgc	924240
atggtttcga	ggcggttttg	ttggatatatc	gaagaaaata	ttcttatata	tcgtcctggt	924300
agctttaaca	ggtttctatc	ttaccaatat	ttttgagttc	ataggattac	aaagtctaag	924360
ttcatctaag	acatgcttta	tttatggact	ctctcctcta	atgtcagcac	ttttttccta	924420
tattcagctg	aaagagaaaag	tgactctcaa	aaaggtttta	ggattatccc	taggcttggg	924480
gagctatatt	tgttacttaa	cctttgggtg	gggaggagac	gattctcagc	cttggacctg	924540
gcaaataagg	cttctctgag	ttctaattct	aggggcagca	agtttagctt	cttttggctg	924600
gactcttctt	agacaaatcg	aaaagcagtc	tacgttatcg	gtcacagcaa	ttaatgcata	924660
cgcgatgtta	atagccggaa	tgctatcaat	catgcactct	gcagtcgtgg	aaccttggcg	924720

tcctttacca	gtgcaagata	tatcgcagtt	tctatacgcg	actttggctc	tagtggtaat	924780
ttctaatttg	atttgctaca	acctgtacgc	caaattatta	agaaagtatt	cttccacttt	924840
cctttcattt	tgtaaccttg	tcatgccact	ttattcaggc	ttttatgggt	ggatattgct	924900
tggggagaag	ggagtctcct	tgggcttggt	gttagctgta	gccttcatgg	tggcgggctg	924960
tcgtctcatc	taccatgaag	agttccgcga	gggctacatt	gtttcttaaa	gtaaagccgc	925020
tttacatgaa	aaagctcggt	atcaaaccga	gctttttttg	atcagatctc	taattgtgat	925080
taattaaaga	tagcagatgt	tgtttgtgtt	tgagagtcgg	caatattttg	tagtgtttgt	925140
aaggcagtat	taaatgattg	catagcttgc	tcttgtaatt	gtcctgcttg	tcctgcttgc	925200
tgaccataaa	ccgaagacat	ttgtttcaag	acttctgctt	gagcctctgc	ttgtcctgct	925260
aaccgctgat	gatgggagac	ttctattcct	gtctgccccg	cagaaagacc	ttcaacagcc	925320
gctgtgagtc	catgcattaa	ttgactcatt	tgcatagagg	aagaaagagc	atttcctgca	925380
aatgatgcaa	cacgcgctcc	ctgagtttca	ctacgttcat	acctctggag	actttttcag	925440
accagttagg	tttattttaag	acttcgccaa	agagtccctc	tgaagctttc	gaagctccat	925500
cagaggccat	ttttgaagct	gctgcggcca	tatcatcggt	taggttcgct	gcagcttttg	925560
tggctgctga	ccccgcagaa	ctcgctgctg	ttgttgccgc	cttggcagtc	gaagccatag	925620
tctgttgaac	agaagaactt	gcagaagtta	aagctttgga	agcagcacct	ccagcagctg	925680
aggcacctgt	ttctttggca	aaggaaagcag	atttttaaagc	cgaggtagct	cctttttgcag	925740
cagagaaaaat	acccgctcct	acagaaactg	taaatcctac	aatgtttaca	ataccactaa	925800
tcaaggactg	ttttgcctgt	gcttctgtag	ctgatgcttg	atggttcgct	tgccttttaa	925860
tagcctctcc	aatagcagga	gcggattcga	cttgtgaccg	gatcgcttgg	ttttgtgatt	925920
ggaatgaagc	tttccaagac	tctccggcag	cattggccat	caaggtcata	actaaaccga	925980
ggagtgtctaa	cgtacccatg	ccttttttaa	gtacaatacc	attgatggtc	tgtgcctcag	926040
gagtaggaag	gctgggtgag	tcataattat	tttgccttaa	tccttagga	ccttgtagcg	926100
cttgtgcgct	tgcagtttta	cttgcgcttg	ctaccgaagt	taggatttta	gatttcccag	926160
attttctcgt	tttttctccc	ttactacttt	tagtagttga	agatgtagct	tctttttttc	926220
ctgtactttg	cgctgaagcg	tcttgaatga	gaccccaaaa	gcctccagca	gcgacttctg	926280
cttgagcccc	ttgctttgtt	acattcttag	tatcgtgacc	gctctgagca	tttctgctt	926340
tttgagagga	ttgtgccaat	tgcgcagcca	atgtgggatc	ctgacttgaa	cttccactaa	926400
ctcctgatgt	catagcaata	catgctcctt	taaaaattat	tggttttatg	ctgcgccacg	926460
atggctccgc	tgattgcggc	atacgcttta	aggatttgag	cgcccagctt	ggtagctttt	926520
tgagtcattt	cattagactc	gcctgtttgt	tttgaggcaa	ttttacttgc	ctgttgccaa	926580
aattgagtga	acatagaaat	catatcagcc	gcagcctgca	gttttccgac	ttcttccgca	926640
aattgagcga	cgttttgttg	catctccgag	agctgcattt	gcataatccc	tttaccgaga	926700
gcaggcgccg	caactacaac	cccaacccca	accgtgaccc	atttactggg	aagagacgag	926760
atgactttcg	agagcttggg	gaagttcttc	gcaatcattt	gagttccctt	agcgaaaacc	926820
ttagagattc	ctttagaaat	ggctttggca	atcgctttga	ctaaagtttt	gataaatgct	926880
tttattccag	atttgacagc	cgctttttata	gccgcgggtga	tcgcttgctt	gacagctgtg	926940
ataacagctt	gtttcacccg	ttggacaaca	gcttgaactg	taatttgtgt	tgctaccgtg	927000
ggtgcggcag	cagctcctgc	tgcacctcca	gctgcccgtg	cacctacagc	agctcccgca	927060
gcgagtcag	cgagtcagc	tccgcatgta	aaaatagcag	caacaataga	aataactgta	927120
atggcaacag	aaaccgcat	catcacagta	ttgacagtat	ccattgttcc	ttcgagatct	927180
ttagacttct	gttcggcagc	cttcatctct	tgggtattctt	ctcgttcttt	atcgattttt	927240
atcgcttgct	tttctagacc	tagtttattt	gtttgggtctg	cttgtgcttg	tgtacttgca	927300
tagttagata	aggcagattt	tgtggcttct	cccaatgtct	gaattgcttt	agcaagcgcg	927360
agtccgattt	cgataacctc	tgatcttggg	gtcaccccg	gcttggggag	ctcaggtgtt	927420
tccaattttg	cggaacccga	acttttccct	gagagggcag	caacaacaac	cgcttcgact	927480
tctttcattt	gcgcggcact	gaggctttga	agtgactcta	aggtagactc	catacttttg	927540
ctcgcctctt	caatagaggt	ctgcatagca	atttttgttg	cagtatttga	tgctgtagta	927600
gcagccgctc	ctgatactcc	agtatcagca	cctgcctttt	gactttctga	ggattctttc	927660
ccagcagcaa	ctccctgttg	tggagctgtt	tctgtttttg	tagtcgagga	agttttgtct	927720
tttccagaag	caccagcaat	agtggcatcg	ctttccatct	cagtgttttt	accctgacgt	927780
gtttgctgta	tttgcttcgt	ttcgttgcca	gacagcttat	cttgttgggg	cacgccttgg	927840
ggtgtcgatg	tcagaacttg	agacatgata	tttttttgat	tgctcaggtcc	tgaagaagat	927900
gaaatagaca	tgtttgtatc	ctaaggggtt	tgattctgca	aagggtttta	ctcagcgctt	927960
ttaaccattt	gtttattaac	tacagtgggt	aggtttttta	atccgtgtac	tactgaagat	928020
aactcctttg	cgaagtggc	atcttcttgg	gcagaagggga	ataatccttg	agttaactct	928080
tcgagatgta	aagattctag	agttccagaa	agagccgcga	tgatgctatt	aatctgattc	928140
ttgtcagtaa	gactggcaaa	tgtctgagct	aagggaagct	ctttatatag	atcagatacc	928200
gcaagttcta	actgctggat	agcagcttct	tgagatttct	ctggtacgcg	ctttacagga	928260
gctgccttag	actgaactgc	cttttttgggt	ttcttgggct	ttttattcat	gattttctct	928320
tagaatctta	ctaacgtttc	tttccgcttt	tcttatttgt	agttgttttg	ctttttcccg	928380
caggtttttt	tgtcggtgct	ttcttagttt	ctccagccat	ctgcttctca	atagatgtt	928440
tcataatttg	gcaacgttct	tttaagattt	tgaattctgg	gttattccca	cagatatcca	928500
tgggtgacgtc	taagaaattg	ttagatttct	cgggttgctg	tagcttcaat	aagctatcag	928560

caatgtagta	aggaggaatt	gggttgtcag	gttgagcatc	gaaagcaagg	aaaaatccaa	928620
aagccgcttc	attatataaa	tgcaattggt	ggtagcagga	gcttaaccct	aacatatact	928680
tgtagttctg	agggtgtgct	gctgccaata	actggaagag	tcctacagct	tcgttgtact	928740
tcccttgaga	atagaatgta	taagctacag	tatagatctc	ctctaagaga	tagtccgaga	928800
gacctagaat	ctgttgtagg	tctagtccat	tgctaagacc	ttcgaagata	ttgcctaaag	928860
cttttttaat	ttcttcttcc	gtaggtacgg	gatggacttg	ttctaagtca	tcagcctttg	928920
ctttcttttg	agcagccagc	tctgctagac	ggttcgcgtt	tttttattga	aagaggctga	928980
agggttttga	ggttgattgg	cattacgagg	agagggcttg	ctcatcgatc	taattcctaa	929040
aataaaatta	ttttgtattt	atgaatcaat	tttaaaatta	atctttttct	aaaaacaagc	929100
ctattgataa	taatatTTTT	attattttta	ttaatctttt	tctaaccctg	tcatttttta	929160
ggaaaaatgg	aaattagacg	gaagctttct	tgacattagc	tttaggggat	tttaatttgc	929220
tggtctcgga	atttaacgaa	ggcacctatg	tctacaagaa	ggcctattca	gttactttgat	929280
cccctgacca	tcaatcaaat	tgctgctggt	gaggtcattg	aaaactccgt	ttctgttgtt	929340
aaagaactga	ttgagaattc	cttagatgct	ggcgccgatg	aaatagaaat	cgaaacttta	929400
ggagggggag	aaggcgcaat	cattatcaga	gataattggt	gtggcttcag	agccgaagac	929460
atccccattg	ccctccaacg	tcacgccact	tcaaaaataa	gagaattctc	tgatattttt	929520
tctttaaata	gctttggctt	tcgaggcgag	gctctaccct	ccattgcctc	gatttctaaa	929580
atggaaatac	aatcttccat	tgaggggggac	gaggggtgtac	gtaccgtaat	tcattggggga	929640
gacatcgttt	cttgtgagcc	ctgtgctcgg	caactaggaa	ccacagtgat	tgtgaactcc	929700
ctgttttata	atgttcctgt	gcgtcgtgga	ttccaaaaga	gcatgcaatc	ggatcgctta	929760
gggattcgca	agctgataga	aaatcggatt	ttatccacag	caaacatagg	gtggctctgg	929820
attagcgagg	gacatcatga	aattcagatt	gctaagcagc	aaggatttca	agaaagagtc	929880
gcctatgtga	tgggagacca	cttcatgcag	gatgccctca	ccatagataa	agaagcaaat	929940
gggtgccgta	ttgtaggggt	gttaggggtct	cccagcttcc	accgtcccac	acgtcaaggga	930000
cagaaaatct	ttattaacga	tcgccctata	gagtccttat	ttatttctaa	gaagggtggg	930060
gacgcctatg	ccttgcttct	gcctctacac	aggtatcctg	tttttgtgct	gaagctctat	930120
cttccctcgt	catgggtgtga	ttttaatgtc	caccacaaaa	aaatagaggc	tcgaattctt	930180
aaggaagaac	ttgtttggaga	ttgtatcaaa	gaagctatcg	tagagactct	agcatgtcct	930240
cctggcatct	tatgtcgtac	gcacaaagaa	atagaagaat	ctgattcggg	gcccttacct	930300
atgtttcgta	tggttgaaac	aagcgatgtg	caagaagaag	agagtgtaga	gtttgatcaa	930360
aatctttttg	catatagtct	agaagatggt	tccttagaga	aacaagaata	tacatctaga	930420
ggacctaaag	cccaaatgga	ttggatata	tctagcgacg	ttcgtttttt	aacttcttta	930480
ggctcgtgtg	tcctggctga	ggatcttgag	gggtgtgcaca	ttattttttac	agctgcagcg	930540
cgaaagcacc	tgttttttct	gtcctttgatg	caagagaatt	ctcgcgatga	tcaatcacaa	930600
gcattactga	ttcctctacg	ccttcagggtg	actcctgagg	aggctttttt	cttctctcat	930660
cacggaagaa	cgttatgcga	cttaggaata	gaaatatcac	aggtaggacc	ttgtgttttc	930720
tctattgaaa	gtacccccac	tgctattggt	gaagaagagc	taaaagaatg	gttatttgcta	930780
ttggcagcaa	ggggctctac	tgatataaac	tcagaggctt	taacagcatt	gatgaaagaa	930840
actttgacgc	aggcaacggt	ttctaatacat	cagcatgttt	ttgatgtttc	ctggctcaaa	930900
ttgcttttga	gtgtagggaa	acctgaaaaa	ggatttgacg	gtgcacgaat	tcgtcgggta	930960
atttttagact	ctgattttat	ggaaggataa	tcatatgtca	cacgatcgta	ttttacgtgc	931020
tcaaagagcc	ctctcagaac	ataatcttga	tgctattctt	gtggaaaaaa	gcgaagatct	931080
tgcttatttc	ctgcatgatg	aagcgattgc	agggatctta	ttgatagggc	agcaagaagt	931140
gatgttcttt	gtctacagaa	tggataagga	cctctattct	catatccaac	gtgtgccttt	931200
gacttttctc	actcaggatg	ttgttgcaga	cttatcgctc	tacgtacaaa	aacagaggta	931260
tcagaaaata	ggatttgata	gtgcctcaac	agtgtatcac	aagtttgcac	agaggcaagt	931320
acttccctgt	ctttgggagc	cttttagagt	cttcacagag	aaaattcgta	gtataaaatc	931380
tgaagaagaa	attagacgca	tgcaagaagc	tgacgctttg	ggatccgcag	gatattgatta	931440
cgtattgacg	ttacttcgag	agggaaatcac	agagaaagag	gtcgtgagac	agctgcgagc	931500
tttctgggct	gaggcaggag	ccgaaggacc	ttcttttctc	cccatatttg	cttttgaggga	931560
gcattcagcg	tttccacact	cgatccctac	agaccgtcct	ttaaagaaag	gagatattgt	931620
tcttattgat	attggagttc	ttctgaacgg	gtattgttct	gatattgacc	ggatgacggc	931680
attaggaact	ccgcattccta	agcttttggga	aagctatcct	gtgggtgtgg	aagctcaaaa	931740
gcgcgccatg	gctcttttga	aagaaggagt	gctttggggga	gacattgatg	cagaagctgt	931800
gcgtgtactg	cgagagcatc	acctggatac	ttatttttatc	catggaatag	gacacggggg	931860
ggggagacat	attcatgagt	accttgttct	tccgcggggga	agtcagggtga	aactggaatc	931920
tggtcatgacc	attactgtgg	agccaggggt	ctatttttctc	gggattgggtg	ggattcgcac	931980
cgaggacacc	ctatgtatag	ataaaaaata	aaatttttagt	ttgactgcac	gtcctgtaat	932040
ctcagagtta	gtttgtttat	aaattaaatt	ggatttagtt	tttaaattta	aattgaattt	932100
aatttgtttt	tataaattga	ttttttttgt	tttttaagtt	atcttataac	tttattttta	932160
acctgcccc	cactatgtac	cagcttcttt	cgatagggtta	tagttttgtg	agtttcatcg	932220
ctctgctttg	gatgctgtgt	tattcacccga	actatgtaac	agattttatat	aggatttctt	932280
tgagtgccga	ggaaagctta	gggggggattc	gagcgtttcc	tcaggcagag	agcctcctgg	932340
gcgagagcctg	tgcttttaaat	tttccagatc	tagaagagag	attgcctgat	ttaaggaaaag	932400

agctgctttt	tctgggcagt	aacgatagac	cagacgcttg	tggtgggaag	ttttcgctac	932460
aactagcctc	ttcaaaagag	tgctacatcg	cggctcttaa	ggagagagtc	tatttgaacg	932520
tcaccaactc	ttctcgaggc	cctgtgtatt	cattcagccc	taaaggggta	cccacagagt	932580
tgtggattga	gtgcttttct	gtgagcgtgg	atggtagagt	agaagttaag	gtgcgcctcc	932640
aaggttttaca	taaggagtta	atttcgaagc	cgcgagattg	tgaaacctta	tttttaaacc	932700
ctccagctaa	taaactagat	tgctgggaga	ttgcgggatt	tagagtagat	gcaagctttc	932760
ctgtaaaaca	aaagatacgt	cgtatcggtg	tggataagtt	tctcttgatg	catgggggag	932820
ctgagtacgc	ggataaggcg	acaaaagaac	gtgtcgattt	tggttctctc	gatgaggaga	932880
attatagtcg	gtaccttgct	ggtggagatg	ttctcctttg	ggatggcaac	tgctggcaga	932940
cctgcggaga	gtttcaagga	gcgagctcgc	gagcgctctc	ttttgagggtg	aagaggatcg	933000
acgataaggt	catgattgcg	gatctatgga	atgtcggggg	tacgcaacgt	cagacgataa	933060
gtcttgtgaa	aggggtgcct	tctcctatcg	aaattaacga	agtgatacgt	gaaatcgagt	933120
tcactgggat	gcgctcatgg	tcaaagccta	tcgttttggg	agggggacaa	aggctgattc	933180
tttctcccga	cgattggata	ctaagaactg	ctaagggttg	ggagaaaactt	tcaagggcag	933240
accagattca	agattacggt	acaggaaagg	taacaggacc	tcttttgggtc	tttggaaagt	933300
tagaaaagga	tttgcagggt	tttgccttgc	gagggcatat	gtttaatgca	cagcgaactc	933360
tcgtagagac	aatcagttta	ccgttaaaac	aaggatttga	gcctgctgtg	gcttctcaag	933420
aagtgtcttc	aaacacacgt	agcgcacagc	acatccaggg	gcgaccaatc	gtgggggatc	933480
atagatgggt	tttttccgta	attctttact	gcatttagtt	gccctatccg	gaatgctctg	933540
ttgttcttct	ggagtggcct	taacgatagc	cgagaagatg	gcttcttttag	agcactcggg	933600
gagaggagca	gacgattatg	aggggatggc	ttcgtttaat	gccaatatga	gggagtatag	933660
ccttcagctg	agcaagttgt	atgaggaagc	acgaaagcta	cgcgcttctg	gaactgagga	933720
tgaagctctg	tggaaaggact	taattcgacg	gattggtgag	gtgcgaggct	atcttcgaga	933780
gatcgaggag	ctttgggctg	cagaaattcg	tgagaaaggg	ggcaatctcg	aggactacgc	933840
cctctggaat	caccagaga	ctacgattta	caatcttggt	accgattacg	gaaccgaaga	933900
ctctatttat	ttgattcctc	aagaaatcgg	agcgattaaa	atcgcaacct	tatcgaaatt	933960
tgtagttcct	aaagagtctt	tcgaagactg	tctcactcag	atcctatctc	gcttaggtat	934020
tggtcgtgct	caggtcaatt	cttggattaa	ggaactttat	atgatgctga	aggagggctg	934080
cagtgttgct	ggagtttttt	cctccagaaa	agatttagag	gcgctcccag	aaacagccta	934140
tattgggttt	gtattgaatt	cgaacgtaga	tgcgcatacc	aatcaacatg	tcttaaaaaa	934200
gttcattaac	cctgaaacaa	cgcattgtaga	tgtgattgca	ggacgtgtgt	ggatttttgg	934260
ttctcggggg	gaagtcggcg	agcttctgaa	gatttataat	tttgtgcagt	cggagagcat	934320
acgtcaagag	tatcgggtga	ttcccttaac	taagatcgat	ccagggggaga	tgatttccat	934380
tctcaacgca	gcatttcgtg	aggatctgac	taaagatggt	agtgaagaat	ctttaggcct	934440
tcgtgtagtt	cctttacagt	atcaagggcg	ttcgttggtt	ttaagtggaa	ccgcggcggt	934500
agtgcagcaa	gcgctgactc	tcattcgaga	gcttgaagaa	gggattgaga	accctacgga	934560
taaaacagta	ttttgggtata	acgtcaagca	ctccgatccc	caagagttgg	cggcattgct	934620
ttcccaagtc	catgatgtct	tctctggcga	gaataaggcg	agtgtcggag	ctgcagatgg	934680
atgtgggtcg	caattaaatg	cctcgatcca	aattgtataat	acagtaagtt	cttctgcgaa	934740
agatggctca	gtgaagtacg	gaaacttcat	cgcggattct	aagacaggaa	ctctgattat	934800
ggtgggttag	aaagaagttc	ttccacgtat	tcagatgcta	cttaagaaac	tagatgtccc	934860
taaaaagatg	gtccgtatcg	aggtgctggt	atttgaaaga	aaattggcac	atgagcagaa	934920
atctgggtta	aatcttctac	gtcttggtga	ggaagtttgt	aaaaaagggt	gcagtccttc	934980
tgtgtcttgg	gccgggggta	ctggcatact	agaattttta	tttaaaggaa	gtacgggatc	935040
ttcgatagtt	cctgggttatg	atctcgcccta	tcaattttta	atggctcaag	aggacgttcg	935100
gattaatgcg	agtccttctg	tagttactat	gaaccaaacc	ccagcacgga	ttcgtgttgt	935160
tgatgaaatg	tcaatagcgg	tgtcttcaga	taaagataaa	cgcgaataca	atcgtgcgca	935220
gtacgggtatc	atgataaaaa	tgctccccgt	aattaatgtg	ggagaggaag	acggaaaaag	935280
ttacattact	ttagagacag	acatcacctt	tgatactacg	ggaaaaaatc	atgatgatcg	935340
tcctgatgtt	acaaggcgta	atattactaa	taaggtgcgc	attgctgacg	gagagactgt	935400
gattattgga	ggtttgctgt	gcaaacagat	gtcagattct	catgatggca	ttcctttcct	935460
tggagacatt	cctggtatag	ggaagttatt	tggaatgagt	tccacatcag	acagtctcac	935520
ggagatgttt	gtatttatca	ctccgaagat	cctagaaaaa	cctgtagagc	aacaagaacg	935580
taaagaagaa	gctttactct	cttcgcgccc	tggagagaga	gaagaatact	atcaggcttt	935640
agcagctagt	gaggctgcag	cacgagcaga	tcataaaaaa	ttagagatgt	tcccgccttc	935700
aggagtatct	ttatctcagg	tagagaggca	agaatacgat	ggctgctagt	attttatctc	935760
aggagctttt	ggatatcctt	ccttatactt	ttttaaagaa	acactgtctt	ctccctattg	935820
aagagagtag	tgaggctatt	actatagccc	atgctaccgc	gacttcagtc	attgctcaag	935880
atgaagtcaa	attgttaata	aaaaagcctg	tgcgtttcgt	tctaaaagag	gaatcggaga	935940
ttctgcagcg	cttacagcag	ctctacagca	atcggaagg	taatgtttcc	gatatgttgt	936000
taacaatgaa	agaggaagat	ggcactacga	tttcggaaga	agaagatctt	ctggagacta	936060
cggatacagat	cccagtcgta	cgcttggtga	actggattct	gaaagaagcg	attgaaagag	936120
gcgcttcgga	cattcatttt	gagccttggtg	aggattctat	gagaatccgc	taccgcatgt	936180
atgggtgtgct	tcacgatcgt	cattccccac	cttcccacct	gcgttcggca	ttaaccactc	936240

ggcttaaagt	cctcgcaaaag	atggatattg	cggagcaccg	tcttcctcaa	gacgggcgta	936300
ttaagatcca	tattggtggt	caggaagtgg	acatgcgtgt	cagcacgggt	cccgtgattt	936360
atggcgagcg	tggtgttctt	cgtatttttag	ataagcgcaa	tgatcatttg	gatatcgcg	936420
gcttgcatat	gcctaagggt	accgaaatac	tcttttaaaga	taccataaca	gctcctgaag	936480
ggatccttct	ggttacagga	cctacaggca	gtgggaaaac	tacgaccctc	tacagtgtat	936540
tacaagagct	taagggacct	ttaacaaata	tcatgacgat	cgaagatcct	ccagagtata	936600
aactgcctgg	aattgctcag	attgctgtga	agcctaaaat	tgggctgact	ttcgacagag	936660
ggttacggca	tttactgcgt	caagatcccg	atataccttat	ggtcggagaa	atccgagatc	936720
aggaaactgc	agaaatcgca	atacaagcag	cattgactgg	gcatttggtg	gtgagcacgc	936780
tccatacgaa	tgacgctatt	tctgcgattc	cccgtcttct	ggatatgggg	atagaatcct	936840
atttggtatc	ggcaacgctc	gttggcggtg	ttgcccagag	gctgggtgca	accatttgct	936900
cctattgtaa	ggtcgcttat	actcctgaga	atcaggaaaa	atcttttcta	gcttctctag	936960
ggaaagatac	agaaatgcct	ttatatcggt	ggcaagggtg	cgtgcattgt	tctgttcagg	937020
atataaagga	agacagggaa	tttacgaatt	tttacgccc	aatacactat	tctgttcaga	937080
agtagcctca	aaccgcccct	atcatatttt	acgagaaact	gcagaacaaa	acggattctt	937140
accgatctta	gagcacggca	tcgctcttgc	tgtatctggt	gagactacct	tagcagaagt	937200
cttaagagtt	accaagcgct	gtgattaggg	agggcggtatg	cctcgatatc	ggtatacata	937260
tttagatccc	aaagagcgaa	ggaaacgagg	atatttgga	gcccttcata	tacaagaagc	937320
tagagaaaag	ctcgcccagg	aaaatatcca	agttttggat	attcgtgagg	tcgccttacg	937380
aagaatgagc	attaaaagta	ccgagctcat	cgtgtttaca	aaacagctcc	tcctcctcct	937440
acgctctgga	ctgcgcgtat	atgaaagctt	ggtatctctc	cgagatcagt	atcatgagca	937500
gaaaatggga	cttttgctca	catcgtttat	ggaaactcta	agatcggttg	ggcttttctc	937560
tcaagctatg	gcagcacatc	cgaatatctt	tgatcacttt	tattgtagt	gtgtcgctgc	937620
tggagaaaag	tggtgggaatc	tcgaagggtg	tctgcaaaat	attattgttg	ttctggaaga	937680
gcgtgcgcag	attaccaaga	agatggctcg	cgcattaagt	tatccttggt	tggtgttagt	937740
atcttctttt	gccgtgatgc	ttttcttttt	gttaggagtg	atcccttcat	taaaagagac	937800
ctttgaaaat	atggaagtca	aaggactaac	aaaaattgtt	tttgaggat	gcgactgtct	937860
ctccgcatac	cggatatctat	ttttaggatt	tgcgagtgtc	ttgattaccg	ttggaatttt	937920
gatgcgccat	cgcattccct	ggaaaaagat	cctagagaag	ctcttatttg	ctttgcccagg	937980
aaccaagaag	tttggtgtta	aggtagcggt	gaatcggttt	tggtccgtgg	catcggaat	938040
cttgaaggga	gggggggacc	taatcgaaag	tctcgacttg	gggtgtgacg	caattcccta	938100
tgacagactg	aagaccgata	tgagagatat	tggttcaggct	gtaatcggtg	ggggatcttt	938160
aagtcaggag	cttgctcagc	gctcttgggt	teccaagctc	gctataggga	tgattgcttt	938220
gggagaagag	tcgggggacg	ttgccgacgt	tttaggatat	gtagcccaca	tttataatga	938280
ggatacacaa	aaaacgttgg	cttcgataac	gtcgtgggtg	caaccctgta	ttctgatttt	938340
tcttggtggc	ctgatcggtg	tgatcatgtt	ggcaatattg	atcccactca	caagcaatat	938400
ccaaacatta	taaagtgtgt	actcagagga	gtcggtatga	aaagacaaaa	gagaaagcag	938460
tccatcacat	tgattgagat	gatgggtgtg	atcaccctca	tagggattat	tggtggtgct	938520
ttagcatctca	atatgcgagg	cagtatccat	aaaggtaagg	tatttcaatc	tgagcaaaat	938580
tggtgcgaaag	tatacgacat	cttgatgatg	gagtatgccca	cgggggggac	ttcggttaaag	938640
gaaatcattg	ctcataagga	gacagttgtc	gaagaggctt	cttggtgtaa	agagggtagg	938700
aaattactta	aagacgcttg	gggagaagat	ctgattgtgc	aacttaatga	taaggggtgat	938760
gatttagtca	tcttctctaa	gcgtgtacaa	agttcaaata	agaagtaact	cttgagtaac	938820
atcatggggg	ctcgacgtaa	acttaaactg	agctttttac	ttatagaagt	cctgtagggc	938880
ctttcttttg	tttggtcagt	gctcttgccc	tgatcagat	tttactacgc	catccacagg	938940
tcttttgagg	aagatatattt	taatttgcaa	ttgccagccc	tgatcgacca	ctgctttcta	939000
tctgtngaag	aaaagatgcy	tcagcaaatg	gcagaaggaa	ctgttctcac	ntcagggaaa	939060
gggcagacag	tttcttttagc	atataccagt	caggggatag	gctatcggtg	cccttatggt	939120
tacaatgtag	atatccgtca	ggaagtcctg	ggtgataatc	ttaagatgaa	agtttgcctt	939180
gccgatgttg	ttgtggaact	tttcccagat	cagaaacaag	cagtatccgt	acagagatgc	939240
ctatgtgtaa	ctctatagct	atgaaaaagc	aaaagcgtgg	ctttgtgctt	atggaattac	939300
tcattgtcgt	cactctaatt	gctttgttat	tagggacttt	aggatttttg	tatcggaaaa	939360
tttatactgt	acaaaagcaa	aaagaacgta	tttataactt	ttatatacga	gaaagccgag	939420
cctacaagca	gctcagaacc	ctgttttagca	tgctcttgct	ttcatcttac	gaggagcctg	939480
gatcattatt	ttcttttaac	tttgatcggt	gtgttttatcg	agatccctaag	ctggcaggtg	939540
cggtacgagc	ttctctccat	catgacacca	aggatcagag	attggaactt	cgtatttgta	939600
atattaagga	tcagtcttac	tttgaaacac	agcgactgct	ctcccacgtg	acccatgttg	939660
tactttcctt	ccagagaaat	cctgatcctg	aaaaacttcc	tgaaacaatt	gctttaacta	939720
taacacggga	acctaagca	tatcctccaa	ggacgttaac	ataccaattt	gcgggtggga	939780
aataagccta	tgcaaccttt	tatctttact	ttactgtgct	tgacatcttt	ggtttcttta	939840
gtcgcccttg	atgctgcgaa	tgctcgtaaa	cgttggtgct	gtgtgcaaac	tatagaacgt	939900
ggagagaact	tcttttccat	aaaacgctct	gtgtgtgctg	aaatcgaata	tcaagaaaaa	939960
tctcgccacg	cctcagcaat	tgaaagaatc	tcaaaagata	aaggcaaagt	cactccaaag	940020
cagattgcca	aagtagctac	taagaaaaag	caaagatacc	gtttattgca	ggttcctttt	940080

tcaaggcctc	cgaataaactc	aagggtataac	ctctatgctt	tgcttagtga	acctcccgaa	940140
tgctatagcg	atacagcatc	atgggtatgct	atctttatctc	gggtacttcg	acgtgcttat	940200
gtagacacgg	gaaatgtacc	tcctggatct	gagtatgccca	tcgctaattgc	tttgataagt	940260
aacaaacaag	agatttttaga	gaggggagcg	cagcttgagc	ccgatgttat	tgaaactcta	940320
acattgcctg	aggaacaagc	cgagattttt	tataaaatgc	tcaaaggggtc	gtcaaactct	940380
cagtcgctac	tgaattttct	gcattatgaa	gagaaaagct	tagggccactg	taagctaaat	940440
ctgatcttca	tggtatccct	actgttagaa	gctgttctag	atcatcccg	tgcttatagg	940500
gaaacgtcgc	tcctgcgcga	tggtcatctg	gaagcgggtga	agcgtcaaga	acatgccatc	940560
caagaacatg	gccaggcagc	tgctttggag	ctttttaaaa	cacgcaccga	cttcgcctg	940620
gagctgcgag	ataagatgca	gttacttcta	agtcgatacg	atctgtctcc	cttattaaat	940680
aaaaaaatgt	tcgactacac	cttaggaagt	gccggagatt	acttattttt	ggtagacca	940740
gatactaagg	caattttctcg	atgtcgctgc	ccttcaaaga	gtattaaatt	ataatttaat	940800
tttaatat	attttaaata	gttttttttg	ataattgtct	taataagtac	tataaaaaat	940860
atctctatag	gtaggaccat	ggcagacgag	accccgaaag	agaactcctc	caaagaactc	940920
tcctcacaat	ttgactcttt	gaagcgtaag	gtgaaagatt	tacactccaa	tcctaaagta	940980
gggaaatgga	agaagtttct	ttctcatcga	gcttgccaan	tatcggtggt	tgcttggtgc	941040
tggttggtat	catcgctgat	tttatttcat	gggctggagg	actgtttatt	gcttggtgtg	941100
tggtcctagg	ttttcacgtt	gaaattcgta	aaatgcttag	caatctccag	agctattcga	941160
ttgctaattg	ccctattaag	aatgcaattc	tctgtggctt	gattttattt	tttgatttaa	941220
acatcccttc	ctttgcagtc	tcgtttattg	ttctctgtgt	cattctttct	tttattacaa	941280
cagcaccgtc	atgttcgacg	tggtcgaaaag	atcattgtga	caaacatcaa	gatacttcta	941340
ataaaccttc	ttaaaactac	tttttcccta	aaggcaaaat	gttgaagccc	tcctttcttc	941400
aactttttgc	cttggttttca	ggcatgttcg	tcgagagctc	acaggctgga	acgtattctca	941460
tggttttaaga	gatgcatoct	tttctatagt	cttgaattta	tagattctta	gattacaaaa	941520
gaatatgcga	gagattccct	aagataatcc	ataaacagtg	cgctaagatt	cgtaagtga	941580
cgcatctcca	gataagagtc	acgataagag	cctaggggat	tagagtactt	gaggggtgga	941640
acctaggagc	ataatgggga	cttctttgaa	ccaagcaaga	gtgaaataat	ctatctgctt	941700
aattatgaac	caccacgcca	gggtgagaaa	gagaagaccc	atgaaagcct	taagggcgaga	941760
gaggaggtag	atgacctgaa	cttgaggtgc	catacggtta	ataatcccta	agaatagggtc	941820
ggacattaac	atcgccaaag	ctgcaggagc	actcagctgt	atggctcatca	cgagacagag	941880
ctggcacatc	ttgatcatag	taatccaaat	cggggcactt	aagctcatca	ctcggcgagg	941940
aaagaacta	tgacttcgaa	tgacttcgaa	agtgtgcaat	aacaaagaga	ttacaatacg	942000
gtgaccaccc	actaaccaaa	aaataatagt	cacgaagtaa	tggtataaaa	tgccatgcgg	942060
agaggtctgc	tcaatggaaa	tcagggatgt	cgcgccctct	aaaccctgaa	tccttgtgtg	942120
gttagtgatg	aaagatcctg	ccgattgtgc	agcataaaaag	ggaaatgcta	aaacaaagcc	942180
tatcacaatg	cctatgatca	tctccttcac	aagtaaaaca	taaaagagat	tgttatccat	942240
gtaattttgtg	atctgcgtat	ccgccaagac	ttttggaaaag	atgattgcaa	gccaagagag	942300
actaatcccg	attttaatat	gggagggaaa	gagctttgtc	cctaagaagg	gagcttagagc	942360
aaaaatagga	agcagacggg	ctaataaaaag	aagaaaaact	gaccaaacat	aggccggagg	942420
atgttgaaag	atagaaatcta	agtaagcaga	acctaggttg	gaaaaaagct	ctggtagaga	942480
gattcccata	agctctttat	ttccatttat	agaagttttg	gaaaatctga	cctgcaaagc	942540
gtaaaatcat	attgctaagc	caccctccag	agatcattaa	ggttccaaaa	atcacgacta	942600
gtttgactgc	aaaagcgaag	gtctgttctt	ggattttgtg	tgcggttgg	aagatcgcaa	942660
ccataatccc	gactatggaa	gctaagatga	tggtgaggtgc	cgaaacaatc	aaaataagta	942720
ataatgattg	gtaggagtac	tcaaaaagaa	cagatttgaa	actagttgag	aaaaatgcta	942780
acacggcacg	tgctcttatt	taaagctgat	cataagccct	tgagcagta	atgtccatcc	942840
gtctaccatg	acgatcaaaa	gtaactttta	aggtaacgaa	atcgatagag	gggataacat	942900
catcatctgc	atcgctacaa	gaacgttagc	agtcactaaa	tcaataacaa	agaaaggtag	942960
atagatcaag	actccaattt	cgaaagcatt	ttttatctga	cccataataa	aagcaggaat	943020
aatgattaca	aagtcggagg	cagtgaggtg	cgctcgaatt	tccgaaggaa	ggttttctgt	943080
gagatcttgt	aaaagctttg	aattttgtgt	tttgaggtgt	tgcgaaattaa	gaaagagcgc	943140
aaaggttctt	tagattttgt	taaagcgaca	aacactgttt	cagcaccttc	tgcatggaag	943200
aggctttgag	gaatggtatt	ggcttcgatt	tccttgcgag	catctttata	catagccact	943260
cccgtgggga	acatcacata	aatagatagg	atgagtgcaa	tccatttgag	gacttgactg	943320
ggaggtgttt	gtgttactcc	taaggcgtaa	cgtaataaga	ctaaagtaat	gataatcttt	943380
agatacgaag	tgagcaacat	gaccaggaaa	ggcgataggg	ccaagaaaat	taagatgatc	943440
gcttgctgtg	taatgtctgg	atacgtatct	gagaaacttc	catctgacag	atggctctcta	943500
gggagaacat	catcagcatt	cagtgggggc	atgtaggaag	gcactgacga	tgagcaaca	943560
ggctgttgta	ctacgttcaa	aggattagaa	ttcgagggag	gaggggtagg	ttgacaacgc	943620
gagggacagg	agttttcata	tagactggcg	tcagaaaaca	gcatgagacg	ctcagcgtaa	943680
aaaaacaaag	ggaaaatcga	aaaatggatc	gcataatagt	gaataccttt	attctttctt	943740
atcctgatca	ttagataaag	aagaagaatc	cgtggatgat	gaagctctag	atggctcgtc	943800
tacagggttc	ttcgctttta	gtatagtcga	gaaagctttt	tctaaggcat	ctaattgtac	943860
atcaagctgc	gcattgatga	tcctgtcttc	agtctcgata	atgcaacccc	caggagtaac	943920

atcagggtttt	gctgtaagaa	ttaaggagtc	agcatactcc	acgatgttct	tgagttcagg	943980
acgacttttc	tcaacaagag	gtaaactctt	gggattgaca	gagagtaatg	atatgtttat	944040
tttgtgtgag	ctctttcaat	gcttgagaaa	taatagagac	aatagtttca	ggatgtaatt	944100
cgagttcctt	cccaatgatt	ttcctcacac	tcgcaattgc	cagaggaacc	aaggcctcgc	944160
gtactcttat	gcgtagattt	ttagtttctt	cttctaagaa	agcaatttgc	ttgctccagg	944220
attcagatcc	ctctttaaat	ccttgatctt	tagcttcttg	acgaatttgt	gcacactttt	944280
gttctgtctc	tgcaacatag	gcttcgctat	cggcttttgt	tttttctaac	agctcttttg	944340
catcaaggaa	agcagacgaa	agcttcagga	gataaaacct	tcttatttgg	ggagacatca	944400
tcactcttaa	aaattaagct	aaaaaacttc	atctttacta	tggcgtagta	tctttgaggc	944460
tgatttacct	cagaagagaa	aacaccgctc	cttttattgt	cgtgttattt	ttctatactt	944520
tgtataaagc	taaactctta	cttataaagc	ttttatttca	ctaagacttt	catgcattgt	944580
tctaggcggg	acttaaaata	atccacatag	ggatgggtcat	accatgtttt	taaagtctgc	944640
tcgacgatat	atgctcgacc	gacatctaac	ctacgtagaa	aataccatag	aaaagaagcg	944700
ttttcttttg	ttaatgcttt	acctaanaac	tctaaccctt	gcttatgaac	gaactgtcgt	944760
aattctgcct	cagtagtcca	agaagaaaga	aaattcgtag	tttctaagt	tttcatcgga	944820
tgagattggc	agtaggtaag	aaagagtctt	tctgtagggg	agagagcatt	cttcaactcg	944880
tcaatcacaa	ccttatccag	aatgtgcttc	aactctttag	caatagaata	aagacctagg	944940
cagttgatta	aagcgatctt	tacaggacct	gtatagtaaa	gtatagcatt	tgctgaggat	945000
gcaggaagaa	agatttcttc	tgtaattcca	caaggacgga	tctttttact	tagcatatct	945060
agaagataga	aggctccgaa	agggtgcacag	cgatgtgggg	ctatagagat	gccaggcagt	945120
aagggtagaa	tttcttgaac	taaaggctct	ggcaaccacg	ctaataattg	accttggatt	945180
tcaggaggga	actctttcat	ggcaatggta	atccatgaag	gatgaattgt	aggtagccaa	945240
ctcatcgtta	aagataaaga	ttttaaaggg	atttcttcgg	gatgaggaga	ttcaacaaga	945300
agatttttag	gaagaaacct	ggagagggtca	tcttccttgg	agtgtctcat	caagatgtct	945360
agagttccaa	aagtgttggc	agtcactaag	caccctcaat	ttcattgctt	ccttctggag	945420
catctttatc	actagagtct	ttatcactgg	tttcgcgatt	tttgctttcc	ccctgtgaat	945480
ctgcatcttc	ttttttctct	ttgtcagcag	ctgtccctc	ggctttcttg	gcttccaagg	945540
cattctttgt	atatggtgtt	gggttgaaga	acccttttgt	acctcccata	gtcataatga	945600
gagtatgagt	tttccaaatg	acccaaagga	gaccacaaga	aataacaaat	aaaatgagaa	945660
tcaagacata	aaaaatgaga	cggaaatttg	tgagcgaaga	cttcgcaaga	ataatacccc	945720
aaacagaaac	ataatcgatt	tcttctgtta	atccccaagg	accattaatt	gtaatatcac	945780
tataantcgc	cgatcgctca	ctacagagac	gttctctggc	acaagtcctg	gaacagcact	945840
tgcaataagg	cgcttaattt	tggaaaccat	aatgctgttc	ggattgtcca	aaacccctcg	945900
atgcttaata	tacacagagg	ctgttaaagg	aagattatct	tcattttctg	tagtgaaggga	945960
aatctgtact	gaggcatcga	caacgccatc	catttttcta	atcgtagagg	ccatctgttc	946020
tgataagcct	tcttgataac	ggattttttc	ctgaagctcg	gaaggaacaa	gaccttgttt	946080
tgcaaaaaga	tctaacaggc	ttgtcccttt	catacgtgga	agaccgcgtt	gatttagaat	946140
ggcaaggggc	tctgtgattt	gtgctgacgg	aaccgcgata	tcccacattt	gtcctagtag	946200
tgtctcgggt	ttagccgctg	cagcttgagg	caatttttgt	gcagccaccc	ctttgcttac	946260
caaaagcacc	acaatctcat	tcgcttctct	gccaggaaga	ccgtgcacaa	ttagagacct	946320
gctgttacag	cttgtacagc	acagcaatgt	cattagaaag	aacaagcaaa	aagaaataga	946380
tcgacgaacc	ataatccacg	catacctttt	tattcaccat	aacaaaaggg	gggattagtg	946440
ccaatcgcg	acataaaatg	gtaatccttg	tcttcttttt	cttcaagcca	cgatattaaa	946500
aatgattttc	atacatacct	ctcggcatgg	tgttccaatt	atgaaaggga	tgtttttttg	946560
aaggtaagat	aaatgctctc	tacctaattg	gatatttttc	agagttttct	ttcctatcgt	946620
tttatgaagc	tctctacctt	tggtgcaata	agagtaattc	acaaactccc	ttacttaagt	946680
cttaggcaaa	ctttttgggt	tgagaatccg	tggtcatttt	aagcatcggt	gttgcggtac	946740
ctacgttacc	tttcgagttc	tttgatggta	taagagttag	gggtaggacg	ttatattttg	946800
gatagtcact	cggaccattg	tggtttccct	tgccctctatt	ttgagataga	aatacatatg	946860
tttcgtgcca	actttggcga	aatcctttta	tataaatata	agagattcaa	ggtttttatt	946920
atggctttgc	tttataatga	aggaaacgta	ctaccgcgac	tttcttcatg	agaactattt	946980
gaaaaacaag	aagagcatgt	ttatgaaaat	ttataaaaact	gcaggggagt	tttttttagc	947040
aatgcaaaa	tggcccttgg	taccggctgg	gtatcgacgt	gttcgaggaa	aagattttgt	947100
tctatccccg	ctcgtggact	tagtgattct	atttccattg	gtaaccacaa	actcccgata	947160
ttcaccttgc	agcatgacat	tcacttgat	ttgttagagt	atagtagagt	gtattcctgt	947220
tgtaagtaca	ttatttggtt	tcggacgatt	ttgtgctgtg	tggtgcgttg	aagggtttct	947280
aggctctacg	tttgataaga	tctatcatat	aattgtcgcc	gttctaggaa	ttcttggttt	947340
gggaattctt	acgttcattt	taagaattat	tttttctgtg	cttatgttgc	ccgtctgggt	947400
cttattttaag	tgttattctt	agcgtacaag	atggcgggac	tcagatcat	agccactagg	947460
attcttgaca	gttttctcct	cccctgcttc	gaggtagaag	cccagacatt	tcctcaagtc	947520
ttatgcaaa	ttgttgata	taagtacaag	agttctagaa	ttttattgat	agctttgctt	947580
tataatataa	ctctcgtcct	agggtctatt	tttattcata	agaaataact	aggacaaaag	947640
gggaagggtta	ttctgaaaat	ttatcaaaaat	gaagaagaat	tttttcgagc	aactgaaagg	947700
tttccatcaa	taggggaggg	gtatctacgt	gttcgaaaca	aaaactctgt	attattttcca	947760



tttgaggatt	taatgcttgt	atgcccctca	gtacctaaag	actttccact	ttcagctttc	947820
aaagtaacaa	ctaagcttat	ctattggagt	gtattagaga	gtatccccgt	cgtgggagca	947880
ttttttttca	gtataggaag	actctttgct	atgtgggtgca	tagaagattt	cccaggctct	947940
atttttttcta	gaatctatca	taccactgtt	gggtgttttag	gaattcttgg	tttaggaatc	948000
atcatgttca	ttttaagaat	tatctttact	ttgcttacgc	tacccttctg	gctcataagt	948060
tgtctaaaat	caagtgtctg	ttgaccaaga	tcgagtcctcg	gtgattgaag	acggtttccg	948120
atagccacta	ggatcactga	ggttccttcc	tctctgagat	aaaaactcat	atttttcgtg	948180
taaagactaa	caaatcagtt	ttataggaat	gcaaagattg	tataaagatc	gagcatcttg	948240
gtcgctctac	tctacagtga	agcacgtgtt	ttatcttgac	tggttagaaaa	gaaaatattt	948300
ccagaattga	ctctttttaca	cgtagttgaa	cttagttcta	ggggatctag	gttttattta	948360
tatttaataa	aacaaaagga	aaaataatgt	gcttataaga	aaatctgaat	cagaaggagc	948420
tttttttgaa	gcaactcaaa	attatcctac	aatacagcaa	ggatatcagc	tggtacggat	948480
tcgtgagcac	aatctttctg	tccgagcaca	ttttgactta	tctctatctc	ttgatgcac	948540
agtccatccc	gcggcttaat	agatagggtg	ttgaattcta	gatgcttatt	tctattttta	948600
aagagtagat	ttctttcggg	gtcttgtcta	aatggaggct	atcaggcgta	tttatcact	948660
cttcttttga	gtgggcccgc	tttggatagt	tttttgaag	cgtatctaaa	attgtaatta	948720
tttatagcgt	acggaattgt	ttgttggagg	ggctaagact	acggagcgca	gttttaagaa	948780
ttttcctaac	aagtttcttc	atcttgggtat	catcggttag	tgtcttgtct	ggatgagaag	948840
atcgcaagga	tgacagtttg	aaaaagcgtt	agaatgtagt	ttttaagatg	tgaatccatg	948900
atctttcaat	atcaagattc	gatgagatgg	atcgactat	gcttggtaac	tgacgctttg	948960
tcttgtacag	aagctaggat	catatcgcca	ttaaaactcg	agcgtaacaa	aggtcctgcg	949020
taaacaaaaa	gacccatagc	ttctccgact	cgacgatagt	aatcaaaagt	ctcgggagtc	949080
acataaacttt	tgacttggag	atgcttacga	gaaggacgta	agtattgacc	tatagtgaca	949140
atacgaactc	ctatggaagc	cagatcttgg	agagtcttgt	tgacttctcc	ttccatctca	949200
cctaactcta	ccatgatccc	ggattttgatt	ttaaagtcgg	ggaggtagtt	ggcagcttgt	949260
tctaacatga	acatagatcg	ggcataggtt	gctttgtgcc	gtactagagg	cgagagcctc	949320
gtacagttt	cgacattatg	attataaata	gtaatgccag	aatctaacag	ggtgtggaga	949380
gcagaaacat	tcccttggaa	atcagaagct	aaaacttctg	tagtcgcttg	agggagttct	949440
tcacgtaact	tttgaatgat	atcgactaaa	ccttgtgcac	caccatcctc	aaggctcatg	949500
cgagccacca	tggtgattac	cacatgcttc	aaccccagtt	ctttcgctga	caaagcaatg	949560
cgctcgggtt	ctgtaggata	tagcgcggtt	gggtgttttag	aatgcccatt	attgcaaaaa	949620
ccgcaacttc	ttgtacagac	atcgccgaga	gcaaggtagg	tggcagtttt	acgagaccaa	949680
cattctgctc	gatttgggca	gagagcttct	tcgcataaccg	ttggcattcc	tgagcgtttt	949740
attgtagcgt	ccgtagcatg	aaatgcagaa	ccttgtggta	agggcctctg	taaccacttg	949800
gggaaacgct	cggaagcgtt	cttccgcact	ctaggttggg	ctgtatttaa	agttgggtcta	949860
catttcatga	cttaggaggg	aagtgtaaag	ggtgatttgt	agcaagttaa	gcaccttcag	949920
cccaaacttc	agagagtgtg	ggatgagcat	gcacggtttc	atatatgcaa	ggtagggtca	949980
gctcattgcg	gatcgctaag	gtcatctctc	caattaatga	tgaggcggtga	ggtcctatga	950040
cataagctcc	gagtatttgc	tggttaattt	catgactcac	aatagcagca	aaaccacag	950100
atgctcccaa	agcaacagct	tttccaactg	ctttaaaagg	aaatttgggtg	agctttgcag	950160
gaagattttg	ttgttctgct	tcttgtagag	atagacctac	catagcaatt	tctgggtggg	950220
taaagatcac	agaaggtag	gcagaataat	ccataacttc	gtgatgtccc	gaaatatttt	950280
tcgcggaat	aacgccttgg	tgcaagcca	catgagcaag	tagccacttt	ccagtgtagt	950340
ctccaatcgc	atagataatt	ggaacattag	tgcgcatggt	ttcgtaacaa	ggaatcacgc	950400
cacgatcgtc	ccggatcact	ccagcattat	ctagccctat	acttgcgtga	ttaaattggc	950460
gaccaatagc	caccaagaca	taatcaaact	cttccacttg	atcgttcaca	gtaatgcgaa	950520
cttgggtttg	ggattcttctg	attgcagaga	tcgaggcttt	ggtaagaatt	cgaattcctt	950580
gtttcgtaaa	tttattcgtt	acgggtttgag	aaactctttt	attgttaacc	gcaagaatat	950640
gatccaaagc	ttctataacg	gtaatctcaa	cgcttaaagt	gtgaaataga	gacgcaaatt	950700
cacagccaat	aacgcgcgcca	ccaataatag	cgagcttttt	agggaggact	tcaagttcta	950760
agatccctgt	ggaactcaaa	attctagagg	agaagggaac	ccctgggaaa	ggacgaggct	950820
cggatcctgt	agctaggata	atatgattgg	ctttgattat	agtcgtgtct	tggtccaataa	950880
ctttaacttc	tgtagaagat	actagagatc	cggttccctt	taagacagta	atcttgttgc	950940
tgcggatcaa	tccttcta	ccttgacgga	tcccctggac	gactgtattt	tttctttttg	951000
ccatcgcagg	gtaatcgatt	gtataacct	caacatggat	gccgaactct	ccgcatgctt	951060
aatgtgagat	acaacattgg	gtccagcaat	gagggctttt	gaagggatgc	atccgcggtt	951120
taagcagggtc	ccccagcct	gtcttcttct	aataagagcg	gtccgtaatt	ttgattgcgc	951180
agcagtgatt	gcggcaacat	agccactagg	tcccgcacca	ataacaacac	aatcaaattc	951240
ttgggtcata	ttctcactca	ctgtaatcaa	gatttcaaaa	agaaccccc	ttcataaatg	951300
catgcatctc	attaagaaga	ggaccctgtg	cttatttttag	acctaagat	taattttcag	951360
cattgctttt	ttcttcgctg	attctgtatt	gaacctcgcc	tatatatccc	agaaaaagca	951420
aacgttccct	cggtaaatat	tgttttcttt	tttaataccc	agaagtatac	ttgcattaat	951480
ggcatttttag	cgacctaaaga	ggtcgtgatt	tcataattga	caagaacgta	ttcgttataa	951540
acaagcatgt	ttaaatggat	gagtttatgg	gggaaatgcc	ataacttaac	cctacagagg	951600



gcatagttgg	atagcaattg	acgaggaaga	atgtatttct	cctcatgatc	atgaaaaaag	951660
tgaaagatac	ctatgccatt	tgctaaagag	acagaaatgc	aaaggacgtg	ttggaagtgt	951720
gaaggcagtg	tatctatgca	cgtgcctcaa	tgtccctatt	gcagcgcctt	tcttcaagat	951780
cctccagtag	cctcaggagg	gttttcttct	tgccacatct	cgttcccaga	aggagcttct	951840
aaagaagaag	ccgaagacct	atgtgccgtc	tcttcagaag	attgggaagc	cgtgcttgga	951900
gatcaaaacc	ctactcaaga	aacgaataaa	caagtgatcc	ctgagtggac	atggttacaa	951960
agttggcctc	ttgcagcctt	attttttaggc	ataggcttgc	tagcgtttgc	ctttctgatt	952020
cttcttttct	ctacagacag	tggattgggt	ttgacttggc	ctaaaaatcg	ggcctatttt	952080
tacggtatta	taggtgctgc	agtcgcctat	cgtggatacc	gtaaaacttc	tctttaatta	952140
gcactaaata	caatttcttc	gttaggaatc	ctcaggggga	agcacacctg	tatcatcttc	952200
tacgggtgca	tctacagggg	actcttcact	gtctgaagtt	ccatgttcgt	ctttgtagga	952260
tagtatagtg	aggagatctt	cccgattcaa	catgtgtagg	atattagaat	cttgagaggc	952320
aatgacctta	tccaataagc	gaattttctt	ctcaattaaa	taatggatgc	gctcttcaag	952380
tgtatcttca	gtaatcagct	tatagataaa	gactgtattt	ttctgaccac	tccgatgcac	952440
acggcttaga	gcttgggttt	ccttggcagg	atccaccac	cggtcataca	taatcaccac	952500
attgcctgca	gtcaggttaa	ttcctgttcc	tgccgcaagt	aacgacccaa	caaacacctg	952560
acaattagga	tctgtagtaa	atgtttcaat	ttcttctctc	cgattcagag	attttctctg	952620
aaatcgaagc	atacttgatc	ccaatttcct	caagatagag	agtaatgatc	cgaatcatgt	952680
ggatatattg	cgagaatata	acaactttgt	atccagcgtt	taaagattcc	ttaagtagct	952740
taacgaaagc	attccacttt	ccagattcgt	aattttttata	ttgatccggg	tctttgaaaa	952800
atactgcagg	gtgatcacaa	atctgcttga	gatgatttaa	gagagcaaaa	atgtgtaaga	952860
aattcgtagc	aggttctctg	ggagtttcaa	gcttttgaat	atgacttttc	tctctttgca	952920
aggtcgcat	atataacttc	tcctgatccg	gagacaacga	acaagcaatg	atagattcga	952980
ccttatcagg	aagctcgga	agtaccagtt	tttttgtccg	tcgcaagata	aaaggacgag	953040
tcaactttaa	taaaagatcc	tgggagggga	taatctcttc	caattcttca	gaagaacatc	953100
gtttggtaaa	caactttttg	aatagagcgt	cagaggggaag	ataattgggt	aagataatgt	953160
ctaaaagccc	tttaaaactct	aagagattgt	tctctatggg	agttcccgtg	agtcccagct	953220
tcatctgagc	gtctatccga	cagaggattt	tgtgaatttg	gctactcttg	tttttagcca	953280
tgtggatctc	atcgaaaacg	acaattgtga	atgctatttt	gtaaaactta	tcgtagtttt	953340
gtcgtagcgt	tccataagaa	gttaacaaga	tatcagcagg	aggtagctca	ctcggtttgt	953400
ttggccccat	gaaagaaaaa	atactcacgc	caggaagatg	attacttaaa	atatgctccc	953460
agtgtggtaa	cacactttgt	tggacataca	attaaggaat	ttcgggcgcg	ctgagggctg	953520
tgaagactga	aatacaatat	ctagttaagg	ctgtagcttg	gtgagtcttt	cctaatacca	953580
tttcatcaca	gagaagccct	gagagtctgt	gattgtataa	gaaccacatc	caaagtaacc	953640
cgctgttttg	atacgggcgg	agctgggtgg	ctgaagaaaa	gagattttgt	ggaatcggag	953700
gtaaacacgc	tgcttttaac	tgtgagaaaa	attgcaagtc	ttcgggattg	gctatagtat	953760
catcagttac	tgatagtggg	gctagagcat	ctaatttaaa	gacgtcagta	atattcgcta	953820
tgacagtgtt	ctcagcgcgc	acacatttct	gcgtagatag	gaactgtttt	aaaaattgaa	953880
acaggttttg	tttcaaatct	aaaaagccag	cctgtgtaaa	tagaaaagta	tgtttacttt	953940
tcaatccttg	ttaaagcgatt	cctatgggga	cagatccgag	gtttgtcttc	agctccaatt	954000
gcaaatggag	aggagaggca	ggatgaggcc	tatgaatcga	ctggatcacc	aattcataac	954060
tttctggagg	gcgtgtctgc	ggatttggaa	ataaaatacg	ctcatgctgc	gcatactgtg	954120
taagaaactg	tgggacattt	tcaggaggaa	tgactctagg	tagaaagcat	aaccttctgt	954180
ggggagtggg	aatcaaagag	aatectatat	cttcgcgata	tagaaataca	ccaaatagcc	954240
aacaacggct	ttccccctaa	ccaacaagaa	taggcttgag	gtcaagtctt	tttccacgag	954300
attgcctgtg	aacttcaata	agaaggtctt	ttaaattagg	gggagaggaa	aagaaattgg	954360
ggagacgtcg	tagtgccgca	tcgttcttta	caatgaaagc	agggatgtct	tgagggttcta	954420
caatgagccc	atcttgaatc	ggcaaatcgt	ttttcttctc	tagaaaagaa	ccttgatttg	954480
tatagtaggt	ccatgtcccg	aaacgtattt	ctgtagaaga	gggatctccg	acatcatagt	954540
ggaataataa	aacaccttgt	tctgtgacat	tataagtaag	atgaccttcg	ggacgttcgt	954600
ttataaatgt	ttggaaaccg	ggctcttgaa	ttagatgccc	cctctcattg	agaaagtctt	954660
caacctgttc	ggatttaact	ataaacgctt	gttttggaga	tagcatcccc	acgacttgca	954720
tcagaccttt	cgtaggacta	tagcaatagt	ttgggtaaat	gagactgcca	ttgtctaaat	954780
ccccaggagt	gacgaggtaa	gcagaaaaat	agaaggagc	gtcacgtagt	agacggatat	954840
catagcgtag	tcgatattct	agagaatcat	agcagagcaa	agaaagcagc	tgatctttga	954900
atttatcagc	gagcaaagga	atcgcataga	tgggaagggc	tatggcttta	gggcctgtga	954960
tcatttcatg	cgtttttgca	acgtatttcta	cagaacctat	tctagtctta	ggatgattct	955020
ctctgtcttt	tttatggata	acaggactta	atgtgaaatt	taccttagct	tcttctgcgc	955080
agaccgtaac	atgttgtaata	ctgatgtcgt	gagatacatt	ctctaaagat	gtatgcgcga	955140
gttccaactt	aggaaatatg	tcttctaatt	taggaaaaatc	caagatttcc	gctttaaaga	955200
ccaggccttg	ccattgaaga	gaaaaatgag	aaggaaagcc	ttgagaattt	tctcctatcg	955260
taagctcagg	cccttcttca	tttaagaaaa	agaatttttt	tagcagtgcg	atagagacgc	955320
ganttcaaga	aagtcttatt	tgtaaatact	gtaggttctt	cagaagcatg	aatggtgcgg	955380
agccaatctt	ggaatacttc	ctcggacaga	cactctattg	ttaacgtgat	atgtggggat	955440

tctagtgtat	aaaccatctc	tccttgagct	tgtaatggaa	tcgagtcgag	gaaaaagtga	955500
gagaagacgg	cataccaaaa	ggaatgacgg	aattttatcgt	gtaaaggggtg	caatcctaaa	955560
gcgtcataga	cagcaaaata	tgcagtcata	aggtggagac	aacactcacc	gtcaggacaa	955620
ctgcaagaag	caaaagttag	cctatcaata	tcttgaagtt	ttaaagtgtc	taaccaatag	955680
ccctctggag	cttcttcac	aggaatgcgt	atggtgtaac	tatcctcaca	aaagtctaca	955740
acgatctcct	tgcgatgttt	aaggagatgt	tgcatcgcat	cctgtcgaaa	gatgggcta	955800
gcttctaaaa	ccataatatt	atgctagcaa	cccgtatgtt	attttaattc	actaacttta	955860
aaacaattgt	aagagagagg	gttaaataaa	acaagactgg	ggagtatcgg	aaattccata	955920
acttgttagc	aatgtttcca	caagccagta	caatcaaagc	tggatagcta	agttgtagca	955980
aaggcaagag	taggtgactt	atagtttcaa	aattcaaaat	agaaattaaa	taggtgggga	956040
taagagtaca	aattactgct	gaagcatagt	tcagtttctt	aaaggaaact	acacgagcta	956100
gaaaatctgc	aacaatacct	actaaagcaa	tttccgtagt	tagacaggca	atgaaaacgc	956160
tgactcctgc	gagaatgcta	tttgggcccta	atgcaatcgc	agagatcctt	cccagaatat	956220
gacctttact	tacattcaca	agtaagcccc	catgacgtgc	agcagataaa	acaaactcaa	956280
gataggctcat	tcctagtaag	atcgcagcaa	gaaagaaacc	taaagctaag	gaacgcttat	956340
tttttttgct	aaactaagag	ggatttcttc	ctctgtagga	tgtttctctt	956400	
cagctacgag	ctgacgtaga	gagatcaaaa	ctatggagca	gaagaaaaac	gctgcaagta	956460
aatccatagt	attgaaccct	tcaatgaatc	ctgccaacca	agcttgacgt	gcgttcggaa	956520
taaattcttg	aaccatgggg	tgggtaggaa	tcataaaaact	gcggatgatg	acccaaagta	956580
aggtaaccaa	cataatcggg	aaaaatacag	atcctagcca	ttgaattaaa	cggctgagct	956640
tgcatgagaa	gatatagata	agcacacagc	aaatcgcact	aaaaataggc	aaagagggaa	956700
tgaaagcact	cttatgtctg	gatagtgaag	tcaatgtggc	atgagatact	gcaatggctc	956760
gagggattcc	accgaagggg	cctatcaaaa	gtataatagc	cgtaataaaa	atcatccctc	956820
gaattcttcc	tatcgagaaa	aagaacttct	ggtagtctcc	agaatagaat	gcacatactga	956880
ctagacctaa	aagagggaacg	catacagcag	taagcatcat	gccgaaatag	gcagaccagg	956940
gatgcgcatt	gtagtgggtat	cccagagcta	agggaaagac	aatattgcca	gctccgaaga	957000
acatagcaaa	aatagatcct	ccaatagacc	aaatggacaa	acttttttta	tcatttggtt	957060
tatgagatgc	gttttttttc	atcttttaaa	taaagtagag	atagtaaagt	gctgagtga	957120
tgagtttaaa	gaatcatgat	cttagaaatc	aaacgatttt	cagtagttag	tttttattgt	957180
actgtgggac	aaaaggtaga	gttacgaatt	cttaaaaagc	taacaactct	aaatttatac	957240
agtttttttt	ataacaaagc	gattttctaa	gtacgggtac	tatttgcttc	ttttgcaaga	957300
tatgaacata	tagggcaatt	gtcaatttta	tgatgtaaa	caggacaata	ctgtcgtgca	957360
taatagatga	gttgcaagt	caatttcggt	gtgttctcat	ggccaaaaaa	gcgagccaga	957420
tcctttttcag	cagcggaggg	gctttttttt	tcagaaattt	tccatcgctg	cgctaaacgc	957480
aaaatatgag	tgtctacagg	gaatgtaggt	tttccatagg	ctatcccaag	aaaaacagaa	957540
gcggtttttc	tgccaactcc	cggaagtgt	gtgagaagag	ccatgtcatt	aggggggtct	957600
ccatgaaaat	cacgcactaa	aatttgagat	aattgataaa	tataggcgga	ctttctctct	957660
ccaaggccac	aaggggcaat	gagctgggtat	agcttccctg	gaggcaaate	taaaatagat	957720
tgggcgctcg	gggcttttgc	aaagagtgt	ggtgtcacgg	aatttactgc	ttgtccgta	957780
gaattcccag	ataagagaat	agcaataagt	agttgaaagg	gagaggacca	cccttctaaa	957840
gatgggtttg	gattgggaaa	tagcgcgttg	agtgttctga	gaataaattg	cttcatggtg	957900
agctattttc	caatgcaaaa	tttactaaaa	atttccccta	aaatactttc	agtaacttct	957960
ttgccagaaa	gcatcccaat	cgagtgaagt	gcctctctta	actccaaagc	aatgatttct	958020
ggagggttga	gatagagggt	tttctgcgct	tctttcagac	agcgagccac	ctcttgtaag	958080
atcatgtgat	ggcgagaaga	aactaaaaac	acttttagagg	tttttccagc	ctcttggttt	958140
tgcatccatt	ggattaaagc	ttgtttcact	tgagtaagtc	cctcaccagt	ttttgctgag	958200
atcgcaaatt	gagggagcga	agtgtcaagg	aattggaggag	gggtgagggt	agctttatct	958260
cataggagga	atgaagggtt	tgtaaaaaaga	attttaggaa	gatcttctag	aggttgctgc	958320
gcatctatta	cccagaggat	cccatccgct	tcttccatag	cagaaaagagc	tcgttcaatg	958380
ccctcttttt	caatgtcatt	gtctgtgtgt	ctttgtcctg	ctgtgtctag	cagtcgggatg	958440
cgtttgccct	gcaagagcca	ctgctcctct	aagatatcac	gagtggttcc	aggaatatgt	958500
gttacaatcg	cccgattttt	ctgaagaagc	gcattgagta	gggaggattt	ccctacgta	958560
ggtttccctg	caaggatcaa	acttggtccc	tgagcaagcc	tctgcccctc	atcaaaactg	958620
gaaataaaa	cttccacgat	atgcagagca	ttttgaattt	tttcttgagg	gacgaggagg	958680
tctggtgtgt	cttcttcagg	gaagtcggct	aggacttcca	aaaacgccaa	tgcttcgata	958740
atcagagtgt	gtatttcttg	aattttctta	gaaaaatttc	cttgaaaatg	cgtttgagca	958800
atccgaaagg	cgtctatatt	ttccgcaaca	atgagatttt	ggattgcctc	tgcttgaacc	958860
aggtcaattt	ttccatttag	aaacgctcgt	tgagaaaact	ctccaggagg	tgaggagcgg	958920
gcgcctaaag	caatcaaagc	gtctaaaatt	tgggagcaag	cgaaaaatcc	tccatgacac	958980
tgaaattcga	ctacatcttc	tccagtgaag	gagcgaggag	agcgcattag	aagaagaaga	959040
gcttgggtcaa	ttaatgtctc	ttcaaaaatg	acttggtccaa	gatgtatcgt	atgggaggga	959100
aagctgacca	cagatccaga	aaaaatacga	tcggcaatga	caatcgcttg	tgggcccagag	959160
agtcgtacaa	cagcaatact	tccttcccct	ggaggagtgg	caatggcagc	aattggtatcg	959220
tgcttttagca	taaaaataga	aaagttaaag	gaactttcgg	atagaatacc	aagttttaga	959280

ttaaagaggt	gaaaggagtt	tggataaata	ttaagactaa	ttcaattgga	atattttcat	959340
taatcttttt	ataatttctt	tttatctgtt	ctagaggctt	tgtgcagaag	ccccaatata	959400
ttgatcgaat	cactaaaaaa	aaagtaatag	aacctatatt	ttatgaaaaa	acaatgctct	959460
tcctatacaa	ctctaagcta	gggaagaagc	tctcagtatt	tctatcaaca	caccccatct	959520
tttctcgaat	ttatggctgg	cttcaaagggt	gttcgtggac	acgtcggcaa	attcgcctt	959580
tcataaatcg	atataagatt	tctgaaaaag	aattgacaaa	gcctgttgca	gacttcacct	959640
catttaaatga	tttttttacc	cggaaattga	aacccgaagc	acgccctatt	gttggtggga	959700
aagagggtatt	catcactcct	gtggatggac	gttaccttgt	gtatcctaata	gtttcgggaat	959760
tcgataagtt	tattgtttaa	tcaaaaagcgt	tttcattacc	caagctttta	ggagaccatg	959820
agttaacaaa	attatagctt	catggcagca	ttgtttttgc	ccgccttgcc	ccctttgatt	959880
accatcgatt	ccattttccc	tgtgattgcc	ttcctcaaaa	gacacgttgt	gtgaatggag	959940
cgctgttctc	tgtccatcct	ttagctgtta	aagataattt	cattttatatt	tgtgaaaata	960000
aacggacggt	tactgtactc	gaaacagagc	agttcggcaa	cgctccttat	ttagaagttg	960060
gagctatgaa	tgtaggctcc	attgtacaaa	cattttctcc	gaaccaaacc	tatgctaaag	960120
gtgacgagaa	gggctttttt	gcttttggcg	gctctacagt	tatcttgctc	tttttgccta	960180
acgctatacg	gttcgataac	gatcttttga	agaactcacg	tatgggtttt	gaaacacgct	960240
gcttgatggg	gcagtcatta	ggtagatctc	agagagaaga	aatttaaaga	ctttaaagac	960300
tttttttgggt	attgcaaaga	gagataaaaag	tcaaaaatgg	cgaattatgt	ggttagtcac	960360
cttgtgggct	ctagctgcaa	gtttagcaat	agcgtgtgtc	gctaaagggt	attaccgctt	960420
tgtttatttt	cgctcgctatg	ctgtgcaagt	tatacgagaa	gtacgcctaa	gtatggagct	960480
caaagaatgg	gcgcttgagc	aacagcaact	cctacctatt	ttaaaaaac	ggctcgatcg	960540
acggcagtg	ttatttgaat	atatgcgcac	tctacgcaag	atgcagcgtt	tcgaggaatc	960600
cgagaaactg	cttgccgaag	cgaagaaatt	gggattgcgc	ggctccctatt	ttttcttaga	960660
aattgcctat	aaagcctaca	ggtttggggc	ttttaaagaa	tgtgcacagg	cgtttgcttc	960720
cgttcctcaa	gatttggttg	aagaagaaga	cgctgcaaaa	tatgcttcag	ctctggtgag	960780
gttaggcgat	ttagatgctg	cctgcagttt	gattgaacca	tggatttctc	ccctatctca	960840
ccaagaaact	tttgtgacta	tggggcacat	ttatttccat	tccaagcgtt	ataaagatgc	960900
tatagatttt	tataatcgctg	cgaatgcttt	gggagctctg	cctgttgagg	tcacctataa	960960
tttagcacaa	gcgtatcgca	ttacctcaag	ctatgcaaaa	gcaggcaaat	tattccgcaa	961020
actcttatca	aatcctgtct	acaaagaaga	agctttatatt	aatatcgggc	tttgtgaaca	961080
aaagctaggc	agaccaggga	aaagctctact	tatttatcag	agcagtgatc	tttggctctg	961140
tggggatgac	ttgctgatga	aatatgcagc	tattggcagc	atggatcaac	gagattatgt	961200
attagcagag	ccctgctggg	aattggcttt	gcgctgttcc	acatttgcta	aagattacaa	961260
atgcgggcta	ggctatggct	ttagcttggtg	tcgattacgc	aagtatggag	acgcagagcg	961320
tgtgtattgt	aatctgattc	aaaatttccc	tgaatgttta	acagcgtgca	aggctttggc	961380
ttggctttgt	ggagttgggt	atgcaacact	acttggttca	gaagaaggct	tgatgtatgc	961440
gaaaaaggcc	gtagaactcg	accatagttg	tgaacttta	gagttattaa	gtgcatgcga	961500
agcacgttgt	ggaaattttg	atgctgctta	tgaatttcaa	tcgtttcttt	cttctcgaga	961560
tacctctttg	caggagaaac	aacgacgttc	gcagattttg	cgaattttac	gtaaaaaact	961620
acctctcaac	gatcatcata	ttgtggaagt	ggatgctctg	cttgccgctt	aaatctgatt	961680
tttttaaat	ttttattcta	tggactacaa	agccctcgtg	gctcgaagat	aacaaaaagc	961740
agaaatcagc	ttcttgggaa	cttttattcg	ttttattaag	taagatcgag	tatggtattg	961800
agaaacgttc	tcgtaaaaga	tggatttcta	gtaattacag	tgaattaaac	gacatatgtt	961860
agggtttctt	aaacgcttct	ttggttcctc	tcaagagcgt	attctaaaaa	aatttcaaaa	961920
acttgtagat	aaagtgaaca	tttatgatga	aatgctcacg	cctttatctg	atgatgaatt	961980
gcggaataag	actgcggaat	taaagcagag	atatcagaac	ggagagtctc	ttgatagcat	962040
gcttcctgaa	gcttatgggtg	tcgtgaaaaa	cgtttgcga	cgtttagcag	gcacccagct	962100
cgaagctctc	ggataccatc	aaagatggga	tatggttcct	tatgatgtgc	agattctagg	962160
ggccattgct	atgcacaagg	gatttattac	agagatgcag	accggggagg	ggaaaaacact	962220
cactgcagtg	atgcctctgt	atttaaatgc	tttaacaggc	aagccagtg	atttggttac	962280
tgttaacgac	tatcttgcac	aacgagattg	tgaatgggta	ggatcggtac	tgcgctgggt	962340
aggacttaca	acgggagttt	tggtttcagg	aactctttta	gaaaagcgta	agaaaattta	962400
tcaatgtgat	gttgtctatg	gtacagcatc	ttagtttggt	tttgattatt	tgagagataa	962460
ttctatagct	actgccttg	aagagcaggt	aggtagagga	tattactttg	ctatcatgga	962520
tgaagtcgac	tcgatcttaa	tagatgaagc	tagaacaccc	ttaattatct	caggctctgg	962580
agaaaaacat	aatccagctc	attttgagct	taaaagaaaa	gtcgcaagtc	tagtgtattt	962640
gcaaaaagag	ctctgcagcc	gtatcgcat	agaagcacgt	cgcggttag	atagcttttt	962700
agatgttgat	attcttccta	aagataaaaa	agttcttgaa	ggcatctctg	aattttgccg	962760
cagcctttgg	ttggtaagca	aaggaatgcc	tttgaatcgt	gtgttacgtc	gtgtacgtga	962820
gcaccagat	cttcgtgcta	tgatcgataa	atgggatgtt	tattatcatg	ctgagcagaa	962880
taaagaagag	agcctagagc	gtctttcaga	gctctacatt	attgttgatg	agcacaataa	962940
tgattttgag	cttacagata	aaggaatgca	gcagtggtt	gagtatgctg	gaggctctac	963000
cgaagagttc	gtgatgatgg	atatggggca	tgagtatgct	cttatagaaa	atgatgagac	963060
cctatcacct	gcagataaga	tcaataaaaa	aattgcaatt	tctgaagaag	acaccttaag	963120

aaaggctcgt	gctcacggat	tacgacagtt	attacgagcc	caacttctca	tggagcgtga	963180
tgtagattat	attgtccgcg	acgatcagat	tgtgattatc	gatgaacata	caggacgtcc	963240
tcaacctgga	cgacgttttt	ctgaaggcct	ccatcaagct	atcgaagcta	aagaacacgt	963300
cactatccgt	aaggaatctc	agacgcttgc	tacagtcacg	ttgcaaaatt	tcttccgtct	963360
atatgaaaag	cttgcaggga	tgaccggaac	agcaattacg	gagtctcgag	agtttaaaga	963420
aattttataat	ctttatgtcc	tccaagtacc	cacgttcaag	ccttgcttac	gcatagatca	963480
taatgatgaa	ttttatatga	cagagcgtga	gaagtaccac	gctattgtta	atgagattgc	963540
gactattcat	ggcaagggga	accctattct	tgttggtaca	gaatctgtag	aggtctctga	963600
gaagctgtct	cggattttga	gacagaatcg	gatagagcat	actgtattga	atgctaagaa	963660
tcatgtctca	gaagcagaaa	ttatagcagg	agcagggaaa	ttaggtgctg	tgactgtagc	963720
tacaaatatg	gctggctcgag	gcacagacat	caaactagat	aatgaagctg	tgatcgtagg	963780
cggctctccat	gtgatcggtta	ctacacggca	tcaatcccgt	cgaattgata	gacagttgcg	963840
tgggctgtgt	gctcgtttag	gagaccctgg	cgctgcgaaa	ttctttttat	cttttgaaga	963900
tcggctgatg	cgactattcg	cctcccctaa	attgaatacc	cttatccgtc	attttcgtcc	963960
tccagaagga	gaggcgatgt	cggaccctat	gtttaataga	ctcatagaaa	cagcacagaa	964020
acgtgtcgaa	gggagaaaact	atactatccg	taagcatacc	ttagagtatg	atgatgtcat	964080
gaataagcag	agacaagcga	tatacgcttt	ccgccatgat	gtcttacatg	cggaatctgt	964140
tttcgatctt	gcaaaagaaa	ttctatgcc	tgtgtctctg	atggtagcat	ccttagtgat	964200
gagtgatcgt	cagttcaaaag	gggtggacatt	gccaaatctt	gaagaatgga	taacctcatc	964260
tttcccaata	gccttaaata	tagaagaact	cagacagctt	aaagatacag	attctattgc	964320
tgaaaagatc	gctgctgaat	tgattcaaga	gtttcaagta	cgctttgatc	atatggtaga	964380
agggctctcc	aaagctggag	gggaagaatt	ggatgcatct	gctatttcta	gagatgtcgt	964440
tcggctctgtc	atggctcatgc	atattgatga	gcagtggcgg	attcatcttg	tagatattgga	964500
cttactacgg	agtgaagttg	gcctacgtac	tgtagggcaa	aaagatcctt	tgttagaatt	964560
taaacacgag	tctttcttac	tgtttgagag	cttgattcgt	gatattcgta	ttacgattgc	964620
gcggcatctt	ttccgtcttg	agctgaccgt	agagccta	cctcgtgtca	acaacgtgat	964680
tctactgtta	gctacgtctt	ttcataataa	tgtgaattac	ggctcgttag	agttgactgt	964740
agttacagat	tctgaagatc	aagattaaga	aataacctag	aaggaggagt	ccttctaggt	964800
atttgtttca	caggctacat	agtttttatt	tttaaataaaa	tgggggtccat	tctgaccaaa	964860
cttggtcatt	atagtagcga	atccagaatt	ttctgcgatt	gccggctatg	aggaactggg	964920
catagtggct	cagtgtattg	tttgctatac	agaaaagaat	gtgcttttgg	ttcttggagt	964980
taggaaaatc	cttaggggcg	ttgagcaaa	tatcaacgtt	tgtagtaagg	agagactgtg	965040
tttttaggag	ttgggtgcag	tcgtattcag	gttctgaaat	gtcttcag	gcaatgttag	965100
accagggaga	cctacttatt	gttcttgggtg	tatagtattt	ttaaatacag	attcaccaag	965160
aacaataagt	aggtctccct	gggtctgtatt	ttcttcaaca	tacacccag	tttcttgata	965220
tttgtctagt	gaagctgctt	cttcagagtt	gtcaagtaag	tcttcgaaaa	tctgatcgtg	965280
gtcgggtgtcg	ggcgtatcgt	attggtcata	gttcagtact	ttaaatctcc	aagaaataat	965340
taattttattt	ttatttcatg	gtaataatat	tttttattat	tttttaacaa	attaattatg	965400
tcttttttgg	ttttcttttaa	attctaaatc	gaaaggtatt	ccatataaat	taaaccagca	965460
tttttaatgtg	tttttttaaat	aatattcata	atgttttgg	aatagagact	ttgcatttat	965520
aaataataaa	aactgcagag	gtgtcgttgt	cttttgatt	gcataataga	tcctcaacct	965580
gcgtccttga	atcacctgag	gatgggttct	atgtagagca	gaagcaagag	ttttattttac	965640
tatcgggtgtt	ggaactttat	tcgatactac	gtgatgtagt	tcatcaattg	cagagaagat	965700
cttttttaaga	ttgcgtttcg	tagtagcaga	gatacaaagc	attttagctt	gtcctaaata	965760
aggatcagta	gcgcgtagat	ctttgcagta	atgctccatg	cggacttctt	caagtaaatc	965820
ccatttggtta	attaatatga	tgtgaggctt	ttttcgttta	gaaattaaag	agaggatgcg	965880
cttctcataa	gaagagagtt	tttgtgtagc	atcaatcaca	agaagacaga	tatcagcacg	965940
agaaatagct	ttttcagttc	gagatgaaga	aatccattct	atggaattct	taacgctttt	966000
catttttcta	agaccgcag	tatcaatgaa	aagatactgg	cggctccttat	gggaatacag	966060
aatatcgata	ttatcacgtg	ttgtcccagg	agtattatca	ataatacaac	gctcttcatt	966120
gagaagaccg	ttaataatag	aagatttccc	tacgttagga	cgtccgatga	gcgctatttt	966180
taatgtcttg	ggagcttgct	gaggagactc	tgggatagtg	cagggttctt	caggggagaa	966240
gccttccgtg	aatacttctg	aaaaatcagg	gaatgtattt	gaagggagag	ccgcctcaga	966300
ttcttcgtgt	tcacttacag	aaagctcctc	aaggccttct	tcttcttctt	cgcgaggttc	966360
tggtaggttg	gctaccaact	taattctttg	aagaagggtg	tcaatgtgct	tatcgtgagc	966420
tgttgaggtc	actacaatat	ctcgaattcc	taatttatag	gtctcatgaa	tttgaatttc	966480
ctcttggcga	ctgtctgctt	tattggcgac	aaggatgaga	ggtttcttta	aggggaaggag	966540
gagtttggct	aggtgagcat	cttcttcggt	aataccacag	cggatatcaa	tgactagcaa	966600
taggacatca	gcttccttag	cgcgggtgag	ggcttgggtta	tagatatgct	tttgggaagta	966660
atcttcagaa	ttgtgatcaa	cacctccagt	atcgatgacc	tgagcaggaa	caccaaaccgc	966720
atggagctcg	ccgtagaggc	gatctcgagt	tgtccccctc	tgagaattta	caattgctaa	966780
agagcgttta	catagacgat	tgaaaagtga	tgactttcct	acattgggtc	ttcctaagat	966840
ggctattttt	agcataatcg	tctctattct	attttttcag	taattaatga	gaaaataata	966900
ggagttaaaa	aattaaagct	aaagagataa	atttctaagg	gttgtaaaag	taggattcta	966960

tttaaattaa	tctacTcca	aaagcctttt	tcttgtaaaa	gcaataaaat	tttttctttg	967020
tcgagacatt	catttttctat	agagagaatc	tcagcttctc	tgagtagatc	gccaaagaag	967080
cttcggggag	agatgccctt	agctatcaga	tcaggagccg	aaacaacggg	ggaggatggt	967140
tttattctta	atatgaattg	ctctaagcgt	gattcgagtt	cttgcaactcg	agagataaaag	967200
tgctgctgtc	tgctcggatc	tttttgtaga	gccgagaaga	gctccaaaaa	tagagggtgct	967260
gtcggagacg	ctaggaaaatg	cgcccaaaat	acacgattgc	cggattgggt	ttggaaatga	967320
gggagtgcct	cgtaccaaga	ttctattaat	ttcaattctt	tattagaaat	tcgtaatctt	967380
ccaaacgcta	ctgttgcggc	ttcctcactg	accccttgga	atagaggcag	taaaaaaaga	967440
atttcaggga	aatgtgttgg	attaaactta	cgggcaaatt	ctatggttgt	tcttaagaga	967500
ctgtaggga	tatcacgtag	ttcaggga	ataaaaaatta	agactttaag	cttgagcaga	967560
agagagaggg	ctccataaag	ctgtctttta	agcatttttt	ttagctcttg	ccagattctc	967620
tccggggata	cggaaatttac	taatgccggg	gcttctttta	taatggcgcg	ttctgtagtt	967680
gggtctaggg	tgaagccgag	ggaggaagaa	aaacgtatgg	cacgtaggat	acgcagttta	967740
tcttctgaga	atcttaaacg	tggatggcct	atagctcgaa	tgactttctt	ttcaatatca	967800
cgagttcctt	cgacaaaagtc	gaaaactttg	tcttcaaaag	gatcgtagta	catcccgttt	967860
actgtgaagt	ctcttcggag	ggcatcttct	cgcatagaag	aaaagatgat	acgatcgga	967920
tgcttccat	ctttgtattc	accgtcagag	cggaaagtgt	caacttcaaa	taggcgtccg	967980
tctgttttta	ctacgatgat	accaaaggca	acaccaatac	tgatgacgtc	tgggaagatc	968040
gtagatacaa	tcgttgggga	tgcattggta	gctatgtcaa	tatcctcgag	agggcgattc	968100
attaacatat	ctcgaacaca	accaccgaca	aaatatgcct	gatatcctgc	attacgtagt	968160
ttgataagaa	ctttttttgc	agcttctatg	gcaattgttg	tcatgacacc	cctaaaatag	968220
gaactaaaaa	gagctaagcg	atagcttctg	gggtccttct	gataattatt	ggcgctttat	968280
tttctgcgat	agtgtcttct	tggatatgaa	tagcttctac	tgtaggatct	gaaggaaatt	968340
caaacataag	gtctctaagg	agatttttcta	ggatcatccc	tagagcacga	gctccagttt	968400
ttgcttgctt	ggcttttttt	gctatagcat	atagggcttc	ttttttgaag	actaaactga	968460
cgttttcttc	tgcgaaatagc	tccatatatt	gtttcacaa	cgcaattgta	ggttctgtaa	968520
ggatggctac	aagctcatcc	aaagaaagct	cttcacagtt	tacaatgcag	ttgaatcttc	968580
cgacaaattc	agggatcatt	ccgaaggcaa	tcagggtctc	ggtttcaact	ttagcaagta	968640
gatggtctct	ggttttttga	gagaggtctg	cttgatcatc	agaaaaccct	atggtagttt	968700
tccccaatcg	ctttgcgata	atcttatcta	ggttgacgaa	agtcgcgcta	cgataaaata	968760
gatattttcc	gtattgactc	ggatatactc	ttggttagga	tgcttacgtc	ctcctttagg	968820
aggaacgttt	gctgtggttc	cttcaacgat	ttttaacaat	gcttggtgaa	ccccttcgcc	968880
agaaacatct	ctagtaaatg	agacgtttgc	tggtgtcctt	ccaattttat	cgatttcate	968940
gatatagata	atgcctcggt	ctgcacgggc	gacatcgtaa	tcagcagctt	gtaataaacg	969000
taagacaatg	ttctctacat	cttcaccgac	ataacctgct	tccgttaggg	tcgttgcgtc	969060
ggctatgggtg	aagggaacat	ctaaaatttt	tgccaatggt	tttgcaatta	atgtttttcc	969120
agatcctgta	gggcctagga	gaagcacgtt	agatttcccg	tagcttacct	gtttgttatg	969180
tagtagagca	cgtatacgtt	tatagtgtat	ataaacagca	acagcgattg	tcttttttag	969240
tctttcctga	ccaatgacat	attcatcaat	atgctttttg	atttccttag	gggtaagcac	969300
cctgagatca	gaaggctgtg	aagggttttc	agaaaactgga	gctgaggata	ttgtagagga	969360
gggtttctta	tctaaaattc	cagagcataa	tttgatgcag	tagtcacaaa	tgtataccga	969420
aggcccagca	atcagtttct	ctacatcttt	ttcagaccga	ccgcaaaatg	aacaaatagt	969480
tagatttttt	ttattcatat	gttctctcta	agtgtacttt	gtatccttat	tagttttctt	969540
cgcagaagtt	accaccttat	caataagtcc	gtaggagatg	gcttctctcg	ctcccatgaa	969600
gaaatctcgt	tcagaatctt	ctataatttt	ttctacaggt	tgtcctgtgc	attcagagag	969660
gatattggca	aggtgttttt	ttagtgtag	aatttcagct	gcttgaggtt	ggatgtctgc	969720
ggatgttccg	ataatgcctc	cagaagggtg	gtggatcatc	atacggctat	ggggaagagc	969780
gtgacgcttt	ccttttagttc	tgcgataaat	aagagggtc	ccatggatgc	agcttgaccg	969840
atgcagtagg	tattttacatc	acaacctaaa	aagcgaatgg	tatcatagat	tgccagttca	969900
gcggtgatgt	agccgcctgg	ggaattgatg	aaaatttgaa	tatccttttt	aggatcttcg	969960
gacatgagga	aaaggagctg	ggcaattact	gtgtttgcga	ggggctccgt	gatttcctga	970020
ccgatcatta	caatacgatc	tttcagaaga	cgggagtaaa	tatccatggc	cctttcacca	970080
cggcccgtat	cctcgacaac	ataggggtacc	agtgtcattt	gcgtttcctc	atcaaataat	970140
tttcagttgt	gtccatacgt	tcccgatcac	gaaatgaccc	taggaacgta	gctaagactt	970200
tttaggctgt	ctacgtcagc	aacaagctta	gacattaaaa	tctcgaattc	tatgtttaag	970260
actttcttgg	gtcaagtatt	ttcctctaac	taaaatttat	gcagaaggag	ttgaagccaa	970320
cagttctgct	ttgcgaagaa	catgttcgat	agctttgcta	taggtcagcc	gatcgcgggc	970380
tgacattaca	agttcttgta	aggtgtcatt	ggaaatatct	ttaggaggtt	gttgtccgaa	970440
gcgtctctct	gaacatacat	ccatcatgta	ttgcagttct	tcgcggctaa	tggtgagttt	970500
ttcatcagag	aaaattttat	gagtcaaaaa	cagtaacttt	aatgcttttg	tagcatcttc	970560
ttctgcttcc	ttgataagtt	ctgattttct	ttttcaagtt	cttcatcaga	acaatatggg	970620
ataagacgtg	cattaagaag	tttttctctt	gtgattaagg	aaatacgttc	ttcaagcagg	970680
gaggtaggaa	gttcaaaatc	tacgagcatg	gcaagagcat	cttcagcttc	agaaaagcgt	970740
ttttgcaatt	gtttatcttt	agcttgcttc	tctagtgtga	tgcgtaattt	cgcttttaaa	970800

tcgtctagag	attctgcttg	tagttgacga	gctttttcgt	catctatctc	ggggatcgag	970860
acttcgatta	cagcggttac	tgtaaagtgt	aaagtatctc	ctcttaagaa	ggattgaatt	970920
tcaggggagg	taattgtctc	aacaacacga	tgtccagtag	aaattcctaa	gaatttttct	970980
ttaaaggcat	cggtcatttc	ttcttcagaa	agcttaaaat	atttgttttc	aaaaatcgct	971040
gcagaggaag	cattctcatc	attactttta	gagacgtgca	aggaaataga	aatgaaatcg	971100
ccttcttggg	aaggacgttc	tacaggagtt	tttggtgcaa	agaacatacc	aatgtttgtg	971160
agtcctttct	cgatatcact	atctgaaatc	tcactagcag	cttcttctcg	aggtaaagaa	971220
aggttttccc	aagggaagtc	agaaattgca	gggaaagctt	ttcataagag	aactctactt	971280
tggctccttc	ttgaagatcg	aattgagtga	ttgagttcga	acggacagct	ttaggcgaaa	971340
gaggacgag	atctccgact	gtagataagg	catgataagc	gtcttgagtt	actagttctc	971400
ctaactcttt	tcttacgtta	gtaggatata	gggatgcaat	tacatcatca	ggggcttttc	971460
ccttgcgga	tcctggaagt	gtaatttctt	ttttaatctt	tttaagagct	tgcttggtga	971520
gtttgttaag	tacttctggg	gagactttta	ctaaagctga	gacaatacaa	ccaggagatt	971580
cttctaaatc	gacggagaa	tgctcattgg	agagactacg	tggcacaaga	caaccctttt	971640
tattagactt	gaaaggaaaa	gcgggtgatg	aggcttgaa	tcacgacctt	cacgttggca	971700
acgtgacgct	ctaccactga	gctacaccgg	caaagaaaa	aatagtttag	atttttgaag	971760
aggttttngc	aacgactaga	gtcttttaga	tcatagaat	tcgtgtctct	tccccctgag	971820
aagggtcttg	ataaaatttt	tcattgattt	agcatgggta	aacagggtaca	agtaagcaga	971880
ttatatttat	cactcttatt	ccagaggaga	aatgcttaat	tttcgcaagt	tacgccggga	971940
tttttcagcc	aatattttac	aagatggtaa	aaaacttttt	gagcaggggg	ctgtgattga	972000
tgcgaaaatc	ctttcgatga	atggagagac	tgtctgcata	agcgctcagg	ttcggggctt	972060
gtacgacaac	atttatgagt	gtgagattga	agttgatcgc	tcgggaatccg	atactgtgga	972120
ttccaactgt	gattgttctg	ataactacga	ctgccagcac	atcgctcgac	tattattcta	972180
tttagagcaa	tattttaatg	agatggtagt	agcctatgct	cgtagtgctg	atttagaaac	972240
ggatcacgag	atcaacgagg	aagtaaaaaa	ggagctcaag	gaaacttttg	tcgctgctgc	972300
cacaaaggaa	gaagagcgta	aagatcgtag	gcatcaaaaa	gagattttta	gagagtatgt	972360
tcacgctgca	aatgctttta	gtgcgaatcc	ttttttccta	cctttagaat	atttagaaaa	972420
ggattctgct	gagcttgctg	tattattttg	ttctgtaaat	gaggatacgt	ttgctcctgc	972480
caatcagcct	atagagtttc	aattagtact	tcgtttaccg	tgctcgttcca	agccttttta	972540
tatctcta	atccgtacct	ttttggaagg	ggtgttgat	caggagccaa	ttgtattgaa	972600
tgggcgtcgg	tttttcttta	cgatgcaatc	gtttaatgct	tccgatcgca	agctaataga	972660
tttattgatt	cgctatgtcc	gttaccctaa	tcatacaacc	gaagagaagt	tattaaaatc	972720
tgcgtatttg	atgcctcctg	cgtttaggtg	gattcttgca	aagatgtttg	aacatcaact	972780
ggcagatcgt	ggaggaggaa	gtttaggggg	aaaagagagt	ttttcagggg	tattctgtgg	972840
aaatcttgaa	gagcctctgt	gttggtcatt	aactccggct	aagatgaagt	ttaacttaga	972900
cttctttgac	atgccttaca	aagcgttggt	aatgactcct	gtgattcttg	ttgatgatga	972960
tgaagttcag	cctgagcaga	ccatgttatt	agagtcggat	gctccaggga	ttattcatca	973020
ttttgtttat	catcggtttt	ctcctcagat	caagcgtgcy	catttacgtt	cctttagtcg	973080
tttgcgagat	atagcaattc	cagaggcttt	gtttggttcg	ttccgtgaga	atgctcttcc	973140
tgtatttcag	gaatatgctg	aaattgcaaa	tgttcacctt	ttgaattcct	ttgtgacct	973200
tccttatgta	catgaggtcc	gggccatttg	tgatatgagc	tatttggacg	gggaattaga	973260
ggcaaaatta	catttccctt	atgggttctt	acgggttcca	gcagcatctt	tggctttgca	973320
atatcaggat	gttcgtgcct	ttattagtga	tgaggggaat	ttagccagaa	atctgggtga	973380
agagcgtaag	atggttgaag	aggctttctc	aggctttatt	tatgatgaac	gcgatggagc	973440
ttttcgtgtt	aaaagtgaga	agaagatcgt	ggaatttatg	acggagacga	tccttgcgaa	973500
tcaacatcgc	attactttta	actgtccgga	aaatctttca	ggtcagttta	tttatgatga	973560
gacgatcttt	gaattatcgt	tccgagaagg	gagcgacatt	aattattatg	aggcagacct	973620
taaggttcat	ggtttattga	aaggagtgcc	tttagattta	ttgtgggact	gcattgtgc	973680
gaaaaagcgc	tttttagagc	ttcctaagc	gggtcagcaa	tctaagggaa	cgcggcgcgg	973740
taagggtgaat	tcgggttaagt	tgcttctgtat	tttagtctta	gacttagaaa	aaattgctcc	973800
tgtggtgcag	atttttaaatg	aaataggatt	ttaaagtttta	gatgacttag	ttcagaagtg	973860
tccttttatgg	agttttaacg	gaatttcgtt	agatcagttt	gaagcacttc	ctgtgaactt	973920
ttccatgtct	gaaaggctta	tagagattca	gaagcaaatt	cgtggtgaga	tcgagtttga	973980
tttccaagat	gttcctcagc	agattcaggc	aacgttacgt	agctatcaaa	ccgagggcgt	974040
acattgggta	gagcgtttga	gaaaaatgca	tctcaacggg	atttttagctg	atgatatggg	974100
acttggaag	actctccagg	cgattattgc	tgttactcag	agtaaactag	agaaaggcag	974160
cggctgttct	tgtattgttt	gtcctacctc	tttagtttat	aactgggaagg	aagagtctcg	974220
taaattta	cctgaattca	ggacttttagt	tattgatgga	gttccttctc	aaagacggaa	974280
gcagtttaacg	gcttttagctg	atcgcgacgt	cgcgattact	tcgtataatt	tattacagaa	974340
agacgtggag	ttatataaga	gctttcgttt	tgactatggt	gttttagatg	aagcgcacca	974400
cattaagaat	cgtacgactc	ggaatgcaaa	atcggtgaag	atgattcaat	cggatcatcg	974460
gttgatatta	actggaacgc	cgatagagaa	ctcggttagaa	gagttatgga	gtctttttga	974520
tttcttaatg	cctgggtttat	tgagcagcta	cgatcgcttt	gttggaagt	acatacgtac	974580
gggcaactat	atgggcaata	aagctgacaa	tatggttgcy	cttaagaaaa	aggctctacc	974640

ttttattctt	cctcgtatga	aagaagatgt	attgaaagat	cttcctccag	tctctgagat	974700
tttatatcac	tgtcatctta	cagaatctca	gaaggagctg	tatcagtcct	atgcagcttc	974760
tgcgaaaaaa	gagctttcac	gtttggtcaa	gcaggaaggt	tttgagcgta	tccatattca	974820
tgtttttagca	actttgactc	ggttaaagca	aatttgctgt	catcctgcta	tttttgctaa	974880
ggatgctcca	gagcctgggg	attcagcaaaa	gtatgatatg	ttgatggatc	tactttcttc	974940
tcttggtgat	tctggccata	agactgtggt	ctttagtcag	tatacaaaga	tgctgggcat	975000
tattaagaaa	gatttagagt	ctcgaggcat	tccttttgte	tatctagatg	gttccaccaa	975060
gaacagacta	gatttagtga	atcagtttaa	tgaagatacc	tagcttggtg	gttttcttaa	975120
tttccttaaa	agctgggggc	acgggcttga	atcttgctcg	tgctgataca	gtgaattcac	975180
tacgacatgt	ggtggaatcc	tgctgtagag	aatcaagcga	ctgaccgagt	ccatcgtatt	975240
gggcagagcc	gttctgtctc	ttcctataaa	ttggtaacct	tgaacacgat	tgaagaaaaa	975300
atccttactt	tgcagaacag	gaaanagagc	cttgtaaaga	aagtgattaa	ctctgatgat	975360
gaggttgat	ccaagttaac	ttgggaagaa	gtattggaat	tgctgcagat	atgattttat	975420
gagtcacat	cgcaatctgt	ttaaacttaa	gaatttttcc	aatcgctttt	acaacagggc	975480
tttgggtcgt	ttcgacaagg	tctttaattt	tttttctggt	aatggtggca	ttgatttagg	975540
cactgcaaac	actttggttt	atgtccgagg	tcggggtatt	gttcttagtg	aaccttctgt	975600
agttgctgtg	gatgcacaga	cgcatgcagt	gcttgctgta	gggcataagg	cgaaagcgat	975660
gttgggtaag	acgcccagaa	agattatggc	agtgcgtcct	atgaaggatg	gggtaattgc	975720
tgattttgag	attgctgagg	gcatgttaaa	ggctttaatt	aaacgtgtaa	ctccttctcg	975780
tagtggtttt	cgcccaagaa	ttttaattgc	tgttccttct	gggattactg	gagtagaaaa	975840
acgtgctgtt	gaagattctg	cattacatgc	tggggctcag	gaagtaatct	taattgaaga	975900
acctatggct	gctgcgatag	gtgtggatct	gcctgttcat	gagcctgcag	cgagtatgat	975960
tattgatatt	ggaggaggca	ctaccgagat	tgctattatt	tcttggggag	gaattgttga	976020
atctcgttcc	ttgcgtattg	ctggggacga	atttgatgag	tgtatcatta	actacatgcg	976080
tcgtacgtac	aatttaaatga	taggtcctcg	tactgctgaa	gaaatcaaga	ttaccattgg	976140
ctcggcctat	cctttagggg	atcaggagtt	ggagatggaa	gttcgagggtc	gtgatcagggt	976200
ggcgggcttg	ccgattacca	agcgtattaa	ttctgtggag	attagagagt	gtttggctga	976260
acctattcag	cagatcatag	aatgtgtacg	tttgacatta	gagaagtgtc	caccagaact	976320
ttctgctgat	ttagtagaac	gtggtatggt	tttagctgga	gggggcgctt	taattaagggt	976380
attagataag	gctttgagta	agaacacagg	actttctgtg	attacagcac	cgcatccttt	976440
gctggcagtt	tgtttaggaa	ccgggaaagc	tttggaaact	ttagatcagt	ttaagaagcg	976500
taaagggaa	ttggtatagt	catggatatg	agcaccaaca	tcaagcatga	aggtctgaaa	976560
tcttggattg	atgaggttgc	taaattaacg	actccgaaga	catacgtctt	tgtgatgggt	976620
cggataccga	gtatgatgag	ctctgcactc	ttatggagag	tacagggacg	atgatccgtt	976680
tgaatcctga	gtttcatccc	aattgctttt	tggtccgttc	gtctgctgat	gatgtcgttc	976740
gggtagagca	atttactttc	atttgcactt	cgacggaaagc	agaggcaggc	cctacgaata	976800
attggagaga	tcctcaagag	atgcgtaggg	agttgcatca	actttttcgt	ggatgtatgc	976860
aggggcgcac	tctgtatata	gttcctttct	gtatgggtcc	tttagactct	ccattttcta	976920
ttgtaggtgt	tgagttaaca	gattctcctt	atgtcgtttg	ttctatgaag	ttcatgactc	976980
gtatgggtga	tgatgtttta	cgttcctttag	ggacttcggg	gaagttttta	aagtgtttac	977040
atagtgtggg	taagccttta	tctccaggag	aggccgatgt	ttcttggcct	tgcaatccga	977100
aatcaatgcg	gattgtacat	tttcaagatg	atagtagtgt	gatgtccttt	ggaagtgggt	977160
atggaggcaa	tgctttactg	ggtaagaagt	gtgtggctct	tcgcttagct	tcttacatgg	977220
caaaatctca	gggctggctt	gctgagcaca	tgttgattat	tggaattacc	aatcctgaag	977280
ggaagaaaaa	atacttttct	gcttcgttcc	cgagtgcctg	tggttaagaca	aatttagcta	977340
tgttgatgcc	taaacttcca	ggttggaaga	ctgagtgtat	tggggatgat	attgcttggg	977400
tccgtccggg	tcgtgacggc	aggttgtagt	ttgtaaatcc	agaatatgga	tttttgggtg	977460
ttgtcctctg	gacttctgag	cgtaaaaatc	ccaatgcttt	ggcaacttgc	aggtcgaatt	977520
ctatttttac	gaatgttgcc	ttgactgccg	atggggatgt	ttggtgggag	ggattaacgg	977580
agcaaccacc	agagccttta	acagattggc	ttggaaagcc	ttggaagcct	ggagggagtc	977640
ctgctgccca	tccgaattct	cgatttacag	ctcctttacg	tcagtgtcct	tcttttagatc	977700
ctgagtggaa	tagtcctcag	ggtgttccct	tagatgctat	tatttttggc	ggacgtcggt	977760
ccgaaaccat	tccttttagtt	tacgaagctt	taagtgggga	acacggagtg	actataggag	977820
cggggatgtc	atcgacgaca	actgcagcta	ttggtggcca	gttaggtaaa	ctccgccacg	977880
atccttttgc	catgcttcc	ttctgtgggt	ataacatggc	atattacttc	cagcatgggc	977940
tttcctttgc	tgagaataga	agtcttaagc	ttcctaagat	ttttggagtc	aattgggtcc	978000
gtaagaataa	tcaaggggag	tttctctggc	ctggttttag	tgaaaactta	cgtgttctag	978060
aatggatatt	ccaaaggact	gatggtctgg	aagatattgc	agagcgcacg	cctattgggt	978120
atcttcctaa	cattcaaaaa	ttcaacctca	atggcttgaa	tcttgaccta	caaactgtac	978180
aagaactggt	ctctgtagat	gctgaggggt	ggcttgctga	agttgagaac	attggggagt	978240
atgtgaagat	ctttgggttcg	gattgtccgc	agcagattac	tgatgagttg	ttgcgaatta	978300
aatcagaatt	aaaagaaaaa	taaaaatcaa	agtcattagt	tatttataag	ttagttttaa	978360
taacaattat	ttcttatttt	ttataaatta	ttttttaaat	aaaattaaga	ataattgatt	978420
attattatct	gataaatacc	gtgacgctac	aaccgagcta	cattaatttc	acccccaatg	978480



tgaccactgc	tttatctggt	ggtaagattg	atacgtcagc	tatcgaactt	tcttgcagcg	978540
ctctattttt	ccaagagttg	caagataaag	ctcagggttt	aaaacatgct	ttgggtttag	978600
ttcaggagtt	aagtgcagag	gcacttcgtc	cgcgccaagt	tcaaacctca	atttcctatc	978660
ttcctacaga	agaatcctca	cgtccaggga	tttctgctgg	aatcatagat	aggacaatgc	978720
cgacctttac	tgatgacgag	gtaaaggcta	tcctccaaaa	ccctaatttt	gaaacgtcta	978780
aaattttcgt	tgagggtctg	gataaggctc	tcaagagtta	tttagattct	gttacccttc	978840
ccgagggtat	agatccttcg	aatcctgaga	gtgctattat	acttaactat	ataacgctct	978900
tgaataatct	taagcctaaa	tttgctgctg	gttcgacacc	aacagacgct	gattataacg	978960
ctctctatgc	gttgccctgg	gattttgtga	aggaaatcga	ggctttgaaa	gcagcggatg	979020
ctcctcctaa	aagtaagggt	catgcttttt	ggcaggagat	catgacaatt	tacaataaca	979080
tgcagggtact	ttcctatcct	gttacggatt	accttaatgt	tcagattgcg	gatctttctc	979140
ttaatattac	cgtctgctcag	gaggtccaac	agtatctaaa	gaacttttat	agcatattaa	979200
aggacatttt	gaatccagga	tggacggatc	cacaggcgac	gcactatcca	gcagatgcag	979260
agtataatgc	tcgcatgctg	gggggtgattc	aaagtttatt	aaatttgagt	gggaactatc	979320
gtcagctgac	tgagaatatg	ctcccccaata	cagatacaag	tcttccccag	gaaattattg	979380
ctcagattcg	tagttttcaa	aatgggtgtga	atgggacgat	aattgcatcc	aacactcttc	979440
tacctactac	catgagactc	gatactctcc	ttggtgttat	ctatacctat	cagtgtttgtg	979500
ccactatttt	tggaaatgagc	tatggaacta	gcactccggc	taagcaaaat	tacatagatg	979560
ctattaatca	agaaaaaagt	tactggcaag	cgcgagcaaa	tggatttgat	gtaactagtg	979620
atcagggtttt	tgaccaatttt	gctactaata	tacagagcgg	cacttcatat	agaggcatag	979680
atctttttcaa	aaataataaaa	gtaaacgaga	tcaatcctat	tttctttaagt	caggctgcac	979740
ctttctttacg	gtatccgtat	aatttgatgt	cacgtagtat	gtatcaaact	atagaggatg	979800
ctgctaatag	atctattacg	gcttttgatg	ggctaatttc	cggttggagt	acacagatag	979860
caacctttcca	aacgcagaaa	aattcttttg	atccttcttt	gttgaagtat	tttgataacta	979920
tgaagcccaa	caaagagtct	tttgtaacca	cagctccttt	gcagatgggtc	tactcttcat	979980
tgatgttgga	taagtatttg	cctacgcagc	agaacgtgat	tgctctctta	gggatacaga	980040
tgacgtattc	taataaggct	gctaagtatc	tcaacgaact	aatcaaagag	atcactacgt	980100
ttcaatctgc	cgatattttat	tattcttttat	ctatatattt	gaaacagatg	aatttgcaag	980160
cggtagcgga	tcctatttgg	aaggctgtgg	gtgttttgaa	tgatgaaaaa	acacgagcga	980220
tggcagatat	tacccgctgc	aataagataa	aagcggctat	tgataagatg	ctcgttgaga	980280
tcaaggcgga	tgcagagtta	tcaaagtcac	aaattcgtga	gcttgtggat	acgttaacaa	980340
acttcaagtc	tcaaagcgac	gatctgattc	gcaatttate	ttgtttactg	ggtttcttat	980400
cagggtctac	ccctaaagct	gtgaatgacc	ctaattgctac	gtatgaggca	tttactgcag	980460
aaatcttcac	agaacctttt	aataatttga	aacggcagtt	agctacattt	gagagttttg	980520
tgattcaagg	tgggcaaaaat	ggaattaccc	cagggtggta	gcaacagctc	ttacaggcta	980580
tggagtcttc	acaacaagat	ttttcaacgt	ttaaccagaa	ccaacagctt	gctctgcaat	980640
tagaatcatc	agcaatgcaa	caggaatgga	ctcttgtaag	tgctgccctt	gctttattaa	980700
accaaattgg	ttcgaagatt	gcgagaagga	ttaaatctta	gtacttagga	aatagaatat	980760
tatgcatccg	aaaaatagaaa	aaagaaatag	ccttccactt	acggcagtcg	ctcctgtgtt	980820
tgaagaatcg	tatcatcctt	ctgtagctac	aactgtagat	ttatgtagatg	ccacgacact	980880
ttcccgacat	cttacagctc	taaaagatgt	gataaaaagaa	gctcgaaact	tagatttagg	980940
gaaggcattc	ctgacatcta	tgaacaggg	ttttataaat	acgggtacgg	aacttgccat	981000
tatacaagca	tctctggcag	atcagagtag	tcgagagtcg	cgtaagaagg	aagagaagat	981060
cttccatcag	cacttaggaa	aggcagcccc	acaagcggca	acagcaactt	caggagtgcg	981120
gcctactgcg	gatcctgttg	ctgataagat	gcctttacaa	tctgcatttg	cctatgttct	981180
ccttgataag	tacattcctg	ctcaagagga	agccctttat	gctcttgga	gggagttaaa	981240
cctatcagga	tatgcgcaaa	atttattttag	tcctctttta	gatatgatta	agagctttaa	981300
ctctgctcct	atcaactaca	atttaggatc	gtacatatct	cagacgagtg	gcactgcgaa	981360
tttcgcgtat	ggttatgaga	tgattttatc	gcgctataac	aacgaagtct	ctcaatgtcg	981420
cctggacata	gcaagtacag	taaaagctaa	agctgcgtta	gcgaacatgt	cggcttctgt	981480
taaagcaaat	gtgagtctga	ctgatgcaca	gaagaaacaa	attgaggata	tcattgccag	981540
ctatacgaaa	tcttttagatg	tgattcatac	acagttaact	gatgtgatga	caaatttagc	981600
atccataacc	tttgtttctg	gtttaaataa	atatgatcct	tcgtatcgca	ttgttggtgg	981660
ggattttatct	atcattgcct	tgcagaatga	cgagaaggta	cttgtcgatg	gtaagggtgga	981720
tatcacgact	gctgtgaatg	aaggaggcct	acttaatttc	ttcactacag	tccttacgga	981780
tgtgcagaat	tatggagact	tagctcaaac	gcaacagctg	atgttggaact	tagagcttaa	981840
ggcgatgcaa	caacaatgga	gtttagtatc	tgcatctttg	aaattattga	atgggatgta	981900
taccacagata	atctctggat	ttaaaaacta	aaactgcaga	cctgacgtaa	tggtgatagc	981960
acgctgatat	ccccaacggc	cttctacact	atagtagaag	ttatttgaga	tgcagcaggt	982020
agttccgaag	cagaagttta	ctctgtcgaa	gtttgtgatt	ttacgaattt	taaattttaaa	982080
attcgtaaat	tgctttttcga	gttctgtgaa	gctatcagaa	ggagcttttc	ttgaagtatt	982140
tcctatagat	acggatgcat	aggggaagcac	atagtcatta	agatacgtag	agatgccgat	982200
gcttgacagc	cattcttttat	agcttaggtt	tccatcagta	gcaccgaaat	agatctcggg	982260
gttggccttg	ttgtaaacga	tgatatagtt	gatgggactg	gaaccgtgac	ggtagtcagc	982320



gctcaccctt	acaaaagaca	ctccatcttt	ccacaatact	ttttgtaaac	tcagacccca	982380
gacaattcca	tagtctgact	ggacttcaat	gagaccatct	gtaacttcag	attctgcatt	982440
taaaggattt	gaagtgaagt	ctctgtgaagc	attgagaggg	aggcggtagt	actgcttaag	982500
tcctccgaca	cgtgcagtga	aggctatatc	taaaagggga	atggcagctg	gggatgtttc	982560
ctgtagagct	atggttgcaa	aaacacagct	cgagctgatg	gagctgttgt	taagatcaaa	982620
gtctacgttt	ttagttgtag	aggtaatggg	tggcgttgtt	cctgtgcctg	aagtcgtaac	982680
ggaggtaatg	acaggggacat	tggtaatatg	ggcactttct	gagaagacat	aatctccata	982740
gaacccaaat	ttgaggcttc	ctgcaagagc	agcaaaaaga	tcgtaactat	tacaaagttg	982800
gaaggcacac	catcccgttt	gctcaggatt	cacacctggg	agtactggag	ctgcagggtt	982860
tccagccctt	aggccatata	ctgcgggaga	agatacaatc	ccgaagaaca	tagagaagga	982920
aagggttgct	aaacgtaaat	gttttagcat	cttgctatct	atgtcaaagg	ggccttattt	982980
gcttttaatg	attaagtcct	ctttaccaga	tggataaaaa	aatgtacaaa	tgaaaagaca	983040
agtgcagggt	aggatcttag	aatgttgtag	gtctcgggtc	tttttttcac	ctggattctt	983100
taattttctg	aaagattata	ggaactcttc	ttttgtattt	ctctgtaaga	ggagagcaat	983160
gccctctttg	agatcaagat	tttcatagag	aacgcgatag	attcccgtag	tgatgggcat	983220
atcgatttta	tgatgtttgg	cgacttggtg	tgcagaaagt	gctgtgtagg	ctccttcgac	983280
taccatccca	atttttgctt	ttgcttggtc	gaaagtaaga	ccttgagcaa	gaaggtgcc	983340
gaaccgtaaa	ttccgactcg	actctgagaa	gcaggtaaca	caaagatctc	caagacctgc	983400
aaggccattt	agagtttctg	gtttacaatc	catgatagcg	gcgagtttac	gcatttcacg	983460
caatccccgg	gtcacaaggc	ctgcttttgc	attgtttcca	aacgataatc	cctcagcaat	983520
cccacaggca	atagcaatca	catttttcaa	agctcctccg	agagcagcac	ctttaatatc	983580
ggtattaggg	tagactcgga	agggtggggag	ggaaaaagct	tcgtggattt	gtttgagagt	983640
ttgtgaatcg	taagcgctga	ctacgacaga	acagggagaa	ccgttttaga	cctcttttagc	983700
gatggaagga	ccactgagat	accctaaata	tggagtcacg	gaatctccaa	gcacttcgag	983760
catgatttca	ctgaggagga	gtcctgtatt	ttgctcgatt	cccttagagg	taattacaaa	983820
ggggaccgag	aggtcagtga	tttgttttaa	ttgctctgct	acgggacgga	ttcctgcgga	983880
ggtcactcct	tctacaatca	tgaagcatt	gtggatcgct	tctttcatgt	ctgtagtga	983940
tgaaggtttt	ggagagatga	caacattggg	agctaaagga	tgacgtcggt	cttcttgtaa	984000
ttgcttgatt	aggtcagggt	tccgggacca	tgccacaaca	ggatatccct	tattcgcaag	984060
tagggaggct	agacaaaacc	cccaaattcc	catacctaag	tagccgatgt	gttgtttcat	984120
gaggcctcaa	aaaatgggtc	ctcgaaaaat	gctttgtttt	cccaatgtag	ggaagttgat	984180
gttgaaggat	aataaaaaatc	agcttctaatt	tcaaattgtg	tgtaggaga	gagctttttt	984240
cctgtgactt	tgtggaagag	ttggcgctct	cgggtcagaga	gagcttgtct	tactgtatcg	984300
gggctatgat	tgccctccag	attttttagg	ggagcaaaagc	actcttgtct	aggatacaca	984360
agagtttgac	aatggctcgt	ataacaaaat	agatcaaaga	taaactcttc	aaatttccaa	984420
gcatttttct	catttaagga	ggtatggcct	agttgcttgg	catgcttgtg	gactttatac	984480
aggggcagct	gttggttaggc	ggcgtggcgg	ataaagtcca	tggagagaca	gtaaagaccg	984540
atatttgcaa	ggcagtat	taattttcca	tcttcattaa	gagcgaatct	ctcgttttgg	984600
ggaatttcag	agtattcgat	aacagaagtt	tttccagaat	catgagattt	tacaagaata	984660
cccacatctt	caatagcagt	ttgacgtaga	gcccgtttta	tggttacctc	gttgtagac	984720
atcgcatgga	atccacagag	ttctacgtca	aaagggaagcg	ctaaaggatt	gtcaatgggg	984780
atcacactta	ccattttctat	gccagcattt	ttccatttct	cccatactcc	tgaagtatag	984840
agaagggttag	ctatacaacc	gttgccattc	ggaccaagag	ctagagtgtc	catatcttca	984900
agaaataggt	ctccagatag	ggtgaggagg	ggccaaagtg	gttggcagaa	aaaatccacc	984960
tgatttggtg	ctaggtggaa	gtagtcgttg	gattcaaaaa	agaacgtgt	ttgtcgggta	985020
ttcaaaggag	aggatcatgaa	tgctagagga	agaggttgac	ctgcaagttt	acttgcagca	985080
cgtacctttt	ctgctacca	ctgaaacagc	ggcttctttt	taataggaga	aacagggaat	985140
aaccttttag	ggccatcgca	cttcaatctt	gagccttgct	cccctgccag	gactacacag	985200
gcaacttttt	tctctttaag	tagcgtagtt	cctgcatgag	ctcgttctgg	atcttctcct	985260
gaagaggcaa	atgacgttat	cggatgaaaa	tctttaagaa	ttgctgttgg	tgaggaaagc	985320
agttgtgtgt	gcttacgaaa	aaaatcaata	tctacagagg	tgagctgctg	aaaaagctct	985380
tgttgttgg	ttggagaaag	ggagggccag	atatctaata	tatgttcttg	atttatggct	985440
ttgagcttat	ctgctagaga	gtttacatgc	atagcagagg	gcgaatatac	cgattcagtc	985500
attacagtta	gccttacgtt	cctatctctt	gaccccttaga	atacttattg	ttcttgatct	985560
tttctgatgat	ttttctgcgg	tttattaatt	cctggagttg	ttgggtgag	atttcaagaa	985620
agcgaagaga	ttcgctctgt	tgtttataaa	gagatgattg	taatgttttt	aagtattcta	985680
ggagtatatc	ataatgtttt	atgttatctc	gagaaataaa	atgtctcata	cgttccaggt	985740
gtaaatcagc	aatcctttta	tttgtagctt	gaatatttcg	tgatactgtt	aaagctaagc	985800
gcttctgatt	atgaagggtg	tctaaatatt	tatggatttt	tacttttaag	attaaagata	985860
ggctcccaag	tcgatctctc	atgagctctc	taatgcctcg	agctgtttta	atgtattgtc	985920
taagtaacag	taactagaca	agggttgccg	taggaaggct	ttgatgctgg	gaaggagctt	985980
cactgcttta	tctaactctt	catcttgacc	gggagtgtaa	gctcctagat	gaatgatata	986040
taaagcttca	ttatatacct	taagtagtga	acgaagctct	tctgcagctg	cataatgatg	986100
gggaagtgc	agtgcctgtg	ctgaccgaga	aagacttgat	aaaatatcga	ttggggggga	986160

ggctaaggct	ttaccttggc	ttgttaggaa	aaagtgtcca	tccaacagcg	atttttaaata	986220
gtctgtaaaa	atatcaggat	gcttcgggta	atataaaatc	gcatacagag	ctgttatgga	986280
ccccctgtca	ttgtttccgg	cacgttctgt	aaattcagat	acatggtgaa	agacagaggc	986340
ggcatattgg	tgcgcagaga	gtgtttctcc	tgcgcgtaaa	gcgacttctt	ggagtgcagc	986400
gatccatcgg	gataaagagt	ccataataaa	taagacttca	tggccttgct	ctcgaaaata	986460
ttctgctatt	gtcatagccg	ctcgccctgc	gattactttt	gttggtgcag	tctcatgggc	986520
aggtgctgca	atgatgatcg	tacgctgctg	tttcagggca	ttgctatgct	tctctatgtg	986580
ttctcggact	tgcgctcccc	gctctccaat	taaagcaatc	acattgattg	tagattttga	986640
tcctaaagcg	attgctgaga	gcagtgaaga	cttcccactt	cctggctcag	agaaaactcc	986700
aatacgctgt	cctttcccta	aggtaagaaa	tgcatacgatt	gctttaatcc	ctgtagggaa	986760
gatctgatcg	ataggttgct	tcatcatagg	ggatggcggg	agagacagaa	gaggttttcg	986820
atgtgtttta	ggaaggtcct	ctttcttgct	aatagggttg	ccgaaagcat	ctaagactct	986880
ccctaaaaga	tgatctgaga	gatgtagaga	gggggggagg	cgtaaaggaa	ggacttctgt	986940
tccaagagct	acagagtgtg	acggagatag	ggacatgaga	agtgtcgtgt	gattgtgaaa	987000
gccaatcact	tcagcaagaa	gattcggatc	tttggttgag	gaaattttgc	agagctcccc	987060
caggcatgca	gagagcccat	cgacctcaat	aagattttcca	gagaccttag	ataatagacc	987120
acaggcacgg	tagggctgcc	agttatgaat	atgaagtttt	tctttattta	gatgattcat	987180
gctgtcaaaa	cagaaagtag	atgggtctagt	tcttcgctga	tttcttgtct	cagaattccg	987240
ttaggggttt	ctattttgaa	tcctgatcgt	ctacaagaag	tgtcagggaa	aaactcagca	987300
tgcttaatca	tggggagttc	gtgggtggag	atccaatctg	taagtgtttt	gagatcctcg	987360
ggatggagaa	atactttgat	gggagtcaga	gatcttaatg	tcgtatgtct	ttggagcgcg	987420
gtagagagga	gcagggccag	ttcttgagga	ttttctagct	tcttatagag	aaatttttca	987480
cagatgagaa	gagccagttc	tagtaggtcg	ggtttttagct	gttgactgt	tttttcgact	987540
tcactaagta	ggtgaatgga	tagcttgcca	aagagatgaa	ctaacgaatg	gagttcttgg	987600
cttgcccttat	cattcgganc	ttcnggaaga	ctgttaggtt	ctgtatccca	aggatcatgt	987660
ggatgaggaa	ggtgagattg	agaaaagcgaa	ccaggagatt	gtgggtgtgt	cacaagaaat	987720
acctaattct	ttaagtttat	atttcagcac	ttgatgtttg	agatcttcgg	gtaatctgtt	987780
taataaggct	tctgctttct	taggggtccag	gtacgaaaga	attaaagcta	ttttttctgg	987840
agattccctt	tgtataatct	ctaacagctt	tgagatatct	atgcctcgtt	ttattttcct	987900
aggttcgggg	gagactctct	cataagcgtg	tcttgcgagg	tagaaactag	ctaaagcaac	987960
aatcatcaag	cttatgacaa	gaatcatact	cccgattaga	acttttgctg	agaacgattt	988020
tttattctgt	aaacgagcga	aagggagggt	ttctatgaca	atatcatagg	agtcgtcana	988080
gtttgataag	aggtagtgtt	tagtatgggc	tacaactctt	tcggattctt	ctttgggttaa	988140
atgagcaata	taattttcat	ttaaagttag	ctgtaatgtg	ggcttctctg	cttttgcgctg	988200
ataccgcaag	agcaaaagtgt	tccttgggga	aaattttccc	caggtaattt	tctaattgtat	988260
ggatgaacag	agaattttaca	gttatagatt	caggaatata	gaggttccct	aagttgtcag	988320
atagggatat	atgttctcgt	ttcaaccag	gaagactgct	gcatagatag	tctgtaattg	988380
agaagagtag	tgaaggagtt	agggactcct	cttttcttaa	agtaagaatg	acagagagat	988440
gcagaggaga	catgacgtca	tcttctgtag	acagagcaat	ggcaactttt	gcagatgcaa	988500
tgggatggaa	ggaggtcagn	ctttttctaa	ctgtcttttt	ttgttagaga	ttctatgagc	988560
ttgggggttc	ccatttgtgt	gagcttcagc	caattgccag	aagttttttc	tgtttttaact	988620
tgagtggggg	ctaaggatgg	gttcgaggat	cttccaaata	aaatagcaca	actcaccacc	988680
ccacctatta	ataggcatcc	taggggagaa	atccccaag	cggtaagttt	ttttgccaaa	988740
ttttgaaaaa	acacaagagt	ccttcataaa	aataaacgaa	acctatggca	ttgttgccat	988800
cgtattcttc	tctatcaaaa	agtaggaatt	attgacaatt	gcactctctc	ttaggattta	988860
ggacttggaa	aattttgaat	gaaaatttta	gagcctacat	tccaaagaat	ggttagagaa	988920
ggatttttaag	ttgctagagg	ttgaatttgt	tggaatcaag	aacacgtgaa	atgaaagcct	988980
ctacaatgat	agagactcgt	atttaggaat	gtagggaatt	ctactaaaag	aagttggggg	989040
gatggctacg	ggtgagaaaag	atttaatgat	gattcatcta	ccttcacttg	aagttcaggg	989100
tagatatagg	ctcttaggag	ctgccctatg	gaattttaag	tagatcctaa	tgacgaagga	989160
catccagaac	aattcccaga	ataggcaatt	gtgacaataa	agttttctag	ggattctaca	989220
gttacttcac	ctccgtccat	agcaatgtaa	gggccgattt	tttctgctat	tgtagcgcgga	989280
agagcataga	gcttttggtc	gtgagtgaga	gcttcccaat	cactctggct	atagggattc	989340
gcgtcttcga	aatcaagggt	catgggagaa	ttttgcaaaag	gaagcgagcc	atcctctaag	989400
gggattttcaa	gacattgctc	aacagctgta	tctaaggcat	caataacaaa	atggtagatgc	989460
gagatgctat	cttcaggaag	agcgggttgg	tgtgcgtgta	cgcgtaagga	tttatcaata	989520
tcatacaagag	tcactcttgta	agcttcgcta	tagctttttcc	cacaaacaag	attgcagaca	989580
gcctccgcta	gtgggattag	ataagggtga	ccaaagtatt	ggaattttgc	atccaggatt	989640
acgccatttt	tcttatccac	aagccaataa	aaagtgcgc	agttgcccac	cagtcgtgtgc	989700
ccctgttttc	cagtgaccag	atgtgcttct	ttagcttcag	catcctcttc	agaaaacgtg	989760
cccgcaaat	gtgggtgtaag	gaattttttc	ataacttttg	ctgatagcga	ggacaaaaaa	989820
atcattgggt	ctagaggtag	ggtcatgagg	aacttccaag	taaaggggta	agatgcttaa	989880
tggcatcatg	catggcacga	gcaagtttgg	aaaactcgag	gtctttactt	ctttctgtaa	989940
gagagaaatg	taaggcactg	tgacataaga	acggggagat	cccacaattt	tgtaacactt	990000

gagctagggg	ctggaatctc	tcgtatccta	aggatggata	gatgccttgc	tgggtggagat	990060
ggaaggcaag	actctctgct	gggatgtcag	gaattgcagc	aacaacgata	ttaggtaatc	990120
ggttctggac	ctcggaaaat	gccaattgga	ttagggggag	gacgctttgt	aactcttgaa	990180
ttagcttttt	acacaaattg	gaggtgtgga	atgtgaaaag	cggagagcgc	gaaatacgtt	990240
cttcacacgc	agtttgcatt	gctgccaccg	cactgaaaca	taaagatgct	gaagtgtgag	990300
gtggaaacca	ggaagaaaag	accctctcta	aagatttacg	aatgaagatc	ccccgatatg	990360
agcccatacc	tccaagagct	gctgaagaga	aagtaatgat	gtcagcgttg	aggatctcag	990420
gagtttagagg	agctcttcct	aaaatgtcag	aaatatccaa	gtgaaggagg	attctgcggt	990480
ctttgcataa	ggagagcaga	ggatctaagg	gttggtattac	ccctgtcaat	ccatgagctg	990540
cagatagtga	gaataacaaa	ctacgtggac	tcaaggtttc	tataagctgt	tcttcaacaa	990600
tcctaccttc	gtgatttact	gttaccagct	cataggtagt	tccgagtcct	tgatggcgac	990660
ataggctatt	aattaaaagc	tgttgatcat	gagcaggaag	aatgatgtga	tttcttcctt	990720
gaaacatgga	cagattttct	acaagggctg	ccaggactat	atgaaccaca	tgagggaat	990780
gagggacaaa	acgaaaaata	tgagagtcct	tcaatccgac	caactgtcgg	atactctcct	990840
ctgtttttct	agctaatttt	aacgcggagc	cggggggtag	agaaaaatag	tccgagtgta	990900
gggcataact	ttcttttaacc	cgctcagaag	gaggaatagc	gacttggttg	tttaaccaa	990960
aaattctggg	tgcttttcga	ttttgtggtt	tttccattga	tatacaactg	gttttcccgt	991020
cggtaattct	aaagatagta	cctcttcctc	acttaatttt	tctagatcca	taatcaaaga	991080
gcgtaaggaa	tttccgtgcg	cagaaacaaa	aacgtttttt	ccattttgca	gttgaggcaa	991140
aataattttt	tcaaagtaag	gcaaggctct	ttgtttcgta	tcatagaggc	tttctccctg	991200
aggaggagct	gtttttagtc	tgcgccctcca	cagcttgacc	cgctcttctc	cgaactgttc	991260
ggctgtttgt	tttttatttt	ttccttgaag	ttcgccgtac	attctttcgt	tgagggcact	991320
agattgatag	agaggaatca	tattgttttc	ttcttcgcga	ctgtagatcc	tcgacatctc	991380
ttttgtcttg	ggatcttcct	gaacaatata	ggggatcttc	ttagagtgtg	gatttgatc	991440
ggcgagtaag	gcggtcatca	gactacgtac	taaggtagag	gtaaagatgc	agtctatagg	991500
caaattttga	atagctcttc	ctgcggaaaa	agcctcttca	attccctggt	ggcttaaagg	991560
aatgtctacc	catccagaaa	ataaattttt	ttcattccat	acagattgtc	catgacgtaa	991620
taaaataaga	agagccatat	gttcctacta	gaatttaggg	tgagaagcta	agcataagca	991680
gaaatcaact	tttgtctagt	agaaaaatata	gaagtaaaaa	aagtttttaa	gcaaagaaaa	991740
gtagaccagt	attgccttgc	ttaggcacaa	taggtgcttg	atatggggta	aacgtgacaa	991800
aagttcgtct	taataaattt	ttagcttctg	cgggagttgc	ttctcgaagg	aagtgtgatg	991860
aaattatttt	ttctggatcc	gtgactgtga	atggctgtgt	tgctgagggg	ccctttgttc	991920
ttgtagatcc	agaagataaa	gtacaggtgg	gaggaacctc	tgttcatctc	actaagaaag	991980
tatatttcat	ggtgcataaa	gctatcgggt	atctgtgttc	ttctgagaag	aagtttctctg	992040
gaactaagtt	ggtgatcgat	cttttcgcac	atcttcccta	ccgtgtgttt	actgtggggac	992100
gtttggataa	agagacctcc	ggattaatct	tagtgactaa	tgatggggaa	tttgcaataa	992160
aaatcattca	ccccctctca	ggaattacca	aaagatctct	tctaaaagtt	agccgcgatg	992220
tctctgcaaa	agatttggga	aaattaatgg	aggggacttt	catagacggc	aaacatgtgc	992280
gtcctgtctc	tgtgactaaa	attcgctgtg	gtacagtaaa	gatcgtcgtg	agtgaaggga	992340
aaaaacacga	gatccgggtg	tttgcagatg	ctgcaggact	tcctatttta	gagctaaagc	992400
gtatccgtat	agggagtttg	gttttaggag	gcttgcgtta	tggcgaatat	cgcgagctta	992460
cagatgcgga	actcgggacc	tacatgaaat	tgtctgacta	acttgttttt	ttatatacta	992520
acctgcaata	gatagagccc	tatgggatat	gttttctatg	tgatcgctgg	cagtatatatt	992580
cttggcatca	gtttgggtgc	ctattgtcaa	ctctactatt	cagtaaaaaag	cgtactattt	992640
tcttggtact	tgtaaacagt	atatgctttg	gaaaagcgctc	atgcgttgct	cgctctctct	992700
caacttgtag	gcgaagaaga	cgcccagctc	caaaaaggaaa	tcgactttct	ctcgcagttg	992760
gacaagctct	cttggcgtgc	gttcctcaaa	aatagctacg	agatcatccc	aacatttcaa	992820
agagatggaa	gaccttcttt	ctgaaagagt	gcagggattc	ctagagtcta	tagaaacgat	992880
tgcagagcac	gatcgagcga	tcttgtgtat	cgaaaacttt	tgggcaagta	aaaatctatt	992940
tgattttgag	attgcagctt	acgaagaagc	tgtggagaag	tatcttaagt	tgcgacagcg	993000
agcccccttg	agacttgccct	caaagttgtt	ccgcttttta	gatgttcctt	cgatttcgatt	993060
tagtagctaa	gctatcggga	agattctcct	gcaacactcc	taggagatgg	tgtataagaa	993120
gtccctcggg	agtctcaagg	tctatgggat	ggccaagaat	ctcttgaagg	gatgttgcag	993180
gttgctcgac	atcttttaaa	gcttgtttcg	tagtattgcc	attgaggccg	atcccaagaa	993240
cgactccaag	aagtccttct	acagggagag	tctctggaag	aactccacag	agcttttctc	993300
catgaaccag	gacatcgtta	ggccatttta	tttttgcttc	tgtaattcct	aaatccttac	993360
ataaggcaac	aacagcttct	gtgcctaagc	gaaagagacg	tgatacatcg	atgtggagggt	993420
ctgtaataaa	aaaacagaag	gtattaagaa	gatccccctt	tgaagatttc	cagctttttac	993480
caaattttcc	tgtgcccgca	gtttgacatt	ttgtggagat	tacagttaat	gcataaggat	993540
cccacaaatg	catataggat	tttgccattg	tggttcgtgga	gggaatttct	tctatttcgt	993600
aataaataac	tttcatattc	tagaaaattg	cagctgtctc	aatagtaata	cgattatgag	993660
atatcataaa	tttttcgggt	atgtgaattc	ttgggttttt	cttgctgtac	ttaccttaat	993720
gctattaagt	gttggtgtca	tttcttcaat	ggatcctaca	gcgatgctgg	tgacctcctc	993780
caaaggcctc	ttgaccaata	aaagtatcat	gcagctcagg	catttcgctc	taggatgggt	993840

cgtttttttt	atctgtgcct	acttcgatta	tcacttattt	aaacgatggg	catgggtact	993900
ctactttttt	atgatttttg	ctctcgtggg	cctttttttt	gttcgctcag	tccaaaatgt	993960
ccatagatgg	taccgtattt	ctttcatcca	tatgagcgta	cagccctcag	aatatggaaa	994020
gcttgtgata	gtgataatgc	tcagttatat	cttggaatcc	cgaaaagcag	atattacatc	994080
gaaaacaaca	gcattccttg	cttgcttagt	tgctgcactt	ccgttctttt	taattttaaa	994140
agagcctgat	ttaggaaccg	cattagtctt	atgtcctgtg	acattgacga	ttttctattt	994200
aagtaatgtc	cattctttac	tagtaaaatt	ttgtacagtg	gtcgtacca	tcggaattat	994260
aggctcgtta	ttgatttttt	caggaatcgt	ctcacatcag	aaagtgaac	cctatgctct	994320
gaaagtcate	aaggaatata	aatacgagcg	actcagcccg	tcaaatcatc	accaacgcgc	994380
gtctctcatt	tctatagggc	tgggaggaat	tcgaggctct	ggatggaaaa	ctggggagtt	994440
tgagggtcgt	ggatggctac	cctacggcta	cacagactct	gtattctcgg	cattaggaga	994500
ggaattcggg	ttgctggggc	tactctttac	tctagggcta	ttttattgtc	ttatctgttt	994560
tggttgtcga	actgttgacg	tcgccactga	tgactttgga	aaactcctcg	ctgctggcat	994620
taccgtatac	ctagcgatgc	acgtcttaat	caatattagc	atgatgtgcg	ggctgctacc	994680
tatcacagga	gtccctctga	ttctaatttc	ctatgggggc	tcttcggtaa	tctctacaat	994740
ggcatccctt	ggtgtattgc	aaagtatcta	tagccatcgc	tttgctaagt	actaactttt	994800
cagcaaaccg	agagcattta	accccacata	accgctagtc	ccctcatgaa	gaattaccgc	994860
gagccataga	ggaatgatcc	ctaacgatgc	aggccaggag	actaaaagaa	taatagcaag	994920
cgctagtcca	aggttctgcg	aaacaacttt	tttcgtttgt	tttgcttttt	gaatgatcca	994980
agggaggggac	gacaaggagt	cgtgcaggag	aacaatatca	gcagcttcta	ttgctgtagc	995040
gcttccagct	tctcccatag	caatgcctac	agtagcttgt	gctaaagcag	gagcatcatt	995100
aattccatcg	ccgaccatca	taatttgacg	ttgtgttgca	agctcgcgta	ttttcgctaa	995160
cttatccctca	ggggtgagat	cgaaaaatac	ctcagaaatt	cctaaaattt	ccgctgtatt	995220
ttcagcactg	actttatgat	ctcccgtgag	catgctcaag	ggatagccga	gatctttgag	995280
atcttgaatg	atttcttttag	cttgaggacg	aggaatatct	cgaaaataaa	atagagcaaa	995340
actattccca	acatacgcta	gagaacaaat	ctccccatgt	tgcttcgcct	gataaatttt	995400
ttgttctata	tcttcaagat	actcagaagg	caccttccct	agtcctgttt	ctaccgcacc	995460
tacaaaagct	tcttgttcat	tgaatatagc	acgaaccccc	tctccaggaa	ctgtaagata	995520
ccgatctgca	ggaagcgagg	ataccttctg	ctccataagg	taagaaacaa	tagcctcagc	995580
aatcggatga	gatgaagact	gctctaaagc	taatactgaa	gggaaaaagg	tctcattttt	995640
agaaccgaag	tagtcgcaac	ctatacagg	aagctcgcca	gtcgttaacg	ttcccgtttt	995700
atccatcact	acagaattac	aaganactaa	acgatctaaa	acacaccgcc	tttcangaga	995760
accccatggt	tcgcacaggc	attgatagca	cttaaatagg	caataggaat	cgcaatgata	995820
aaagcacagc	gaagcgtgc	aataagaaac	gctagggcac	ggtaaaatgc	actctgaggt	995880
cctaacaatg	gaattggaag	aaataaagga	acaaaaagg	caattccaca	ggcaattgca	995940
aaaatagaga	gagcatatac	tgaagaatat	ttatctaagc	gttgctgtaa	cctaggttta	996000
gagttctgtg	cctgaatgac	taaattgata	atatgagcga	tggtagaatc	cgatcccgtta	996060
cgtaagacac	gaagatcgaa	actcccttcc	atattatggg	ctcccgcagg	aacaatcgac	996120
cctggatgac	aggatttagg	aactttttct	ccagtaagat	gcatgaggtt	gatagaagaa	996180
gaacctatgaa	ggattttctcc	gtccaaaggc	acaacctcgc	cacttttaat	gcgtaggata	996240
tttccaacct	caatcttggt	gattgcgact	ttttgtaagt	tgccatcttc	taagacaagc	996300
caaccgcgtg	taggagcgag	ctgcttcaaa	gagactaaag	tgctctttgc	tttcccgcgt	996360
accatctgtc	ccaacgcttc	tgaatcgca	aacaagacaa	gaagcaaggc	tccttctaaa	996420
gctcctccaa	taaaaataga	gccgaagggt	gctgatgtca	tcaaaatata	aatgttctact	996480
accttttgac	atatgttaac	taacgactta	atcagagcag	gagtgccagc	aagaaaaaat	996540
gtaaatacta	caaataagtt	agagagattt	tttgcatgga	gccagaaact	tagaagagca	996600
atcaagtagg	tccctaaaga	taaatacgcc	gatttttaag	gaagattgtg	actcaatttg	996660
cgatttttgt	tagatagaag	gggactcgta	tcttcagaca	tccctgattc	aaaaaatgta	996720
ttcactactt	ctgcagaaaa	tgaagtgaia	aacaaacggg	agaacacgta	gcgacctgtt	996780
ataataattt	cattaatgat	gagataatac	tcgcggaagt	gatgaagatc	cctaacaccc	996840
aaaccatttc	ggaaatttta	tcgtttttta	gaatttttagc	tttttaggaag	gaaagaacca	996900
gaaccataag	agcagaaaag	acccctgcaa	gagtgtagct	gatgcatagg	actagtggga	996960
ggaaaatggc	aagcccacat	agacctccta	atattctaga	tcctccttga	atcaggggat	997020
gaggaagatc	ttctttttcga	atgtaaagct	cttctcgaat	catcgtatct	agtagtaggg	997080
tagaatcgga	acagacatat	tctaccatct	cttgaggagg	agggtcttta	aacccttgat	997140
tctcaaaaca	aatccggagt	tctatttttt	cttgttcaaa	attctcttca	atctcgtttt	997200
tctcttccag	catagaacga	tgcgagagtt	ccatataggc	ccaagctttt	cttgctttta	997260
agcatccgtg	gtaaaatgtc	cagccaacgc	ctaaagatat	taaggatttt	acttgaagcg	997320
cacgattcgt	aggaatttaag	aaaaacaacg	tccgaatgaa	aaaaataaaa	acgccagtag	997380
ataaagcatt	attagctaag	tgatagaaaa	accctttaaa	ggttgtatgg	ggctcccctt	997440
tacagactct	gtgcttgtct	ctaacatgct	ttatgtggte	ctctggagtg	cgtgatttaa	997500
agtggtcatt	tggatcctga	gtcataattt	tccttagaat	ttgatgctgt	ctacagtctg	997560
atgtgttctc	actggctctt	gggaagaaga	atctccaacc	ctcctaaata	aggacgaagg	997620
acttcaggaa	taaccacaga	gccatcagct	tgttggttat	tttctaaaat	agctaccaag	997680

agacgtgggtg	ttgccagacc	tgaaccgtta	agagtatgaa	caaactgtag	tttcccttgg	997740
ctatcttttat	agcgtgtccc	agagcgccgc	gattggaaat	ccgtacactg	agaaatagaa	997800
gacacttcat	aaaaagcttt	ttgtcctggc	aaccagacct	cagcatctat	agtcttggat	997860
nctgtaaaag	acatatcccc	cgtagaaagc	aaagaaagac	gataaggcaa	cttgagctct	997920
gtcagcattt	cttcaacaat	actaagcatt	ttttcataag	caatatcatc	ttgattgggt	997980
gttgtaaagg	caaacatttc	taccttatgg	aattgatgca	cccgcacaag	tcctctctct	998040
tgagctectg	cagcacctgc	ttctcttcgg	aagcacggag	tgacgcagc	atagtaaaga	998100
ggaagtctct	tttctgttaa	aatgtcttgg	gaacgaaacc	cattaagaac	gacttccgca	998160
gtggggatca	gatagagata	ctgctctccg	tcctcaacac	gatagtattg	tcctcatcaat	998220
ttcggaatct	gcccagagcc	aaataaaaatt	tctttcttca	ctaataaggg	gggaagccag	998280
agctgaaatc	catgagctgc	ttgcttctgt	aacatatacg	taagaagagc	ccattccaga	998340
agaacaccac	gatttttata	agcaggccat	cctgatcctg	tcgtttttgc	tgctgcttgg	998400
aaatctaaga	tgtctaactc	ctgatttagc	tctaagtgat	gcttcggagg	aaagggaaat	998460
ataggaagg	ccccaacact	tttaatgact	tgatttcccg	ctttgtctct	ggatacagga	998520
atgtcgctcag	cagggttaatt	aggaagatgg	ctcagcaatt	catgtagtgt	agcgtttttt	998580
tgatcgagg	gctgctcaat	tttttcaaga	tccgcagcaa	gagtctctac	ctcttgaatt	998640
aagtttgtcg	cgtctacccc	ttgctgttta	gctttatgta	tatcttgaga	taagaggcgt	998700
ctttgtgctt	gtaaagtttc	tgaatccgtc	ttgagttgac	ggacctcttt	atccaaggag	998760
agtacagggt	ctaaagaaat	ttttggatct	tttttacgaa	gtcgagtctc	acattcttcg	998820
ggagtcttgc	gtataatttt	tatatccaac	atgcttgtct	cattgttaag	tagaagtgtg	998880
caaaagttag	agtatatgga	agatttctct	gagcaacaac	tcttttttat	gcggcgtgct	998940
atagaaatcg	gagaaaaggg	tagaatcaca	gcccccccaa	atccttgggt	aggggtgtgtg	999000
gtcgttcaag	aaaatcgcac	cataggggag	ggatttcatg	cgtatgctgg	aggacccac	999060
gctgaagagc	tcgccataca	aaacgcctct	atgcctatat	caggatccga	tgtctatgtt	999120
tctctagagc	cttgctctca	ttttgggtca	tgcccccat	gtgcgaactt	actaatcaaa	999180
cataaggctc	ctagagtttt	tgttgcctct	gttgatcctg	atcccaaagt	cgcagggtcaa	999240
ggaatcgcca	tgctacgtca	ggcagggatt	caggctctatg	tcggatttgg	agagagcgaa	999300
gcacaggcgt	ctctacagcc	gtatctatac	caaaggaccc	acaacttccc	ttggacaata	999360
ttgaaaagt	ccgcaagtgt	tgatggtcaa	gttgccgatt	ctcaagggaa	gtctcaatgg	999420
attacttgtc	cagaggctcg	tcatgatgtg	ggaaaattgc	gagcagagtc	ccaagccatt	999480
cttgtcgggt	ctcgtacgg	tcttagtgac	gacccgtggc	tcacagcaag	acaacctcag	999540
ggaatgctct	atcccaaaca	gcctctacgt	gtcgtcttag	acagtcgtgg	gagcgtccct	999600
cctacatcaa	atgtctttga	taagaccagt	ccgactctgt	atgtaaccac	agaacgatgt	999660
cctgaaaatt	ataataaaagt	tttagattcc	ttagacgtcc	ccgttttact	cacagaatct	999720
accccatcag	gagtggatct	tcacaagggtc	tatgagtatc	ttgctcaaaa	aaagatacta	999780
cagggttcttg	tagaaggagg	caccacacta	catacgtctt	tgctaaaaga	aagatttgtt	999840
aattcttttg	ttcttttactc	tgggcctatg	attcttgggg	acaaaagag	acctctagtc	999900
ggagtattag	gaaatttgtt	ggaatctgcc	tctcctctaa	ctctgaaaag	ttcccaaatt	999960
ttaggaaatt	ctttgaagg	cgtatgggg	atttccctc	aggttttcga	gcccataagg	1000020
aattgaaagg	aaaggatttt	tagagtagca	tgcttagcat	cggaaatccgt	taatgcgagg	1000080
gagtcaatga	tagaaactcg	agaagaggta	ggctctgcaa	attttgtttc	tttagaacga	1000140
gctattgagg	atttaagagc	aggaaaattt	gttattgttg	ttgatgaagc	ttcgagagaa	1000200
gatgaaggcg	acctgattat	cgccgggagaa	aaaattacag	ttgaaaagat	gacgtttctt	1000260
ctccagcaca	ccacaggagt	ggtttgcgct	gctttaagcc	aagaacgtct	cttaagcttg	1000320
gatcttctct	ccatgggttaa	ggataaccgt	tgccgtttta	aaactccctt	cactgtatcc	1000380
gtagatgctg	ctcacgggg	gactacagga	gtttctgccg	cagatagaac	caaagtcgtt	1000440
cagttattag	cagatcctaa	gagcaaacc	gaagatttta	ttagccagg	acactttttc	1000500
cccctagcaa	gttctccagg	aggagtgtta	aaacgagcag	gtcatacaga	atctactgtt	1000560
gacctaatgg	agttggcagg	actgcagcct	tgtggtgtac	tcgcagaatt	agtgaacgaa	1000620
gactactcta	tgatgcgatt	gcctcaaatt	ttagagtctg	caaggaaaca	taatattgca	1000680
gtgattcccg	tgacatcgat	cattgctcat	cgcagtctct	ccgatcggtt	ggtttctaaa	1000740
atctcttcag	cacgcctccc	tacaattttac	ggagacttta	cgattcatgt	ctatgaatcc	1000800
ttattggaag	gaatgcaaca	tcttgctttg	gtaaaaggca	atgttgctgg	aaaaagtaat	1000860
gtcctcgtac	gtgtccactc	agagtgtgtc	acaggagata	ttttaggatc	taagcgtgtt	1000920
gattgtggag	aacaatttag	ttcagcaatg	tcctacattg	ctgagaaggg	aactggtgtt	1000980
cttgtttact	tgcgagggca	ggaaggccga	gggatcggtt	tgggccataa	agtacgtgct	1001040
tatgctttgc	aagataacgg	ttatgatact	gtagatgcaa	acttagctat	gggatttccc	1001100
gtagactcaa	gggaatatgg	cataggagca	caaattcana	ttgatctcan	gttgacaacc	1001160
ataaaaattaa	tcactcataa	tcctcaaaaa	tattttgggc	ttcaagggtt	cggacttagc	1001220
atcacagaaa	gagttcctct	tcctgttcgc	atttctgaag	acaatgagca	gtattttaaga	1001280
acaaaacagg	aacgtatggg	acattggcta	gatctcccat	gctgtaacaa	tcgggtacaa	1001340
taatttttag	gagtatatga	aaacattgaa	aggacatttg	tctgcaaaga	atctacgtat	1001400
tgctattgtc	ggctcctgct	ttaatcaagc	tatggctgat	gccctagtgt	ctggtactca	1001460
ggaaactttt	ttgaagtttg	gagggagcga	ggacggcctg	atgactatcc	gtgttcccgg	1001520

agctttttgag	attccctgta	cgatcaaaaa	actttttatct	tctgaaagaa	agttcgcgatgc	1001580
tattgtttgca	tgcggtgtcc	taattcaagg	agaaacagac	cattataacc	aaattgtaaa	1001640
tcaagtagcg	gcagggtattg	gtgctctctc	tttggaattt	tgtcttccca	taaccttgctc	1001700
catagttgca	gctccttctg	cagaaatcgc	ttggcacaaga	tcagggtatta	aaggacgtca	1001760
tttgggagtt	tctgggatga	cgacagctat	agaaatggca	acgttattca	ctcaaatcta	1001820
gttcttgtaa	gaacgtatac	gtcccacaaa	atttgtggga	ctcttccctc	tacagattga	1001880
tgctgacagc	tccattttaa	tggatgcgaa	ctgcgatact	ctcagcaaa	acatccaagc	1001940
ctcccgaaga	caatgtcgtc	tcagaaaaat	ctaacacagt	cccttgcggg	agaagttgtt	1002000
tatttagcat	ttctctatga	gaacgtaagc	tttttaccac	taaggatagc	attgtcaggt	1002060
ataattgacg	tagacgattt	tctggactta	ccgtagatcc	atgagtcgcg	accgaaagtc	1002120
ccgcaactaa	actgggaaga	ccacgaaatg	ttaaaggaat	atgctctcct	tgtactgtat	1002180
agaaactgtt	aacaagattc	tcagcttcat	cagaaggtaa	atttttataa	ctccacgcca	1002240
aagtactcgc	ttccgacgga	gagagattca	ttaatgttgc	taagcgaacc	aaagtcagt	1002300
ccgttcgaga	ggttccctca	aaacctaaac	gattcgctcg	ataagtaaaa	taacgagaga	1002360
atgcctcttc	tatagtcgca	tgctgctgta	acatggaaa	tagaggagca	aagtttatat	1002420
agaactcttg	agaacagttc	ttgtctccac	aggatctctaa	gcaatacagg	tacaaatcta	1002480
agatcgcaag	agaccgacgt	gttctccaa	cagaaagcag	ctgcgcacta	ggaacctctg	1002540
ttaagttcag	tagagaatcg	tagttgcccc	aacgtcttag	agataacaag	acttcttgct	1002600
gttctggaga	aagcctcgca	taagaaggac	aaagttcagg	gaaagtcgca	aacacatgta	1002660
acgcctttgc	gtaaaagctc	tgtgggcacg	agtctgtgaa	ataaggctta	aacgtggtga	1002720
cagcttttgc	agagcagcct	acatgtctga	gcacgatcgc	tgtttctaaa	attctcaagg	1002780
tattatcgaa	actcttagga	gaatttataa	agaacaataa	ttgtttgtgc	gccgtctgga	1002840
attgcttaaa	tgctacatct	ccttcttcag	aagggaggat	ctgagagagc	tgcatgtaag	1002900
attgacgaga	ccccgtgata	aaaagatgta	ggtgaatcat	actgcgaatc	gcaatgtcta	1002960
aagcggggac	ttttttatta	aagagctttt	cagaataggc	catatcgata	ggagtcgatg	1003020
tgagaagagg	agccccctca	gattccgtaa	gccaaagaag	ctcaggatac	tgacgtagtt	1003080
tttgttctat	ccaaacctca	gaaccaat	taacctttgt	ctgcgagttc	gtctgtagag	1003140
atccttgggg	gccagcatag	ccgatagaat	tgcatcccat	aagtaaagct	aatgggaaaa	1003200
ccaagacttt	gatttttaaga	atttttaaca	tggaagcctc	ttctctatca	cgttgctttg	1003260
ttaatatctt	taaattttaa	gagattaact	aaaaacccca	ttttgataac	aaaatgccca	1003320
ataacaaatc	aacttgagaa	acgcaaggac	gttttccctc	gaagaattaa	agattccaac	1003380
ataaggattt	agttatgtta	ataacttaat	aatttatttt	tgtaataaat	aggccttttt	1003440
aaaaggaaaa	tgtgttataa	tctttaaaa	ttaattttta	ttttaactaa	aaataatgaa	1003500
aagagtcatt	tataaaacca	tattttgcgg	gttaacttta	cttacaagtt	tgagtagttg	1003560
ttccctggat	cctaaaggat	ataacctaga	gacaaaaaac	tcgagggact	taaatcaaga	1003620
gtctgttata	ctgaaggaaa	accgtgaaac	accttctctt	gttaagagac	tctctcgtcg	1003680
ttctcgaaga	ctcttcgctc	gacgtgatca	aactcagaag	gatacgctgc	aagtgcgaagc	1003740
taactttaag	acctacgcag	aaaagatttc	agagcaggac	gaaagagacc	tttctttcgt	1003800
tgtctcgtct	gctgcagaaa	agtcttcaat	ttcgttagct	ttgtctcagg	gtgaaattaa	1003860
ggatgctttg	taccgtatcc	gagaagtcca	ccctctagct	ttaatagaag	ctcttgctga	1003920
aaaccctggc	ttgatagaag	ggatgaaaaa	gatgcgaagg	cgtgattgga	tttggaatct	1003980
tttcttaaca	caattaagtg	aagtattttc	tcaagcttgg	tctcaagggg	ttatctctga	1004040
agaagatatt	gccgcatttg	cctccacctt	aggtttggac	tccggggaccg	ttgcgtccat	1004100
tgtccaaggg	gaaagggtggc	ccgagcttgt	ggatatagtg	ataacttaac	cttctaaagc	1004160
tctctacaac	taagcttcct	ttccccaaaa	caatagggaa	gggaagccca	gaagtttttc	1004220
tctttggcct	tcctgaattt	tcataatcaa	tcgcaacagg	agagacaatg	ttatatttta	1004280
tagaacagct	aaataaaactg	agtacgtcgt	tttgtgtatt	ccctatgatc	ttattgttag	1004340
gggggttctt	gacatggaaa	ttacgcgggt	tacagttcca	cgggttaaag	ctcggcttta	1004400
acttgatgct	tcaaaaataaa	ttggatgata	gttcatcaaa	agctaacgaa	gtttcttctg	1004460
acgaagctgt	agccggaatc	ctagcaggaa	attttggcac	gggaaatatc	gccggaatgc	1004520
tgctgcctta	gcttgtggag	gtccagggcg	cctggctctg	gtctgcttgc	agccctctct	1004580
ggagctatcg	tccaatatgc	tggctcctat	ttagggtcaa	aatataggaa	acctgaaggga	1004640
aatacaggag	aatttatagg	aggaccata	gcctgcctcg	cttttggcat	gcgtaaaaaa	1004700
atactcgag	gattctttgc	tttattcact	atcatgacag	ccttctgtgc	aggaaactgt	1004760
gttcaggtaa	gttgtatcgt	tcctctctgt	gcagaaggaa	ctccaggaaa	actcctcgtt	1004820
ggaattctac	tagctctcgt	agtgatcccc	gtgttagcag	gaggaaataa	ccgtatatata	1004880
agattctctg	ctcgtgtgat	tcccttcata	caggattttt	actgtatttc	ttgcggggatc	1004940
attctcttcc	aacatgcctc	ggctattctt	cccgcaatca	aactgatatg	ctcttcagca	1005000
ttcggcatta	aagccggact	cgctggaatc	ggaggctata	ctctttcgca	agtcactctt	1005060
acagggatta	accgtgctgt	catggctaca	gattgcggca	gcggaaatgg	atctattttg	1005120
caagcaaata	caaaaagcaa	aaatcctgtt	gtagacggac	tcgttactct	agtcccccca	1005180
gtcattgtga	tgggtgtttg	ctctattaca	atgctcgttc	taattgtctc	aggagcttac	1005240
agctcaggag	cccaaggaa	tctaattggtc	atgagtgcct	ttaaaaatag	cctcggctct	1005300
ctaggtagtg	tgattgttat	tctcgtctatg	gccctattcg	gatatacaac	aatattgaca	1005360

tggtttgctt	gcgcagaaaa	aagtttacaa	tatatgatcc	caggaagacg	agcaaatcta	1005420
tggttgaagg	ctatatacgt	cttgatcatt	cctctagggg	gtgttatcga	tatgcgtatg	1005480
atttgggcct	tatctgacac	aggtttttct	ggtatggtca	ttctgaactg	catagctcta	1005540
atcgccctac	tgaaagatgt	actatccaca	aaccgcgatg	ttgctttgct	taaagaacgc	1005600
gagtgcctcg	ttgcagatcc	tgtgcgtaat	ctagatgctt	aaaggagaag	aatcatgcaa	1005660
ttattgtccc	cagcgtttgc	ttatggcgcc	ccaattcccta	agaagtatac	atgccaaaggc	1005720
gcagggattt	ccccccctt	gacttttgta	gacgtccccg	gtgcagcgca	aagtcttgct	1005780
ttgattgtcg	aagaccctga	tgttccctaaa	gaaattcgta	gcgatggcct	gtggatccac	1005840
tggaatagtct	ataacctatc	caccacaatt	actaatcttg	ccgaaggagc	tgaaatcttc	1005900
gctgtgcaag	gattaaatac	ttctggaaag	cctgtctatg	aagggtccctg	tcctccagat	1005960
aaacagcacc	gctaactttc	tttactctat	ttgctcttga	cgtagttctt	ccagaagaag	1006020
aaaacgtcac	ccgtgatcag	ctatatgaag	caatggaatt	ccatattata	gaacaagcag	1006080
agttaatggg	aacttacgag	aaaagttaga	atttattcct	cttcaggaat	aaattcctct	1006140
cgcttcttcc	tgtgtttcca	atatagcggg	ccatagtgat	agcaaatctt	ttggcccgca	1006200
tatatcggtg	ctattgtcct	gataatcacg	tgaaacaatc	cctcactgaa	aaccccgata	1006260
gcttcgcgat	taggttgctt	gctgtgattg	ataaaacgtg	tgacgtttcc	ctgcttccca	1006320
ctatcaatag	taaaatatct	taaagtgaat	aaaggcatcg	gataacgaaa	acaataatcg	1006380
ttctcatcca	tccaaattgc	ctgccggtga	cgcaaaattc	ccgtgtattc	tcgatatat	1006440
gtccaaggag	caatttcatc	acgagcaaaa	actccatacc	ctacgtgcgc	attaatccaa	1006500
cagacagaaa	ccggtggagc	tgaggagcat	aatagatctt	gcttgtgtag	ttttcctaac	1006560
cacttggtcta	gaggagaaat	caaacgacgt	ttttccgatt	tgtgacaaa	agtctcaatt	1006620
tgctgttcta	ccttccagtt	agaaaaaact	aaagaaggaa	gaaaccgaaa	atgaagaagt	1006680
tcactcgctc	ggtctaaaaga	atacggctgg	ctatctcgcc	aatcattggt	caaagaaatg	1006740
tgtatagaag	aaacaaggttc	cgtagttacc	gtggacatgc	aacctcaaga	cgagaaaagt	1006800
atattggaga	tgtaatgccc	tgcgctaattg	caatttctgg	tgctatagaa	gtgatagaag	1006860
ctatcgattc	agatactgta	gaaagtgcta	gctccgcagt	gttacactcg	gtagacaggt	1006920
gagcaagata	taacttcttt	aacttcggag	tgataatctt	ttgtaaaagc	tgaccacact	1006980
cttggttaga	aatatgacct	aatttactca	atacacgctt	tttgtaaaca	tcaggacgtt	1007040
gagattgacg	taccaattca	ggggaatgat	tggactcaat	taataagtaa	tcacaatcat	1007100
agagttcatg	tgtgatccaa	gaggtgaccc	aacctaaatc	tgtgcaaaaa	cccagtttct	1007160
cttcgcgata	atgaaaaata	aaagccacag	gatctacagc	atcatgaggt	acattgaacg	1007220
tctgtacttc	gagatcttga	aaacaaaatg	aagaccctgt	ggaaaatatt	ttgaattctg	1007280
gatggctatc	tagtagatgg	cataaagcac	gagccgtctc	caagttgcaa	acaatgggag	1007340
tggtatacgc	cttaacaaaa	cttttaatcc	cggagatatg	atcagaatgt	tcgtgcgtaa	1007400
caaaaattgc	ctgaatatct	tcaggatcga	tattcataga	gagtaattcc	cgagtgcga	1007460
cttgcttgct	cactccctaaa	tcaataagaa	tcttacaaga	atccgtgcct	agataagcag	1007520
aattcccttt	ggatccagaa	gctaaaggga	aaaaaccttg	catgctaacc	ttccagagga	1007580
ttctgtatca	ggatttgacg	aggcttagct	ccttccgaag	gccaataat	tctagcttct	1007640
tcaagttgat	caattaaact	agctgctcgg	gcataaccaa	tttttaattt	tctttgaagg	1007700
aagggtggtg	aagcattccc	cgtctgtaaa	attaagggtt	tcgcctgagc	aaataaaggga	1007760
tctttttctc	cagagttatc	agaatcagaa	tcatacaaa	catggaaaaga	aggaatcaca	1007820
tattgtgtag	ggaatctaga	acatagatct	tgaatgactt	tgtttatgtc	ctcatcacia	1007880
atgtaggcac	cctgagctcg	tatagttcca	aaaacagaag	gaagaagtac	aagcatatca	1007940
ccatttccca	tcagattctc	tgaccaggt	tcataatga	taattctgact	attcacttta	1008000
ttggagacct	taaaagaaat	tcgagagggg	aaatttgctt	taattaaacc	tgtaattacc	1008060
tctcttgaag	ggcggttgct	tgctaaaatc	agatgaatcc	ctacagctct	agccatctga	1008120
gctaagcgaa	tgataggagt	ttcaatatct	tgggatgacg	agagaagcaa	atcagataac	1008180
tcataaatga	tcctaccat	aaagggcata	gtttcacgaa	tctccctgtc	gtaagaagcc	1008240
tcaatcgttt	tattgcgagt	gcgggagtta	aacgcttgta	tattgcgcaa	acccaaatat	1008300
ctcaaaatct	cataacgaga	ttccatttcc	ttaactaacc	aaactaaagc	attgtacact	1008360
tctcttgatt	cggtaatcac	aggagataac	atatgaggta	attgcgaata	cccagtgagc	1008420
tctacttttt	taggatcaat	aatgacgagt	ttaatttcag	aaggtaagggt	cgtcataatc	1008480
atagacatga	caatcggtgt	aatacataca	gatttccag	atcctgtagt	accagcaata	1008540
atgagatgag	gcatcgtagc	taaatcagcc	caaagattgt	caccatttgc	tttcttccct	1008600
aacaacaagg	gaatctgcaa	tttacgattt	gtcttctgat	agtcttctaa	taaatcacga	1008660
aaattcacag	cttgaggaaa	aggtgtggga	atttcaatac	ccacagcagc	tttccccgga	1008720
atcggagcaa	taatccgtat	gctcgaagct	tggagtttta	aagctatatc	attttctaaa	1008780
gatttgattt	tctgaacctt	aactccagaa	tgaggtaaca	cttcaaaagc	tgctaattgtc	1008840
ggctcctgaac	agatgttgcc	aagggtccgca	tcaattccaa	aactcgtaag	agtcgtgttt	1008900
aaaatcagag	cttttctctc	tagctcagct	tgtaaggagt	cgggacgagc	ttctctgttt	1008960
ttactaagta	aatgatattg	cggaagatca	ttttcaggga	ctgctaaact	ttttaattta	1009020
ggaagagccg	ctcttttctt	gcctttggat	tccttacta	cagtgagggt	cgaagatagc	1009080
gcaattgttt	tccttctctt	cgctttattc	tcttgaggct	caacaaattt	tgtcaggaaa	1009140
cgcttgcaag	gatgaggagt	taggaaaaag	gactctttct	tagaaccggg	gatctcttcc	1009200



tgaggtaagg	gagaaataga	cccattcttaa	atgatagtct	cagaaactcg	acgtggcgaa	1009260
ggttgcgatt	tcgtacaaga	aaaaggattc	ttggaaacaa	aaggaaccga	aggcttagga	1009320
agatagtttc	gcctatttat	taattttttt	aaatttttga	aacaagtttg	gaaaaaagag	1009380
caaaaagcct	ttttgacccc	gtcttgaaag	gtnttttttt	ttaataaagc	aatgcctgcc	1009440
gcaaagataa	aggacggaga	atagcatcac	gaatccaaaa	attagagcag	ttcctacaga	1009500
cccaattaaa	tgttttagac	aaaaagattg	gccttcgtaa	aacagataga	aagggattcc	1009560
acccacataa	gagacaggag	gaatattccc	taaaataaac	tttggagagc	gtgtatctaa	1009620
taaagcagga	agcgttccta	ctggagataa	catggataag	agaatcgagc	aacaaaaggg	1009680
gagagaaaga	aatgccgcag	ctttatagaa	gaaaagcggg	cgaggagtc	ttctgaagta	1009740
caaaaaagat	aaccaaagaa	aatatanagg	gataaaaaat	gccgcggcac	caaagaaata	1009800
aagtagaaaa	gaactaaatg	accaacctaa	tagacctatc	caattctgtg	tgacgggctg	1009860
atctctatga	aaactccata	gactgagacc	agaaaaacac	gcgaaaaata	aatataaact	1009920
ggcttttagct	gctaaaggca	aagtcggaag	acgaggggtg	ctgctctttt	ttctttctct	1009980
tatcatgggc	tacataagat	tctaagtatt	gtcgagcttc	gttatagatt	tcgttatatc	1010040
aagaaaaaca	aaagaaacaa	agaagataaa	gagggcgaa	gacggggcct	gaaccgcga	1010100
ccttcggaac	cacaatccga	cgctctaacc	agctgagcta	cgttcgccaa	accatataaa	1010160
attaaggaaa	atattagctt	cagcttgaaa	tttagccaag	ataaaaagggt	cagaatagga	1010220
aatctcaatg	ttctcactaa	gataagtagt	atgaatttct	tgaaaaacag	caaacataac	1010280
gttctttgaa	ttcaaataga	aaaccaggac	agggaaaacc	ggagctcatt	gcgaatagaa	1010340
ataggggtta	tgaataaaaa	tgcatatttt	ttttcgcgaa	atttttagccc	ttacagcccc	1010400
ttctggagca	gaaaatgggt	ttttgcaaaa	aaagaaaaaa	ataaaaagca	aacgaaatgc	1010460
gttgcgaaaa	aatgcccatt	ttttatagga	tggtgctttc	ttcttaagtg	aaacaaacaa	1010520
agaagaagag	tccacacttc	gatgtggata	cgcaacgaaa	gtttgagtat	ctgtagttaa	1010580
taggttttta	aatttttctt	cttaacaatg	caaatgagat	agaatgcagg	ccagtataaa	1010640
atgcttgtag	ggatcttttg	aaggatctgt	taattttttt	tattttttct	gagaatttga	1010700
tcttagttca	gattgaacgc	tgccggcggt	gatgaggcat	gcaagtcgaa	cggaataatg	1010760
acttcgggtg	ttatttagtg	gcggaagggt	tagtagtaca	tagataatct	gccctcaact	1010820
tggggataac	ggttggaaac	gatcgcta	accgaatgta	gtgtaattag	gcatacata	1010880
tatattaaag	aaggggatct	tcggaccttt	cgggtgagga	agagtttatg	cgatatcagc	1010940
ttgttggtgg	ggtaaaaagc	caccaaggcg	atgacgtcta	ggcggattga	gagattgacc	1011000
gccaacactg	ggactgagac	actgcccaga	ctcctacggg	aggctgcagt	cgagaattct	1011060
tcgcaatgga	cgaaagtctg	acgaagcgac	gccgcgtgtg	tgatgaaggc	cttaggggtg	1011120
taaagcactt	tcgcctggga	ataagagaga	ttggctaata	tccaatcgat	ttgagcgtac	1011180
caggtaaaaga	agcacgggct	aactccgtgc	cagcagctgc	ggtaatacgg	aggggtgctag	1011240
cgttaatcgg	atttattggg	cgtaaaaggc	gtgtaggcgg	aaaggaaagt	tagatgttaa	1011300
attttggggc	tcaaccccaa	gtcagcattt	aaaactatct	ttctagagga	tagatgggga	1011360
aaagggaatt	ccacgtgtag	cggtgaaatg	cgtagatatg	tggagaagaa	ccagtggcga	1011420
aggcgctttt	ctaattttata	cctgacgcta	aggcgcgaaa	gcaaggggag	caaacaggat	1011480
tagataccct	ggtagtcctt	gccgtaaacg	atgcatactt	gatgtggatg	gtctcaaccc	1011540
catccgtgtc	ggagctaacg	tgtaagtatt	gccgccttag	gagtacactc	gcaaggggtg	1011600
aactcaaaaag	aattgacggg	ggcccgcaca	agcagtggag	catgtgggtt	aattcgatgc	1011660
aacgcgaagg	accttacctg	gacttgacat	gtatttgaca	actgtagaaa	tacagctttc	1011720
cgcaaggaca	gatacacagg	tgctgcatgg	ctgtcgtcag	ctcgtgccgt	gaggtgttgg	1011780
gttaagtccc	gcaacgagcg	caacccttat	cgtagattgc	cagcacttag	gggtgggaact	1011840
ctaacgagac	tgccctgggt	aaccaggagg	aaggcgagga	tgacgtcaag	tcagcatggc	1011900
ccttatgtcc	agggcgacac	acgtgctaca	atgggttagta	cagaaggtag	caagatcgtg	1011960
agatggagca	aatcctaata	gctagcccca	gttcggattg	tagtctgcaa	ctcgactaca	1012020
tgaagtccga	attgctagta	atggcgtgtc	agccataacg	ccgtgaatac	gttctcgggc	1012080
cttgtagaca	ccgcccgtca	catcatggga	gttggtttta	ccttaagtcg	ttgactcaac	1012140
ctatttatag	gagagaggcg	cccaagggtga	ggctgatgac	tgggatgaag	tcgtaacaag	1012200
gtagccctac	cggaagggtg	ggctggatca	cctccttttt	aaggacaagg	aagggtgttt	1012260
ttaacaaccc	gactagggtg	ggcaagtatt	ttatattccg	cattctatct	cttttgcatt	1012320
gttaagggtg	ttttcaaaaac	attcagtata	tgatcaagta	tggttatgta	ataatcatgg	1012380
taacaagtat	ttttcacata	taataataga	cgtttaagaa	tatctgtctt	taggtgaagt	1012440
taacttgcat	ggatcaaaaa	tttacagacc	aagttgttaa	gagctattgg	cggatgcctt	1012500
ggcattgaca	ggcgatgaag	gatgcgttta	cctgcagtaa	tcttcgggtg	gctgggtatg	1012560
agctatgacc	cgaaggtatc	cgaatggggc	aaccgcgatg	actaatagtc	tatcattata	1012620
tggtgaatac	ataggcatat	aaggcgacac	ccgctgaact	gaaacatctt	agtaagcgga	1012680
ggaaaagaaa	tcaaagagat	tccctgtgta	gcggcgagcg	aaaggggaac	agcctaaacc	1012740
atatttttaa	tatgggggtg	tagggctgat	aacatgggat	cttaagtttt	agttgaatac	1012800
ttctggaaaag	ttgaacgata	caggggtgata	gtcccgtaaa	cgaaaaaaca	aaagacgcta	1012860
atcgatacct	gagtagggct	agacacgtga	aacctagtct	gaactctggg	agaccactct	1012920
ccaaggctaa	atactagtca	atgacctata	gtgaaccagt	actgtgaagg	aaaggtgaaa	1012980
agaacccttg	ttaaggggagt	gaaatagaac	ctgaaaccag	tagcttataa	gcggtcggag	1013040



acctataact	cttcgagta	atgggtgacg	gcgtgccttt	tgcattgatga	gccagggaggt	1013100
taagttaaac	ggcgagatta	agggattttac	attccggaggt	cgaagcgaaa	gcgagttttta	1013160
aaagagcgtt	ttagtcgttt	gatttagaca	cgaaccacaa	tgagctattt	atgaccaggt	1013220
tgaagcattg	gtaagacttt	gtggaggacc	gaaccagtac	atgttgaaaa	atgtttggat	1013280
gagttgtgaa	taggggtgaa	aggccaattc	aaacttggag	atatcttgtt	ctctcngaaa	1013340
taactttagg	ntagcctcgg	ntattaagtt	ttttgggggt	agagcactga	atttctaggc	1013400
ggggcctacc	ggcctaccaa	cggaaatcaa	actccgaata	ccaaaagcga	gtccgggaga	1013460
tagacagcgg	gggctaagct	tcgttgctga	gaggggaaca	gccagaccg	ccgattaagg	1013520
tccctaattt	tatgctaagt	gagtaaggaa	gtgataattc	taagacagtt	ggaatgttgg	1013580
cttagaggca	gcaatcattt	aaagagtgcg	taacagctca	ccaatcgaga	atcatcgcg	1013640
caataatgat	cggggctcaa	gcataaaacc	gacatcgcg	gtgtatatta	tgtatacgcg	1013700
gtaggagagt	gtagtattca	gcagtgaagg	tataccgaaa	ggagtgcctg	agcggatact	1013760
agtaaagatc	catggcataa	gtaacgataa	aggaagtga	aatcttcttc	gccgtaagcc	1013820
caagggtttc	agggtcaagc	tcgtcttccc	tgggttagtc	ggccccctaa	tcgaggcaca	1013880
aatgcgtaga	cgatggagca	acagggttaa	tattcctgta	ccacctaaaa	cttttagcaat	1013940
ggaatgacgg	agtacgttaa	gcacgcggac	gattggaaat	gtccgtatca	caatgagact	1014000
ggttagtagg	caaattccgt	aacacaagg	cgggttgctg	ttaagggaaa	tcttcggagg	1014060
aactgatagt	gtggcgcaag	gctttcaaga	aataatttct	agctgttgat	ggtgaccgta	1014120
ccaaaaccga	cacaggtggg	cgagatgagt	attctaaggc	gcgcgagata	actttcgtta	1014180
aggaactcgg	caaattatcc	ccgtaacttc	ggaataaggg	gagcctctta	aggtgattac	1014240
ccagcgggat	gagcctcggg	gggcccgcga	gaaatggccc	aggcgactgt	ttaacaaaaa	1014300
cacagcacta	tgcaaacctc	taaggggaag	tatatgggtg	gacgcctgcc	caatgccaaa	1014360
aggttaaagg	gatattgtcag	ccgcaaggaa	agcattgaac	ccaagccctg	gtgaatggcc	1014420
gccgtaacta	taacggtgct	aaggtagcga	aattccttgt	cgggtaagtt	ccgacctgca	1014480
cgaatgggtg	aacgatctgg	gactgtctc	aacgaaagac	tcggtgaaat	tgtagtagca	1014540
gtgaagatgc	tgtttaccgc	caaaaggacg	aaaagacccc	gtgaaccttt	actgtacttt	1014600
ggtattgatt	tttgatttgt	tatgtgtagg	atagccagga	gactatgaac	actcttcggt	1014660
aggagggtgg	gagtcattgt	tgaaatactg	gtcttaacaa	gttgggagtc	taacattact	1014720
ccatgaatct	ggagaatgga	cattgccaga	cgggcagttt	tactggggcg	gtatcctcct	1014780
aaaaagtaac	ggaggagccc	aaagcttatt	tcacgtggtt	tggcaatcac	gagtagagcg	1014840
taaaggata	aaatagggtg	actgcaagac	ttacaagtcg	agcagagacg	aaagtcgggc	1014900
ttagtatccc	ggcgggtgga	agtggaaatc	ccgtcgctta	acggataaaa	ggtactccgg	1014960
ggataacagg	ctgatcgcca	ccaagagttc	atatcgacgt	ggcgggttgg	cacctcgatg	1015020
tcggctcatc	gcacccctgg	gctggagaag	gtcccaagg	tttggtctgt	cgccaattaa	1015080
agcggtagcg	gagctgggtt	caaaacgtcg	tgagacagtt	tggtctctat	cctttgtggg	1015140
cgcaggatac	ttgaaaggag	ctgttcctag	tacgagagga	ccggaatgga	cgaaccaatg	1015200
gtgtgtcggt	tgttttgcca	aaagcatagc	cgagttagta	cgttcggaat	ggataagcat	1015260
tgaaagcatc	taaatgccaa	gcctccctta	agataaggta	tccctatgag	actccatgta	1015320
gactacgtgg	ttgatagggt	gggtgtgtac	gcacagtaat	gtgttttagct	aaccaatact	1015380
aataagttcc	tagacttggg	ttttatcata	taaaaagctg	aataagcttt	tttggtgaat	1015440
tagtcgattt	atgcaagttt	actaaagact	cttcttaagc	gtctattagt	atacgtgaaa	1015500
atacgtttaca	agatttagct	tggcgatact	ggagaaagg	atacacctga	taccattccg	1015560
aactcagaag	ttaagccttt	tatcgctgat	ggtactatac	acaagagtat	gggagagtaa	1015620
gtcgttgcca	agctttctat	tatatgtttc	ttaatacata	attaagaatt	tcaaaaggag	1015680
ataatttttt	tatcctcttt	ttttttgctg	ttttttgata	aacctattta	cccagcttgt	1015740
ttcatattta	aaagtgattt	cattgttttt	aaaataaaaa	attcgtctga	cacatgccc	1015800
ttcctataga	taattcctct	cgcaacctac	aagaagttcc	agaaagccta	gaagacctcg	1015860
aacaacacgc	agaagaatct	cttactcatc	aaaagtgcag	aaagcagttc	tttgcaactg	1015920
tctctagcct	cctcagcaat	ttctagtaga	gtagaacaac	tatcttccct	cgtcttagga	1015980
atggaaaatt	cagattttct	ctctttaaga	gacgttccct	tcttctcagc	tatctacgaa	1016040
tcttcaacac	acacacctgt	ccccactcct	ctagttggcg	tgggatatat	caacgggaag	1016100
caatcaggat	actacgatac	acaaagagaa	tctcttcacc	tcagccaatt	gttagggaag	1016160
cgaagagtgg	aagttgtcta	taaccaagga	aacttcattg	aggcctcttt	gctaaatctg	1016220
tgccccagaa	gacctcgaag	agatccctct	ccaatttctt	tagctctatt	agagctctgg	1016280
gaagcatttt	ttttagaaca	ccccccagg	agcactttta	atccaatatt	tttttggtaa	1016340
cggagctttc	tatgttcgcg	aagctctccg	cctaactccg	catgcacaga	atatagtgct	1016400
cgttgggtatc	tgtccttctc	tatatccaga	acatcctcgc	tccttttatt	atcgtgtttc	1016460
tggagatata	ggctcccgat	tcgacgatag	aggatttgta	aactctggag	tcgaaacctt	1016520
gccatactct	tcaggcagct	ttgggatttt	ttggatctcg	tttacgggat	ccacatttaa	1016580
ttttgtctatc	gtaaataacct	ttatgccaac	tgcagggatc	aatgaagtct	ctagacccat	1016640
gacacaagat	acagaaactt	cattgataga	aatgagagac	ctaagtgaac	aacaagaagc	1016700
gaataacaca	gattcttttag	agcaagaaga	gagcttaatg	ggtattgtag	gacatactgt	1016760
gggaggagtt	tccatgaccg	tgacctccag	tccaaatata	ttttatcgta	tacaaacact	1016820
tctgggactg	ccagagactc	ttgcagaagc	tgaagaaaat	cctaccttcc	caaattctac	1016880

tatagatagc	cttgacagaaa	taatgatgaa	cctcgtaagg	atctctgatg	ctgtctctat	1016940
tttctggatt	tttcctatcg	tagatactac	atataatgga	gttttattag	ccgtctgtat	1017000
cggcttcttc	ggaatcaatg	ggatttggtc	cacgttccct	atgcttacga	atccacgctc	1017060
tcgctcgagat	agatggagga	atttacgcat	catggttctt	tgctatcggt	ctttgggaag	1017120
cggatgaat	ctctttgatc	ttagcaataa	tgtgcgcatg	gcagcacgta	ggcatgtgac	1017180
atcatgtaca	gtagctctct	atgctatggt	cactctatct	ggatggacag	tagcaataca	1017240
agatgctttg	caatatgggt	tccctagcgt	tcgggatgcc	ttctatagat	attgcttacg	1017300
ccacagatat	tgcttaactc	aaagaaacga	agactctctg	caaactacag	gaacgcgctt	1017360
tcagggttacc	cgtacacatc	tagaagatca	acagatgggtg	gcttctatct	tgaatttgag	1017420
tgtttttggg	ctcttttttg	gattcgtagg	gctaatagacc	acgtttggag	gattagaaat	1017480
ctcaccatct	tgctgggtggg	atgcagcaaa	taaccgaacg	gtagggtatct	tttagactcc	1017540
aatgtttacct	tttctcaagc	tttaagtagt	ggctgtgtct	atgcagtcag	ccaatcggtg	1017600
catatgatct	tttgcttctt	ctctattatc	ttatatacga	tgtctctact	ttctcttcta	1017660
agaagacgtc	gtcgtcaata	aagaaaaacc	agatccacta	gcttccaaaa	tcatacaaga	1017720
taatcgaact	gcgctcgacc	ccatagtcac	caagaagttt	aagaatactg	ctatttgtga	1017780
gcggtggacc	acatacgtag	taaagatagt	cttcaggatt	atctaaccata	cttaattgac	1017840
ctagattaaa	gtcccgaat	aggaagtttg	tctttgtagg	gtcatcttta	tcccaacctg	1017900
cagcaatata	ttcaggaaga	ggctcagaaa	ggactagggtg	ataatggaaa	ttgggaaact	1017960
gtcgttctaa	attttcataat	tcttcttggt	aaatgttctc	ttttaatgag	cgcgccccat	1018020
accaaagatc	aattttctctc	ttggaatgct	tgtttaaaag	taaatctagg	atgtggctcc	1018080
taccaaaga	tgaacctgct	cctccaatta	ggaagattaa	agggcggtcg	tcattcttca	1018140
taaaagattc	tccataaggc	ccagaaaactg	taattttgtc	tccagggtttt	aaggagaaca	1018200
cataggagga	acagactccc	caagggatct	ctgaattagg	ctttccatta	atgaaaggag	1018260
gcgtagcaat	acgtatatta	aacttaattg	taggaagctc	ggcaggatag	gaagctaaag	1018320
aatacgcttt	gttggcagaa	tccgcaggaa	gttgactgtt	gtctataact	tgactcaata	1018380
gatgaaagt	gtcccgagtc	ctgtaatact	caggagccat	agtttgcttc	caatcggaag	1018440
agttcgtttt	atagctcggt	actgtaattt	gtaagtagcc	cccaggctta	aagggaatag	1018500
gtttattttg	gtctacagca	acaacaagtt	ctttaataaa	ggtagccaca	ttgtcattag	1018560
agataacagt	gccctcccaa	gaagaagcat	ttaaatatct	ctcttcaatt	tctaaactca	1018620
tgctcggtg	aactttgcac	tggcaggaaa	ggcgccagcc	ttcctcgagt	tgtctttttg	1018680
aaaatgtaga	acggtccggt	tctaaaggct	catcagcatt	tttaacaacg	cgaactttac	1018740
attgcttaca	ggtggctttt	cctccacaag	gggagggaat	aggaattcct	gaacttaata	1018800
atgaaactaa	gagagtctga	ccactttcga	cagtttttgt	cagttcttca	ttgtcggtta	1018860
tctttaattt	acaagggtgt	accttaatga	aaagcttgcg	agatagaagg	atcacacctg	1018920
caagaatcac	gccaatggcg	caaaagataa	gactagcaat	acaaatgaaa	tagaggcctg	1018980
aaagccaagt	cataacgata	aaaatcccag	actttatgaa	aagctcatag	agtcaaatca	1019040
taacttagcg	cataaaaaag	caataaacct	taagacaata	aataagaaat	cccacgatnt	1019100
taatcggtgg	atgaaagtct	caaaagaaat	tccttatgat	ttgttatcgt	taggcttgag	1019160
gatttcagaa	atagctcctt	ttaaaacttc	tacttttcca	gaagcaatat	ttaaaactac	1019220
cgtgtgctca	cggatatcgt	caacagtgcc	gatgattccc	atggcagtg	ctttatctcc	1019280
tttagcgaga	tcattcttac	gcttttccat	ggcctttctg	cgtttttgtt	cgggacgcca	1019340
taagataaaa	tagaaaaata	gaatagcaat	tgccaacatc	acggcagggt	gcacaaaagt	1019400
attttttgat	tgagctgctt	cttcttctgc	aaacaggggc	aaagagctca	gtaaacataa	1019460
gaaaacatgt	cactatacga	gaaagcatgc	aatcacctta	acttgggtta	attcgaagta	1019520
agattatcat	aatagggaagc	gagcattcaa	tgcttttccct	agagatcgat	ctctctttct	1019580
agtaaaataa	tattttctag	gtgcgtcgaa	tagggaaatt	ggtcaatagg	ctgcatcttt	1019640
tttatgcat	atcccccaga	gattaggtcc	gcgcactctt	gaaactgtgt	tttagggttg	1019700
caagagatat	agacaatttt	tggagatcct	atagctaaaa	tatatattaag	tactttactt	1019760
tgcataccac	aacgtggggg	atcaataata	atgacatcag	gagctttaca	attttcatte	1019820
ctttttgcaga	acgctttcgc	atcttctaaa	tagacttcta	cgcaatcttc	tttggtattc	1019880
gctttgatgt	tctcctgagc	cgaagctaca	gcacagggaa	taatctcaac	gccaatcaca	1019940
tttttgacat	agggagagag	cataatccct	atagttcctg	ctccacaata	gagatcaaga	1020000
agcgtttccg	aaccctcggg	gtttataaac	tctttcgcag	tttctataat	tttcgctgcc	1020060
tgagtaatct	gaggttgga	gaaacttctg	ggacgcaaac	taaaagaggc	agagttaccg	1020120
tcactaggta	aggacagttt	ttgctgtatc	gagggggctc	cgtatagcag	tttagtttca	1020180
taatatgtag	aaatcccacg	tgcagctacc	ttttcttccc	aatagatcga	tgctatgttt	1020240
agagaagacg	ataggagaat	ctctttccat	tcattctatac	aggcttcggt	taccctatat	1020300
tctggagttc	ctgatgttgt	taggatcacc	ataaagtttt	gctgcgggct	ccccgtacgg	1020360
acggtgagtg	tgcataacga	gcctttgttt	ttagggggga	agtagcccat	aagctctggg	1020420
tgcttatccc	accattcgcg	agtgagtttt	aaaatatcca	tagtctgctc	atggataagc	1020480
agacatgtag	tcactggaat	tcctttcttt	ggttttgtag	agctgatgaa	tcctaaactt	1020540
ttttctcctt	cataagtttg	aaaaaaggag	aattccattt	tatttcttcc	tcttaaagag	1020600
ggagaacatg	ggatgatagg	agcaatcata	tccgagggaa	ctaaaggagc	gaataactga	1020660
tgaaggagtt	cttccttttt	ctttaaggag	tcagaataat	tggactgagg	aaacgagcat	1020720

cctccacata	caccaaattg	tggacaattt	tgcatggtag	acatagttaa	gatagaagct	1020780
tagtttttgt	tagagaggta	atctgagaac	tagacaacaa	ttcacaagga	ccttcatttc	1020840
gaatccctag	atgagatact	tgaaagggtg	tttgagaata	tcaaaagcaa	aatggaaatt	1020900
ttatcacgaa	ggaaaattat	atctctacct	ttttaaggaa	gaacncctag	gtagcacaga	1020960
gaaaaatttg	ggcataaaaa	agaggatgag	tagaaaatta	cccaccctct	aaacgaaatc	1021020
aagctaaggc	gaattatttt	ctaaatccgc	gtgctttgga	aggtttttta	actttttttg	1021080
cggctgtctt	tttagatgca	ggtttagaag	ctttgactgc	tttgctagtt	ttagctgcag	1021140
cagcagagct	tttttttagg	gctttttttt	cccgagtttt	ttttactttg	gcaggagcct	1021200
tagttgatgg	cttacgtttt	aataaaccag	atttctctgc	ttttatagat	tcttttctgt	1021260
aaagtttcgc	aactttttct	aatttttatag	agtctgtgcg	tactctttga	gctgctgcct	1021320
tgtttccctt	ctctgcttta	gctaagtcgt	gttggatgct	atccagcagg	tctttcattt	1021380
tttttgccgt	atcttttagc	gccatgaaaa	gcgtccctta	gtcgtgtgtt	taaactattt	1021440
ttacttgttt	taatttttaa	ttagtttggt	tgttcaaatt	catgcaacca	tttttttagag	1021500
aaaataagac	ttttgtaagt	tattgttatt	ttgttatgag	aacacacttc	tttgtttctc	1021560
aatgtgttaa	tttataaaat	gtttggaaaa	taaaatggag	aacgtatttg	tatcaatttt	1021620
aggatttggt	tttttttttc	gtgttttgag	tgatcattgg	gaacgtagtt	tctatagatc	1021680
tgtagcatgt	agagaaaaac	atattttctt	atcctttact	ttcgagaaat	gtctgtctata	1021740
gaatgtagtt	caaagaatgc	taccccccaa	tatatcacc	taccttattt	ctgagacctt	1021800
aaaggaatag	aagtatttag	atgaagaagc	gtttgacact	gatttcagga	aatttccac	1021860
tgattcggct	gagcctcatt	tttgcgtaa	atatgcactc	agcattaata	tcagggaaaa	1021920
agcagaaaatc	ctttggtcat	tgctgtgcag	agcgggttct	tgccgacaga	gagactttga	1021980
attgtgaaga	actctttgca	gattttattg	tagtccgcga	gtatctcttg	aagtgtattc	1022040
ctgcccgtga	ttggggaaact	gttggtgtct	ttcttcagaa	actcctagcc	ttacgcttgc	1022100
gtaaagggtga	ttgtgactat	ggagtgaaaa	tatggcaccg	gttgaatcca	gagcaggctc	1022160
cgaaggatgc	taggaaagac	ttgcagatct	ctataggctg	tcacgaatct	ttgcaagatc	1022220
ctttgcgaga	tggtgttgat	cagcttttca	tgcatagcgg	ttatgaaaac	cgtaaacagg	1022280
acttgctttt	tgagctctac	accgtgacat	acaaaaaagc	tatagaattg	gcaaaaagagc	1022340
atatgctttt	agctaaagaa	caaggggatt	gccctcacc	agagatagt	caaatagaaa	1022400
tggttgccagc	attggaaaaag	ggatcgtgta	tgcaaatata	agtagcaca	gaagctcaag	1022460
aaactttttt	gcaaaaaaca	ctgcttgctt	gtttgtctga	aattgcctat	actgaagcta	1022520
aactcttgca	tgctttactc	acaccctact	gtgaagtctc	tcgtactaat	gaggtggata	1022580
tggtatgctt	ggtagctgct	atagctagag	tccttttcgc	acgggaaaaa	gcgattcctg	1022640
gtgtcttact	gagccatgcc	ttacaacacc	atctagaatc	cacattacta	tactatgcat	1022700
aacttgaagt	tcttattgat	cacggagcct	ataaagactt	tgcatcgcta	gagcgtttgc	1022760
acttctcttt	attagaactt	tatcatcaaa	agcatcccta	tttcccagaa	tatgggtttt	1022820
tagagaaggg	tgatgctgtc	tttgctccctg	aatacgagag	cgctgagaaa	gttttcttac	1022880
ttctaggtgc	atattttctat	gctaaaggga	ctacttttgc	tagagcatat	gaatatctag	1022940
agattataga	tcccgtctga	aaactaggag	agaagtcgga	agaatacttt	ctccgtgctt	1023000
ggtgtattgc	ttatgttcag	aatcattacg	taggattatt	tttagcatac	gctgtgcaaa	1023060
ataagagttg	gggacgcgaa	gagtcaggta	accatccctaa	gttttctttt	acctaccgtc	1023120
agaaaaagac	tgcatgtgag	gatatgctct	atccacatgg	ggaaaataag	ggcagctctg	1023180
atlttgctaga	ttctctctgt	tctttatcgt	agcttttcaga	gatttatagc	cgctgtatct	1023240
cgatccaaag	agtcctatag	gctgtacccg	tataagaaat	ttgtagggat	gcgcaagatc	1023300
atgatatgat	taaataatag	aatgttacct	tagaagaaat	atcgccctca	ctctgtccaa	1023360
accaagtccg	caattttagaa	aaacgtaatt	atcgccctca	atcgccctca	ctctgtccaa	1023420
cagaatatga	taaagcttta	gcctttttgg	gagcccttca	cacaatacgt	tgctatgagg	1023480
ggtctctcat	tgaaagttca	gatgtggatg	aagccggaat	tcaagcgttt	tctgaagaat	1023540
ctttatattt	tcacaatcca	gatgctatag	ctatgcttcc	agtacgacct	aaaggagctc	1023600
gtaattcttg	gcaaacggca	ctgcgactcg	tttgacgttt	ccatggggat	agcctatatt	1023660
ctaatacacgc	taagtattgg	gatcaccttg	tgctccgtcc	agatgccttg	aagcatctgt	1023720
tttttggtta	tgaccttcaa	gaatatctca	ttggcaaaga	gcttggtatac	tatttacaag	1023780
ctgtattttgc	ggaaactcttc	cctaaatctt	cgctgctttc	tgtaaaagct	cttgaagagt	1023840
gctatagcga	atcctcggct	ttgaggaaaag	tcggatgggt	ggcgatatatc	tattatatgg	1023900
tcactgagat	ttcttggtcg	ggagagcata	tgaagacatg	cttttctcag	gcagttcata	1023960
tgaagttaga	tcttgctgat	acctacatct	cttttagcaa	tcccaacta	catttcctta	1024020
ttcttgagga	ggtttaaggaa	gattggcaag	tcgccagtca	agagggattg	gcctatgcgt	1024080
agggagagga	ctgttactta	gctatggaac	tgcgatgggt	tcttgagcat	gtagaaaaga	1024140
actttcagtt	acatgagacc	gcacacttgt	ccaatcatct	gtctctacag	agaactctgg	1024200
atttaatttc	cccacgttct	tacagagact	attatggcga	catgatatgc	agaagctata	1024260
ggttggtgcca	gcgtttcttc	ggtgtgtaaa	tcacagatag	tttttaaatt	tcctggtaag	1024320
catcgattca	gtcctggggc	tgcaatattt	tgacctacaa	catgttggtg	catgcatcc	1024380
tgaggttaga	tacgtctctt	cctttctaga	aagccaacag	tattcaggta	ttctgagaga	1024440
tgagatgaaa	ataaagcaaa	agcatctggt	ttttgattga	gagaagggag		1024500
gctgctatcg	caaaggcatg	agcttctgat	tcccgcatt			1024560

agcactgttt	tccctggcgt	acttgcgga	agatttgaga	attccaaacg	attcccaaga	1024620
ggggaagctc	gtctgcaa	agcatgccat	aacctttggg	aagcgaaaag	ttggcgat	1024680
gccaacctaa	gctgatgcta	gataaattcc	aaggagaaac	tcttttagat	aaattttcaa	1024740
ttccatagtt	aggaagcaat	acaggaagct	gctggagagg	tctgtataa	attaccatat	1024800
cggcaaaaaa	cgtctctgaa	ggtgtgggta	cacaagcttc	ttttgggtgaa	caatcgatgt	1024860
gagtcacact	agtagaaaac	ttccatgttg	cggggagttt	ttcttggata	gtagtaatca	1024920
aagtccecat	ggaaggagat	agagatgcaa	gatatctgtc	ggtcttagac	tttttggggg	1024980
atctattttt	aagataactg	cgtaatagag	accgctgga	agcttctctc	tttgctagtt	1025040
caggaaatgc	catgtgtgtg	gagagaatgc	tgctatggcc	tgcgcgatg	gctgtgatta	1025100
gtggatctaa	tatatagctt	gtaaaatttt	gtgaactatg	tcgctttaag	aaatcctgaa	1025160
cggaaactatc	ttgagtatag	caagggtgcac	ggaagtcctt	aattaaagaa	ggaagcaggc	1025220
cctttcttag	gagagtcag	gtggatattt	tacgggcctt	ccctctgtag	tagacaaaagc	1025280
ggttttttgc	tgacgatca	ctgaagatca	aggaattttg	gagaccaagt	tcatggataa	1025340
gttttagagt	atactctccg	tctccccggg	tgaggaatcc	tttaggtccg	aggtcaaaaag	1025400
aaaacccttg	aggggattcc	gtgcggacga	agcctcctgc	gtaggcttct	ttatctaaaa	1025460
caaggatttc	cgcttggggg	aatttcttat	gaagccacca	acctgcagca	agaccagaaa	1025520
ttcctgcgct	tataatgatt	gctctcttca	cacaaaacct	cctctctgct	cagtttctca	1025580
acatttttat	atagaagctg	agaaacattc	tttttttagat	accttattga	gaaaatagtg	1025640
atcgaaagct	gtggcaatga	ctctgacaaa	caattctcca	agaggagtta	ctttcaaaga	1025700
gccaggactg	ttatggatga	gacctgtagt	ttccatactt	atcaagcgat	cacgactttc	1025760
tataaaataa	gtatcaaaact	catatccaaa	aagggtgaaa	aactcttcct	tattgatcgt	1025820
aaacgtgcac	atcagcttat	ggattgcccc	ttttctaatc	cgatcatcct	cggtaagaat	1025880
tttacttttc	acagtggcaa	atgttctctg	aagcaccgta	ttgtgatatt	cctcaagggt	1025940
ttttgcattt	tgtagataaa	ttccacgaat	gaagcttgta	gaagtcattc	ctaaccggag	1026000
cagatcttct	tctgggggta	gagaataccc	ctgaaagtgtg	cggattagag	ttttgttttt	1026060
gaaagcgagg	gtaagaggat	catggggaag	agagaaatga	tccataccga	tgccctgata	1026120
tctgtctttt	gtaagtaaat	gccgggattg	agaataaatc	gcgaatttct	cttccataga	1026180
aggcatatcc	gaagctttca	tggtcttttg	gtgcggcttg	atccatggaa	ctgaggcaaa	1026240
agaaaataaa	gcaagacgat	ctggatacat	cgctaagata	tcttgaattg	ttttagaaaa	1026300
ggactccttg	gtttgttttg	gaagaccata	aattaagtct	atattgatac	tttgggaaggc	1026360
gagttcctta	aatttttctg	atgcctttta	agattcctca	tgcgattggc	gtcgtcgtag	1026420
agcttcttga	acatcagctt	gggtatcttg	aaccgcttaag	ctaaccctat	taaaacctac	1026480
gttctgaaag	aaatctgctt	tttccatgtc	gtttctttaa	gaacgaggat	ccacttcaat	1026540
agcaatttct	tcagcatgtg	aaagatcaaa	aagcttatgg	atgtggtcaa	aaagcagggt	1026600
aaacaactcc	ctggagagtc	tgctaggggt	gcctcctcca	aaatgaatcc	tggtacactg	1026660
aggccggaat	cctatggctt	caacgacaag	tttcatctct	tggtatagg	tggtgatata	1026720
agcttctaca	atatcttcac	gacgattcaa	aacaacagaa	caaccgcaat	acaaacacat	1026780
ggattggcag	aaggggatat	gaaaataaag	agagagaggc	tgagnattnt	ctctaantct	1026840
ttggaacgct	agaagagctg	gagccgcac	ggaaggttcc	cattctaaag	ctgtagggta	1026900
gcttgtgtat	ctgggcgcgg	gttgatgaag	tccttctaag	aattttaaag	tgacgttgaa	1026960
cataagaaac	ttaccaattg	acgttttcta	aaggtgttct	aggaagaatc	ccatgtccag	1027020
aattaaaaat	gaagtttaga	tatgttctta	aaggaacaag	gaaggcttct	acatagtgtg	1027080
ataattttct	ttggggcaat	aaaaatattg	ccggatccaa	gtttccttgt	agggagagca	1027140
taagattttt	ttgtatgcga	tgaaggtcca	catgataatc	aggatggagt	gtatcggctt	1027200
gcgtggcttg	cagagtataa	aaattttctt	caaaacaacg	acaaaataaa	ctcacaggaa	1027260
tgccctgctc	tttaagtttt	gctatcagac	gacggttttg	ttcagtcaca	tagcgtgtaa	1027320
agagtgtcga	agggagacgt	agactcgaag	attcaaaaag	ctgcacagca	gcagctcctg	1027380
cataccattg	tgtttttaga	taaatagcag	tcccttcgat	aattgtagag	atgagctgat	1027440
caaatttttc	aggatacaca	tagagaaaag	acatggtcct	agaaaaatct	ttggaagcac	1027500
ctccatcaat	taagtagcag	gcgagtgtga	agggagatgc	tgcaaaaaca	atcagcggaa	1027560
caggaaagtt	ttgcttaaga	gttcgaatcg	cgtccaaaag	atagctaaag	atgggttgtg	1027620
gatcggaagt	gaaagtgaag	ggttgtctct	gagaaaattg	tatgcgcgga	ccaggagcaa	1027680
agtcataaggt	cacagcaaaa	ccatccaaga	tggtataggat	atcagcaaaag	agaatagcag	1027740
catctacatg	tagcaacgag	ggccctaaaa	gcgtagctct	acaatagctt	cagtattatg	1027800
gaaaaaggtt	ttaaagattg	ggatcctttc	agctcttggt	atggaggcat	gtaccttctc	1027860
acctgtcgtg	atagccatat	gggaggtatg	gagggcagtt	gagattttta	aagatcaaaa	1027920
aaagcagaca	tagagtccca	attatgaagc	gttgattaag	aagccccctt	ctatggactc	1027980
aatgacttct	ttgactagaa	gttcaggagt	tggtagataga	gcatagggca	aggttttctt	1028040
tgtctgttca	gatttgctaa	ggcatttttg	cacatataaa	gcattcgcag	ttcccttaat	1028100
gctagaaatg	ccatgctgca	aagcaaatag	gcgtattttca	gcaagggcaa	aaagccagca	1028160
gatctcttga	ggtaatgggc	caaagcgatc	tcgcattttct	tcttgtattg	cggtaagctc	1028220
ttcagagctt	tcagcattac	caatcttttg	gtaaaactca	atgcgcacgc	atccagtttc	1028280
gatgtaagta	tcaggaatac	gcgaattgtg	aggaaattct	attttcacat	cgctgttgaa	1028340
aagtaggggg	gacgtgtgtt	tttttaaagc	tgaaacagct	tttttttagta	atttgcaata	1028400

cåaatåaac	cctatagtcc	cgatatgtcc	cgactgatcg	gttcctagaa	tattccctgc	1028460
accgcggatt	tctaaatcat	ggaggggcaat	cttcattcccc	cctccatatt	cctgcttatt	1028520
taaagcagcg	agtcgcttcg	ctgctggccc	agacaacctg	tctaagttag	gaactagaaa	1028580
ataacaatag	gcctttttat	tccatcgccc	gacacgtccc	ttcattttgat	ataaatccgc	1028640
cattccaaac	ttatcggcat	gatctatcaa	aatgggtattg	gcgttttgaa	tatcaatccc	1028700
gttttctatc	agtgcagtag	caacgaggat	gtcggttttc	tgatttttga	atttcgtaaa	1028760
gatattagag	aggtccctcag	ctcccatttg	accatgagct	acgccaatac	gagcctcagg	1028820
aatcagattg	cgaatggctc	cagcaagagt	atagatgctc	tcaatccgat	tatgaatgac	1028880
ataggcttgt	cctcctcgaa	ggagctcgtg	ccttaaagcc	gctgtcaatg	tttctgtatt	1028940
atgctccatg	acaaaagtac	ttacaggcaa	cctatccaag	ggaggcatgg	caatcacaga	1029000
tagatcacga	gctcctgata	gagacatgtg	caatgtcctt	gggatgggag	tcgcagatac	1029060
tgtaagacag	tcaatcatgg	gatagcgctc	cttcagattg	tccttaactt	taactccaaa	1029120
gcgttggttct	tcatcaataa	ttaataaacc	agggttctta	aactctaggc	ttttgttaat	1029180
gagtttgtag	gttccaatga	taatgtcaat	ttgtcctgaa	gctacttgct	cacagatgag	1029240
tttttgact	ttggcttggg	agaaacgtga	aagcacagca	atttcgatcg	gcaatcccg	1029300
cattctttct	ttaaaagt	catagtgtg	agttgctaaa	atcggttggtg	gaaccataac	1029360
aatgacttgt	cgatggccat	cgcaaacagc	cttgacagca	gcccgcagta	tgacttcagt	1029420
tttcccaaag	cgagcatctc	cgcaaattaa	tctatccatg	agttttggag	acatcatgtc	1029480
attgtaaatc	tgatcaatag	tctttaactg	atcggggggtt	tcttcatagg	gaaacgtttc	1029540
cgaaacttg	attacggact	ctccgtgagg	agggtacaca	aaagcaggag	ttgtcgaacg	1029600
ttgtgcttct	aactgtgaaga	gcttctctgc	gtagacaatc	aaagattttt	cagtaagatc	1029660
tctagagcgc	ttccatttctg	aactatttaa	atgatggaga	tcggcagctt	tatcagaagt	1029720
cccaacatac	cgagagatca	gataggcttg	gttcgaagga	acataaagcc	gagctttatc	1029780
tgcatattct	aaaacaagat	aatccgtttc	aatattcaga	tggttcgggt	ttttttctat	1029840
tcctaggaat	tttccaattc	cattatgaat	atggacaaca	gtctctctcg	gaatcggaac	1029900
aaaaacttct	tcagtagtca	ctgaaaagtg	agtgcgttgt	ttttgcctac	gcaatacttt	1029960
tgtagaagca	aactcggata	gggaaatcgc	tgcaaaggct	tcggtttacta	atgcaaagct	1030020
ggaagttaga	ttccctgttt	tttcatagat	ttccacatcc	ccacgagcta	cagtctctgc	1030080
tagagcacgg	gcctctttta	aagatttctg	ttttgtgctg	tagatggcta	attttaaggg	1030140
ctttccatga	ggaggcatat	attcttgaag	atgctgtagg	aaagcaagta	gggattctc	1030200
atcgttctga	ataatttgct	caggatacag	tatagggaac	gcttggcgac	tcgcttccat	1030260
gtttcgggtga	aatgcttcga	tgatgacgcg	gttttccttg	agattcttga	cgtaggaaa	1030320
cggagtctcc	gagaaataaa	cttgattaga	cgtagaaatg	cgatcgtaga	gagtgccaat	1030380
agagaaaaat	ctatctggaa	gggacgaaag	tgttccagaa	atatccgcaa	agtcattctc	1030440
tagaatttct	aagttatcaa	agagatagag	aggaggggtg	ctgaaatagt	ctaatagtga	1030500
atgagaatag	tttccctccag	aggcctcttc	tgtgtacgct	ggagagatag	aaattttaga	1030560
gacttttctc	gtcgatagct	gatccgaagg	attgtaagat	ctgatagaaa	tgatcttctc	1030620
tccccaaaa	tctatcctaa	aaggctctgg	cgaggataac	gggaaaaatat	caacaattcc	1030680
tccgcgacaa	gaaaattctc	ccttttcgct	agttagcatg	acctgagaat	atcctaaact	1030740
tttacagagt	tccgtagtgt	cttctggatc	taagacatct	ccaactgcga	gatcaagatg	1030800
ttgttgactt	gtagcttggtg	gagaacgggt	tttttctaaa	agagctttta	atgtagtga	1030860
acagaatata	ggagccctgt	gctgattcaa	gctgtaaaga	agatgatctc	gcttccccac	1030920
agcatctatg	ttactaatt	ttggagagag	atcaatttca	gaagagggaa	attctacagg	1030980
agcttggtct	aaaaaggctc	ttaaattttc	aaagagatca	tcaagacgtg	cgggtgtcgt	1031040
aatcataatt	acagaagcac	gacagtcag	aaacatcttt	gctgcaagga	atgccgtggc	1031100
tcctggatga	atatttttcta	atagtaaagg	aagtgtttcc	cttttgaatt	ctttggaaat	1031160
agaaaaatct	aaattaactg	ggttgaaatc	cattgccata	aagtttcatt	taataacttct	1031220
gttgctggga	gagcgggagc	actaccttgg	gccgattgat	cttttctctc	ccagegacca	1031280
ccgcaaggag	taagaacagc	tttcaataaa	tcctgagcat	ggacgccttg	tgtgataagg	1031340
tcgtcagaga	ctcgagatag	tacaatatat	ttcccathtt	tctctgttgt	ccacagagaa	1031400
attagttttt	ctggaatcct	ttgatgcaaa	cattgtgcgt	actgctgcaa	acggtgggtc	1031460
tcagtgtctg	cgagatgatg	cacgaggcaa	gtgattcctt	gacgttgatg	acaattgtgg	1031520
attaacttgt	ctaattttgt	ctgaatcaga	ctgttttcta	actcatttaa	ccgtttgtct	1031580
tggtgtttgc	gctcatctaa	agttgcagtt	agcctggaga	caactctgac	cctaggagact	1031640
tgtaatagcg	tacaatctct	tctaataact	cgctttgttg	gtgtactgta	gcttcggcctt	1031700
tttctccagt	gacgcctca	atacggcgga	tgcccatggc	cacagcatgt	tctttggtaa	1031760
tccggaagaa	tccgatatcc	ccagtagctt	ccgcagtcgt	gcctccacaa	agttcatgag	1031820
agtgccttgc	agaaactaca	cgaaccacat	cgctatactt	atccccgaag	aattgcttga	1031880
tttctgatga	gttcatcaca	tcagaataga	gagcttcacg	aatatctaca	ggctcattct	1031940
cccggatact	ttcattgact	agagtctcaa	tacaaagaag	atcttcagggt	gaaattgcct	1032000
gggggtgagt	aaagtctaaa	cgaatttttg	tatcgtaaac	ataggagcct	gcttgacgga	1032060
tgtgatcacc	caaagtgtat	tctaaagctt	tgtgtaatag	gtggcaggca	gtgtgattgt	1032120
tggcaatcct	ctttctacga	taacgattta	cctgagcagt	cactgcagct	tctacagtca	1032180
gacttccttg	ggaaattctt	ccatgatgta	cgattaaccc	ggcttttgga	gatgtcgtat	1032240

gggtaacaat	aaaggtcccc	tcactacaaa	agatctcccc	agaatctcca	acttgtcccc	1032300
ctttttctgc	ataaaaagga	gaaactttta	atacaatagc	accctcttgc	ttctcttgaa	1032360
gcgaagaaac	tatgtgatct	ttagaaatga	tagcttcgat	gaacgtatca	caagagagat	1032420
gatcataccc	tataaattct	gaagttaaat	gtagtccatt	gtagatagat	tccgaagtcc	1032480
cttgggattg	aactacgttt	tttctagaac	gttcttttagc	ttcttgctct	aacttatgga	1032540
aggtatccat	gtcgacacta	tagtcgtaat	ctttagctaa	caaagaaatc	tcacatcaatgg	1032600
gcatgccata	ggtatctttg	agcttgaaaag	catcttcacc	tgaaatgcaa	gaggaggaag	1032660
aagaactttt	caaaaacttgc	tgtagaaggt	ttcctccacg	gtcaagagtt	ttaaagaaac	1032720
tttcttcttc	taaagtgagt	actttttgaa	tttgggatag	cgaattcttt	aattcaggggt	1032780
aggcctctcc	catagcatct	gctaattgagg	gaacaatttc	tgctaagaag	ggattgcgaa	1032840
accctaaacg	ccgtccatag	tttacggatc	gtctcaaaat	ttttcttaga	acatagcctc	1032900
gctcagtgtt	tcctggaagg	agaccatcag	cgatagcaaa	agataaagaa	cgtacatgat	1032960
ccgcaattac	ccggaaagct	gcaccactat	catcgggatg	atagactttc	ccagagagct	1033020
gctcagtctt	tgcaatcagt	cgcgcaaacac	atccgcttca	aaaacagtgt	gcgtcccagc	1033080
aattaaagag	acaagtctct	ctagaccagc	tcctgtatcc	acatgtttat	taggtaaagc	1033140
aagtaaagag	ccttcgctgg	tacgattgaa	ttccatgaa	actaaattcc	aattattctaa	1033200
gaaacgctct	ccatcagtat	cgtcaagggg	agaagaggcg	tttccaaaac	tggggccacg	1033260
atcaaagagg	agctcggaa	aatagccaca	ggggcctgtg	tttgccatgc	tccagaagtt	1033320
gtctttgtct	gtaagacgga	aaatacgatc	tgtaggaaga	tatgcttccc	aaagagcaaa	1033380
tgcttcatcg	tctttttcat	gtacggtagc	gtaaatcctt	cgggattaaa	attaaaaaca	1033440
gataaagaga	cttcccaagc	aaaggcaatc	gcctctgctt	taaagtagtc	tccgaaagaa	1033500
aaattcccta	acatctcgaa	gaaggtgagg	tgcttgaag	tatgaccac	attatctagg	1033560
tcgttgtgtt	tccttccagc	tcgaatacat	ttctgcatg	ttgtggctcg	agagtgcctc	1033620
accttctctt	tatttaggaa	aatatcctta	aactgattca	ttcctgcatt	cgtaaaaagg	1033680
atcgagggat	cattgtgagg	aaatactgga	gaagagggaa	gaatgggatg	gtggcgggta	1033740
gcatagaatt	ttaaaaaatt	ggagcgaata	gtattgctta	acatgaaaaa	gaactctcaa	1033800
cggcagcggg	tttgcagatt	ccttgccatt	ataggagagt	tctttatttt	cgtctctatc	1033860
cctaattttt	agttaaaaaa	ctttcctgtt	tattattgag	atttgatcga	aaattcattt	1033920
gtttttgaaa	gaattacaag	gtaagagttc	cttgcttttt	gcttggggat	ttcctatagt	1033980
tgctgctttt	acatagaagg	tctccagggg	ttacttatga	tcaataaaga	attagatatt	1034040
ggtatttttag	gaaaaattgc	tggggctatt	aaacaaatta	gtattgaatc	catccaaaag	1034100
gcctcttctg	gtcatccagg	acttccccta	ggatgcgcag	aacttgctgc	ctatttatat	1034160
ggttatgtcc	tgcggcacaaa	tccacgtgat	ccccattgga	ttaataggga	tcggtttgtc	1034220
ttgtcagcag	gtcatggatc	tgctcttctc	tattcttgtt	tgcatcttgc	cggatttgat	1034280
gtttccttag	aggatcttca	ggaatttcgc	cagcttcact	cccgaactcc	cgggcatccc	1034340
gagtacggcg	aaactgtggg	agtcgaagca	acgacaggtc	ctctgggaca	gggattaggc	1034400
aatgctgtcg	gcatggcgct	ctctatgaag	atgttggaat	cccgaattcaa	tcgcccagga	1034460
catgagattt	ttaacggaaa	aatctattgt	ttggcagggg	atggctgttt	tatggaggga	1034520
gtcagccacg	aagttttag	ctttgcaggc	tctttaaatt	taaataatct	tgtggatc	1034580
tatgactaca	ataatgttgt	tctcgatgga	tatcttaattg	aaattagtgt	tgaggataca	1034640
aaaaaacgtt	ttgaagccta	tggctgggag	tattatgaaa	ttgatgggta	tgattttacc	1034700
catattcatg	agacattctc	gagcatcaaa	cgggggcagg	aacgtcctgt	attagtgatt	1034760
gcacatacaa	ttatttggtca	tggttcgcct	aaggaaggga	caaataaggc	tcatgggtct	1034820
cctttaggag	tcgaagggac	tcatgaaaca	aaacagtttt	ggcatctccc	tgaagaaaag	1034880
ttttttgtcc	ctcctgcagt	aaagaacttc	tttgctcata	aaatacaaga	agatcgaaaa	1034940
gcacaggagc	aatggctgga	tgaagttcgt	gtttgggtcaa	aacagttccc	agaattacac	1035000
gaagaattcg	ttgcgttgac	ctctcataag	ttacctaaaa	acttagaatc	cttgggtcag	1035060
agtgtagaaa	tgccagactc	tatagctggc	cgggctgctt	caaataaact	gatccaagta	1035120
ttagtacagc	acattcctta	tttgattgga	gggtccgcag	atctttcaag	ctcagatgga	1035180
acttggattg	cgaatgagaa	agtcatccat	acgtatgact	tctctggaag	gaacattaaa	1035240
tacggcgctc	gtgagtttgg	tatggccaca	atcatgaatg	gttttagctta	tagccaggta	1035300
tttcgtcctt	ttgggtggaac	attttttagtt	ttttctgact	atatgcgtaa	tgcaattcgc	1035360
ttggccgcat	tatctaaatt	accagtcac	tatcaattta	cccatgatcc	tatatttgtt	1035420
ggagaagatg	gacctacgca	tcagcctgtg	gaacaattga	tgtctttgcg	cgcgatccct	1035480
ggattgtatg	taatacgtcc	tgccgatgct	aatgaagtta	gaggagcggtg	gattgcagga	1035540
ttaaagcaca	caggtcctac	agtcattgtc	ttgtcgcgac	aagcattgcc	cacactgcct	1035600
gctgcgcac	ggccttttaa	agatgggtgta	ggctcgtggg	cttatattgt	cttaaaagag	1035660
tcaggagaaa	aaccagacta	tactctcttc	gctacagggt	cagaagtttc	tttagctctt	1035720
tctgtagcta	aagaactcga	acacttggat	aagcaagtgc	gtgtagtttc	tttcccttgt	1035780
tgggagcttt	ttgaagctca	agatgtggac	tacaaacaga	gtattgtagg	cggagatctt	1035840
ggaattcgtg	tctctataga	agcaggatct	gctttggggg	ggtataagta	tatcggatct	1035900
gaaggtttac	tatcgctatg	gatagattcg	gatactcagg	agcttctgat	gatgtatcag	1035960
aagaatgtgg	ctttactaca	gagcaaatcc	ttcagaggat	tctctctcaa	tagtcactgt	1036020
cggaagtttc	agagccgcta	gccatagtgt	catcggcttc	tccaacttcc	atatgaggta	1036080

atcctcgata	ctgttgatcc	ttcttatggt	cagaagctgc	tcgttttagc	atgacttttt	1036140
caagggtctc	tatgacttct	tgtcctgtta	agatgtggtc	ttccgtataa	gtattaaaga	1036200
tgaagttccc	actggacttc	gttttgattc	cctccttcct	taagggaaga	tctgaaatca	1036260
ataataacgc	tccaatgggc	aggtttctac	ggtatccggc	agcaaaaagt	gtcgcacact	1036320
ccatttcagc	ggattgagct	ttggtttcgt	acagtttttt	tctaaatfff	ttgttaaatt	1036380
cccaaaagcg	aatgttggtc	gtgtgggtaa	tgccaatatg	gtagtttgcc	ttcttatctt	1036440
ctaaaacttc	agttgttgct	ttctgtacaa	caaaatttgc	aagagccgga	acttcaggag	1036500
ggaaataggg	gtctgaagta	ccctctccac	gtatgctagc	tacggggaca	aagtaatctc	1036560
caacctgata	atgagagcgt	aagcccccac	acattcctaa	cataagcgct	gctttgagat	1036620
caggaagaaa	tgaacataag	tctatagtta	atgcagctcc	tggagaccct	agtttaaagt	1036680
ctaaaattga	agttttaaga	tgaggagcat	gggcagcaga	aaacatagaa	ccctcaaaga	1036740
cgggcacccc	atgaagtttt	gcaaagggtt	ggatatagta	agagaagttc	gtgagtaaga	1036800
gataaggaca	aaattgcttt	acgctagagc	cagaataacg	ttctaacata	tcttgagcaa	1036860
tcctggattc	agaagtatgt	ttggacacac	gctctccttt	gtaatgtttt	cttctcagat	1036920
tcttagcatt	cttatcggtt	ctcgggtcatt	aaaaaaatcc	tagaaatcaa	aagatagaa	1036980
tctgataagg	gacagctgca	atcattttaca	tagaaggaga	gtccttcgat	tcctgatgta	1037040
cattcttctg	gacaaaggag	aaaaagctcg	ataacataaa	tcgaagaaaa	ttaagaaata	1037100
gattgcttta	tgggttcgtg	aagtactagt	gaattccgtg	tgggattaag	aatagaaatt	1037160
gatggtcagc	cctacttgat	tttacaaaat	gattttgtaa	agccaggaaa	aggccaggct	1037220
tttaatagaa	tcaaagtaaa	aaatttttta	actggcagag	tcattgaacg	aacctataag	1037280
tctggagaat	ctgtagagac	tgcagatatc	gtagagcgct	ccatgcgctt	tctgtatact	1037340
gaccaagaag	gggccacgtt	tatggatgac	gagacctttg	agcaggaggt	tgtcttctgg	1037400
gagaaactcg	agaatattag	acagtgggta	ttagaagata	ccatctacac	cctagtttta	1037460
tataacgggg	atgtggttgc	tgtagagcct	cctattttta	tggagcttag	cattgcagaa	1037520
acagctccag	gagtgcgtgg	agatacagca	tcagggcgtg	ttttgaagcc	agccgtgacg	1037580
aatacaggag	ctaagatcat	ggtccctatc	tttattgatg	aagggggaatt	ggtcaaagta	1037640
gatactcgta	cgggaagcta	cgaatcccga	gtttctaaat	agattgccgt	tgtaggaaaa	1037700
gtatttcttt	tttacagtgc	gtaatatgga	agctaagaaa	atcaaagagc	tatctaaaga	1037760
agctcaattg	ctaaaaaaat	taagagagaa	gtctcggggt	cttgatgaaa	agaacaagcg	1037820
caaagcttgg	gttgctaagc	ttgtagctat	gccagagtct	atccgagaga	tagagaaaga	1037880
agagcgcgta	gaaactcctc	aattatttca	agctatagca	gagaagattt	tagaagaagg	1037940
tgtttagtca	cctgaatctt	cctgcatcat	tctataactt	ctgacagtcc	caagttgctt	1038000
cattagcaat	ttctaaagg	gcatcaaaat	ctaagagatt	tttcaaaatc	atagtgtgca	1038060
cctgatattt	ttcaggatac	aagtctataa	catggaaacg	tgaattcggt	ggtagagaga	1038120
tcgacccgct	attgagaata	taagagggcg	aagtgtccgc	acaattgtaa	acagcagctt	1038180
ggtgttcgtg	accgtgtaga	taaaggcgta	ccttgggata	tttcttcaaa	acgttttgaa	1038240
gatgtgtatt	gttgataaga	tcagtactgg	gattttgtga	agagagcaga	ggataattgt	1038300
ttgcaatgat	gacattctct	tcaggggaaa	gagagagcaa	aaagggttca	atagccgaaa	1038360
tctgtgctaa	atgcaccact	ccatttgctg	aaaaccatcc	attcaaacia	gaacaatcta	1038420
ataaaattaa	ccaccaatga	tcagtgatct	tgtgaaagga	caccttattc	tgttgagact	1038480
ggtcatttgg	gaagtgggtg	taaaacgttt	gttggtgcaag	agatttcagg	gtgtagacat	1038540
cgtggttgcc	aggcaaaagg	taaaccgagg	aatgcttagc	gagagtttca	acgaaatgct	1038600
tagcgagtaa	gaactctcca	tccatagccg	tgaggggagaa	atctcccgtg	atgcacacgc	1038660
tatccgctcc	aagagatcgg	actaccttag	ggaaacgctg	ccctatagtt	gtagcttgaa	1038720
aatggactaa	cccaaatacc	ttgcgcagaa	gtccttttag	ccttttatta	aagcagtga	1038780
cgggattgac	agggagaaca	tgaaaatgta	catcggaat	gtgaataata	cgatgcacat	1038840
gtcggggctt	ttcttgcata	ggacgtgggt	tacttttgtt	ttcttgatct	actgtattag	1038900
aatctagggg	aaaatttctaa	caacaaagat	cgatctctaa	ggagaagccc	ttagagtcaa	1038960
gattctaagg	ggctatccca	aatgattgat	accaaggggt	ttattaattt	tataagagaa	1039020
gatcagagcg	tagaaatctc	atattgattt	tctaaaatta	aaattttaga	agagagaacg	1039080
agaatcgctg	tatctaaggc	ttgggctagg	attgtagatg	tcgtagctaa	cgaatctaag	1039140
attccaccag	caataagatc	ttcaatttct	ctagaaaaca	cactgattcc	taggcttggt	1039200
gttccaagtg	aggagagctt	agcaatcacg	gcacccccat	ccaagtctgc	attggttgcc	1039260
aagagcttca	gaggagcaca	acaggccttc	tgtaaagagag	aaattgcaat	actattctca	1039320
tcagcatcat	ctttaggagt	ccctaagggt	aaagatgcac	agaacaatgc	aacgcctcct	1039380
ccaggaacat	ccccacgact	taaagcagat	tccataatct	taagagcgag	ggatatataa	1039440
ggttcgttat	cttcatcagt	aggaagaatg	gctaccgaac	tttgagagcct	atttgtgctt	1039500
ttgattagcc	ttttttttgt	ttcaaggcat	gaggctcgtg	gtatttcttc	tgctaattgt	1039560
cgcgtcttta	aggctcaggac	ttccggggata	tgtaggccctc	caatgagtg	cgtttgtgac	1039620
tctgagattt	ctatagatag	acaggaccct	aaagtgaaca	tctcaggagc	taaaacatga	1039680
gatgcttctt	ggcaaggaca	aatgtgggtc	ccagtaataa	aagcaaatatc	ctcgggcta	1039740
tcttgatttg	tagtagagag	ttgaggaatg	gtgactacag	ttacttgcaa	gagcccttgc	1039800
aatttggttaa	caacaagggt	agcaagtacg	tctggatcga	tatcttcaca	gaaaatgatg	1039860
aggtgctggg	tttggttctga	aatttcttgg	agtaggggaa	gtaaggagtg	aatcatagag	1039920



atcttttctat	ctgtgatcag	aattagagga	tgagcaattc	tagttagacg	agacgctgta	1039980
tcagaaacaa	aatacgtcga	agcataccct	gcaggaattt	taaatccttg	aaagacatcc	1040040
atggaagttt	tgctgttttc	tctctcctta	gtgatggaga	taagaccctc	agggcctacc	1040100
acagaaaaag	cattgtaaaa	atgatcgga	atgggtgggca	tgtgtagaga	agaaaaaata	1040160
atattgcgaa	cttttagagc	atctttaata	ggccaagatt	gttgttgtaa	ggcttcctga	1040220
agcttttctc	cctgcaattt	taaagaggca	atgagcttgt	gtgtggagat	tcccttttct	1040280
aaagctgcat	agctttcctg	taaaattgca	tggagtaaaa	taagtccagt	agtcgcgcg	1040340
tcgctgtgtt	ccttatgaat	tttattcacc	atagctttcg	caaaatctac	accgagattt	1040400
tcataggaat	tcgaaagtcc	tgtttggtgaa	atagcgtaga	agccacgctc	tttaagaaa	1040460
gaagttgggg	agagggattg	cttgggacca	tacgatccct	ttactatctg	gaaaagttaa	1040520
tctatccctg	aaaaaagttt	tttatcagca	ttgtaattag	ataatttttc	ctgttcggac	1040580
atgcaaacc	ccagtagacg	taaaattttt	acactacca	gtcgtttttt	agttcacat	1040640
accttcagta	ggaaaggtgg	caccggaat	cgaaccggg	atagaggctt	tgaggcctc	1040700
ggccttaccg	cttggctatg	ccaccaaggg	ggaggatgag	aatccttagt	ttaagcgaaa	1040760
gaagatttta	tggttaagcga	gaagtgcgca	taattctaga	gactagggaa	atcttagtcg	1040820
tttttgagag	atgcaattgc	attttagttc	tcttaaaaaa	gaggttatgt	aatcaacct	1040880
ataagggtag	ttgcattctt	gtctgcattt	taaatatagt	acttttttagt	gtaggtccat	1040940
ccttctggta	gggagttcag	acttttctaa	accatagatg	ctgtaggcaa	aatttatatgc	1041000
gagctatggt	gcttgaagat	tggtgtctct	tgatgctatc	agatgtctct	tgctcgaagt	1041060
gtgataaaaa	aattacagga	tttgctatag	atagccagaa	agtgcagcct	ggggatctat	1041120
tttttgccct	tcctggaaat	gcaacagacg	gtcatcaatt	tttaaaacat	gccgcaaccg	1041180
caggagctgt	tgccgcctg	gtttcccatg	actaccaagg	agatagcttt	ggtctagaat	1041240
tgatccgtgt	tgatgatacg	aaatctgctt	tgcaagaagg	aggatccaat	caatgcaatt	1041300
tattccaagg	cacccttggt	ggaatcacag	gatctgttag	gaaaacaaca	accaaagaat	1041360
tctcaaaaac	aatcctaagc	tccatctata	aaactcacgc	aagccctaaa	agttataatt	1041420
cacagttgac	ggtaccttta	agcctcttga	tgccggaagg	ggacgaagat	gtgatgattt	1041480
tagagatggg	ggtctctgaa	ccaggaaata	tgcaagatct	ccttcggatc	gtccagccag	1041540
agatcgcagt	gatcacgcat	attaatgacc	aacatgcgat	gcatttcccc	caaggcatcc	1041600
aagagatcct	aaaagaaaaa	agctatatct	tacaaaaaag	taaactacaa	ctgctcccca	1041660
aagattctcc	atattaccta	gatttaagggt	cctgttctcc	tactgccgaa	aaatttttct	1041720
tttcttttaa	cgatccctct	gcagattttct	gctacaaggc	aattagtggg	gactctgtag	1041780
tcattccaac	tcctgaagaa	aattattgtc	ttccgatagc	ttttctttac	aagcctgcat	1041840
ataccaactt	attaattgct	gtagcactct	cttggatctt	agaagttcca	gaagagggag	1041900
tgatacgctc	tctacctgaa	ctgaagttgc	ctcctatgcy	ctttgaacat	agcatgagaa	1041960
atggaatgca	ggtcatcaac	gatgcataca	atgcatgtcc	agaagctatg	atcgctgctc	1042020
tcgatgctct	acctttacca	agtgatggag	ggaaaatcat	cttaatttta	ggccatattg	1042080
ctgaattagg	caggatttca	gaagaaggac	atgcttttagt	agctgaaaaa	gcagcttctc	1042140
gaggagatat	gatatttttt	attggggaaa	agtggatccc	agttcaaagt	gttttaaaaa	1042200
gctattcttg	tgaagtgagc	tttttctcct	cagctcaaga	tgtaaagac	attttgaagc	1042260
aagtggcacg	ctatggggac	gtgattctac	tgaaaggttc	tcgtgccctc	gctctcgaat	1042320
ccttatttagc	ttgtttttaa	tttcttagga	cgaagtatga	tccctttaat	tccaatgttt	1042380
ctaaaacagt	ctctattttt	ttctttggct	ttgacagggg	tgaccaccct	tgtgcttaca	1042440
gtatctctgg	gtgttcctgt	aatgaaatgg	ctgaaaagaa	aaaattatcg	tgattacatc	1042500
cacaaagaat	actgtgagaa	acttgaaatg	cttcacaaag	ataaagccga	ggttcctacg	1042560
ggaggaggag	tcttactttt	tatctcggtt	attgcttctt	tacttggttg	gttgcccttg	1042620
ggaaaatttt	caacatgggt	ctttattata	ctcctgacat	gttatgcagg	tctgggttgg	1042680
tatgatgata	gaataaaaaa	taaacggaaa	cagggacatg	gactgaaggc	aaagcataag	1042740
ttcatgggtc	aaattgccat	tgagcttttt	acactcattg	ctcttcctta	catcttacgga	1042800
agtaccgaac	ccttatggac	tctcaagatc	ccttttatgg	aagggtatgt	ttctcttccc	1042860
ttttggctag	gaaaagtctt	ttgcttagga	ctcgctcttg	tcgctattat	agggacaagc	1042920
aatgcagtaa	atcttaccga	tggtttggat	ggacttgctg	caggaaccat	gtcctttgct	1042980
gctctgggct	ttattttcgt	agctctaaga	agttctacaa	ttcctatagc	tcaagatgtg	1043040
gcttatgttt	tagctgctct	tgtaggggct	tgtatcggat	tcttatggta	taatggtttc	1043100
ccggcccagc	tcttcatggg	agataccggg	tactacttct	tagggggcct	gctagggagc	1043160
tgcgctgtta	tgctgcgcgc	agaatgcac	ctagtctgtg	tcggaggagt	ttttgttgct	1043220
gaagcgggat	ctgtcattct	acaagtactt	agttgtagat	taaggaaaaa	acgccttttc	1043280
ttatgctctc	catgcatca	ccattatgaa	tatcagggcc	tcccagagac	taaaatcgct	1043340
atgcgctttt	ggatctttag	ttttgtatgc	gcagggtctag	gtatagcggc	tgtcttatgg	1043400
agatagatat	gtgtcagcgc	attcttattt	tagggactgg	aatcacagga	aagtcggtag	1043460
caaggttttt	atatcagcaa	ggacactatc	tcataggagc	agacaattct	ttagaatctc	1043520
tgatatcggt	agaccatttg	catgataggc	tactcatggg	agctagcgag	tttcttgaga	1043580
atatcgacct	tgtgatccgc	tctccgggaa	tcaaaccgta	tcatccgtgg	gtagaacaag	1043640
cagtatctct	taagattcct	gtcggttact	atatccaagt	tgctttgaaa	acaccagaat	1043700
ttcaaagata	tccctccttt	ggcatcacag	ggtctaattg	caagacaaca	acgacattat	1043760



ttcttacc	ctctttaa	actttagg	tccctgct	agctatgg	aatatcgg	1043820
tgccatac	agaccacat	ggacaacc	gagttcgt	tgtagaaat	agctcatt	1043880
agctagca	ccaagagg	catatccc	cactttct	atctgtgt	ttgaactt	1043940
ctcgtaac	cctggact	catcgcaac	tagatgcct	ttttgatg	aaacttcg	1044000
tccaaaaa	cttgcgtc	gacaaaaac	tttgggtg	ggaggagt	tccttggg	1044060
attcttat	aattttact	gaagaaatt	aggagatt	agataaagg	gatgcatt	1044120
aaccaata	cttgcacat	agggataac	attgcgcag	ttatgcttt	gctaatag	1044180
ttggttgg	ctctccaga	ggttttct	aggcaatt	gacatttg	aaacctgc	1044240
atagacta	gtaccttgg	aaaaaagat	gcgtgcact	tattaatg	agcaaagc	1044300
caaccgtg	agcagtag	aaggctct	tggctgtag	gaaagatg	attgttatt	1044360
tgggtggc	agataaagg	ggagatttc	ctgccttag	ttctgtatt	tcccagaca	1044420
ccaaacat	cattgctat	ggtgagtgt	gacagaca	agcagatg	ttatcagaa	1044480
agattcct	gacgctct	aaagattta	aagaagcgt	gtccatag	caaactat	1044540
cacaagagg	agatactgt	ttattgtct	caggatg	aantttgat	agtttcaa	1044600
ttttaaaga	cgcggant	ctttaagct	ttgatcaga	gaaatgcag	cagtgcagg	1044660
aatatgaat	gtagagac	ggtaataac	gctgtcgt	tgaatgct	attgtctgt	1044720
gctctttt	tcacatcaa	gcgtattgg	gtcaaggac	atgacgagg	attccgta	1044780
tttgcttct	gcaaggtt	acaagcagt	gtttcaga	aaaaagtc	agaaaagc	1044840
gtagtcgc	aagtgcct	ccgtcctat	gctaaagag	ctctagct	acagtttat	1044900
gaaagtaa	cggttatt	aaccacacca	cccgtgcct	ttgttagcg	aaccccaga	1044960
gtgcctact	tggcagtt	gcctcagc	gttcgtgag	cagtaaaag	ggaacaag	1045020
ccttatgct	ctgttgtag	gaaaaaagg	gattttct	aacgcatt	gagagcaa	1045080
catactacc	ttgcaaaa	gatgcagat	aatgatct	ccaccacca	acttaaaat	1045140
ggtcaggta	tcaaaagtc	tacgtctca	gatgtcag	acgaaaaaa	tcctcaaac	1045200
cagaccgca	accctgaaa	ttattatat	gtccaaga	gggatagcc	gtggacaat	1045260
gcattgcgt	accatatt	attggatga	ttgctaaaa	tgaatgat	cgatgaat	1045320
aaagcccg	gccttaag	tggagatc	ttgcgcata	gttgatcta	gcagtcct	1045380
agcatgaa	ggtttgtt	ttcctgttt	ttaggaat	tttctctag	gctgattat	1045440
gtttttgag	cttcttcag	agaagtatt	gaccgctct	tagaatgt	tacacata	1045500
gctctcat	gccagggt	ctatcttat	cttggcttg	gagtcgcac	gcttctct	1045560
atgatgga	ggagagatt	cttaaaaa	agtctctgt	tgttttcag	agctgccta	1045620
gccttaate	gtgtgttt	tccaggata	gggatatt	gtaatgggg	aagacggt	1045680
ttgggggt	gtcagcta	gattcaacct	tcggaatt	tcaagtac	cgtcctata	1045740
gtcgtctat	atttcctac	attctcttc	ctctatcag	aacaactga	aatgtttct	1045800
aaacttac	caattttat	tattccgatt	cttttgatt	ctatagaac	cgataacg	1045860
tctgctgt	taatttcag	atccctgatt	cctgtgttt	tcatgacct	agtgcgcct	1045920
cgctactgg	ttctaccac	tctgtgcgt	ctcatagct	gaggagcc	tgcttatag	1045980
atgccctat	tgcgctacc	cttaaacgt	taccttcac	ctgaactcg	catcaaagg	1046040
agaggacat	agccgtat	agccaaaat	gccgcagg	ctggaaaag	actaggaaa	1046100
ggtcctgg	ctagccttc	gaagcttacc	tacctccag	aagcccaaa	tgactatatt	1046160
gccgcaat	acgtcgagg	gttcggatt	ttaggtat	tcgtcctcat	acttttgt	1046220
atgtgcttg	tttacggag	gtatgcaat	gctataaaa	catcatcact	agaagggt	1046280
gctttggca	tggctcatt	tttgattatt	agcatgca	catttatg	tttaggagt	1046340
gtttcagg	tgcttcct	taaaggagt	aaccttcct	tttttagcc	aggagggt	1046400
tctcttat	caaatatgt	tggagtcac	ttgttatt	aggtatat	tgaagaaa	1046460
tcgaaaagt	gccttggct	taggagggt	aggaggcc	attgtccc	ctctctcgt	1046520
aaaggaagt	ttttctcgt	aaggaatag	cgtattact	ctagggaa	gtctcaaga	1046580
ccatcctct	ttgcaacag	gaatcagct	tcgggaaat	cctcaggac	ttcctacagt	1046640
ccttaatcc	ataaagat	tgagcagg	cttttctct	tgttcagg	acctgaaag	1046700
aagaaaagg	cttaaaaatt	ttgacctga	cctggtcata	ggatttgg	gctaccact	1046760
tcttcccg	ttgctcgc	gactgtccc	taaaattccc	ttatttct	acgaacaaa	1046820
tctagtct	ggaaaagta	atcaattgt	ttcccgcct	gctcgagg	ttggagtga	1046880
tttctcccc	gttactaac	acttccgct	ccccgcaga	gaggtcttc	ttcctaaac	1046940
aagcttctc	ttaggaaag	ctatgatga	gcgatgtac	aatcatacc	ctacaatt	1047000
tggtgttgg	ggttctcag	gagcacag	attaaata	tgtgttccc	aagctctgt	1047060
caagctagt	aataagtac	caaatatgt	cgctcatcat	attgtagg	ctaaaagt	1047120
tgttatga	gtgcaacat	tttacaat	tggagaggt	ctctgctgt	tgaagccgt	1047180
cgaagagca	ctcctagat	tcttgcttg	cgcagatt	gtcatcagt	gggcaggag	1047240
cacaatttt	gaagaaatt	tttgggcaa	agttcccgg	attttaatt	cctatccag	1047300
agcttatgg	catcagga	ttaatgcta	attctttgt	gacgtctta	aaggggga	1047360
tatgatcct	gaaaaaga	taacagaga	gctattagt	gaaaaagta	cgtttgctt	1047420
agactcccat	aacagagaa	aacaacgca	ttccctagc	gcgtatagt	agcaaagg	1047480
aacaaaaaca	ttccatgcat	tcatttgtga	atgcttatag	gttcattata	tgaaggga	1047540
tcctcagtat	catttttat	gtatcgggt	tataggaat	agcgctttag	ctcatattt	1047600

gcttgatcgt	ggctatgagg	tctctggaag	cgacttatat	gaaagctata	cgatcgaaaag	1047660
cctgaaagct	aaaggtgcga	ggtgtttctc	aggccatgat	tcctcccatg	ttcctcatga	1047720
tgccgctcgt	gtttatagct	caagtatagc	ccctgataat	gtagagtatc	ttaccgctat	1047780
tcaaagatca	tcacgtcttc	ttcatagagc	agagctcttg	agtcagctta	tggagggtta	1047840
tgaaagcatt	ctgggtttcag	gaagccatgg	gaagacaggg	acctcatctc	taattcgagc	1047900
gattttccag	gaagctcaga	aagatccctc	ctatgctatt	ggaggactcg	ctgcaaactg	1047960
cctgaatggg	tattctggat	catcgaaaat	cttcggttgc	gaagccgatg	aaagtgatgg	1048020
gtctttaaag	cactacactc	cccggtgcag	agtcattaca	aatatagata	atgaacattt	1048080
gaataattac	gctgggaatc	ttgataacct	ggttcaggta	atccaggact	tctctagaaa	1048140
agtaacagat	ctcaataaag	tattctataa	cggggattgt	cctattttga	aaggaaatgt	1048200
ccaagggtat	tcttatggat	attcaccaga	atgtcaattg	catatcgttt	cctataatca	1048260
aaaggcatgg	caatctcact	tttcctttac	ctttttaggg	caggagtatc	aagacattga	1048320
gctcaatctc	cctggacaac	ataacgctgc	aaatgcagca	gcagcctgtg	gagttgctct	1048380
tacctttggc	atagacataa	acatcattcg	aaaagctctc	aaaaaattct	cgggagttca	1048440
tcgacgtcta	gaaagaaaaa	atatatccga	aagctttctt	ttcttagaag	attatgctca	1048500
tcacctgtga	gaggttgcac	ataccctgcg	ctctgtgctg	gatgctgtgg	gtttgcgaag	1048560
agtcacgcga	atttttcaac	cacatcgatt	ctctcgttta	gaagagtgc	tacaaacctt	1048620
cccaaagct	ttccaagaag	ctgatgaagt	catacttaca	gatgtctata	gtgccggaga	1048680
aagtcctaga	gagtcctatca	ttctttccga	ccttgccgga	cagattcgta	agtcctctta	1048740
tgtccattgt	tgttatgttc	cccatggaga	catcgtagat	tatctacgaa	actacattcg	1048800
cattcatgat	gtctgtgttt	ctctaggagc	tggaaatatc	tatactattg	gagaggcttt	1048860
aaaagacttt	aaccctaaaa	aattatccat	aggactcgtc	tgtggaggga	aatcttgcca	1048920
acacgatatt	tctctacttt	ctgctcaaca	tgtctctaaa	tatatctctc	ctgaattcta	1048980
tgatgtgagt	tacttcatca	taaactcgta	gggcttatgg	agaacaggaa	aggattttcc	1049040
tcactttatt	gaagagactc	aaggggattc	gccactttct	tctgaaatcg	cttcagcttt	1049100
agcaaaaagc	gactgtttgt	ttcccgtgct	ccatggccca	tttgagagg	atgggtacgat	1049160
ccagggtatt	tttgaaatct	taggaaaacc	ttatgccgga	ccctcactat	ctttagcagc	1049220
aactgcaatg	gataagctgt	taacaaaacg	aattgcatca	gcagtgggtg	ttcctgtagt	1049280
cccttaccaa	cctttaaatc	tctgtttctg	gaaacgcaat	ccagaactat	gtattcagaa	1049340
tcttatagag	acattttctt	tccttatgat	tgtaaaaact	gcacatttgg	gatctagtag	1049400
tgggatattt	ttagtccgtg	ataaagagga	attacaagaa	aagatctcag	aagcatttct	1049460
atatgacacg	gatgtgtttg	tggaggaaag	tcgcttaggg	tctcgtgaaa	tcgaagtgtc	1049520
ctgtatccgc	cattcttcta	gctggatttg	tatggcaggg	cctaataaac	gctgtggtgc	1049580
tagtgggttt	attgattatc	aagagaaata	tggatttgat	ggcatagatt	gcgcaaagat	1049640
ctcttttgat	ttacagctct	cacaagaatc	tttagattgt	gttagagaac	ttgcagagcg	1049700
tgtctaccga	gcaatgcaag	gaaaagggtc	agctcgaata	gattttttct	tggatgaaga	1049760
ggggaattat	tgggtgtcag	agggtcaatcc	tattccaggga	atgacagcag	ctagcccatt	1049820
tttacaagct	tttggttcacg	caggatggac	gcaagaacaa	attgtagatc	actttattat	1049880
agatgctcta	cataagtttg	ataagcagca	gactatcgaa	caggcattca	ctaaagaaca	1049940
agatttaggt	aaaagataat	aaaaaaaacta	gagatctttt	tattaaaatc	tctagttttt	1050000
acatgtaaac	aaaagcagac	gaataactac	gattaaaggt	ggttactaca	ttcgcaagaa	1050060
tgatgcata	tgccctcttc	ttgttcttct	tgattaaagt	cttcgctcgt	atgacagtgt	1050120
ccactgcagc	agggtgtcaga	ctcgccgaaa	gtatcttcag	tagagttaga	agagtcatta	1050180
tcacagatgt	aatcttgatc	agcaatcaca	tcagttccat	tttcaggctg	aaccaaatct	1050240
atctgcactt	tcttttttaa	tctagaacat	acacgtctaa	gaatcgttct	tagcgcatgt	1050300
attgtgttcc	ctcttcttcc	aataattttc	ccaatatcct	ctgctgcgac	acgaatttct	1050360
aacttaatat	attcgttatc	ctcgtcttca	atagaacgaa	tttcaacagc	ttcaggatta	1050420
gtaactaaat	tcttaacaat	atatgctaca	aactcttcca	taaagtccaa	attaaattga	1050480
gatatagaaa	gaaaaaaaaca	taactctatg	tttttaaagt	tcctgaagaa	aggatagata	1050540
ttcaaaatga	aaaagtcaat	gtctaactctg	aaagcggagg	cttctctgga	tagctgagaa	1050600
tcgttaacca	attcaagtac	ctcggatccc	catttttcaat	aggaaatagt	aagacttcag	1050660
gaacctcata	gccagagaac	tcctgaatag	caagacaaat	ttccgagaag	cgtatgtcta	1050720
tcgatttgat	ttgtatatga	tgttcttcag	actcacatag	cttgccctcc	catagatatg	1050780
tcgatgtgcc	tttagggaat	acatgcacac	aggaagcaag	acgctctgta	atcagatgtc	1050840
tagctaagga	gcgagcactt	tcctccgaag	ggaaagatgt	aagaataaga	acagcagtc	1050900
tagagctttt	aataataaga	aatttggaaa	acgcaaatca	tagacatatt	gtttttcgct	1050960
ctcgattaca	ggactttttt	tcatgtgctt	atacaggtct	aaggcacgat	ctaaggctct	1051020
aattgggnagt	cttaacagac	tgcttgaaga	gagcgtcact	ataattttct	cagggtatgc	1051080
atcagatnaa	gataaatcaa	tgaattttcgg	agactccata	gcaagctcct	taagaagaat	1051140
cttggtaaaa	agcatttttt	ctttagggag	tttttgcatt	tttaaatctt	cttgagagaa	1051200
aaaaatctga	gggagattca	gagaggggaa	gtacgggttg	ccaagaaagc	agctcccttc	1051260
gagattgcat	aacgtattag	atcggttccc	aacataagca	ataggtgttt	gtaagggtata	1051320
gaaaattgta	atgcccttat	tatcaggaga	tttttctata	actaaagagg	aaaaaatccc	1051380
aagagcatgc	aagctcgact	cagcttcttt	aatagagaat	tcatggagat	atgtagggtgc	1051440

atccgcagaa	agacgtaaat	gttctgcaat	cgcagtagga	gggactttgg	atagagtggg	1051500
ggaaactaaa	aataggttcc	taatgggaga	aggattgaat	ttagataaag	acagttcagg	1051560
gagaaataac	caacaaaatg	taggaacaca	aacaagggaa	ctcaaaacga	tcaggatcga	1051620
agcataacat	aaagagtatt	gaggacccgg	agggaaaagc	gttttgaaaa	aacgtcttat	1051680
catgagctca	ttgtttttta	ttatgatcat	aaataatatc	gctaataatt	acgagattcc	1051740
tcttgaggag	attactgatg	aatttatcag	ctaaagaata	cggagatatc	attgtttatt	1051800
atttacaagg	atcttttagat	gccgtctcag	tgcctagtgt	tcaagagtat	ttagagcagt	1051860
ttatacagaa	gaaacatctt	aaaattgtct	tgaattttac	agatgtctcg	tatatcagta	1051920
gcgcagggat	tcgtctactg	ctgtctaatt	ttaaattggg	tcagagcttg	ggaggaaaaa	1051980
tgtgcctatg	ctgtgtcaaa	gagagtgtaa	ccgaagtcac	gcggattgcc	aggtttagac	1052040
aaatgatctt	gctctgccag	gtctgaacag	gaatgtttta	gtaagttata	ntttctctat	1052100
atgcttccct	ttgaattcga	gtttaatata	acttcttctc	ctgaatgcga	cgtatgcctt	1052160
gacctcaga	agttattttg	aaagctatct	aagcgtacga	tcgtcttgct	ttcaggacct	1052220
acaggatctg	ggaaaactga	tgtttcttta	gcattagccc	ccatgattga	tggagagatc	1052280
gtctcagtg	attctatgca	agtataccaa	ggcatggata	tcggaactgc	aaaagtatct	1052340
ctaaaagcta	gacaagagat	tcctcaccat	ttaatggaca	tccgacatgt	tcaagagccg	1052400
tttaagtgtg	tggattttta	ttatgaagca	attcaagcat	gccaaaacat	tttatcaaga	1052460
aataaagttc	ctatttttagt	tgggtggctca	gggtttttatt	ttcatgcctt	tctttcaggt	1052520
cctcctaaag	gtcccgcggc	agatcctcag	atacgagaac	agcttgaagc	gatagcagaa	1052580
gaacacgggg	tttctgtctt	ttatgaggac	ctacttctta	aagatccaga	atatgtctca	1052640
acaatcacta	agaatgataa	aaataaaatc	attcagaggat	tggaaaattat	ccaacttaca	1052700
ggaaaaaaaag	ttagcgatca	tgaatgggat	atcgttccca	aagcttcaag	agagtattgt	1052760
tgtcgtgcct	ggtttctttc	ccctgaaaca	gaatttttga	aaaataatat	tcaaatgcgt	1052820
tgcgaagcta	tgttgcaaga	agggctgcta	gagggaagtc	ggggattatt	gaaccaggga	1052880
ataagggaaa	acccttcagc	attcaaggcc	attggatatc	gagaatggat	agaattcctt	1052940
gataacggag	agaaattaga	agagtacgag	gaaacaaaaa	gaaaatttgt	atccaatagt	1053000
tggcattata	ctaaaaaaca	aaaaacatgg	tttaaactgt	attcgatatt	tcgagaactt	1053060
ccgacattag	gcctctcttc	ggacgcaatt	gctcagaaga	tagctaaaaga	ctacttactg	1053120
tacagctgat	gtgttgataa	aagggtattt	tctccacagg	aatgaaacct	tcagatcgaa	1053180
tgatattaca	gatttcttct	tcagagctct	gtatcgacca	tcctgtagct	ttatgcacgc	1053240
tttctgtctaa	aataaccctt	ccaaaatcat	cagctccgta	atggagagct	ttcgtctcta	1053300
agctttttacc	ctcgccaaac	catgaggctg	ctacgtgatc	aaaattatcc	agaaagattc	1053360
tgccccaaag	taaaatgcgg	taataagttt	caatagaagc	ttgttgagga	acgttacgtc	1053420
ttagggccgt	attcccagggt	ttataactcc	aggggataaa	actataaaaag	ccagggcagc	1053480
tatcttgagc	atcacggagt	gtttgaagat	gtataaggat	atcttctggg	ttctccacat	1053540
gccccaaacat	cattgttgct	gttgtgcgaa	agcccatgag	atgggctaac	ttatgtagat	1053600
tgatccagcc	cccaggctgc	attttttttg	gagagatgat	ttttctaact	ctctctgaaa	1053660
gaatctcagc	cccgcctcca	gggatggtag	gttgccccgc	atcccataac	ctttggagac	1053720
cttgctcaat	actgatgcca	gagaccgggc	aagcatgttc	gatttctact	gcagaaaaga	1053780
aatgaggatg	gatggaagga	aattcttgaa	cagtaatgcg	tacgagttct	tcaagataat	1053840
cgatgcctaa	ccccgggtgc	acaccacctt	gcagtaaaac	agttttgact	cctgaactta	1053900
cataacgctg	taataggctg	cgaacttcat	caaaagataa	tagataagcg	tcgggagatt	1053960
taggctttct	gtagaacgca	caaaacgtac	aatctatttt	acaaatatta	gtatagtttg	1054020
gattggcatc	caaaacataa	gtaacttcat	ttgaaggata	tcgttcttta	cgaatcgctg	1054080
ccgcacgctc	ttgtaatctc	tcgatagggg	acgaaacaaa	tagtcttaat	ccttcttcaa	1054140
atgaaaattct	tttacataaa	ttcataaaat	aattgacgtt	aaagattgct	agcagcagac	1054200
tttaagtttt	aacaatttta	tttgtcaagc	cccacacctt	agttgtttat	atggataatt	1054260
cagacaacag	ctttcatact	ttggaaacgg	agcaggatc	gtttttaaac	gatgaattag	1054320
cagtccaaga	agtggcgtct	acagaaaagc	cagaaaattt	tgatgcgaca	ttatgtttcg	1054380
ctgatgagat	tcaagagctc	ccctccccag	aaaagaaagt	tgtttttatc	ttgaataaga	1054440
tgaggggaagc	cttaacagga	tcactctcaag	gctcagactt	aagggtgttt	tgggatttaa	1054500
ggaagcaatg	cctccccctt	tttaatgaaa	tcgaagatac	cgcgaaacgg	gcagatcatt	1054560
ggcgttggtta	tatcgagttg	actaaggaag	gccgtcatct	caagggtctt	caggatgaag	1054620
aagggtcttt	tgtcgttggt	cagattgatt	tggcaatcac	atgtctagaa	aaagatattc	1054680
ttaagttcca	agaaggaaca	gaagataaaa	ttttcaaaga	tagagaagat	aatttcttag	1054740
aaagccaagc	tctagataaa	catcaggctt	tttataagca	gcatcatacc	tcattgctat	1054800
ggttaagttag	tttttcttca	aaaatcatag	atctccgcaa	ggaactgata	aatgttggga	1054860
tgcggatgcg	gttgaagagt	aaattttttc	aacgtctctc	taatttagga	aatcagggtg	1054920
ttcctaaacg	aaaggaactg	atcgaaaaag	taagtcaaac	atttgcagaa	gatgttgatg	1054980
catttgtcgc	taaatatatt	attggatccg	ataaagaaac	attgaaaaaa	acggtttttt	1055040
ttttaagaaa	agaaatcaaa	aaccttcaac	acgcagcaaa	aagacttttt	gtctcatcgc	1055100
atgttttttgc	tgaaacacga	ttgaaactca	gtaagtgtcg	ggatcagctc	aaggggatgg	1055160
aaaaagaaat	tcgccaagag	caaggccgct	tacgtgttgt	atctgctgaa	aattcaaaag	1055220
aagttcgcca	gatgttagct	gaggctctct	ctcttcttat	tgagggaaat	gatctgagta	1055280

aagttcgttaa	agacttggag	ggcattttcta	agaaaaattcg	agctcttgat	cttacgcacg	1055340
atgatgtcat	ctctttgaaa	aaagaaatgc	aacaattatt	tgatcaatta	cgagagaaac	1055400
aagacgcggc	agagcattcc	tatcaagagc	aattagctaa	agataaacia	gtcaagaaag	1055460
aagcggctcg	ctctcttgct	gagcgcatca	caacattctc	aaaaacttgc	tccgaaggaa	1055520
cattacttcc	gaatctcgag	aagaatggca	gacattgaaa	gagctcttag	gtaaaatgtc	1055580
ttttttacct	cctcctgaaa	aaattttctt	agataatcaa	ctcaatcttg	ctcttcaaac	1055640
tattgttaac	ttctttgaag	aacaacttct	ctcttctcca	gattctcgag	aaaagcttgt	1055700
gaatatgcgc	caagtattga	agcaaagacg	agagcgtcgt	caagaactta	aagataaatt	1055760
agagcaggac	aaaaaattat	tagggctctc	aggattagat	tttgatcggg	ccatgcagta	1055820
tagtgcctta	gttgaagaag	acaagcgtgc	tcttgaagaa	ttggatgcaa	gtatttttaga	1055880
attgaagcaa	cagattcagc	aattgctatg	agaagaaact	gtatatatgc	ttttgattta	1055940
gacggaacct	tattgaaggg	gaatagcagc	tggagttttt	attgctacgg	cttacttcaa	1056000
ggtttgtttt	cctataaaaac	gttgccccc	tgcatttacc	gcttttttag	atttaagttt	1056060
ttttttggga	tcttccatcc	ttctattatt	cgatagtaac	tcgtctactc	tcttctgttc	1056120
cctgtgatga	tctttatgaa	gttgccctga	attttgtatc	gactctgacc	ggctccgatt	1056180
tttatgtctc	tgtttttagaa	aaactagaag	aagcttttgc	agataccaca	ggacaggcga	1056240
tcttttttcc	tcttctcca	gactttattg	tccaccccat	agcgcagcaa	ctcgggatta	1056300
gttcttggtg	tgctgcgtgt	tatcgcgcatc	agtctgcaga	acagacgac	tataaaaaat	1056360
gtcttacagg	ggataaaaaa	gcgcaaattt	tgagttatat	taaaaaaatt	aatcaagcaa	1056420
gaagccatac	cttctccgac	catatttttag	atcttccctt	tcttatgctg	ggagaagaga	1056480
aaaccgctcg	tcgcccctcag	ggacgactca	agaaaaatggc	aaaaaaatat	tactggaata	1056540
tcgtttaatt	ccatttataaa	aaaagctcga	ccttatcttg	gataatcgag	tatcctaaag	1056600
ctggttttat	ggattcattt	tgttttgatc	tattgaaagt	agctgctaaa	gctattgacg	1056660
acaaaaaagg	gaataatctg	gttggtctag	atgttagaac	aatcttcggaa	tttaccgatt	1056720
attttgtttt	tggtgaaggt	agtgtgaatg	tgcatgttaa	ggcttttagca	aatactatcg	1056780
tagaagagtt	aaaaaagcag	aaagttagtc	ctcttcatgt	ggaggggata	acggatggta	1056840
attgggtggt	gatagattac	ggattttatcg	tcgtccatgt	atttgtctct	gaaattcgtg	1056900
gaaaaatatcg	tttagaagag	ctatggaagg	acggattttat	tgtcacatcc	aagcttttag	1056960
cttcttaatg	gagtaagggg	ctacatgagt	aaaaaacgcg	tagttgttac	aggattcggg	1057020
gttgatatctt	gcctcggtaa	tgaagtagat	acctttttacg	ataatcttct	tgccgggtgc	1057080
agcggcgctac	gaccaattac	atcctttctt	tgtaggaggt	atgccactcg	ttttgcccgc	1057140
tggatcccag	aattcaatcc	cgagccttat	gtagataaaa	agcaagcacg	tcgtgtcgac	1057200
cccttttatta	cctatgccat	ggtagctgct	aagaaagcga	tcgctatgtc	acgttgggat	1057260
aaagaccatc	tgcttccga	tcccgtgcgt	tgtaggagtga	ttgtcggctc	tggaatgggt	1057320
gggctctcta	ccctagacca	agggatggaa	agactcttag	ttattcataa	aaaattatct	1057380
cccttcttta	ttccttatat	cattacaaat	atggccccag	cacttattgc	tatggacttt	1057440
ggtttgatgg	gccccaat	ttctatatca	actgcatgtg	ctacaggaaa	ttattgtatt	1057500
gatgccgcct	accaacattt	agtatctggg	cgcgctgata	tgatcatctg	tggtgggtacg	1057560
gaagctgcag	tgaaccgtat	tggttttagag	ggtttttattg	ctaactcgtg	tctctctgag	1057620
agaaacgatg	ctccagatca	agcttcacgt	ccttgggata	gagatcgtga	tggctttgtc	1057680
ttaggagaag	gagcaggaat	tcttggttta	gaaaccctag	agagtgtctt	acgtcgcgat	1057740
gtccttattt	ttgctgagat	gttaggaagc	tatgttacat	gcgatgcctt	ccatattacc	1057800
gctcctagag	atgacgggtga	ggggattact	gcgtgcgtgc	ttgggtgctt	aaattccgca	1057860
ggaattccta	aagaacgtgt	caactatgtg	aatgctcacg	gaacgtcgac	tccattaggg	1057920
gatctttctg	aagttctagc	tgtaaaaaag	gctttttggct	cccatgtacg	aatctccgc	1057980
atgaactcca	ctaaatcatt	gatagggcat	tgtcttgag	ctgctggagg	tggtgaagcc	1058040
gtcgttgcaa	ttcaagctat	ccttacggga	aagcttcac	ctacgattaa	ttgggataac	1058100
cctatcgcag	aaattgaaga	ctttgatgta	gttgcaata	aagctcaaga	ctgggatatt	1058160
gatgtagcga	tgtccaactc	atttgggttt	ggtggacata	attcaacgat	attattctcg	1058220
aggtatgtac	cctagttatg	atgaagacaa	aatatgagta	ttcttttggt	gttattccta	1058280
taaaattttt	tggcaccctc	gataagaaca	cattaaaagc	ttgttttatt	tgccatactc	1058340
gaggaaaaca	ttggggattc	cctaaagggc	attctgaaga	taagggaagg	cctcaagagg	1058400
ctgcagagag	agaattggta	gaagaaaccg	gactaagtgt	tgtaatttc	ttccctaaag	1058460
ttcttatcga	acagtattcg	tttaataatg	aagaacaagt	cttcgttcgc	aaagaagtca	1058520
cctattttct	tgctgaagtt	cgtgggtgaca	tccatgcaga	tcctatggaa	atttgcgata	1058580
gtcaattgggt	atccttgcaa	gaaggactcc	gcttattaag	tttctctgag	ctacgagatc	1058640
ttaccgtaga	agcagataaa	tttattaata	actatctttt	ctcttcttga	ttttcaagga	1058700
gagggaaacc	ctctccttag	acattaattc	acttcagcag	tgtctccaat	ataggataag	1058760
taatcctcgt	gagcgagctg	tatcaccttt	tgtgcttctt	tcttcccgtg	aatccccacg	1058820
atttcaattt	ttgcagggct	acctttaatt	aaatgattgg	gagtcgcttt	atatgttagg	1058880
aaatagtgtt	ggatcatatc	taatactgtg	cctggacagt	ctgaaatate	ttcgatctca	1058940
gcaaagacta	aatcgtcctc	taaaacagca	ataatcttat	catcagcttc	tccagaatca	1059000
atgatgcgaa	gacctcctat	aggacgtgct	tgaagtaaaa	tatttccatg	atggatattt	1059060
ttttctgtaa	gaacacagac	atccagaggg	tctttatcac	cttggaattcc	ttcgcgacgt	1059120

gtttgttccc	cgctatagtt	cccagaagca	gtgccacagt	atgtttgagg	cagtaaacca	1059180
taaaggcagg	gacaaaagtt	agaaaatttt	tgagggtctgt	ctactttgag	caagcctgta	1059240
gccttggtcta	attcaaattt	tacagagtca	taaggagtaa	tttctatata	acaacacagg	1059300
gactcataat	tatcctgggt	taatgtaggg	ctgtgccaa	gatgtgcaac	atataatggt	1059360
tttttagaca	taagtaactc	tcaatataaa	atttcctata	caatcgggtt	tagtgaattt	1059420
agactaacac	ggagaaaagtt	ttaagagaag	tgtctgctca	ggcctaattg	acttttaatt	1059480
aaaagtagtc	aataatttta	ttttctaatt	aaacctcact	aatttatgaa	atactcactg	1059540
aactttaaag	agatcaaaat	agatgattat	gagcgtgtta	ttgaagtcac	atgttcaaaa	1059600
gttcgtcttc	atgcaattat	tgctattcat	caaacggcag	taggaccgcg	cttaggtgga	1059660
gtgcgagcct	ctctatatct	ttcttttgag	gatgcgtgca	cagacgctct	tcgcttggtt	1059720
cggggggatga	cctacaaggc	aatcattagt	aatacaggaa	caggcggggg	gaaaagtgtt	1059780
attattcttc	cccaggatgc	tccttccttc	actgaagaca	tgctgagggc	ttttggccag	1059840
gctgtgaatg	cttttagagg	gacctacatc	tgtgctgaag	atcttggtgt	atctataaat	1059900
gatatttcta	tcgttgctga	agaaactcct	tatgtgtgtg	ggatcgctga	tgttagtgga	1059960
gatccttcta	tatacaccgc	acatggcgga	tttttatgca	taaaagaaac	cgctaagtat	1060020
ctttggggat	cttcctctct	tagagggaaa	aaaattgcga	ttcagggaa	aggctctgta	1060080
ggacgacgtc	tattacaatc	gttggttttt	gaaggcgccg	aactttatgt	tgctgatgtt	1060140
ttagaaagag	ccgttcagga	tgctgcaagg	ctctatgggg	ctacgattgt	tcctacagaa	1060200
gagattcatg	cattggaatg	tgatattttc	tctccttggt	ctcgtgggaa	cgtgattcgt	1060260
aaagataatc	ttgcagattt	aaattgtaag	gcgattgtag	gtgtcgcaaa	taaccaactt	1060320
gaagatagct	cagctggaat	gatgctccac	gaacggggaa	ttctttatgg	ccccgactat	1060380
ttagtgaatg	ctgggggatt	gcttaatgtg	gccgcagcaa	tagaaggaag	agtctatgct	1060440
cctaaagaag	tgcttcttaa	agtagaagag	cttcctatag	ttctaagtaa	gctatacaat	1060500
caaagtaaaa	ctacaggaaa	agacctgtga	gctttatcag	attccttcgt	ggaagacaag	1060560
ctcttggcct	atacgtcata	gagcaataag	cttatccgtg	gggacaacat	tgagttgggt	1060620
ttgtaacgct	gctaattgtg	tctcatgggt	ttcctgggtc	ccagaagcaa	gaatcactgc	1060680
gtgattatct	aagaccaaac	tttcttttct	atattctaaa	ggggctccta	aagcatccgt	1060740
gactctaccc	ccagcttctt	caacgaggaa	ggctccagg	acgtgatccc	aagcacgagc	1060800
gggagaatca	ataaaaggg	agcgaatgaa	aaaatctacg	gcgccttcag	caactaaagc	1060860
atacttatat	tggttttcta	cacgacgagg	actcggagtg	ttggggagac	ccaggcttag	1060920
cttacgtgtt	gcatgatgct	gttgattcaa	tgacgtcaac	gaagcctcac	agaattgttt	1060980
tgtttggttt	ctatcagcat	aaacaaagcg	tctatctaga	ttttgagaat	gaacaataga	1061040
aagaccattg	cctttagctg	ctgaatatag	tttaaattgtc	tgattatagg	cagggcatgc	1061100
catgaccgac	aaaatcggtc	gatactcata	aattagtgtg	atagcaacgg	caaaagcacg	1061160
atgtctgata	aaacctgcag	taccatcaat	agggtcgaca	agccaaaata	aagaagtcgg	1061220
agatggagga	gggaccagg	tagaaattaa	gtcatctctt	gagactgaag	aagttaacag	1061280
gcgtgtaaat	tttaagattt	cagggatttt	ttcgttgtct	tgatcaggat	atagagtttc	1061340
ttctccaata	aaaggaatat	tgggaaaggc	ttttgcaagc	tgttgtttta	gataatattg	1061400
actgccgtaa	tcagcagcgg	tgataaaaaga	accatcggat	ttttcccaa	aaggaaccaa	1061460
acgggtgctcg	cttcgatagt	ttagtagttg	tgtagtgatt	tccgtaacta	cagactcaac	1061520
gatgttctga	tagttaggca	actcggagtg	catagaattt	tcctcaagta	tctagataag	1061580
aatgttagca	aaagttagga	ttatgttaaa	cttcggggagt	agcactataa	tagatagcat	1061640
agtgtttaca	aaaaattctt	tttccctaag	taaggggaac	ttatgcta	caagctatgg	1061700
cgagctactt	atgaagggat	gtatacattt	cttggtgggtg	cgttgctaaa	gttgcgctac	1061760
cgtatgcaag	ttgaagggtg	ggacacctta	aacataaatc	ctaagcagg	gtgtttgttt	1061820
cttgccaatc	acgttgacga	agtggaccct	attatcttag	aatatctatt	ttggagtcga	1061880
ttccatgttc	gtcccatggc	ggtcagatgt	ttgtttcata	gtcgcgttgt	tcaatgggtt	1061940
ttaaattctg	taagatccat	tcctatccct	caacttggtc	ccggtaaaaga	gagtaagcgc	1062000
tctttagaac	gtatgaacgt	atgttatgaa	gaagcctcac	gagctttaaa	tagaggggaa	1062060
agcctccttc	tttatccttc	aggaagggtta	tcgagaacag	ggaaagagga	aatcggtta	1062120
cagtattctg	cttatgtgtt	attacataga	gttatggaat	gcaacgtggt	tttagtcaga	1062180
gtttcaggct	tatgggggag	tgcgttttcg	cgctataagc	agaactctac	acctaagtta	1062240
ggccctgcgt	ttaaagaagc	ttttcgagct	ttactgcgtc	gtgggatttt	ttttatgcct	1062300
aaaagggttg	taaaaattac	tctatgtcaa	gtagatcatc	tttttttaaa	gcaatttcca	1062360
acaaaacaag	acctaaatac	ttttttgggt	tcttggttta	aatcaaggag	atgacaattt	1062420
gcccatagaa	gttcctttac	gcataacgag	gaagttacga	cgtatgcacg	atcaacggaa	1062480
taggggtcat	aacaaccata	atttaagggt	gcgacctgga	tctacattat	tggaagcttt	1062540
tttaatatata	tgttccgaac	atgaagagg	aattgcctgt	tttgacgaac	atctaggctc	1062600
actctcttat	cgagaacttc	gcaatgctat	aattgctgta	gcaattaagg	tctccaagtt	1062660
ttctgaagat	agagttgggg	tgatgatgcc	cgcatctata	ggagcattca	ttgcctattt	1062720
tggcattctt	cttgcgggga	agactcccgt	aatgatgaac	tggagtcagg	gactcagaga	1062780
gctacgtgca	tgtacaaaaa	cagtagagg	tcgacgtgtt	cttacttcac	agcagttcat	1062840
caaacattta	actgaggtcc	aagggttcgt	agaatatccc	tttgatctta	tgtatatgga	1062900
agatgtgcgt	aaacgccttt	cctgggtggga	gaagtgcggg	ataggggtgt	attctaaatg	1062960

ctccgctccct	tgggttgctca	gaatcttttgg	agtttcaggg	gttgagagcg	atgatactgc	1063020
tgctattttg	tttactttctg	gaacagaaaa	acttccaaaa	gcagtccttc	taaccataa	1063080
gaattttaatg	gaaaatcagg	aggcatgcct	caaatTTTTc	gacctaata	cacaagatgt	1063140
catgtttggca	tttctccctc	cttttcatgc	ttatggattc	aatagctgtg	gcttggttcc	1063200
tttactgatg	ggcgttcatg	tagtattcgc	ttcgaatcct	ctaaacccta	aaaagttagt	1063260
tgagtttatc	gatgataaaa	aggtcacctt	ctttggggagc	actccggtat	ttttcgacta	1063320
tattctgaaa	acagcaaaaa	aacaaaattc	ctgtttggag	tccttacgac	ttgttgtgat	1063380
cggcggggat	gcattgaaag	ataccctcta	cgaagaaact	aagaaattac	aaccacaaat	1063440
tgctctctat	cagggctacg	gtgctaccga	atgttctcct	gtaatttcga	ttactacgaa	1063500
agaaagtcct	aggaatccg	agtgtgtggg	aatgccgac	gaagggtatg	atgtgctgat	1063560
tatttctaaa	gagactcata	ttcccgtatc	ctcggggagaa	cagggattga	tcgttgttcg	1063620
tgggaactct	gtattttcag	gatatcttgg	gaaccatgaa	catcagagtt	ttgtctcctt	1063680
agggtggggat	cagtgggtatt	tgactggaga	tttgggtcat	ataggctcta	gcggggatct	1063740
atTTTTtagaa	ggtaggctaa	gccgatttgt	aaaaatcgg	ggagaaatgg	taagcctaga	1063800
agcttttagaa	agtatttttgc	atgagcattt	tactgaaaat	caaaatgaag	acgcaggttc	1063860
cctagtgggtg	tgtgggtattc	ctggggataa	ggtaaggctg	tgtttattta	ctactcttgc	1063920
tacaacaata	catgaagtaa	atgatatctt	aaaaacgct	gaaaccagta	gcatagtgaa	1063980
gatattcgtat	tgcatcagg	ttgaaagcat	tcctatctta	ggcattggga	aacctgatta	1064040
cgtttcatta	aatgctctgg	ctgtttcatt	atltgggtaa	gtagccgttt	ctctgggtag	1064100
gttgatacat	agttagtttg	caaggagagt	ttcttgacta	ccagtgatgt	tatagatttt	1064160
gtaacaaatg	atTTTTctagg	tttcgctcgt	tctccacaa	tatactgtga	ggtaagtaag	1064220
cgtttccaaa	tacattgtca	gcagtttctc	catgagaagc	tcgggatccg	aggttctcgg	1064280
cttatggtag	ggccttcttc	agttatcgac	gatcttgagt	ctaaaatcgc	aagctatcat	1064340
ggagctccta	atgctttcat	agtcaatagt	ggctatatgg	cgaacctagg	cttatgtcat	1064400
cacgtatcac	gatctacaga	tgtccttttg	tgggatgaag	aagtgcata	gtcagtagtg	1064460
cacagcctat	ctgcaatctc	tgggcaacat	catacttttc	atcataacaa	tctggaacac	1064520
ttagaatctc	tattacagtg	ttacaggata	agctctaagg	gaagaatttt	tatctttgtc	1064580
tcttctgtat	attcttttag	ggggacttta	gtcctcttg	agcaaactcat	agcactatca	1064640
aagaagtatc	atgcccactt	aattgttagat	gaagctcatg	ctatgggaat	ttttggagac	1064700
gatggtaaag	gactgtgcca	tgccttaggt	tatgagaatt	tttatgctgt	attgggttact	1064760
tacggaaaag	cttttagggac	gatgggagcc	tctttattaa	cgctacacga	agtgaagtac	1064820
gatttaaatgc	aaaattctcc	gcccttgctg	tattctacat	ctttatctcc	tcatactcta	1064880
atltctatag	gcacggcgta	tgattttcta	gcctctgaag	gggaaatcgc	acggaagcaa	1064940
gtctttaagt	taaaagagca	ctttcatgag	tgtttcgact	ctcatgtctc	aggatgtgtg	1065000
cagcctatat	ttttaccaca	cacctgcttg	gaagaagcaa	tttctgtttt	agaaactaca	1065060
gggatccatg	taggcgttgt	tgcctttgct	aagcatcctt	tcttacgtgt	gaacttgcac	1065120
gcttacaata	ctgtcgatga	agtgaacctg	ttggctcaag	ttatgaagcc	atacttagaa	1065180
aaaagtagtc	ataggggtcca	catcaatcat	gaatttcacc	tttgccgaga	gctttgccag	1065240
cattaaggcg	tgatggagtt	tcttattcac	tggaatgaca	taagcactct	taattaaaaa	1065300
ctgatagcgg	aacgtatcct	tgatttttaa	atgaccgcaa	ggagtcactg	gcacttagtg	1065360
attcgtgctt	tctagtgcct	cttttagaat	gttatggact	cgggtggcct	cttcccaagt	1065420
ctgcttggga	catttcccca	tgaaaataca	acggataaga	cggataaatg	gaggatactc	1065480
acagagttcg	cgacctgtga	tttcttgact	ataaaatgcc	gagtagtcct	gacgcatagc	1065540
actatgaatt	gtgggatggg	caggaagaaa	ggattggatg	agaatttctc	caggtaggtg	1065600
gctccgaccc	gacctacctg	ctacctgtgt	aatgagctgg	aagacttgct	ctgaagctcg	1065660
gaaatcaggg	atatacaatc	cagaatctcc	atlttagaatg	accgcgagtg	tgactgcaga	1065720
gaaattcatg	cctttggcaa	tcactctggg	gccgatcaaa	acatctgctt	ttcctgttgc	1065780
aaattgcctg	agtaacgttt	catggctccc	cttgaatttg	gtagtgtctg	aatcaatacg	1065840
gatggtagct	atctgaggaa	aaatctgctg	gagaattttt	tctatttttt	ctgttctctga	1065900
gcctcgatat	tgcaacgtca	tagttccaag	acatttttgg	caagatttgtg	ggaggtcttt	1065960
agggtaggag	ttgcatagat	ggcagagaag	cacatttgca	tatttatgga	agggtgagac	1066020
catgtcacaa	tgagggcatt	tcaatgtatg	cttgcaaaca	gtacaagaga	cgttgggtatg	1066080
atatccccga	cgattaaaga	aaatcaaaac	ctgctctccc	acttccagac	gttcggctat	1066140
tttctttaac	acaggctggg	aaaatagaat	cttggttttt	gacttttccc	tctctaagtt	1066200
catgttgata	agagaaaattt	ttgcgggatg	agcagcagct	gctcttgaag	agagccgaga	1066260
cagaacgtac	ttgccagata	gcgcatttag	atagctttct	aagctgggag	tcgcacttcc	1066320
taaaaccaca	gtagcatgag	cgagtttgcc	tcgcattaca	gcgacatccc	tggcatggta	1066380
gcaaggagga	ctttccggtt	gttttataggc	gggatcgtgt	tcttcatcta	caatgatcag	1066440
tcccagattc	ttcatggggc	agaaaagagc	agaccgtgg	cctatgagga	tacgtaggga	1066500
tcttcggaag	cttggcgcca	cgtgcgactt	ttgatcgctg	tcgctaagct	tgtgatggag	1066560
aacacctaca	tccttgccaa	agcgcgcttt	aaataatgag	actgtctgca	ctgtgagagc	1066620
gatctctgga	acaagaagaa	ttgtactttt	cccttgttta	agagcctcgc	ttgttgctcg	1066680
aagatagatc	tctgttttac	cacttctgt	aattccgaaa	agtaaatgtg	tatggaattg	1066740
tgaggttttt	agtgaggaaa	aaattttatc	tatagcactt	tgctgttcag	gatgtaaatc	1066800

cttaggagca	ggcgggaaaa	aggttaggag	gtcttcttga	agctctaact	gcgctgcac	1066860
tacaatatca	agaatgcccc	gcttttcaag	agaatgaatt	ggagattgcg	atactttggc	1066920
agtctccata	agggaagata	aacccgggtg	ggacgcatgt	tgtagtagaa	tttttaaaac	1066980
agccccctga	gaaggatgta	aaactttctaa	ttttgcaaga	atctcttttag	tttttgcttt	1067040
actttgcttt	aagacgacac	ggtagtgtcg	cttaggctga	atcacattcg	aagagatagc	1067100
gggaagaaat	aatttttagag	ttttcccaag	aggagcaaag	tagtattggc	tgatccaaaa	1067160
tagcaagtct	agaagatctt	gaggaaggac	aatctctgaa	tcggataatc	ctaagatagg	1067220
taaaattttc	ttacattggg	tcgttggttt	tatttgataa	ataactccaa	ctttttccc	1067280
cccccgtaaa	gagatagtaa	cagcagttcc	tttagtaatg	tgctctagat	tttcaggaac	1067340
gccataatcg	agtaccttgt	tgatgttaga	gcctacgatg	acttcggcgt	ataggcgaaa	1067400
ggtagacgat	tcaatatagc	ccatagattt	cgtttttagct	gtgaatcttt	ttcatactct	1067460
agtgaagaat	agaggggaag	aaagatacat	ccattttgtg	tcagagattg	atgataatca	1067520
gttgtaggaa	ttttataacg	gatcacattt	aaaggggcta	gagctaaaaa	aaaattgggg	1067580
ttgtttacga	agatattcgt	cttcgcatga	atcaaagtca	actttgtagg	gaaaagttgt	1067640
tgcgtaagaa	tttttgctaa	tctgttaaaa	aacagcactt	cttcgttggt	ttcttcataa	1067700
acaaaaatag	agcaggggat	cttcggagca	ggaagactac	aatcttttaa	agcgggatat	1067760
ttctctttta	aaatagcatt	ttgtgacagg	tctggatgca	gaggaacaca	tttccaatct	1067820
gaaggcttag	tcttttcttg	agaaagattt	gtcgggtggag	gaggggtgat	tggttggggt	1067880
tctgcattgg	ggactttctac	agcttttctca	ggtatagaag	aaacacttgc	agagattgca	1067940
gtattcggaa	gagttacatt	caggagagat	gcaagtgttg	gatagagttc	ctcagaataa	1068000
cgatccaaaa	gttgacagag	agtgtcatga	aaattttgag	agttttccat	aaatagccaa	1068060
tgtttctaaa	aaagagaggt	acgttttggt	accataaaaa	ggagagctct	ctgtggataa	1068120
gaatttctat	tcttattttta	tcctaaatca	gataatagtg	tcatacatac	caacaaactt	1068180
attcgacacg	tttttttaag	gatagtgcac	tgaatttttg	gttgcaagga	tgtgtctttg	1068240
tcgggtgtct	gctattgact	ttaccttggt	gtgctgcacg	aagacgtgct	tctggagaaa	1068300
tttgcaacaa	actcgtccta	tagcagctgc	aaatctacaa	tgggagagct	atgcagaagc	1068360
tcttgaacat	tctaacaacg	atcacaaacc	tatttgtctt	ttctttacag	gatcagactg	1068420
gtgtatgtgg	tgcatataaaa	tgcaagacca	gattttgcaa	agctctgagt	ttaagcattt	1068480
tgcggtgtg	catctgcata	tggttgaagt	tgatttcccc	caaaagaatc	atcaacctga	1068540
agagcagcgc	caaaaaaatc	aagaactgaa	agctcaatat	aaagttacag	gattccccga	1068600
actggtcttc	atagatgcag	aagggaaaac	gcttgctcgc	atgggatttg	agcctgggtg	1068660
tggagctgct	tacgtaagca	aggtgaagtc	tgctcttaaa	ctacgttaag	ggattttata	1068720
acttattttt	gagaccttcc	ttttttaagt	tgaatgtgag	aaactttcta	caaacccttg	1068780
gattaggata	aggtctcaaa	aaagtgcgta	ggatattaat	caggttgctg	agactttctg	1068840
ttttcagaat	ctaaataatt	agagatcact	gctgctaate	tgtctactac	atttggtactg	1068900
agaggattta	gatggagaag	atccctttcg	ggtataggaa	tttttagtccc	cgaggttttt	1068960
acttcaggaa	gctctagaaa	aggtgttnct	acgcaatttt	ctctttcgaa	gaggccgtcg	1069020
ctaattgagtt	cttgatcatg	attagagttg	taaatgaaaa	tttcgggaca	acgcaatctt	1069080
tcgctagggt	tcacagagtc	tatgttccaa	ccaacgagtt	ttataatcgc	ggaagctatg	1069140
ggcttacaaa	tttgattcgc	gacatctgtc	agagagcgag	ggccccgac	ttttacaaca	1069200
atccatgcaag	ttccatcact	gccatcagtg	acctcacgat	ctagagcagc	agcttggaac	1069260
ctagttccca	aagagtatcc	gaaagctatg	atttgattgg	ctttaggacc	tgtctcttca	1069320
tctcgtaggt	agcgtacgca	tgcttgatac	gatttaacca	gattttctcg	tttcgcttct	1069380
cctttgctgg	acataattcc	aggatagttg	aacacaagaa	gattcgagcc	ggttgctttg	1069440
gctagctggg	gtagagagga	atcgccccga	tcgaacaggt	tttccatcaa	tccagagttt	1069500
ccttgagaat	aaagaatcca	cctgtgggga	agagcatgag	gtatctttat	agctaagcta	1069560
tcaaccacca	aatcgtcata	ttgtataacc	acacgatcgg	cagctgagat	ttccttaagg	1069620
cttaggagtt	gtttaatatg	ggacagaaaag	gtcattcgcc	gaattgccac	agctgttttt	1069680
gacatgctct	gagatatgat	agaagatggg	agaatgaaaa	actgacaggt	tttcttgagt	1069740
accacacaata	acgctaaggg	aaggaacaga	atgattgaga	taataaactt	cacaatatct	1069800
caaatcgctc	ctagaacttt	aaataaggtg	ggatgggcct	tccgtctttc	agaagctatc	1069860
tctgtttttt	ttgaagagaa	catgattaaa	gacggctttg	gatccgtctc	tagaatcgta	1069920
tcatacagaa	agttttattg	ggtaggggat	gggatcatac	aagagtccta	aatttttaggt	1069980
acacagagta	ttaaagagaac	aaaagaaaaa	gaatacgcac	tataattttt	taattttttc	1070040
tagagagact	ctcaaggatt	gcttcagcaa	gcttttgat	tgtagggtgt	ttcagagggc	1070100
ttgagtggag	tagatttacc	tctcctataa	attttttact	cctggcaaat	gggggttcgtt	1070160
ttattgcatg	agcaagagta	aactccggga	gcaatgcggt	atcatcacca	acttctgaag	1070220
ggcgaaatcg	atccgcagaa	taaacaagaa	tttctgggca	aggaagctct	cggctgtttt	1070280
tttccgcac	cattttccat	cgagcgagga	ctgcgatgag	ttttcctatt	ggcccgaaga	1070340
aactattagc	agctgcgggt	aaagagtggg	gagcacggtc	tttgactgct	acccaagaag	1070400
tctcgctatt	tgtaaaagga	ttttttgcaa	agctgcagac	tggactaccc	ctcctaagga	1070460
atatacctagg	tgatgatttc	gttagcccca	gggccctgaa	ttttatcttg	taggtacttt	1070520
gcacatagat	tatgactgtc	gctaggttct	ctaagttcaa	ttttcctgtg	ctcgacttaa	1070580
ccccaggata	gttgtaaaat	aggatattag	cgcttagcag	tttagctaac	tctttccagg	1070640



agagaaacaa	ggaatctttc	aggcctatca	tgtcttcgag	gaaatctcca	cttcctagag	1070700
aaatcagcag	ccaacgttta	ggccttgccg	tactgaaatg	tattgctaaa	gtatcaatgg	1070760
taagatggtc	ttgttggtatc	gtgattcttt	tactttccga	gactgctggg	tctttgaaag	1070820
agggatctag	attctttaca	aaataatctt	gtatttcctg	ttccaaacga	tactttttaa	1070880
agcagggtttt	caagacgctg	taaagcatcg	aagaacgggg	gaaaagagcc	aaggaacata	1070940
ctaattgaca	taaccaataa	attcccaggg	gcggaataat	cagaccgatt	aagagtttga	1071000
aaattttaac	aatgatcgta	acaattttgg	tgagtatggg	gtgcttctta	ctaaagtcac	1071060
ttaactgctt	ggcgtgtgtt	gacgaaaaat	aggaaactgg	atgaggattt	gaaaatattc	1071120
ctgacaaaaa	atcagacctg	tttgaaagat	tcaaaagagt	gaatgcgaaa	tccttacgtc	1071180
tctaactctca	agggactggg	gacgtcaggt	caaacaaagt	tcagtgttat	cggcggctgt	1071240
ttttcgcgct	tatattataa	cgggtgcctt	agaaagatta	aatagttaag	tgccttttaa	1071300
tctgattctt	aaggagcatc	ccttctttct	aagagagctt	tttcaaaatt	gggtgtggcaa	1071360
gagccactct	tgttttgctg	tcgatgggat	cgatatcaga	cgataatcgt	acttctataa	1071420
attcttttatt	ttgaacatag	ggactatttt	ttatcgcatg	agcgagagta	agttcagggtg	1071480
ctaagagctt	gttctgtctg	actgttgatc	ttcgttaagga	atccgtagga	tagagaaaaa	1071540
tttctaggca	gggaaggctt	tggcttctct	ctacggcttt	gggtccccag	ccaaaaagac	1071600
gagctactag	ctttcctatg	cgtctgcaac	tgtggaaacc	ttctggagat	ataaagagag	1071660
gacacctatc	tttgactgct	atccaagtat	tatcatcggt	tgcaacaatc	ttctgggtctc	1071720
gcaatgcttc	tgcttgtatc	aaacctccta	gggagtaccc	ataggtaatg	atttcttttg	1071780
ctccagggcc	ctgttcttta	tctttaagggt	atcttgtaca	aatattatga	gctgatgcta	1071840
gggtcctttag	gctgctgctc	cctgtgctgg	acatgactcc	ggggtagtta	taaacgagta	1071900
tattggcccc	tatcaacttg	gcaaatcttt	gccaagaatc	aaagatctcc	ttacaagcga	1071960
tttcttccaa	gctacagtca	cttcctaaag	aatgagcat	ccaacgattc	gtaggtgctt	1072020
gtgaaaggca	tattttccaaa	gtgtcgatga	gaacattatc	ctggaggata	ggaactcgct	1072080
tcattggaagc	aacgcggttt	ttcggaggaat	aatcttgcaa	agcacgcaaa	taattagttt	1072140
ttaagggtttt	agtgttgggt	tgcttcttga	aaatttttaa	taaattcttg	gaagggagaa	1072200
tcgagtttgt	acaaagcgtt	tgacatagcc	agtagattcc	taaggggaagg	atgatcagcc	1072260
ctatcagaac	tttaaaaaatt	ttaataatta	cagaagcaat	ccgtgtaagc	acgggatgcc	1072320
tgtcttttaa	ctcatgaagt	ttttgggcgc	gtgttgaaga	aaaataagtc	gcttgtggag	1072380
aagggtggga	atgtaaaaata	tcctcaacaa	acgcattact	tcctgtgaatt	ggagccatga	1072440
acttttctcta	taaaatttaa	gttcttttta	cggaaactact	tggtttttga	tttgttcgta	1072500
tagagggggg	gggttcagggt	agaatgttgc	cgatatggag	tcgtctagag	caggcttcaa	1072560
tgtctgtcca	caaaagtttg	tggtcttttc	tttattgcca	tccaagaact	gatctagctt	1072620
tacagtttag	aagattttca	ggaccgaatt	ctaagagaat	aaattttaag	caataaggga	1072680
ataaaaaaga	atcatatctt	cactcggttc	tgactttgta	aagaagttaa	tcctcattct	1072740
tgattacacg	aatctaacca	actataaaca	aatttttttg	aggagaaaat	ttcttctact	1072800
gttttggect	gaactcaagt	tgtttatcta	aaagaactta	aaaaatacaa	cagctctttc	1072860
tttagaggat	acagaaagtc	gagttataga	tagagatttt	actaacttaa	ggataaatat	1072920
taaaatattt	atttaatat	ccaagagttt	ttatttgata	gtttctattt	ttaattttaa	1072980
tttattaatt	ctttaaaata	agatgagcga	gtcgcgcccc	tgctcgacag	gattcgagat	1073040
gggtccccat	acgcaggctc	atcatgccct	tgatacgcgg	agagtcattc	taacgatagc	1073100
cgcctgtctg	cttttaattg	caggaatcgt	gttgggtggc	ttaggtgctg	cagcaatcct	1073160
gcctctgctt	tttggagtca	ttggagggaat	gattcttatt	ctgttttctt	cgatcgccct	1073220
catttattta	tacaagaaga	caagggagggt	ggatcagatt	gctctggagc	ctcttctctga	1073280
gatgatttct	aaagatcaaa	gcattataga	ttttgtaaag	acacgagact	atgcatcttt	1073340
agaaaagaaa	gcgacctttg	cttataactca	tactcattat	tacgatggaa	gcatggctct	1073400
ctatagggag	atccctagat	ttatgttagg	ctcttatctc	gcgcttcgca	aagacatgga	1073460
ccgccaaagt	cttttttgaa	gaaggacatc	catgttatgt	tgctcgccag	gcttttaatt	1073520
cagggaattcg	actctatcgt	cagttatttg	acatagaata	tttaacgaag	ctatacaaaa	1073580
acaaggatta	cgatcctgag	catcgacaaa	gtttaaaaag	cctaatagat	tggaatgaaat	1073640
gcgaagacca	tggggaagac	tttttgcgtc	aacatcgggg	ctgtgactac	ccatcttctg	1073700
gctatacggg	aatgtttttc	aaacattctt	aagtctttgt	ccgcacccctg	aatcttgcat	1073760
ctagaatttc	tttttcataa	tctcatcctt	catggttttag	aagattttgtt	ttgggtgtgtc	1073820
ttagttcacg	caaaaaagtg	ggagagactt	gtaagggaga	cttctttaac	taaatgacta	1073880
tcgattgaaa	gaaggagttt	tgtattttaga	aaagcgtatt	cttcttaaat	tttttactga	1073940
tacatacata	gaatgtatag	aagtatcaga	atcttcaaaa	gactcagagt	gatcaacaac	1074000
agtggatcca	tttatagaag	taaaacaaga	gctgtactac	catttagaat	ataggccttg	1074060
gttttgctcg	gggaaaattcc	atgatattctt	tctttatgaa	tctaaagttt	tcctagagcg	1074120
aagagagtc	aaaactcagt	aagctatata	aaatttgccg	tgtaatttaa	gcatcagata	1074180
ctctgtctgg	tgggatcggc	ctgcttttta	caactttaga	tagatagatt	ttagagtcctt	1074240
gggttgga	agcgatatct	atacaaacat	actagaggaa	agaatgacgg	cgagagcaga	1074300
atatttagac	catgaggatt	ttttatatag	gagtcacaaa	cttcaggaac	tttctgagtt	1074360
gggtgtagtc	ctttatcctt	acgagtttcc	tggagttttt	tcatgcgaag	atattaaaaa	1074420
aacgtttgct	agtcaagagt	tagggaatag	tgaagctgct	atgagtaggt	ccactcctag	1074480



agtgcgtttt	gctgggcgtt	tggttctttt	ccgtgcgatg	gggaaaaatg	cttttgggca	1074540
aatttttagac	cataatcaaa	ccatccaagt	gatgttcaac	cgtgagttta	cctccgtaca	1074600
cggactttct	gaagatgctg	agattactcc	gattaagttt	atagaaaaaa	agtttagattt	1074660
aggagatata	cttgggatcg	atggctattt	atttttcacc	cattccggag	agcttaccgt	1074720
tcttgtagag	actgtaaccc	tactttgtaa	atccttactt	tcggtgcctg	ataagcacgc	1074780
aggtttgagt	gacaaagaag	tccgctaccg	caagcggttg	ttagatctaa	tttcttcaag	1074840
agaggtttag	gatacctttg	tgaaaagaag	ctatattatt	aagcttatcc	gtaattatat	1074900
ggatgctcat	ggatttttag	aggtagagac	tcctatatta	caaaatatct	acgggggagc	1074960
agaagctaag	cctttcacaa	caacaatgga	agctttacat	tcggagatgt	ttttaagaat	1075020
ctccctggaa	atcgctttga	agaaaatcct	agtaggagga	gctcctcgta	tttatgaact	1075080
cggtaaagtc	ttcagaaacg	aaggaatcga	tagaacacat	aatcctgaat	ttaccatgat	1075140
agaagcgtat	gctgcttaca	tggactataa	agagggtcatg	gtccttgtag	aaaatcttgt	1075200
tgagcatctt	gtccgtgctg	taaatcacga	caatacctct	ctagtctatt	cttattggaa	1075260
acatggcccc	caagaggtag	attttaaagc	tccttggtat	cgtatgacaa	tgaagaaaag	1075320
tatcgcgacc	tatgcaggta	ttgatgttga	cgttcacagt	gatcagaagc	ttaaggaaat	1075380
cttaaagaag	aaaactacct	ttcctgagac	tgcatttgcg	acagcttccc	gggggagtgt	1075440
gatagcagcc	ttatttgatg	aacttgtctc	tgataattta	atagctcctc	accacattac	1075500
agatcaccct	gtagagacaa	ccccgttatg	taaaactctg	cgttccggag	ataccgcatt	1075560
tgtagagcgc	ttcgaaagtt	tttgcttagg	gaaagagttg	tgtaatgcct	attcggaaact	1075620
caatgatcct	atccgtcaaa	gagaactcct	ggagcaacag	cataactaaa	aagaactcct	1075680
tccggatagt	gagtgtcatc	ctatcgatga	agagttttta	gaagctctgt	gtcagggaaat	1075740
gccccctgca	ggaggatttg	gtataggtgt	cgatagactt	gttatgattc	ttacaaatgc	1075800
tgcattctata	cgcgatgtgc	tgtatttccc	tgtaatgcgg	cgcttcgatg	cagagaagac	1075860
gaattaaagg	ggcttaactt	taggccctga	cttagagtct	tcgacaagga	agcctgcggc	1075920
aagtattctca	tcacgtaagg	tgtctgccat	cgcccaattt	ttagtttttc	tagcttctct	1075980
acgttctgca	acaagttgca	ttacggtttc	tgggatgcac	acgcttgtgg	ttagaggaag	1076040
cacaccaagt	acagtatcga	cttttttaag	agtgtctaag	atatagagag	agtcggcttt	1076100
agaaaagtgc	ccttggtcga	tcaaggtgtt	gatttcgtga	acaaaatcga	acagagatgc	1076160
aaatcctgta	gaaacattta	agtcattagc	aagagctctt	gagaaagctt	ctatgaattg	1076220
actgctagag	tccaaggttc	tgggaagggg	agattcccca	gggagatcta	cgccttcaag	1076280
tcgagaaaac	aaatctttta	agcggcgtaa	ggcatgccta	caggcaagga	gagcttcttc	1076340
tgtaaagttg	agttgcgtac	gataatggct	ttgcagttag	atatagcgta	cttcttgacc	1076400
agtaaattcc	tgggtggagaa	ggtctcgtag	agtgaggaaa	ttccctaagc	tctttgacat	1076460
tttcttccca	tcaataagca	gatgttccga	atgcagccaa	tagcgtgcaa	aggggttccc	1076520
tgaaagagcc	tcagattggg	cgatttcatt	ttcgtgatga	ggaaatatat	tatctacacc	1076580
tcccgcattg	atatccaaag	aatctccaag	aagttccatc	gccataatcg	aacattctaa	1076640
atgccatcca	ggtcttccta	ttcccgaag	gactttccca	ataaatgacg	ccatcacggt	1076700
ctggattgta	tgttttccac	agtacaaaat	cacttgggtt	ttctttgtca	tactctcag	1076760
cagaaattct	ggagcagcag	cgtaagctac	ttagatccag	atgagagagc	ttcccataat	1076820
ttggaaaacg	gtttagagaa	aaatatacgg	aagcatcctg	acctatatag	gcgattccct	1076880
gctctaagag	ctttgtaatc	gcttggatca	tttgagggat	gtagtgtgtt	gcgtgtggat	1076940
agaaatctgc	tctagcaata	tttaaagtat	cgagatcttc	aaaaaaggct	tcggtatatg	1077000
gctgcgtgta	ttcttgagc	ggaatatatt	ttttcgaggc	tcctgctatg	gttttgtctt	1077060
ctacatcagt	aatattcatc	acatgggtta	cagagtagcc	aaagaatact	agagtgcgtt	1077120
tgagaatatc	ttcaaagaca	taagttcgga	agttccctat	gtgagcgtag	tcatacacgg	1077180
taggaccaca	agtatatagt	cttacagggg	tgtgattggg	gaaaaaaagt	cttttttttt	1077240
gagatgctgt	attgtagaaa	tagagaccct	cgatatgaga	aaatgccata	actgtatcac	1077300
tcttgactca	ggagtttggt	gttatataga	cagagagaat	ttaacgctcag	tctcttcggc	1077360
ctatccctaac	aaaataaatt	ttctagatct	atgatttttg	ctttcgaaaa	tcttatagga	1077420
gaaaagatag	caaatttcct	tcttttcaaa	agaaataaaa	aatcgcataa	atattcttag	1077480
aatttcatat	ttattcatgc	aatagaagct	aaactttttt	tagtagcgaa	gttcaacggt	1077540
tttaagtagt	gtttttttatt	tcgttttaat	aaaaaaaaga	ctatacaaca	agagtcgcta	1077600
gaaagatggt	ctcgaggcat	atctggcccc	ccctgaatag	aataaaattgc	gtcctaattct	1077660
taggaaaagga	ggaggtagcc	cgtgatccctg	ttacaaaata	tcaaaaagatg	ttccttaaaa	1077720
cagttgaagg	tcttggtctac	tcttttggtg	agcttgagct	tacctacgct	agaagcagcc	1077780
gagaacagag	attctgattc	tattgttttg	caacctggatt	atcaggaggc	tttgcaaaag	1077840
agcaagggaag	cagagcttcc	tttgcttggt	attttttctg	gttccgattg	gaatggccct	1077900
tgtatgaaaa	tccgtaaaaga	ggtgttgga	tcacctgaat	tcatcaaaag	agttcagggg	1077960
aagtttgtct	gtgtggaagt	ggagtatctg	aaacatagac	cgcagttgaa	aacattcgct	1078020
agcaaaatct	tgctttgaaa	tctaaattta	aaattaatga	actgccctgc	atgattttgc	1078080
tctcacatga	ggagagagaa	atctacagaa	taggttcttt	tggtaatgag	acgggttcca	1078140
atthagggga	cagtctttgt	catatcgtag	agagtgatcc	ttactaaga	agggcggttc	1078200
ctatgatgac	gtcgctatct	ttatcggaac	tgcaaggta	taccgactt	gctgaagagc	1078260
tctctcataa	agaattcctc	aagcatgctc	ttgagcttgg	ggtgcgcagt	gacgattact	1078320

tcttttttate	tgagaagttt	cggttatttg	tagaagtg	caaaatggat	tctgaggagt	1078380
gtcagagaat	taaaaaacgc	cttctcaaca	aagatcctaa	aatgaaaag	caaaccatt	1078440
ttaccgtagc	cctgatagag	tttcaagaac	tggcaaaaag	atctcgagct	ggtgtgcgcc	1078500
aagatgccag	ccaagtcac	gtcctctag	agagttatat	ttctcaattt	gggcagcaag	1078560
ataaggataa	cttgtggcgt	gtagaaatga	tgatagcgca	gttttactta	gattctgatc	1078620
aatggcatca	tgctttgcaa	catgcagagg	ttgcctttga	agctgctcct	aacgaggtgc	1078680
ggtcacacat	ttctcgctct	ttggagtaca	ttcgccacca	gtcgtagctt	tcgtttttcc	1078740
aagacgatgt	aacccctctg	ggatttgatt	tataaaatcc	tggagaagtt	ttgaaaagac	1078800
agggcgctgt	ttatgtccct	tggggaaaac	aacaatttga	caattgggaa	gttgggtggcg	1078860
gacatgccga	aatacttcac	gaacgacacg	tttaaaagag	tntctttcgt	gagctttgcc	1078920
aaatttttta	gatacagtaa	tacccatcct	acaagtcccg	ggatgcctag	aagggaccac	1078980
gtagaaagtc	gcctgactac	cacgacaaca	aaaacctgaa	cgcgtaatgt	aaagaaattg	1079040
ctttcttttc	aaaacgcggg	attgtttttg	taaggtgagt	gggtgcacga	aataactaaat	1079100
tataaatcga	ctagggaatg	cctaccgtgg	cggcggcgac	gattcaaaag	ttttcttcca	1079160
tttcttgtgg	ccatacgagt	acggaaaccc	acagaatttc	ggcgtttcct	tttgcctagg	1079220
tgataagtcc	gttttcacagt	gtcttccat	aattccttgc	ctcattcacg	gttgagtctt	1079280
actaaagagg	ctttgcccg	aatttttagaa	gatttatatca	ataaagatca	ataagaagac	1079340
atcggctttc	ttccaactta	tctaagaaaa	ttcgagagat	gacagtctgg	tattgtcaaa	1079400
aaagctccta	ggagattaaa	ttggttcctt	gttgtaactt	agtatgcttc	tcctttttat	1079460
gagaagtga	ggtaatatct	catgaaagtt	agttcatctg	ttaaggctga	tccatctaag	1079520
ggggacaaat	tagtccgccc	taaaggacgt	ctttatgtaa	ttaataagaa	agatccaaat	1079580
cgaagcagc	gccaagcagg	acctgcacgt	aaaaaataat	ttaaaaattt	aggtaaaacg	1079640
catggcgaaa	aaatcatcag	tagcaagaga	agctaagcgt	cgacgattgg	tagaggctaa	1079700
ttttaaaaaa	cgatccgacc	ttcgtaaaat	cgtgaaaagc	ttgtctgtta	gcgaagaaga	1079760
aaaagaaaaa	gcccgtatct	ctttaaataa	aatgaagaga	gatacttctc	ctcacgttt	1079820
gcataatcga	tgcttattga	caggccgtcc	tagaggctac	ttaagaaagt	ttgctatctc	1079880
tagaatctgt	tttagacaaa	tggttcttat	gggagaaatc	cccggcggtta	ttaaggctag	1079940
ttggtagtct	attctgatta	gagccccaac	cctattttaag	gacgtggggc	tttattttga	1080000
tgcttctttc	aaagcctgtt	gtagtgatgg	aacatccttc	actcgttgcc	aatctttcat	1080060
tccttttttc	catacccaaa	tttcttctgg	atacgttttt	ccctttaaaa	gtacgacca	1080120
ctcctcaaaa	gatatcggac	ctacgttttc	tctatcttta	tttaataaaa	accacttctc	1080180
tgtatcgata	acgatttctt	gaagatctcc	cgatagggtt	atctcgtcat	tacctgttaa	1080240
actttttttc	aaatcatcaa	aaagatcggg	gttatcaaaa	ggatcgtttt	gtggcttttc	1080300
taaagcgttt	cgacgagaag	gaagaagaag	aaggacaact	agaccaataa	atccaaaaaa	1080360
tgctcctgca	aaaaaccagc	caataacatt	tcgttttttc	ttatctgcta	tgtaggcaga	1080420
tagacaacct	agaatcacat	aaaataataa	aatcgaaata	gggagcatag	tgcgtagcgt	1080480
acctgaaaga	ttaatagtct	gtcactaacg	cctattattt	ccatgtgttg	tatttctcgc	1080540
tagagaaata	gggcacgttt	cataaggaaa	cgtagaaaat	acaagtctta	aattaaaaat	1080600
atcagttcaa	gaagaacaat	ttcagaactt	ttctgatgcc	atatagtagt	gaaaaagaga	1080660
aggtagactct	atagacgtta	aagtggataa	aaaaactcat	aggcaagagt	gcgacttttt	1080720
ttctttacta	gcagagcgtt	aggggaacct	agaagttgga	tctaattggat	gtagcatatt	1080780
aaccgctgga	cgattagact	gtcgctaaca	cttattattt	ccaccgtgtt	atatttcttt	1080840
agtgaagaaa	tagagctcat	tggaggagga	aaaatggaaa	aacaaaattt	aaaattagat	1080900
gtcaaagaga	ttgagtttcc	tgaacggta	ttcagccgtg	atatcgaaac	tcgtgttatc	1080960
caagtaatta	ttttgcattg	tttagcaaaa	attaacggtg	tttccctcct	cggaggaaat	1081020
ctaatagacg	ctctgttcgg	tagagatatc	gaaagaatga	aggggatcta	tgtagaacag	1081080
gattcaaaaa	atcatctggt	caaagttcgt	gtcgaaagtga	acgtagatta	cgggtgtttc	1081140
ataccagaga	aaacagaaga	aatccaggga	tgcattgttt	cagaaatttc	agaatatata	1081200
ggacttcatg	tggccgctgt	ccacgtgac	attaaagggg	tgacacaacc	aaaagatcgt	1081260
attgatgaag	aaattgaaga	ggaagtctct	gttcaagatc	ttccttcacc	tgaagacttc	1081320
ttacttgaga	attctgaagg	gtagacttaa	tcagatttgt	tgaagtcttt	ttgccttgca	1081380
agaagcactg	caatatcttt	cttagtttag	ccagggaatag	cttcagctc	ttcctgggag	1081440
ctaagcatta	cctgtttcca	acttttaaat	ttctgcaaca	atcgtttttc	ctttacctct	1081500
ccgattccag	ggattttttc	ctgttcaaat	aaagcctttc	ctcttttttt	cctgtgctta	1081560
ctaatacgcaa	agcgatgtgc	ctcatcacga	aggatctgaa	aaaattgtaa	taaattagaa	1081620
gtcgggggaa	gagaaaaaac	ctctgggaac	gtctcgcgaa	aaatcttctc	cttatttaac	1081680
cctcgactat	gtattacttt	ttcttttgcg	atagtaacaa	cctgaatttc	tgtaagattg	1081740
agagtttgga	ttattttttt	tgtcttggtta	tagtgcgttt	ttcccccatc	aaccacaatc	1081800
atatcaggaa	gagctgtggt	cagtgaatga	aaccttcgta	agagcacttc	ttctaataga	1081860
gccaaagtc	tctgagtcct	ttcagaatct	atggaaaacg	tacgatattg	cttgggatcg	1081920
aaccatttat	tttcaaatac	aatgtacact	ccagtagcgt	gagcaccttg	catatgagca	1081980
ttatcgtagc	attctatccg	atacggatat	tgtgacatcc	gcagtattat	tcttaaagtc	1082040
ttggtagggg	agcttgatga	aggaagtgtg	gttgctgcat	acgccttggc	attgcatag	1082100
gctagatcaa	gaagttcttt	tccatatcct	gtttttggag	aacgtaggcg	gggaggagac	1082160

tccgcattca	atacgttagga	gagagtagga	aattctaggg	gaagagggtgt	cagaattttct	1082220
ttaggaatgt	aggggttggt	aacataatat	tgcaaaataa	aagaggagag	caagtcttga	1082280
tcttcttgag	cattctcaaa	gaaagagaaa	tggtcggtccc	caagaagctt	ccctgagcgg	1082340
acagtaagta	gcgtgaggat	ggtgctgtgt	ttatgtctgt	aaagaccaag	agcatcaata	1082400
ttttgaaaat	gaaatttttc	cacctgttgc	tttgccatag	cttgcttaat	tagggacaac	1082460
gtgcggtagt	aattcgagc	ttgctcaaat	tctaagttat	cggaagcctt	ttgaatcact	1082520
ttttctaagt	ccttgaccac	ttcttcgac	tttcccttaa	gaaagaggat	cgccttgctt	1082580
aagggttcctt	gatattcttc	aggagtgcga	tagccgacac	aaggagcaag	acagcgcttc	1082640
atgtcataaa	gaatgcaagg	gcgtttcctt	aaggcaaaact	ctcgatctga	acaagtcttc	1082700
agaggaaaacc	attggctgat	aacctctaag	agagtgtggc	aggcttcagc	acttacataa	1082760
ggggccaaaaa	tcaattgtcg	ttgtgaagag	gttatcgctt	tcgtgaggat	agcttccact	1082820
ttggggccacg	aatgtgacag	ggaaatcgca	aggcagaaaa	aggttttatc	atctttgagc	1082880
aacacattgt	atttaggatg	gtgctgcttt	atcaaattgt	tttctaaaag	gagggcctca	1082940
gtttcattcg	acacaacaat	agtttcaata	gacgcggtct	ttttcatgag	aaaagggatg	1083000
cgttctcgag	agtcctcttt	ctcatgaaaa	taggatgcta	agcgattttt	gagattttta	1083060
gccttgccaa	tgtagaggac	ttgatcatgg	acatccttca	tcaggtagac	tccaggagag	1083120
gaaggaaatga	gtttgagaga	aaaatcctca	atgcgcataa	ctagaataat	gtcagttggt	1083180
gcatcttatc	ttgagcaggg	cgtgtaattg	attccggggc	ttctaattgt	cttaggatct	1083240
gctgagctct	cgataccaca	caaaggggaa	agccagcaag	cctggcgaca	tgaatgccga	1083300
aacttttttg	tgaatgtcct	tgagaatctc	atataagaaa	acaggctgcc	ctgctttatc	1083360
tttaactccg	gcatgaaaaa	tttcaacgtg	cggacaatgg	tcttctaaag	tcgtcaattc	1083420
tttataatga	gttgcaaaaa	gcgtcttagc	tttctttttg	tcagtgaata	ggaggtagct	1083480
tacaacagct	tgagcaatgg	caaggccatc	ataagtagct	gttctctctc	ctacctcatc	1083540
taggatcact	aaagagcggt	ccgtggcatt	gtgaaggata	ttcgcagttt	cggccatttc	1083600
taccataaaa	ctagacattc	cttttgagag	gttgtctcca	gcgcctatcc	tggtaaaaat	1083660
tttatcaatc	actccgatgt	gagctgattt	tgccaggata	tacgacccca	tttgagccat	1083720
aatcacaaga	agagctatct	gacggatata	ggtagatttt	cctgccatat	tagggccagt	1083780
aagtaagatc	attcgagttt	gagagccacg	catttccagt	tcattgggaa	taaattttccc	1083840
tgtgtctaca	agagtttttg	ctacaggatg	acaaccacga	taaatacata	aggtgtcact	1083900
catatctaca	cgaggacgac	aatagccctg	agcatgtgca	agatccgcaa	gagaaatgat	1083960
gtagtctaga	tcagcaagac	tttgagatag	agccaaaatc	tcagtgcgta	actgtaggat	1084020
gtgtgagcaa	agatccttga	agaattgctg	ttctaaagtt	tgaagttttt	cagagatatt	1084080
agacatatca	tcttggaatt	gctgcagctc	aatagtagta	aacctttctg	catgcaatcg	1084140
tgattgccga	cggatgaaat	ctttaggaag	ttgaggagca	aactcgctgc	tcacttcaat	1084200
ataatatcct	aaagcctgag	caaagcagat	tttgagtttt	ttgatccctg	tttctttacg	1084260
aatgcgttct	tggtattccc	aaatccattc	ttgagaatgc	tcttgattgt	ggcgtaagcg	1084320
ctttaaatca	ttgtggaact	catccacaaa	aatattttcca	tcagaaaact	ggagagggag	1084380
gtcgccgttc	aaggactttg	aaagcagtg	aattaaggag	gctagctttg	tatctaacga	1084440
gcatttatct	ataagaatt	ctggaagatg	cgcagaagcc	agttgttcgt	agatttgagc	1084500
tccctgagaa	aaagaatctc	tgagtgtccc	gatatctcta	ggccctgcca	atcctgtggt	1084560
cactttggtc	atcagtcgtt	cgatatcacg	tacttgacaa	aggtacgttt	tgatattttt	1084620
tcttaaagtc	acttgccgaa	gaaaaattct	acagcatctt	gacgtacaag	gatctcctta	1084680
gggttataga	aaggactgat	caaaatttga	cgtaaaagtc	ttccccccat	aggtgtgctt	1084740
gtatgatcca	tgatacgtaa	gagagaattt	ttcccctgag	gatcattcaa	gggagcgagg	1084800
agctcaaggt	tcacttgaga	tgccgtatct	attaataact	tttgctgttt	tccacgcgtt	1084860
tggggaaatcg	caatatgttt	cgtaggtaat	aaaagtttat	cttgatata	agagagaagg	1084920
cctccagcag	cggtgatcgc	tgggacgagc	cctttcaggc	caaatccatc	tagggaggcc	1084980
acttgaataa	gcgttgtaag	tttttgagag	gcgaacttat	gttcaaaggc	ccagtcgcga	1085040
tacgtagata	agggtcagctt	gaggtgttgt	tgcaactgca	tgacaatagc	agtttcttta	1085100
ttataaaatt	tggttacacga	gagcacttca	gaaggagcaa	gacgacagat	ctcgtcaaca	1085160
agctctttgg	tattctcaca	ttcttcaata	aagaaagatc	ccgtagaaaag	atctaaacaa	1085220
gcaaaaccaa	acagagaccc	gatacgagtg	atagcaacaa	tatnattatt	gaatttttcc	1085280
tggagcaggg	tggaggatag	caaagtgcga	ggagtgcaca	atctctgaat	atccccggcc	1085340
atgggaccga	tttttttact	ctctttttct	tttgaggctt	cgccaaattg	ttctgcacaa	1085400
gcaactttga	atcccttgcc	gatgaggcga	tccacatagg	tatcaacagt	agatacagga	1085460
atcccaactca	taggaattcc	ctgtcggtgt	gttaaagtaa	gttccaaatg	ttgggataaa	1085520
agaaccgcat	cgtcataaaa	agcttcgtta	aagtctccca	tccgaaataa	aagcacagaa	1085580
tctccagctt	tttctttaca	ctgatgccat	tgttccatca	tcggggtagg	ttttttttcc	1085640
gtcataaact	attcgcaatg	tacgttattg	ttttcatatc	cattaggatt	caaattgtatt	1085700
gagctaattg	attactgctt	tattaccgtg	gctttttgta	acggttgctt	tgactataca	1085760
agaaagtaga	gttttctgaac	gagcctctaa	aattcctgag	agacagcctc	agttgtataa	1085820
ctagagtggg	agtttaagaat	gctgcattac	gagccggctc	ccttgagaaa	agataaacag	1085880
gatgggatat	gaattccaag	gcaattctcg	gtagtaaatc	cttccctggg	atgctgtaaa	1085940
tagaaaaatt	ctttttataa	gaattcccta	atataaaaaga	aattcatcca	gaaagaaaag	1086000

ctgcattaga	caaaataacag	aggtaaatta	ataattgggg	agagtctctt	tattttatag	1086060
agcctcagtc	tttttaaact	aagaaatctg	taagttaaaa	ttgcagcata	accaagttgc	1086120
gtaccgctat	gtatacggaa	gagagcttag	ataacctgag	acacagtata	gatattgtgg	1086180
atgtcctttc	ggaacacatc	catttgaagc	gctccggtgc	aacatacaag	gcatgtttgc	1086240
cttttcatac	agagaaaaca	ccttcgttca	tagtcaatcc	tgcggttgca	cactaccact	1086300
gctttggatg	tggtgcacat	ggagatgcc	ttggcttctc	catgcagcac	ttgggatact	1086360
cttttactga	agccattttg	gtattatcta	aaaaatttca	agtagacct	gttctccaac	1086420
ccaaggattc	cggatacacc	cctcctcaag	gactgaaaga	agaattacgt	cacatcaaca	1086480
gtgaagctga	aacttttttc	cgttattgct	tgtatcacct	tccagaagcg	agacacgctt	1086540
tgcagtattt	ataccatcgg	ggattttctc	cagatacaat	cgatcgattc	catttgggtt	1086600
atggaccaga	acaatctctt	tttctacaag	ccatggaaga	aaggaaaatc	tcacaagaac	1086660
aactgcatac	tgcaagggtt	tttggaata	aatggttttt	gtttgcacga	agaatctctt	1086720
tcctgtccac	gatgcgctag	gacataccat	tggattttcc	gctaggaaat	ttttagaaaa	1086780
ctcccaaggg	ggtaagtatg	tcaacactcc	agaaactcct	atattcaaaa	agtccaggat	1086840
cctctttggg	ttaaattttt	cacgtaggag	aatagccaaa	gaaaanaaag	tcactcctagt	1086900
ggaaggacag	gccgattgcc	tgcaaatgat	agattcagga	tttaattgta	cagtggcagc	1086960
tcaaggtaca	gcattttacag	aagaacatgt	gaaagagtta	agtaaattag	gagttttaaa	1087020
agtcttcccta	ctcttcgaca	gtgatgaagc	aggaaataaa	gcagcattac	gtgttgggga	1087080
tctttgtcaa	actgctcaga	tgtccgtatt	tgtctgtaag	ctaccacaag	gccatgatcc	1087140
cgattctttt	cttatgcaac	gaggaagctc	aggactcatt	gctttattag	agcaaagcca	1087200
agactatctt	acgttttttga	tcagtgaaaa	aatgagttct	taccggaagt	ttggccctag	1087260
agaaaaggct	cttctagtgt	aagaagcgat	tcgtcagatc	aagcattggg	ggagtcctat	1087320
tcttgtatat	gagcatttaa	aacaactagc	ctccttaatg	atggttccag	aagacattggt	1087380
attgtcttta	gcaaaccctc	aggtaacagc	cgaaccacaa	aatattccca	taaaacaaaa	1087440
agttcccaag	atacatcctc	atatgtgat	ggaaacagat	atcttgcgtt	gtatgctttt	1087500
ttgtggatcc	aatactaaaa	ttctctacac	agcgcaattc	tactttgtcc	cggaggattt	1087560
caaacatccc	gaatgtagga	aattgtttgc	gtttatgatt	tcctattacg	aaaaatatcg	1087620
gaaaaatggt	ccctttgatg	aagcctgtca	ggtactttct	gattctcaga	ttcttcaact	1087680
gttaaccaag	cggcgccctaa	acacagaagc	tctcgatact	atcttcgtac	aatctcttca	1087740
aaaaatggca	gataggagat	ggcgagagca	atgcaaacct	ctctctctta	accaaaatat	1087800
tcaggataaa	aagcttgaga	ttttggaaga	ctatgttcaa	ttgctgtaaag	atagaacaat	1087860
aatcacactt	ctagatccag	aaagttagct	cattccttaa	cccagctctt	cttttgtaaa	1087920
gaattcttgt	ttttctaaat	ccccgggatt	tcttagatgt	ttcctaattt	ccttggagga	1087980
ggaacctgca	atgatgtgcc	tttcaataaa	ccggaaagcg	gcgtaattcc	tattaaaagc	1088040
aacttactta	taattttattg	aaattttaat	aaatataata	taaaatgttg	tttcgttttt	1088100
atttttatta	ttagtttttt	atgaaatctt	ttaagttttt	gttgccattt	ttaagtgtta	1088160
ttctttgctg	tggaaacct	ctctcttctc	cacgctccag	agcaatttca	gtgaccgaat	1088220
ccattggaat	gtcggcagtg	aagactcttg	ttctatctga	gaaggctcat	gaattcttag	1088280
agggaaatcg	atatggagtt	ggagcatcta	gtattctccg	cgactggcaa	acacaacagt	1088340
ggtagaanaa	agaatcctta	ttagcacaaa	atgaggtgat	gtaaatttga	gatattttca	1088400
cttacaaggt	atctttgcct	atttatatcg	gcgacctgtt	ctctatagct	tagcaagtat	1088460
gattttctct	actgtagtct	ctaaaattca	tagcttgacc	gcgatctagc	tttccaactc	1088520
tcatactctt	atctatctcc	aaaaaataga	ttttataaaa	ttataagttt	aattctatct	1088580
gtttgcaatt	tgataaaatt	gattatctgt	gataaactac	tttaacttta	aataaagatt	1088640
tttaaatata	aattatgatg	caccgttatt	ttattccttt	attagcactt	ctcattttct	1088700
ctccttcttt	agtcagggca	gagctacaac	caagtgaaaa	cagaaaaggg	gggtggccta	1088760
cacaactttc	ctgtgcagaa	ggttcgcaac	tcttctgtaa	attcgaagct	gcctataata	1088820
atgcaattga	ggaagggaag	cctgggattt	tagtcttttt	ctctgagcga	cccacaccag	1088880
aatttgccga	cttaacgaat	ggttcatttt	ctctctctac	gccaatcgcc	aagggtttta	1088940
atgtcgttgt	gttatgcccc	gggcttatca	gtcccttaga	ctttttccac	caaaatggga	1089000
tcctgtgatt	ctctatatgg	gaagttttct	agagatgttc	cctgaagtgg	aggcagttag	1089060
tggccctcgc	ttatgttata	tcttaataga	tgaacagggt	ggggctcaat	gtcaggctgt	1089120
cctgccttta	gaaacaaaga	attagagtat	atttaaaaac	aaaattttgc	cactctactt	1089180
cggacataat	tttgatcaat	taaggaggca	ttacatgcgt	atcgactat	ctctactttc	1089240
attattaatg	atatcccta	tcttcggaga	ggaaagtgcg	cctggttcag	aagacggcaa	1089300
cagtaataacg	caggagatag	tcggatctca	ggatacacag	gtatgtcttt	atcattccta	1089360
tgaacagggc	ttgcaagcat	cccgaatcga	aggaaagccc	ctgggttattg	tagtactttg	1089420
caattctggg	gatgatggcc	aggcatgcac	catagggtta	agtgaacat	gtgaggaggt	1089480
cctttctgta	ctttcaggat	ctattttttc	cgagtttagct	aacttcgctc	tacttgctcc	1089540
ttcaggagtg	aaccactca	tttatcctcc	aattgaagat	ccgattctcg	cagagattgt	1089600
aaagtttaag	gagttgttca	aagatgagtc	tttccctaca	ggattaagta	ttattgttgt	1089660
tgggtgcact	ccagaaggac	ctgggtgatc	catagaagtc	agtccgggtt	cgttaccggt	1089720
agaggaagaa	gagacgctac	caagtgaaca	aactacagaa	gtagagagca	gctctgaact	1089780
tcaatcagaa	gatccageta	tagcataacc	aagatcttcc	cttaataaaa	gaaagcgctc	1089840

gtaggattcc	tcccacgagc	gctttcttta	tctaaatggt	atgaaattat	acagctacag	1089900
attcccaatg	acacaaggaa	aacttatcca	tagcagtaag	taatagcgaa	atccgtaagt	1089960
tgcggtattg	accatcatca	ttagcaatat	gcacagtatt	cagaaaatcc	tgaatatcat	1090020
tggaagatc	agcaagggat	aagaaatatt	ctaaaaaggc	atgtgctgaa	gtttccttag	1090080
gaaatccagg	gaaagcatca	agaacttgct	taaaattaga	ttcacgatcc	ccaagaactt	1090140
caatagggga	cgaagtcatg	gagagtttta	aagaggaaag	aatcttcttt	aaacgattgt	1090200
gagtggctgt	aatcactgct	aatttttctg	tatgctcttc	ctttaatagc	tgaagggctt	1090260
cagcagtatc	taaaatctca	ataggatttt	ncgttgacga	atctataaga	acagcagcaa	1090320
tctcatcctt	acgaaaactct	agggatccca	taaatgtttt	taaccgaccc	caaatgaatt	1090380
caaggatttc	gtgtatagtc	ttggacttat	cccagacctt	ttcttcaatg	gtgctaggaa	1090440
aatgggtccgc	tagacgatct	aaaagagaag	caagatctat	agggagccga	gaggcggata	1090500
ctagtgttaa	cacttctaag	gattgacgac	gtagtgcata	aggatcatgc	gatgacgtag	1090560
gcttaagtcc	taaaataaag	caagcaagca	agttatccaa	acgatctaaa	agagaaagaa	1090620
gagttcctat	ggttgagagc	ttttgaccca	tagtaatgtg	tcgtagggtgc	tctcctacag	1090680
caaccgcaga	cgctgtggga	agattcgcat	gcttcagata	atactctccc	atgatcccc	1090740
gaagttcagg	gaattcattg	acgacagccg	acactaagtc	agctttgcag	tattggatgg	1090800
caatgtctag	gtcctcggaa	gccgctaaag	agggaaaaag	agagaacact	ctttggtgtg	1090860
cttttaaacg	ctctaccttg	tcatataaag	aacccaaagc	ttcaaagtat	gtcacagact	1090920
tgagcttttc	aataaagggt	gttaaaggag	tctgtaagtc	ttgtttgaaa	agaaattctc	1090980
cgtcagttag	acgaggagtg	agtgcctttt	catttccttc	aatgattgta	tcatctggag	1091040
aattatcaca	aactacaata	aaaaagttag	aaatagctcc	agaagagggt	tcgtgggtag	1091100
ggaaataactt	ctggtgattt	accatctcag	ctataagtaa	ctctttcggg	aaagcacaaa	1091160
attgctcggg	aaattgcccc	caagagacaa	aaggggtgct	cgacaggaag	gtagcttctt	1091220
caattaaacg	gggaagagga	atcgacagaa	ttgtatcaga	actatgagct	cgtagccctt	1091280
gttctataat	catgacgacg	tctttttgtg	aaactacaac	acacgcttgc	cttaagggtt	1091340
ctacataatc	ttgaggagag	gaaatcgaaa	tttttctcgg	atctaattga	cgatgaccaa	1091400
aagaattttct	tgaagctatt	atagtaccga	gagtgtattg	taagatgtgt	tctccataaa	1091460
gagcaactag	ccaacgtata	ggcggggcat	actcgactcc	gctgttatcc	caaaccatct	1091520
ttttagggaa	tttcatcctc	tgaattaata	aaggaagttc	ctgcattaag	atatcagcag	1091580
ttcgtaacct	tatctcagga	tgtaatagga	ataaatattc	agaaccgttg	actgtacgga	1091640
tagctaagga	agcgtgacgg	gaaagatctt	gataatgaga	aatatccaca	ccctgagaag	1091700
caaaaaactg	ctggccttga	ggagacacat	ctccatcagg	agaaaaataa	gacgtcagca	1091760
taggaccttt	tttctcaaaa	gccttctgca	cgacctcagg	agctacgttt	ttaacaagca	1091820
aagccaaccg	tcgtggagag	ccaaggacct	ctaacccttc	ataaacaata	ttatgatcag	1091880
taagaacctg	gcgagctaac	gattctagtt	gttgatttcc	aataggaaca	aaagtcgcag	1091940
gaagttcctc	agaaccaatt	tctagtaaga	gatcctctgt	agatgaaatc	ataggaacta	1092000
cagattctga	tgtttcttta	ggctcagatg	ttgaagaaag	actaagtaaa	ggataattta	1092060
aagaagcacg	ccactctaca	tagctatccg	caactaaacg	agtttaattga	cggatacagag	1092120
caatataacg	tgtacgctca	gtaacagaaa	tcgttccccg	agcatcaagg	atattaaaag	1092180
catgcgacgc	tttgatcacg	aagtcataag	caggaacaga	aagaccattt	ttaagagttc	1092240
ttaaagcttc	ctcagcgaaa	tcttcgaaat	gcttaaacca	catctcgggtg	tttgcatagt	1092300
caaaattata	ttcactccaa	gctttttcag	aagcttggtg	aatttggtcca	tacgttaaag	1092360
tgtcattcca	taagacatca	taaataagag	ttttcttttg	caaatacatc	gcaattcttt	1092420
caatgccata	ggtgatctcc	ccactgatag	tatccaaagg	tttactccca	atggcttgga	1092480
aatagggtcaa	ctgggtaatt	tccatcccat	tgagccacac	ttcccaacct	aagccccag	1092540
ctccaatggg	aggggttttc	caatcgatc	gaataaaacg	gatatcgtga	tcacgaaggt	1092600
ctaaaccaat	ggcccgtagc	gattccgtat	agagtcgagag	aaaattttca	ggcacgggct	1092660
ttaaaatgac	ctggagttga	tgatagtttt	gtagcgggtt	cggtatgcacg	ccataccgac	1092720
catcttgctg	acgccttgaa	ggttctacat	aagcagcctt	ataggggtca	ggtcctaagg	1092780
ctcgtaagaa	cgttgcagga	ttgaatgttc	cagcaccaac	ttctaaatcg	tatccttgat	1092840
ggatgacgca	cccttgctcg	ctccaaaatc	gtaagatagt	cgcaatcata	gactgtaagg	1092900
tgaggggatg	ttctgacaca	aatgactcca	aggtataaca	ttttttcttt	tgacattctc	1092960
cttagctaaa	gcgggagatt	cttggtttcat	tgaaggtagc	atagatttta	aagctacagt	1093020
cacaccttct	ccacaagcgt	agattttccgt	gtgtctcagc	gtacgtgtta	ggatgagtat	1093080
ataccttttg	aaaaatactg	cagtacagaa	aaccaaaaga	aaataacgac	atagatttaa	1093140
caagatcaga	gaacaagtgt	ttaaaacatc	atttccattc	taattaaatt	atatgaagat	1093200
tttttacctt	ttgacctaaa	aactctcttg	agtaattctta	agaacaatcc	tgtgagcaga	1093260
tgtttggtat	ataacactca	attttgagtt	attttcatag	tgcttgacaa	tattttcaat	1093320
aatttagaaa	aattagaaaa	ttttctattt	agcttagagc	aagagggttc	tcgatataca	1093380
aaaatggatc	atgagagcaa	ttgattttta	ggaaaacacg	acttcctttt	aaattcaaag	1093440
ttatcctcga	tcttgatgaat	aaaataacta	taggggttcc	ttaagtaagc	tagaacaaaa	1093500
aatacgcaga	ctgtgatttc	agtgccttcc	tcttagtaag	gcactcatct	catggacaga	1093560
caagaaccat	atattagggg	agtagggtgg	ggctaccta	ttacatcact	ttttccagac	1093620
tctttattac	accgattttc	atgatcctgt	atttaaaagg	aaaatgggtt	ggaatcactc	1093680

cagtagtggt	gccttacgtg	ctgttagctc	tcctggcaat	ctctgagtta	acagacgcta	1093740
tcgatgggta	tgtcgcaaga	aaattttcac	aggttaccga	tttaggaaaa	ctcctggatc	1093800
ctatggcaga	tagtatctac	agaatttcta	tctacctaac	ttttacacag	cctccagtca	1093860
atttaccttt	gcttctggta	ttcatcttcc	tagcacggga	ttctgtaatt	agtactttgc	1093920
gtactgtatg	tgctttccgt	gggcgtgttg	tcgctgcaag	ggctagtggg	aaactaaaag	1093980
ctatactaca	aggagtcagc	ttctttcttaa	ttcttttggg	tatgattcct	cactccctag	1094040
gacttctttc	tcagaatgga	ttggaaatct	ttgcctcagt	tacggtttca	atcatagctg	1094100
tgtattctat	agcctcagga	atcgaatact	tctggatgaa	caaaaaacttt	ttatcccaaa	1094160
gagctaaaaa	aaaagattca	gaaaagaatc	atgagagtaa	agattgataa	agattttacgt	1094220
aatgccttagc	catggcatct	aagccagagg	cccgaagcat	tcccgactca	atcaaattca	1094280
accaaagctc	aggctcctga	cgatacgtcg	ttacagcggt	gctaagcata	gcccgaat	1094340
cattaaaatt	gtttgtatca	aagaaagtga	aaccattttac	cccaggaatc	actgtatcag	1094400
caagccctcc	agtttttacga	actaaaggaa	ctgtgcccata	acgcatcgct	atcagctggg	1094460
taagtccaca	agcctcccta	tgtgaaggga	tgcagatcat	atcggcagca	gcataagtta	1094520
gcctggctaa	aggatcatta	aagtccaaga	tcaaacgaat	gttgggggag	ctcgctaaac	1094580
aatcttgtaa	gttacggaac	tcattaagaa	gaacctcatt	ttgacttgct	ccaatcaaga	1094640
ttaaaggcata	actgtgctcc	atagcatgga	gaataatctc	tttcataaat	tcaggacctt	1094700
tttctctaac	aatgcgtgag	atcacacaaa	tcaaaggaaa	atagtctgaa	ctgatcccca	1094760
acttctcata	taataaccgt	ctgttctctt	cttttttagt	aaagagaacg	tcagggttcgc	1094820
ttaataggct	tgcacgttac	tgtacagcta	aagcaggatc	tgtcttcggg	ttccaaacgt	1094880
cttcatcaat	gccattgatg	atcccagaaa	atacagaatt	tcttgctaga	atcgcatcat	1094940
gaagttcgta	atcagaatag	tcgtttataa	tttcttgcac	ataagtaaga	gacactgtcg	1095000
taatgtaatc	cgaacaatag	agagctccct	tcattagaac	agaagtttgc	ggatcgcgaa	1095060
atagttggta	gtgactcaaa	tgaaaatcat	caatttgcca	cgctgctaata	agctgcgtac	1095120
tacaataccc	tcgataacca	aaattatgga	tagtaaaagac	aatcttcgaa	tgcacagggt	1095180
ttaaagggtt	ttttaataaa	cccgaagta	aacctacatg	ccagtcatgc	aagtgcacaa	1095240
tgtcagcagg	atccgcttct	tgaagataag	ctgcagctgc	agctgcaaaa	gcagagaaac	1095300
gtacaacatt	attctcagag	tacacggacg	tggttgagaa	aagctctatt	tgtgaatcca	1095360
acgtaattat	agtaagcgta	agaccctcgt	aagaataaga	aattgcagag	gcttgctgct	1095420
tgccataaaaa	ttcataatag	aaagaacgct	cggaaagaac	ttgagacgaa	gagaatttgg	1095480
aaattaaagg	ataatgaggg	agaagtactt	ccacatcatt	ttgtttcgct	aactccttag	1095540
atagactagc	tacagcatcg	cctagaccgc	ctactttaac	gattggagtg	aattctacag	1095600
cgacttgttac	gactctccct	aaagctataa	aatatcccat	atcaagggag	1095660	
aaggtaaaat	ctcaagacca	aaaaagagag	ttttttatca	ttttcttatt	ttcaaaaact	1095720
gaagattcgt	taaaataaat	cctttctggt	ggggtgtggc	caagcggtaa	ggcagcgggt	1095780
tttggtaccg	tgcacggag	gttcgaatcc	ttccacccca	gagtcctttt	cttctccttt	1095840
tggttaactgt	attcttttagt	tgtctcttct	tacaagaagg	atatacgttc	aattcttttaa	1095900
ttagggaaaag	tattgacttt	ttccaaactg	gagatataat	tttgcctcga	aaactgtcga	1095960
tagacgtcca	agacatgaca	gtgattggcc	ctctaagaaa	atagtgttgg	actctcagag	1096020
tgaatgcata	gcgcacagct	cttttagctc	agaaataaac	attatggagc	1096080	
ttgtagttac	agctcgagag	actggtaaga	aatcttttct	taagaaaatt	cgctcagcaag	1096140
gtggaatccc	tgtgtagta	tattctgcag	gcaagagcct	tgcgaatatc	actgtggatg	1096200
cacttggtgt	taaaaagttt	ttatcgaatt	tagaaagcgg	agccctatct	tctacgggtc	1096260
tttctttgtc	ttatgaaggg	cgtataatta	aagctctagt	taaagatata	caatatcaaa	1096320
tcaccaccta	cgatgtaatt	cacctcgatt	ttgaagaact	cgtagaagat	cgctcctgtaa	1096380
agttaaaatat	tcctatccgt	tgtatcaatg	ctgtagactg	tattggagtg	aaactcgggtg	1096440
gatcttttacg	acaagtgatt	cgtgccgttc	gcgtagtagt	caaacctaaa	gatattgtac	1096500
ctttttctaga	acttgatgtg	cggctctgtt	gactttctca	aacgagaaaa	ctatccgata	1096560
taaagatccc	tgttggaata	gaaacaatta	cacctttgaa	agaagtcgct	ataaccgtct	1096620
ctagaagata	atattggctaa	gctcattgta	gcgataggga	accctaggca	tggttatgca	1096680
aatactagac	ataacgcagg	gttctctatt	gctgatagggt	tagtggagga	gctccaaggc	1096740
ccccatttta	aaccgttatc	aaaatgccat	gctttaatga	ctctcgtaga	gtcttcttca	1096800
gggccttttg	tttttattaa	accaacaact	tttgtcaatt	taagcggtaa	agccgtgggt	1096860
ttggctaaaa	aatatttttaa	tggtgtctct	agtcacattc	tagttctcgc	tgatgatgtg	1096920
aaccgttcgt	ttggtaaaact	tcgcctttgt	tttaacggag	gaagtggggg	acacaagggt	1096980
cttaagagca	ttactgccag	cttgggttcc	aatgaattat	ggcaattacg	gttcggtgta	1097040
ggaagacccc	tcgaagaggt	gttgagctat	ctaatttcgt	tttaggaaag	ttttctgaag	1097100
aagaaaatct	tcagttggga	tccatatatt	ttgaggcac	tactctattt	accgagtggt	1097160
gttcgaaatt	ttaaatggct	tgagaagttt	ctgaaataat	tttagtgagc	tgagatatct	1097220
taaggataat	aaactactct	atctgtctgt	gtttaggagt	ttttaatggg	aaaaaaagaa	1097280
aatcaacttt	acgaaggcgc	ctatgtgttt	agcgtcactc	ttagtgaaga	agctaggcgc	1097340
aaagcttttg	ataagggttat	ttcaggcata	actaattacg	gcggtgaaat	tcataaaaatt	1097400
cacgatcaag	gacgtaaaaa	actagcgtat	accattcgtg	gagctagaga	agggtactac	1097460
tatttttattt	atttttctgt	ctctcctgga	gccattacag	agctttggaa	agagtatcac	1097520

ttaaatagaag	atctacttctg	tttcatgact	cttagagcag	attctgtaaa	agaagtttta	1097580
gaattcgcc	ctctacccga	ataatttgtt	aaggagaaaa	tatgaataag	cctgttcata	1097640
ataatgaaca	cagaaggaag	cgtttttaata	aaaaatgccc	ttttgtttcc	gcagggttgga	1097700
aaacaataga	ttataaggat	gttgaaacct	taaaaaaatt	cattaccgaa	agaggtaaag	1097760
tattacctag	aagaattaca	ggtgtttctt	ccggtttcca	aggcgtgcta	tcccaagcaa	1097820
tcaaaagagc	tgcgccattta	gggttgttgc	cttttgttgg	agaagattaa	tttaaaggaa	1097880
gaagaatgaa	acaacagcta	cttttacttg	aagatgttga	tggattagga	cgtagtggtg	1097940
atttaattac	cgctcgccct	ggatatgtcc	gtaactatct	tatccctaag	aaaaaagcag	1098000
tgattgctgg	tgcaggaact	ctgcgtttac	aagctaaact	taaggagcaa	cgcttaatac	1098060
aagcagctgc	tgataaagca	gattccgaaa	ggattgtctc	ggctctcaaa	gatatacgtt	1098120
tggaattcca	agtacgtgtt	gaccctgata	acaatatgta	cggatctgta	accattgcag	1098180
atattattgc	agaagctgct	aaaaagaata	ttttcttggg	tcgtaaaaaac	tttccctcatg	1098240
cccactacgc	tattaagaat	ttgggcaaga	aaaacattcc	tttaaagcta	aaagaagaag	1098300
taaccgcaac	cttattggtc	gaagttacct	ctgacaatga	atagctcact	gttttggttc	1098360
aaggaaaaaca	aactgaggaa	aatcaagaag	gctaatacgt	agggtagaaa	agtttggttat	1098420
aaggatatca	tgaataactt	ttctcccgca	aagttaaacc	tttttttaaa	aatatgggga	1098480
aagcgtttcg	ataattttca	cgagctcaca	accctttatc	aagctataga	ttttggagac	1098540
acactttctt	taaagaatag	catgaaggat	agtttgagca	gtaatgttaa	cgaattgctt	1098600
tccccctcga	atctcatctg	gaaaagcctc	gaaattttca	gaagagaaac	acaaattcac	1098660
caaccagttt	cttggcacct	caataaatct	attccccctc	agtctggctt	aggaggaggc	1098720
agtagtaatg	cagccacagc	cctctacgct	cttaacgagc	atttccaaac	ccatattcct	1098780
ataacaacat	tgcaactttg	ggctcgagaa	atcggaagcg	atgttccctt	ttttttctt	1098840
caggaaacag	attagggaaa	ggctggggag	aacacctctt	ctctataaaa	aaactcaacc	1098900
ataaacataa	atatgtttct	tatctcgata	atcaaggaat	accacagaa	aaggcatacc	1098960
aatccttact	tccacaagac	tatagtacag	gaaatcataa	cgctgtttc	tatggtgaaa	1099020
atgatctaga	aaaatccgta	tttctgtatac	ggacagactt	gaaaaataaa	aaacacatgt	1099080
tagagaggat	gtggagtctt	ttcgaaagcc	atgtgcttat	gtcagggttca	ggagctaccc	1099140
tattcgtttg	ttatctagaa	gagttagaac	aagattcaaa	agtatcctcc	caaattccata	1099200
gcctaataca	acaaacccaa	ggaattcccc	ttagccgtct	ttatagggaa	ccgcattggt	1099260
attctctaaa	gcaatctact	tacaaaaaca	gcccgtctaga	gtgttttcag	ccacagatat	1099320
gattttattt	gcctctacag	aaagtgaagt	ttctgcttgg	caaaatccat	gaacattacc	1099380
taaactcgcc	ttttccttca	gcacagagaa	tataagagta	gaagcttcgg	aaattttcgt	1099440
tactttttta	gcagtcgttt	catctgcttt	aggaagtgt	atcttgtaag	acataaataa	1099500
accctcacat	tctcttcccta	cttaaaggat	ttttttattt	taaacaattt	cttttataaa	1099560
tgtgttttag	cttcttaatg	tgaaatttct	atttctctac	gagaagaaaa	ccagagatct	1099620
tcctaaattt	tttgaccctt	tctttttact	gtgaatacct	ttatgtctac	gcataagtat	1099680
taacttagct	cgctctgggtc	tctatgatcc	tgccctccata	ctcttattct	ttgaaaaatag	1099740
gcgcgcgagt	gctctttttt	tgttccatac	tgcacacatt	ctgtactccc	tggtcttaca	1099800
ctctatgtca	gtcttacgaa	cataaaaaac	ttgttttccc	agaatgctgg	aaacgctatg	1099860
cccggttgtc	agaactcttc	agaatcctaa	gtagagtaga	aattgtattt	ttcttgtggg	1099920
cagtaccctt	gttcttctgg	tttctatata	ccgaaggata	caggatttcc	atggcctatt	1099980
ttaatagtag	aaattatgga	ttcgctgtct	tcattatggt	gatcctcatt	ttactagagt	1100040
cccgccttat	agtatatctt	gcagaacttg	tgctctcctc	aattgcaaaa	ttaggaaaaa	1100100
cctctcccaa	atcctgggtg	tggacattga	tgatcgcacc	accacttctc	tcctgtctcc	1100160
ttaaagaaac	aggagctatg	attatcggtg	cgactctact	tatgagacat	ttttatgttt	1100220
ttactccgtc	aagacgcttc	gcatacgcta	ctattggact	tctgttttct	aatattttcca	1100280
tagggaggat	cacaagctat	gtatcctcaa	gagctctctt	ccttatcttt	ctctgactaa	1100340
aatgggaaca	ctcgtttttt	ctttcccaact	tcgcatggaa	agctatcgtc	gctatcctaa	1100400
tctctacaac	aatctattat	tttatctttc	gaaaagaatt	taaaaagtcc	ccagatatcc	1100460
ctagtgacaa	agatcctagc	gttgaaaaag	tgccctgggtg	gatcatctgt	gttaatatta	1100520
tttttgctgg	ttctataata	ttatcacgat	ccacaccctt	gttcatggga	gctctactac	1100580
tcttttactt	agggttttcag	aagttcacta	tcttttatca	agatccaatc	aacctttcca	1100640
aggatatgcta	cgtaggactt	ttttatgccg	gattggtagt	cttcggagat	cttcaagaat	1100700
ggtgggtgct	gaatctaattg	caaggtctgt	cagatttctg	atacatgaca	gtttccata	1100760
cgctgtccat	attcttagat	aatgcacttg	tgaactatct	agtacataac	ctctccgtag	1100820
ctacagattg	ctaccactat	cttgtagtcg	caggctgcat	ggcagcaggg	ggacttaccc	1100880
tagtctccaa	tatcccaa	atcgtgggat	acctcatctt	aagggtccgca	tttccctcat	1100940
cgacaatcca	tatgggatgg	ttgtttctcg	gagctttagg	cccctccata	atttccctgg	1101000
gagtcttctg	gttattgaaa	aatgttccag	aattcctcta	ctgttttttc	aggtaaacta	1101060
aagataaaaac	aaaggcataa	gatatgatct	tatgcctttg	tttttaagag	gtcttctgag	1101120
tgccacgtat	atagacgcta	gtttgcgtcc	ctagttcatt	gctaaggaaa	cactgacagt	1101180
attttaagaa	ctcttcggtat	gttaacggtt	cggaaatagc	aatcttcaag	ctgggagtcg	1101240
aaaactccac	aaaaggccgc	tcaaagtcta	gagaaaataa	cgccgagttc	atcatgtcta	1101300
aggaatgctc	aggctccaag	attttattga	tatacgcttt	gcgtatgttt	gcgaatttct	1101360



cttgcgatat	tccaaatttc	tcaggagaag	ctgagacctt	gttaaggaac	agagaagttt	1101420
tagcaagaag	ctcttcagga	gaatacgcac	ccgaacggat	atagagaaat	ccaaacggcc	1101480
tggaagcaaa	ctctcgatag	cgcgcaccca	ccatataacc	caattgctgt	tgcgttctaa	1101540
gctcctcaaa	agtaattgtga	tgcaaccatt	caaagagcat	ctccgcacaa	accttccctt	1101600
gtatagacgg	ggaactctta	tcttgaagta	ataagagcat	cccgtttgca	gttaacggat	1101660
agtcattgatg	gatctcagaa	atttcctgag	actgtagctc	gtaataaaaag	ggctttgtag	1101720
catgcgaaga	tcgtgacgca	gtgaaaactt	gtagcatctc	aagataatct	ttcttctgct	1101780
gctcagaaaag	gttccctaag	accataactt	caagatgtac	actgttgaaa	aggttcgagg	1101840
caaacgcttg	gaattcagaa	aaacttaact	tctcaagagc	tgatagctta	gtagtattag	1101900
aatacgtctc	cttcataact	tgtgaggcaa	gctcatcaag	cccagaacga	accggacagt	1101960
tgagcaaagc	tccttgataa	agctctaaca	actgcttttt	atatactaag	aatgtctcat	1102020
acctaattctc	taaattaggt	aatgaggtta	aaattgagtt	taacaatgca	gggactgttg	1102080
ttgtgtaccc	tgaaactctt	aaatcaatac	catcaccacc	taaagcagaa	gtaaaagaaa	1102140
aaccagcttg	cgttgcgagg	taatactccc	tcaaaagctg	atgggtcaca	ggctaagcaa	1102200
tagagctccg	tagcaactag	aaattgaggg	gaggacctcg	aaatctgagg	agagcggatg	1102260
cgaattctgac	tggagagttt	cgggtgctgta	tagtagtggt	cctcgcaatg	gtacagagtt	1102320
aatattatcat	cttggtaact	gagtgacagga	gcaaaaggaa	attcttgttt	tttcagtagg	1102380
tgtagaccag	gaagagtcac	ctcttttagga	ataaacagat	tcggctttgg	aagagctatg	1102440
ggcttttagtg	actgcacctt	tccataatcc	tgaacaccgt	ccagagcttt	tacatagtag	1102500
gtcatgtcaa	aaataggatc	gtggagctga	gtcgcttctt	cccaatgctc	agagttctta	1102560
ctagataaga	caaaacgtgc	ttgttcagga	tcagagacta	aattaagaag	agcagactcg	1102620
tcttcagaag	agtatttagg	atacacaagg	ctatgataag	gatacgtaga	tagatcctca	1102680
ttgcccgaag	atacaatctg	cttacaagc	agatcaaaac	atggactttt	ggaactgtaa	1102740
cagtagttta	aagcattaat	tgtagaatt	tcttctaacg	tatagttggg	aatcccggtg	1102800
tctgaatat	atcgaagata	ttggaaggta	ctatcaataa	cctgagaata	gtgtttatcg	1102860
cctttctccg	taagctcata	gctaataatg	aattctccag	tatttaaaga	acttctaaag	1102920
aattccacgt	ctaaatccgt	aattagctgc	tcgtttttca	ataaagagac	taaactgttc	1102980
ttactctcat	ttcttaaaac	ttcagcaaga	gccttgtaac	agcctaaagg	aatcggtatg	1103040
gaagattcat	aaatatgcc	gtaaatttct	agattagagg	taggctgaat	cgcttggtta	1103100
atatagagat	tctttaatga	cgaggtgtca	ccagaaggaa	gaaaagggtc	ctgtctttca	1103160
taattttttg	atctaggaat	ctgagaaaaa	atcttttga	actgtttctt	tgcttttagag	1103220
agcggagctg	atgtgtaac	aatagcacac	atattctcag	gagaataatg	tagcttaaac	1103280
cattctgcc	ttttctctgt	agtcactggg	gtgaggggtg	aagcattccc	acaacccaaa	1103340
cgtgcgcagg	gatggccctg	aggagcaaca	agctgctgaa	tgcatgcac	acgtctccca	1103400
tcagaaaagag	gatgagcagc	gaattcttga	tgtactgcgt	acttttctct	atcaagatct	1103460
tcttgacgaa	acttcggatt	aataaataga	tgaacaaatt	gggtctaaagc	atcagaaaac	1103520
gcagaatgtt	ctactgaaaa	tacaaagact	gttttatttg	ggtaagtga	agcattatgc	1103580
acccattat	tttcgcttaa	aaatccaggg	aaaccagaga	cctcaggata	cttttcattt	1103640
ccaagaaaga	cacagtgttc	tgtgaagtgc	gccatcccag	gatactcttc	aggatcggca	1103700
tattttcctg	ttttcacaa	gagtgctgct	cccgaagtag	gaagattagg	gtcggaaata	1103760
ataagaagag	ggagcccgtt	actacaaata	atcttttcaa	ttttctggtc	cgcagcggca	1103820
ggagtggaaa	cttgtaaagg	gcactgattg	gggacgactt	tgaactgctg	ttcacacgat	1103880
gttatggata	gggaagtgca	aattaaaata	gggacaaaaa	agtttccaaa	acatctttaca	1103940
attcctcgta	tagatttttt	acaaatagaa	aatacttttt	ctgctcttaa	tggtcttttg	1104000
gcgtgtttat	cgcaatgaat	aagttcctct	tttgaacata	atgcatacaa	aaatagttct	1104060
gctccgaagt	tgaagaaaac	aggagcaaa	aaaatggctc	gctgctcccc	aattgcattc	1104120
tctattttcg	gaggaggggg	gagaatgtca	taggttttta	aagcaaaagg	ataaaaatgt	1104180
gtcgtttgat	tagaagcctt	agctaataaa	cgaaacactt	caatgctttc	tggagagaat	1104240
tctgaaggat	ataatcttcc	ttccgcattt	tttctgtcac	gacctcctgc	aggggctacg	1104300
taaataaatt	tgctctcttc	atttaacaag	gtcttttaata	tttgcatgct	tttctgatta	1104360
tgaagaagct	tttcttcccc	gagttctggt	ggagtggcaa	tatgacgctt	agaataaata	1104420
cataataaat	cacatcccat	gctaaatggg	cgtgctaggg	gatcagaagt	gactcggctc	1104480
ccagctacaa	aaatcatggt	ctccattaac	tcaggatgcg	tcttgccata	ggcataatac	1104540
atgagttgtg	gatcgcatte	tgtctgggtg	tttgcaagg	gaacaacatt	atctccccta	1104600
gcaatgtatt	cttctatttc	cttaaggcgg	tgtaggttta	aaattcgaga	gtttttatcg	1104660
tcaatgacta	gagaaaaaaa	atctatactc	aaacgaaata	gatctatagg	agctcgaatt	1104720
tttttatgat	acggaggggaa	aatgaaaggg	tttttcaagt	cctcgatgat	aaccttgacc	1104780
cattgtaaac	atagcacctc	agcttgatca	gctgcagctt	ttttgtagc	tgcatcgatg	1104840
taattctgat	gaaaaacaga	aaatttctga	tataaaggct	ctgggagata	ctgggttatca	1104900
aaagcatagc	gtaaatacct	agaaaactgc	atgtatattg	ccctataaat	ctatactttc	1104960
ccctgtaatg	agagagaaga	attggtagtg	gtttaaatga	accgagtcgg	atgtattgat	1105020
ctgaagttta	gctttttaatt	gcttagccaa	atgatcatc	tcattgtcat	cgttttcttg	1105080
tttcataatg	cttgcaattt	ctggatgcac	aacaagacaa	agatgagagt	gttctttgtg	1105140
attaataacc	tttttcaaat	ccctctcaat	ctcgatgacc	acactttcag	gtgttttaat	1105200



aàtggcgttg	cgcgtgcagt	agggacatag	agtgaataat	gtctgcatta	gagattccccg	1105260
atttctctgt	ctggtcacat	caacaagacc	aaattcactc	atgcttaaaa	tagtacagcg	1105320
agcagcatcg	tatttcatat	gttctttcaa	tcgttccaaa	acacgtcgct	ggttcttacg	1105380
agatttcata	tcgataaagt	caataatcac	taatccgcct	acattacgta	aacgcaactg	1105440
tctggcaatt	tcttcagctg	cttctaagtt	gatttggacc	agagtttctt	caactccact	1105500
ttctaactgt	gtgcttcttc	ccgaatttac	gtcgatagtg	tgcatggctt	ctgttttgct	1105560
aaaaaaciaa	taaccaccgc	tggacagcca	aatttttctt	cttgtcgcct	tatcaatttc	1105620
tttctctata	ttgaaacgct	caaacatcgg	aatagaatcc	cgataatact	ctatcttgat	1105680
ggaagcatcc	ggagagtatt	tttttaacat	atgtttgcac	ttttgatacg	tagcataatc	1105740
atcaataagg	agtcgcttgt	agttcttatc	gatacaagta	atcacagctt	tttttagtat	1105800
gtccgtctca	gaataaagca	agcaggggtg	ctctgtggaa	tagaattttt	ctaaaattgt	1105860
tttccaagtg	agtaacaagt	cgtgggcctc	attaatgaga	gcttcagtag	aggctgtagt	1105920
gctcgctgta	cggcaaatca	aacccatgtc	ttgaggcatt	tcaaagaac	gaatgagctg	1105980
ttttaactgc	tctctcatat	ggggatcttc	aatttttcga	gaaacacctc	ggtagggtga	1106040
gtttggtaaa	agtaccaa	aacgtcccgg	aatggagatg	ttagaagtta	agcgagctcc	1106100
cttacttcca	ataggctctt	tgactacctg	aacgagaacg	gggctgtcta	atttgagaaa	1106160
ttcttcaatg	ggagcttctt	cagaagaaag	aagaggagct	tcagaagctt	cttcgggaag	1106220
agcatctaca	tccatctcga	acatctgttc	aaacttcttc	gaattctcta	aaatatcaga	1106280
gatatgaatg	aaaccattct	ctctctcatc	aatattaata	aacgcagatt	ggatatttct	1106340
cagaatgttg	gtaacacgac	ctcgataaat	attgcctttg	agctgacgaa	ctttctttct	1106400
ctctatagtt	agatcaaaaa	gttgaccatt	tttcagatgg	gcatagcgaa	tttctttcga	1106460
ttctatgttg	agtaaaattt	cattttccat	gactttcctt	gtgcctatac	catatctctg	1106520
agcttactta	ttctgtttgg	gaaaagagtg	gtttctagac	gtcgaaactt	aaatttctaa	1106580
ctgctcgtga	gataagttac	gttggtgatt	ataaagaaaa	taggtaaaaa	attctacaga	1106640
aatggctttt	tgattctttt	taaaaataat	taggttattt	taatttaatt	cttttcaact	1106700
gtaggctctt	gttttctata	atcattgtct	ttggtaagct	atctttctaa	tcctcaaaaa	1106760
gccttggttc	taggtagtaa	aggttttagt	atggactgtg	tcgataattt	aaaatttatat	1106820
atttttcggt	tgaaactacc	tggagatacg	gaacgcacat	gctattctat	tagccctgaa	1106880
tacattcgtg	agaaggggga	agaagagctt	ttgaattctc	ccatcgaggt	ggaagggctt	1106940
ctgggacgca	tagatagtga	ccaatggatt	ctctcgctaa	gcctaaagac	tcagctaggt	1107000
ttatgttgcc	cagtgtgtaa	caattttttt	tcacactcgg	tctgcttgcc	agatcttcaa	1107060
cgtgtgatat	ctcatgatga	ggtaggttcg	ggagtctttg	attgtagacc	tttgattcgt	1107120
caggagctcc	ttttagaaag	cgattgtttc	gaagagtgtg	gtgggcaggg	ctgccccgaa	1107180
aggaaaaata	tcttaaaatt	tttggaagac	agaaaaaac	atgaggggaa	taatcccttt	1107240
gagtatttat	aaaaggtaag	gaacatggcg	gtaccacgca	atcgacatag	taatgcaaga	1107300
aagaatatcc	gaagaagtca	cgatgctaag	aaggcttgct	acgcagcaaa	gtgcagcaat	1107360
tgtaagcatg	cccttcttcc	tcatactata	tgcccttctt	gtggatttta	taacggtaaa	1107420
gccgttatga	ctgtagaaaa	gaaataaatc	ttatctgatt	tatgggaagt	gcaaattggc	1107480
atagatttaa	tgggagggga	ccattctcct	cttgttggtt	ggcaagtgtc	ggttgatgta	1107540
cttaaatctc	aaagttctac	tattcccttt	gcatttactc	tttttgcttc	cgaggagatt	1107600
cggaagcaaa	ttcaagaaga	atttatatca	gatctgcctc	aagagaagtt	tcctaagatc	1107660
atttctgctg	aaaattttgt	ggctatggag	gactctcctc	tagcagctat	ccgcaaaaaa	1107720
tcctcatcca	tggcttttag	attggattat	cttcaggaag	ataaaactcg	cgcttttata	1107780
tccacagggg	atacaggggc	cttaggtaca	ttagcacgtg	ctaagattcc	tctatttcct	1107840
gccgtatctc	gtcccgcatt	acttgtttgt	gttcctacaa	tgcgaggtca	tgagctcatt	1107900
ctagatgttg	gtgccaatat	ttctgtaaag	cctgaagaaa	tggtaggttt	cgctcgtagt	1107960
ggacttgctt	atcgctcagt	tcttggcgat	tctaagattc	ctacgatcgg	attgcttaat	1108020
attggttcag	aagaacgtaa	aggtacggaa	gcccacgcc	agacattccg	tatgctgcga	1108080
gagacatttg	gcgaactttc	ttaggcaata	tagaaagcgg	tgctgtcttt	gacgggtgct	1108140
cagatatagt	tgtcaccgat	gggtttacag	gaaacatctt	ccttaagact	gctgaggggt	1108200
tatttgagtt	cttgacagct	attctagggg	ataaaactga	agcagacatt	caacgtcggg	1108260
tggattacac	attttatccc	ggctctgtag	tctgtgggtc	ttctaaactt	gtgatcaaat	1108320
gtcatggtaa	ggcgtgctgt	tcttctttgt	tccatggcat	tttgggctct	ataaaacttg	1108380
ctcaagcacg	cctatgcaaa	cgcattttgt	ctaatttgat	ttagttaact	acattcaatt	1108440
tttgcttctc	ctgtatagct	tttcttttat	tgacgggatc	ttgttgatag	tgctacatat	1108500
tttgcaaaat	actttataaa	cacctctcag	gtttaagggt	gcaatggtag	cgaaaaaaac	1108560
agtacgatct	tataggtctt	cattttctca	ttccgtaata	gtagcaatat	tgtcagcagg	1108620
cattgctttt	gaagcacatt	ccttacacag	ctcagaacta	gatttaggtg	tattcaataa	1108680
acagtttgag	gaacattctg	ctcatgttga	agaggctcaa	acatctgttt	taaagggatc	1108740
agatcctgta	aatccctctc	agaaagaatc	cgagaagggt	ttgtacactc	aagtgcctct	1108800
taccaagga	agctctggag	agagtttgga	tctcgccgat	gctaanttct	tagagcattt	1108860
tcagcatctt	tttgaagaga	ctacagtatt	tggtagctgat	caaaagctgg	tttgggtcaga	1108920
tttagatact	aggaattttt	cccaaccac	tcaagaacct	gatacaagta	atgctgtgaag	1108980
tgagaaaatc	tcctcagata	ccaaagagaa	tagaaaagac	ctagagactg	aagatccttc	1109040

aaaaaaaaagt	ggccttaaaag	aagtttcatc	agatctccct	aaaagtcctg	aaactgcagt	1109100
agcagctatt	tctgaagatc	ttgaaatctc	agaaaacatt	tcagcaagag	atcctcttca	1109160
gggttttagca	tttttttata	aaaatacatc	ttctcagctc	atctctgaaa	aggattcttc	1109220
atttcaagga	attatctttt	ctgggttcagg	agctaattca	gggctagggt	ttgaaaatct	1109280
taaggcgccg	aaatctgggg	ctgcagttta	ttctgatcga	gatattgttt	ttgaaaatct	1109340
tgttaaagga	ttgagtttta	tatcttgtga	atcttttagaa	gatggctctg	ccgcaggtgt	1109400
aaacattgtt	gtgaccatt	gtgggtgatg	aactctcact	gattgtgcca	ctggtttaga	1109460
ccttgaagct	ttacgtctgg	ttaaagattt	ttctcgtgga	ggagctgttt	tcactgctcg	1109520
caaccatgaa	gtgcaaaaata	accttgccagg	tggaaattcta	tccgttgtag	gcaataaagg	1109580
agctattgtt	gtagagaaaa	atagtgtctga	gaagtccaat	ggaggagctt	ttgcttgccg	1109640
aagttttgtt	tacagtaaca	acgaaaacac	cgccttggtg	aaagaaaatc	aagcattatc	1109700
aggaggagcc	atctctcag	caagtgatat	tgatattcaa	gggaactgta	gcgctattga	1109760
attttcagga	aaccagctct	taattgtctc	tggagagcat	atagggtcta	cagattttgt	1109820
agggtggagga	gcttttagctg	ctcaagggac	gcttacctta	agaaataatg	cagtagtgca	1109880
atgtgttaaa	aacacttcta	aaacacatgg	tggagctatt	ttagcaggta	ctgttgatct	1109940
caacgaaaca	attagcgaag	ttgcctttaa	gcagaataca	gcagctctaa	ctggagggtgc	1110000
tttaagtgc	aattgataagg	ttataattgc	aaataacttt	ggagaaattc	tttttgagca	1110060
aaacgaagt	aggaatcacg	gaggagccat	ttattgtgga	tgctgatcta	atcctaagtt	1110120
agaacaaaag	nattctggag	agaacatcaa	tattattgga	aactccggag	ctatcacttt	1110180
tttaaaaaat	aaggcttctg	ttttagaagt	gatgacacaa	gctgaagatt	atgctgggtg	1110240
aggcgcttta	tgggggcata	atgttcttct	agattccaat	agtgggaata	ttcaatttat	1110300
aggaaatata	ggtggaagga	acttctggat	aggagaatat	gtcgggtggtg	gtgcgattct	1110360
ctctactgat	agagtgcaca	tttctaataa	ctctggagat	gttggtttta	aaggaaacaa	1110420
aggccaatgt	cttgctcaaa	aatatgtagc	tcctcaagaa	acagctcccg	tggaaatcaga	1110480
tgcttcatct	acaaataaaag	acgagaagag	ccttaattgct	tgtagtcatg	ggatcatta	1110540
tcctcctaaa	actgtagaag	aggaagtgcc	accttcattg	ttagaagaac	atcctgttgt	1110600
ttcttcgaca	gatattcgtg	gtgggtggggc	cattctagct	caacatatct	ttattacaga	1110660
taatacagga	aatctgagat	tctctgggaa	ccttggtggt	ggtgaagagt	cttctactgt	1110720
cggtgattta	gctatcgtag	gaggaggtgc	tttgctttct	actaatgaag	ttaatgtttg	1110780
cagtaaccaa	aatgttggtt	tttctgataa	cgtgacttca	aatggttggtg	attcagggggg	1110840
agctatttta	gctaaaaaag	tagatatctc	cgcgaaccac	tcgggtgaat	ttgtctctaa	1110900
tgggttcagg	aaattcgggtg	gtgccgtttg	cgttttaaac	gaatcagtaa	acattacgga	1110960
caatggctcg	gcagtagcat	tctctaaaaa	tgaacacgt	cttgccgggtg	ctggagttgc	1111020
agctcctcaa	ggctctgtaa	cgattttgtg	aaatcagggg	aacatagcat	ttaaagagaa	1111080
ctttgttttt	ggctctgaaa	atcaaagatc	agggtggagga	gctatcattg	ctaactcttc	1111140
tgtaaataat	caggataacg	caggagatat	cctatttgta	agtaactcta	cgggatctta	1111200
tggaggtgct	atttttgtag	gatctttggt	tgcttctgaa	ggcagcaacc	cacgaacgct	1111260
tacaattaca	ggcaacagtg	gggatatect	atttgctaaa	aatagcacgc	aaacagccgc	1111320
ttctttatca	gaaaaagatt	cctttggtg	aggggccatc	tatacacaaa	acctcaaaat	1111380
tgtaaagaat	gcagggaacg	tttctttcta	tggcaacaga	gtccttagtg	gtgctgggtg	1111440
ccaaattgca	gacggaggaa	ctgtttggtt	agaggctttt	ggaggagata	tcttatttga	1111500
agggaatata	aattttgatg	ggagtttcaa	tgcgattcac	ttatgcggga	atgactcaaa	1111560
aatcgtagag	ctttctgctg	ttcaagataa	aaatattatt	ttccaagatg	caattactta	1111620
tgaagagaac	acaattcgtg	gcctgccaga	taaagatgtc	agtcctttaa	gtgccccttc	1111680
attaattttt	aactccaagc	cacaagatga	cagcgtctca	catcatgaag	ggacgatagc	1111740
gttttctcga	ggggtaccta	aaattcctca	gattgtctgt	atacaagagg	gaaccttagc	1111800
tttatcacaa	aacgcagagc	tttggttggc	aggacttaaa	caggaaacag	gaagtctcat	1111860
cgtattgtct	gcgggatcta	ttctccgtat	ttttgattcc	caggttgata	gcagtgcgcc	1111920
tcttcctaca	gaaaaataaag	aggagactct	tgtttctgcc	ggagttcaaa	ttaacatgag	1111980
ctctcctaca	cccaataaag	ataaagctgt	agatactcca	gtacttgccg	atatcataag	1112040
tattactgta	gatttgcctt	catttgttcc	tgagcaagac	ggaactcttc	ctcttctctc	1112100
tgaaattatc	attcctaagg	gaacaaaatt	acattctaat	gccatagatc	ttaagattat	1112160
agatcctacc	aatgtgggat	atgaaaatca	tgctcttcta	agttctcata	aagatattcc	1112220
attaattttc	cttaagacag	cggaaaggaat	gacagggacg	cctacagcag	atgcttctct	1112280
atctaataata	aaaatagatg	tatctttacc	ttcgatcaca	ccagcaacgt	atggtcacac	1112340
aggagtattg	tctgaaagta	aaatggaaga	tggaaagact	gtagtcgggt	ggcaacctac	1112400
gggatataag	ttaaatcctg	agaagcaagg	ggctctagtt	ttgaataatc	tctggagtca	1112460
ttatacagat	cttagagctc	ttaaagcagga	gatctttgct	catcatacga	tagctcaaag	1112520
aatggagtta	gatttctcga	caaagtgtctg	gggatcagga	ttaggtgttg	ttgaagattg	1112580
tcagaacatc	ggagagtttg	atgggttcaa	acatcatctc	acaggggatg	ccctaggctt	1112640
ggatacacaa	ctagttgaag	acttcttaat	tggaggatgt	ttctcacagt	tctttggtaa	1112700
aactgaaagc	caatcctaca	aagctaagaa	cgatgtgaag	agttatatgg	gagctgctta	1112760
tgcggggatt	ttagcaggtc	cttggttaat	aaaaggagct	tttgtttacg	gtaataataa	1112820
caacgatttg	actacagatt	acgggtacttt	aggattttca	acaggttcat	ggataggaaa	1112880

agggtttatc	gcaggcacaa	gcattgatta	ccgctatatt	gtaaatcctc	gacggtttat	1112940
atcggcaatc	gtatccacag	tggttccttt	tgtagaagcc	gagtatgtcc	gtatagatct	1113000
tccagaaatt	agcgaacagg	gtaaagaggt	tagaacgttc	caaaaaactc	gttttgagaa	1113060
tgctgccatt	ccttttggt	ttgctttaga	acatgcttat	tcgcgtggct	cacgtgctga	1113120
agtgaacagt	gtacagcttg	cttacgtctt	tgatgtatat	cgtaagggac	ctgtctcttt	1113180
gattacactc	aaggatgctg	cttattcttg	gaagagttat	ggggtagata	ttccttgtaa	1113240
agcttggaag	gctcgttgga	gcaataatac	ggaatggaat	tcataattaa	gtacgtattt	1113300
agcgtttaat	tatgaatgga	gagaagatct	gatagcttat	gacttcaatg	gtggatccg	1113360
tattattttc	tagttcgatg	tgacagggct	tcaatcaaaa	aaaaggggta	cttttagtaa	1113420
ccctttttta	tttctcttaa	tgcttatagt	tcgatgatct	ttaatacata	gagcaagtag	1113480
gcgatacaag	ctttattagg	ttcataggtc	tctgggtcca	ttaagagtgt	agaaaagacc	1113540
tcggtatgag	cggaagtttg	aggaagccgt	aaggatgcat	ataatatatc	tagagcaaac	1113600
tcacggatta	aagctttggt	ttctggatct	gctttttgca	tggattttaa	gacgctatta	1113660
acaagttgat	ttccagaatt	taaataacta	tttaggaaaa	gagcagctga	caaatcagcg	1113720
tcttctctgc	cttgatgtgt	gtccactgta	gtttgacgta	aagttagggc	gccgagagta	1113780
tcttgtaggt	gttctgtaac	tagaccgaga	tttttcccat	ggaagaattt	catagtgttg	1113840
atcacatgcc	attgtagttt	ggctgctgac	tcgtttcgta	gaacttggtc	tattgcctct	1113900
gtgtaacgct	caccgtgttg	ctgagccgca	aaccgatact	cttcagcatc	atcaccatct	1113960
tggatggaca	tcagctctcg	ttcttttaac	tcttgaaccc	aaatcagaag	ctgattgtct	1114020
ccttcattag	ctatactata	gagtcctgta	agagatctgg	ttatgacttc	ttcccaagtc	1114080
ggcttacaag	tcttgcaaga	acttgcaata	aataaggccg	cttgcatttt	ttcctttgta	1114140
ctaggagttt	tgggtaaaga	ggactttcca	gtaagagctt	cttgaggag	ctgatcaat	1114200
attgggaacg	tctttttatc	aggattacta	tcatgtctgt	ttttcagtc	ctcaaagtac	1114260
ttcagcatgt	gctttccattc	tggagttagc	acgcctagag	actttaatac	ttttttcagt	1114320
tgtgagcata	gatccggaat	cttcgcgatg	gcttcttggt	tntcttgctg	cgaaattgct	1114380
actagtctat	ttaaaaaggg	attaggttaag	ggtgctttgc	ctacactttg	ttcaacaatt	1114440
ttaaaagagc	gaagtttggt	atcctcaaaa	agcaacgctt	gcaaagcgaa	aatgaagggg	1114500
tgaatgacct	cattcgtttc	ttcagtagta	ggttcactta	aatcctctac	gattttttta	1114560
gggggaagag	gcatgaagag	acgaagacct	gctacgatga	gattcaccgg	taaaagaatg	1114620
ataaacagta	ctgaagtaat	aataaatgct	aggatgttga	gaatcaccca	acataaggga	1114680
ccaccagagc	acccgcaggg	attcagttat	ttttttgaca	tactgaatag	gctagaagga	1114740
tgtaggagct	gagccacggt	ggttaggcgt	gtttgacacg	cattttcttc	caagataata	1114800
agttccgctc	tccgaggata	aatcggcgaa	gtttttggaa	ttaaattgta	ctttgctatt	1114860
aactctgcag	gggaaaacaa	agagatgggg	ttagacatat	gcatcttgga	gttatggatt	1114920
aagtagaaat	attttattat	actttctaag	attgattgtt	attcaattaa	tttttattta	1114980
gaaatactat	aaaaaagtag	ctcaaaacga	attgttttat	acttatttat	gagttcttaa	1115040
agaacttggt	ttaagaaacc	taaatattca	tacagcggga	agtgtgtcaa	aaattctttt	1115100
taaaaactct	tcagaagcta	tttgccctgt	cgtcatcact	ttacataatt	tgccgagtc	1115160
ctccttttgt	ttttctttag	agccatgttg	atttagcaaa	tctaaagcgg	tagcagtttc	1115220
ttctggatga	aaatcttttt	tccctccaat	gaactctgga	aaaatcacgg	agttcataat	1115280
gatatttggt	aaggaatacg	cgggcacaaag	aatttttaaaa	atatattttg	ctaagaatgt	1115340
gtcaaaaggt	cgaagtcgac	acatgactat	tgtgggtgtt	tgattttaagg	cagtttctaa	1115400
gactatagtg	ccacattttg	ctagtgcaca	atcacagctt	ctcatgagct	catagcggaa	1115460
attcatgggg	atgatttgac	tatgctgaca	tccttctgct	tttagagtat	cttcaatgat	1115520
ttcgtcgtac	ttagcgcttg	atgaggaaac	cacaaattga	tgtgtttgag	atagcgatga	1115580
atttagaaaa	gcttgtacct	ggatccgtaa	atttcggctg	atgtcaccac	gacgacttcc	1115640
aggaaacgca	gcaacaatag	gacggtcaga	attaaaggaat	ttctctttcc	aagaggcctg	1115700
ttctttgtag	tcagagatct	cctcaactag	ggggtgtcct	aaatacacag	tctcaagaga	1115760
tgtgtttttg	aaaaggcctt	cttcaaaagg	aaggatcagt	aggagcatat	caagatgttg	1115820
ctctagtatg	cgttttcttt	tggggcgcca	tgcccaataa	ctcgggcaaa	cgtaatggat	1115880
gatttttctc	cgatacccat	gtttttctcag	cttttttaatt	aagagaaggt	gaaaatcggg	1115940
gaaatcaatg	aagataagag	tcgctggcct	gtgttttgat	atcgttttta	ggattttgctg	1116000
gtaatttcga	tataatctaa	ataatgacct	cagaacttca	gcaaactcctg	aaacttgaaa	1116060
ctcctccatg	tttagaatgg	gctggagacc	ttcttgcgc	attgcaggac	ctccaacacc	1116120
ccagaaccgt	atgtttggat	agagagactt	tatggattgg	attaacttac	cccccaaat	1116180
gtcacccgta	gcttctccag	cagagagaaa	gcagtgtgta	tccaaataag	gagtcgaacg	1116240
ttgttcttta	taaaagagac	gtaaatttgc	gatggacggg	aataatccac	agccatagca	1116300
caggatgttt	ataggatctc	cgatgcgaat	gaagtacacc	agcgccagca	atcccccaag	1116360
aagtccaatt	ttccaaaata	gtaaggggaa	atcttttagta	ttattcgatt	ctatgtagaa	1116420
ccattggatt	aaaaaacgac	ccgaaaaaat	agcaagccct	aaacagccta	taagatgccca	1116480
agaaagttgt	gcaggaggaa	gaggaagatg	gaagatatta	ggagaggcca	tccattccat	1116540
gttcacatag	aggaaaggca	gagtcacgaa	caccacgcta	agagccatca	gaactaaggt	1116600
cgctcgaaag	gaaatcggtc	gagaggaagt	aatatttagg	tttctgaggt	agataattaa	1116660
gttaatgaca	tgaagtacag	tcacaggaaa	ttggctttga	attgtcccgt	ggacaatcat	1116720

caaagtggct	cctattgaag	agagaatcca	aaagcttcga	ggagcataga	cctctttgcg	1116780
ctttttactc	agccaccact	gtattgagaa	ggcactccca	aaaaaaagac	tagcaagaaa	1116840
tcctagggga	taaagcagat	aaactaggcc	agaagggatc	atgttttagac	ctacttttga	1116900
gaatgagaat	cctttttaca	cttaagtgtt	tgatgatgac	gtatccaagc	aacatacact	1116960
ttatcgagct	taggatacac	tatactacga	atttccaata	aagataatgc	ttctaagaac	1117020
cttgtgtgat	gtaaaagttt	cttattaaag	aagagcgctt	tttttgtagg	gatcagggga	1117080
gtgagctctg	actgcatttg	taaaattaat	gctgtcagga	taaaattctt	ttttgagcaa	1117140
cttgtgaacg	agtcagcaaa	gaattgttct	aggaaatttt	tgatataatc	aaaaacggat	1117200
gtcaaagaca	aatacgggtg	cttctgatgc	ttataacgga	cattaaagtt	cactaaagga	1117260
aaaaggaata	tagccatcag	ctgatgacga	tcatactctg	cctctttttt	tagtattttg	1117320
tcacttagag	cttttaggta	ggtggctggt	tgctcttcta	gtgcgcgatt	taagcggaat	1117380
gccttatcca	tatagggaaa	aaggatctca	agaagatggg	tctctattag	cagttggaaa	1117440
aagtctcttg	cggctccgga	atttaacatt	ttgataagtt	cttcgaagac	ccgtgcccga	1117500
gaacttttaa	ttagctcttg	gcgacaagca	attaaagctt	cttgagtttg	cgtttctaca	1117560
gtaaacggcg	accgtgataa	aatctttaac	agtctcagca	tgcgtagctg	atcttgcttg	1117620
aatcttgtaa	agggatcgcc	gatagtgcgc	aaataacggg	tccttaaatc	attaacgcca	1117680
ccagtatagt	ctataatctc	ttcatgctcg	ggatcgtaaa	acaatccatt	gattgtaaaa	1117740
tctcttcgca	agacatcttc	ttcaggagtc	ccccatagat	tatctttagt	aatcaagaca	1117800
tcttcacggy	tgcttcccga	acgaaatggt	gaaacttcaa	taatctgctt	agagaatcta	1117860
atatgggcaa	gacggaaacg	cttaccgacc	aaaatacaat	ttttaaagat	agctttaatt	1117920
tcttcagggt	tcgctgaagt	ggagatatca	aaatccttcg	gcgtgggtatt	taataacaaa	1117980
tcctaatgc	aacccccaac	aatataagcg	atataccctg	ctttacggag	ggttttgatc	1118040
actgacaggg	cgtgaggaga	gaaatctttg	agtttgatgt	tatgggttaga	aacagaaatag	1118100
atcgtaggag	ttaaagtgat	attagatttt	ttttttaaca	attctaggcc	tctaccagag	1118160
agaatattgt	tttcgcagac	cattattata	gttattaaga	gttaaaagtc	ttggaagaaa	1118220
aagagtgtgt	agtttgcgtc	tacttccatt	ttaaaatccc	aacatagcaa	aactagggaa	1118280
gttttcaagg	ataaaaatga	aaaacaaaag	atgttttcta	tagagattcc	tcttcaattt	1118340
ttaattatat	atggatcatt	cttaagactc	tagcatccac	agaacccggg	agagagctct	1118400
taaatgcctt	gatcctgggg	agcagaaaag	atgtaaaaag	catggaataa	aaaatatcta	1118460
gtttctgaca	gaattcaatt	atagaacttt	acatccattg	gagagttctc	tatagaagat	1118520
cgaagtattc	ttcgagaaga	gtactacagt	cagaggctac	ttctttttac	ttatagttta	1118580
ctgcttataa	attcgctttt	atttgtgcgt	gtagaagtga	aaagatacgg	agaataggaa	1118640
tagatttttag	gagaaacatg	caacaaagtg	tcagaaaact	ttttggtaca	gatgggtgtg	1118700
gaggacgagc	aaattttgaa	cctatgacag	tggaacgcac	tgttttatta	gggaaagctg	1118760
tagctagagt	acttcgtgag	ggtagatcgg	gcaaacatcg	tgttgtagta	ggcaaagata	1118820
ctaggctatc	gggatatatg	tttgagaacg	cattgattgc	tggtcgaatt	ctatggggat	1118880
agaaactttg	gttcttggtc	ctatccctac	gccaggagtt	gcgtttatta	cacgggccta	1118940
tcgagcggac	gcagggatta	tgattttctg	ttcacataat	ccttacaggg	ataatggaat	1119000
taagattttc	tctttagaag	gatttataat	ttctgagtt	cttgagcagc	gtattgaaac	1119060
catgggtgag	gaagctgact	ttggtccatt	acctgaagat	cacgcagttg	ggaagaacaa	1119120
acgtgtgata	gatgctatgg	gacgctatgt	agagtttgtg	aaagcaacat	ttcctaaggg	1119180
acgcacttta	aaggggttaa	agattgttct	agactgcgct	cacggagctt	cttataagggt	1119240
agcaccttct	gtatttgaag	agctggatgc	agaggtcatt	tgttatgggt	gcgaacctac	1119300
aggaatcaac	atcaatgaac	actgcggagc	tcttttccct	caagtcattc	aaaaagctgt	1119360
aatcgaaacat	caagcacatc	ttgggattgc	gctagatggg	gatggagatc	ggattatcat	1119420
ggtggatgag	aaggggcata	ttgtcgatgg	agatatgac	ctcagtatat	gtgctgggtg	1119480
tcttaaaaaa	agatccgcac	tacctcataa	ccgtgttggt	gccacgatta	tgacaaattt	1119540
cggagtcttg	aaatatttgg	aaggattagg	cctacaggta	ttcacctctc	cagtagggga	1119600
ccgtcatggt	ttgcacgcca	tgttagaaca	tgaagtgacc	ttnggagggtg	aacagagcgg	1119660
acatatgatt	ttcttggaact	acaataccac	tgagatgga	attgtctcag	cgctacaagt	1119720
tttgcgcat	atgatagaaa	gtgaatctat	gctctcagat	ttgacagccc	caattgtaaa	1119780
aagtccccaa	acattgatca	acgttgctgt	aagagagaaa	attcctcttg	aaaccatccc	1119840
tttaattgaa	agaaccttga	gagatgttca	agatgcctta	ggccccctctg	gacgcatatt	1119900
attaagatat	tctggaaccg	aaaatatatg	cagagttatg	ggtgaagggtc	ataaaaaaca	1119960
tcaagtagac	tgcttgccca	aggctcttgc	ggatggtatt	gatgcagaat	taggtacagg	1120020
tagtagagag	tgtgcgggta	ttgctgggat	atttggtat	ttgggaaacc	aagatgggtg	1120080
gtctattgtt	ctagaaggct	tggaacaggt	agaatatcgt	ggttatgatt	ccgcagggtc	1120140
tgctgctgta	gttgaacaag	agctttttat	tagaaaaact	gtaggtcgtg	ttcaagagct	1120200
ttcaaacttg	tttcaagaaa	gagaaatccc	tacggcatca	gttattggcc	ataccggttg	1120260
ggcaactcat	ggagtgccta	ccgagattaa	tgctcatcca	catgtggatg	agggaaaggtc	1120320
gtgtgctgta	gtccataatg	gaattataga	aaatttcaaa	gagttgcgac	gcgagctgac	1120380
tgcgcaaggc	atttcatttg	cttcagatac	cgattcagaa	attattgttc	agctgttttc	1120440
tctatattat	caagagtccc	aagatcttgt	gttcagcttt	tgctcagact	tagctcaact	1120500
ccgaggtagc	gtagctgcgc	tttgattcat	aaagatcatc	ctcatagcat	tctttgcgct	1120560

tctcaagaga	gccctttaat	tcttggttta	gggaaagaag	agacgtttat	tgcttcagat	1120620
tcgcgagctt	tcttcaaata	tactcgacat	tctcaagcct	tggcctccgg	agaatttgct	1120680
atagtttctc	aagggaaaga	acctgaggtt	tataatttgg	agcttaagaa	aatccataag	1120740
gatgtacgac	aaatcacctg	tagtgaagat	gcttcggata	aaagtggcta	cggctattat	1120800
atgctgaagg	aaatctatga	tcagccagaa	gttttagaag	gtctgattca	aaaacatatg	1120860
gatgaagaag	gacatatattt	atctgaattt	ttatcagatg	ttcctatcaa	gagttttaaa	1120920
gaaatcacga	ttgttgcttg	cgggtcttcc	tatcatgctg	gttatctcgc	taaatatatt	1120980
atagagtcct	tagtttcaat	tcctgtacat	attgaagtgg	cttccgaatt	tcgctatcga	1121040
cgtccctaca	taggtaaaga	tactttgggg	attttgatca	gtcaatcagg	agaaacagct	1121100
gataccctag	ctgctttgaa	ggaattacgt	cgcagaaaca	ttgcttatct	cctaggcatt	1121160
tgcaatgtcc	cggaatcagc	aattgctctt	ggtgtggatc	actgtctgtt	tttagaagcg	1121220
ggggtggaaa	tcggtgtagc	tacgacaaaag	gcttttacct	cgcaactctt	gttgcttggtg	1121280
tttttggtt	tgaaattagc	aatgtacat	ggtgccttga	ctcacgcaga	acaatgttcc	1121340
tttgccagg	gattacaaag	cttaccagat	ctctgtcaaa	aacttcttgc	ccaacgagtc	1121400
tctccattct	tgggcgcagc	cttactccta	tgaagataag	tttctttttc	taggccgtag	1121460
gttgatgtat	cgggtgggta	tggaggctgc	cctcaaactc	aaagaaattg	cttatattga	1121520
agcgaatgcg	tatcctgggtg	gagaaatgaa	acatgggccc	atagctttaa	ttagcaaagg	1121580
taccctgttt	attgcatttt	gcggtgatga	tattgtctat	gaaaagatga	taggcaacat	1121640
gatggagggt	aaagctcgtc	atgctcatgt	gattgctatt	gtcctgaat	ctcgtgaaga	1121700
tatcgctgca	gtttctgata	aacagatctt	tgccccagat	tgcatttttc	tcgctgtctc	1121760
tgtgttatat	actatagttg	gtcaagtgat	ggcatatgct	atggcgtag	caaaaggaat	1121820
ggagattgac	tgtcccagaa	atcttgccaa	gtctgttact	gtagagtaag	tacttcacag	1121880
tagtagacct	cgcaatccta	tgatgaaact	ctttagaact	tgtcttaaga	gtgcatatga	1121940
aatttaggta	tacgttatgt	caaataaagt	tctaggtggg	tccttgctta	ttgcaggttc	1122000
tgccatcggt	gctgggtgtt	tagcagttcc	tgtattgacc	gcaaaaggcg	gttttttccc	1122060
tgcaactttt	ctctatattg	tgtcctggct	ttttctatn	cctcaggcct	ttgccttctt	1122120
gaagtcatga	cttggtatgan	agaatcaaaag	aacccagtga	acatgctttc	tatggcggaa	1122180
tctatttttag	gtcatgtagg	caagattttct	atatgccttg	tctacttggt	tctcttttac	1122240
tcctactga	ttgctatttc	tgcgaagggg	gaaacatctt	atgccgcgtg	tttaattgtc	1122300
aaaatttagg	aatctcatgg	attcgtcacc	ttggccctct	aggttttgct	atattgatgg	1122360
ggcctatcat	tatggcgggg	acaaaagtgt	ttgattactg	taatcgtttc	tttatgttcg	1122420
gcttaactgt	agcttttgga	attttctgtg	cccttggtat	tttaaaaatc	caacctagct	1122480
ttctgggtgcg	ttcctcatgg	ttactacaa	taaacgcatt	tcctgtgttt	ttccttgctt	1122540
ttggattcca	aagtatcatt	cctacgttgt	actactacat	ggacaaaaaa	gttgtagatg	1122600
ttaaaaaggc	aattctcata	ggaacgttga	ttcctcttgt	tctctatgtc	ttatgggaag	1122660
ttgtgggtttt	agggtgctgtc	tctcttccga	ttctttccca	ggctaagata	ggtggatata	1122720
ctgctgtaga	agctctcaag	caggcccatc	gtctctgggc	attttatatt	gctggagaac	1122780
tttttggtct	ctttgctttg	gtctcctctt	ttgtaggagt	tgctctcggt	gttatggact	1122840
tcttggcaga	cggtttaaaa	tggaaataaaa	aatcacatcc	caattttcaa	ttttcttttt	1122900
aacattttatt	attccccttg	cttgggctgt	ttgttatcct	gaaattgttt	tgacctgtct	1122960
taagtatgct	gggggattcg	gggcgcgcgt	gattatcggg	gtattcccaa	cattgattgt	1123020
gtggaaaggg	cgttatggca	aacaacatca	cagagagaaa	cagttagtgc	caggaggaaa	1123080
gtttgcttta	tttttgatgt	tcttggtgat	agtaataaat	gtagttagca	tttatcatga	1123140
gctttaaatt	tgttttgctc	tatttttcaa	tttcaagtga	gcaaatagga	nnnttctatg	1123200
ggactatatg	atcgtgacta	tatacaagat	tctcgagtgc	agggaacttt	tgcttcaaga	1123260
gtctatgggt	ggtgacagc	agggctaact	gtacttcat	gtgttgccct	gggtctttat	1123320
ttttctggat	tatacagaag	tttattttct	ttttgggtgg	tggtgtgttt	cgctacgcta	1123380
ggcgtgtctt	tctttatcaa	ctctaaaatc	cagacactat	cggtagttgg	tcaagtgatg	1123440
gcatatgcta	tggtgttagc	aaaagggaatg	gagattgact	gtcccagaaa	tcttgccaag	1123500
tctgttactg	tagagtaagt	acttcacagt	agtagacctc	gcaatcctat	gatgaaactc	1123560
tttagaactt	gtcttaagag	tgcatatgaa	atttaggtat	acgttatgtc	aaataaagtt	1123620
ctaggtgggt	ccttgcttat	tgcaagttct	gccactgggt	ctgggtgttt	agcagttcct	1123680
gtattgaccg	caaaaggcgg	ttttttccct	gcaacttttc	tctatatgtg	ctcttgctt	1123740
ttttctatgg	cttcaggcct	ttgccttctt	gaagtcata	cttggtatgaa	agaatcaaaag	1123800
aacccagtga	acatgctttc	tatggcgga	tctatttttag	gtcatgtagg	caagattttct	1123860
atatgccttg	tctacttggt	tctcttttac	tcctactga	ttgcctattt	ctgcgaaggg	1123920
ggaaacatct	tatgccgcgt	gtttaattgt	caaaatttag	gaatctcatg	gattcntcnc	1123980
cttggccctc	taggttttgc	tatattgatg	gggcctatca	ttannncggg	aacannantn	1124040
attgattact	gtanantttt	ctttntntnn	ggcttanncg	tnncttttgg	aatttnctnt	1124100
gcccttggat	ttttaaaaat	ccaacctagc	tttatgggtg	gttcctcaat	ggttaactac	1124160
aataaacgca	tttccctgtgt	tttttctntg	ctttttggat	tccaaagtan	cattcctacn	1124220
ttgtactact	acatggacaa	aaaaagtttg	agatgtttaa	aaggcaattc	tcataggaac	1124280
gttgattcct	cttgttctct	atgtcttatg	ggaagtgtgt	gttttnaggtg	ctgtctctnt	1124340
tccgattcct	tcccaggcta	agataggtgg	atatactgct	gtagaagctc	tcaagcaggc	1124400

ccatcgttct	tgagcatttt	atattgctgg	agaacttttt	ggcttctttg	ctttgggtctc	1124460
ctctttttgta	ggagttgctc	tcggtgttat	ggacttcctg	gcagacgggt	taaaatggaa	1124520
taaaaaatca	catccatttt	caattttctt	tttaacattt	attattcccc	ttgcttgggc	1124580
tgtttggttat	cctgaaattg	ttttgacctg	tcttaagtat	gctgggggat	tcggggccgc	1124640
cgtgattatc	gggggtattcc	caacattgat	tgtgtgaaaa	gggcgttatg	gcaaacacaa	1124700
tcacagagag	aaacagtttag	ttccaggagg	aaagtttgct	ttatttttga	tgttcttggt	1124760
gatagtaata	aattgtagtta	gcatttatca	tgagctttta	atttgttttg	ctctattttt	1124820
caatttcaag	tgagcaaata	ggagggttct	atgggactat	atgatcgtga	ctatatacaa	1124880
gattctcgag	tgcaggggaa	ttttgcttca	agagtctatg	gggtgatgac	agcagggcta	1124940
atcgtaactt	catgtgttgc	cctgggtctt	tatttttctg	gattatacag	aagtttatatt	1125000
tctttttggg	gggtgtgggtg	tttcgctacg	ctaggcgtgt	ctttctttat	caactctaaa	1125060
atccagacac	tatcgggtttc	tgctgtaggg	ggccttttcc	ttctctactc	aacattagaa	1125120
ggaatgtttt	ttggaacctt	acttcctgtc	tacgctgctc	aatatggcgg	aggggtgatc	1125180
tggggccgctt	ttggatcagc	agccttggtta	tttggcttag	cagcagtata	cggagcgttt	1125240
acaaaaagcg	atcttactaa	aattagtaag	attatgactt	ttgctttgat	aggactcttg	1125300
ctagtgaact	tagtctttgc	tgtgggttgc	atgtttgtat	ctatgccttt	aatctactta	1125360
ttgatttgct	atctagggct	cgtcatcttt	gttggattga	cagctgctga	tgcgcaagca	1125420
attcgctcga	tttcttctac	tataggggat	aacaatacct	tgagttacaa	actctctttg	1125480
atgtttgctc	tttaagatgta	ttgcaatgtc	atcatgggat	tttgggtatc	gctgcagatt	1125540
ttctcatctt	caggaaaccg	agactaaaca	acgacttaga	tcttttctac	ttcaggaaat	1125600
aatttggttta	gaaaaagatc	taagtcgaat	tcattaagat	ccttttaaaga	ttccccataa	1125660
ccaataaact	ttgtggggat	tttcagtcgt	ttagctatatt	gaaatagggg	gccacccttg	1125720
gcagagccgt	ctacttttgt	gaagataaga	ccagaaaggg	gaacaacatc	atgaaatacc	1125780
cgcacctgct	ctatagcatt	attccctaag	gtagagtcca	agtcataaaa	aatttcattga	1125840
ggagctccct	ctagagcttt	gccgcaaacc	gagactatatt	tggaaagctc	tttcataaga	1125900
ttgccatgta	catgcaggcg	acctgaggta	tcaataatga	ctctagagta	cccccgggcg	1125960
attgcagatt	gaatcccatc	aaaggcaata	gcagcagcgt	cccccccggg	ttgtccagag	1126020
acaaagccac	agccaagttc	gttggcccag	agtcgtgcct	gggtccatgcc	agcagctcga	1126080
aaggatatccg	tggctacaag	catgacgctt	tcagatcgct	ccttgtagta	atgagcaagt	1126140
ttggccgctg	ttgtcgtttt	tcctgagccg	ttgggtccaa	gaagtaaaga	aacaatcggt	1126200
ctgggtctggg	aactttgtga	agcttgagaa	ggaagacctt	ctagagactc	gcgaagttaa	1126260
actgtaatca	gatctttgat	agtagatgcg	tcagcttttt	tagtccgacg	taatcggtca	1126320
cacaattctt	cagtaagctc	agtacccaaa	tctgcttcat	aaaacaaact	ttcagcatct	1126380
tctataagat	ctaaagatat	atttttttta	aataaagatt	gaagcttggt	tctaaagaat	1126440
ttgaacattg	ctaatagcaa	agttagtgtga	agtaaaagaa	atgatacaag	ataagaagga	1126500
aaaagcaaag	agttattttat	gcatcttcat	gagtaccaag	ctaaagatct	cttagcttct	1126560
tacgatgtgc	ctattccccc	ctattgggta	gtgtcttcag	aggaagaagg	ggaacttctt	1126620
atcacaaagt	cgggattaga	ttccgcctg	gttaaagtac	aggttcatgc	tgagggtcga	1126680
gggaaacatg	gtggtgtcat	tggttgcaaaa	tcctcagcag	gcattttgca	agccgtagct	1126740
aagctcttag	gaatgcattt	tactagtaat	caaactgccg	acggatttct	ccccgtagag	1126800
aaagtcttga	tttcaccact	tggtgtcata	caaaggggat	attatgtcgc	agtgattatg	1126860
gatcgaaaac	accgatgccc	agttcttatg	ctttcaaaag	caggagggtat	ggatatcgaa	1126920
gaggtcgcac	actcttcccc	agaacagatc	ctgacattac	cactgacctc	ttatgggcat	1126980
atctatagtt	atcaacttcg	tcaagccact	aagttcatgg	agtgggaagg	agaagtgatg	1127040
caccaagggtg	tccaattgat	caaaaagctt	gcgaagtgct	tttatgaaaa	tgatgtctct	1127100
ttattagaga	tcaatccttt	gggtgttgact	ttagagggtg	agctacttgt	cctcgattct	1127160
aagattacga	tcgatgacaa	tgccctatac	cgtcatccca	acttagaagt	attgtatgac	1127220
ccctctcaag	agaatgttcg	ggatgtccta	gcaaagcaaa	ctggattgtc	ctacatcgct	1127280
ctaagcggaa	atatcggttg	cattgtgaat	ggcgccggac	ttgccatgag	taccttagat	1127340
attttaagc	tccatgggtg	gaatgctgcg	aatttcttag	atgtcggagg	aggggtctct	1127400
caaaagcaaa	tccaagaagc	tgtatcttta	gtattgtccg	atgagagcgt	gaaagtgcct	1127460
tttatcaata	tcttcgggnn	gattatggac	tggtctgtag	ttgcctccgg	gctcgttgca	1127520
gttatggaaa	caagagatca	agtgggttct	acagtcattc	gtctcgaagg	aacaaatgta	1127580
gaattgggaa	aagaaattgt	tcagcaatct	gggattcctt	gccaatttgt	ctcttctatg	1127640
gaagagggcg	ctagacgcgc	tgtagaactg	agtatgtaga	tttaggagat	acatgttcca	1127700
ctcactaagt	aaaaatactc	ccatcatcac	acagggaaat	acagggaaaag	caggttcatt	1127760
tcatactgag	cagtgccctc	cctacgggtac	gaatttcgta	gggggtgtga	ctccaggcaa	1127820
aggggggaacc	ctttggctag	acctgccagt	ctatgattct	gtacttgagg	cgaagcaagc	1127880
tacagggtgt	cgcgcgacca	tgatttttgt	tccaccacct	tatgccgccg	aggccatcct	1127940
agaagccgaa	gaggccggaa	tcgaacttat	tgtttgtatt	accgaaggga	tccctgttcg	1128000
agatatgctt	gaagtggcta	gagttatgga	caacagtact	tcacagctta	tcggcccgaa	1128060
ttgtccagga	attatcaagc	ctggagaatg	taaaattgga	attatgccag	gatatatcca	1128120
cctgccggga	aatattggag	tggtctctag	atcaggaact	ctgacatacg	aggctgtttg	1128180
gcagctcact	cagctcaaaa	tcggccagag	tatttgtgta	ggtattgggg	gagacccctt	1128240

caatggaacc	tcattttattg	atgtctttgca	ggcgctggag	gaggatccct	atacagaact	1128300
gatttttaatg	atcggggaaa	tcggcggttag	tgccgaagaa	gaggccgcgg	cctggatcca	1128360
agcacactgc	acaaaacccg	tggttgctttt	tatttgctggt	gttacagctc	caaaagggaa	1128420
acgcatgggg	catgctgggg	ccatcatctc	tggaatttct	ggggatgcca	aaagtaaaat	1128480
acaagtctta	cgtgaatctg	gagttactgt	agttgagtct	cgggcccata	tcggaaaaac	1128540
tgtagacgct	gtattacggg	caaaagaact	ctaattgctta	atcatctaac	ctacaagtac	1128600
aaggttcgct	taatcctttg	gattggggagc	tctctacttt	aatgaagatc	ttgtgcttgg	1128660
ggactcattc	ttgCGCctag	ttcttattca	tgtcttacgt	cgctatttcc	ctgtgggtaa	1128720
ggaaaatcag	aaaaagagac	ctattcgcaa	gttataaagt	atttacttga	aatattattt	1128780
ccctcatcta	ctagctcttt	aagaactagc	caagggtgga	tagaagtgcc	ttcaaggagt	1128840
gctctggcag	ccatatctaa	gtgtgtgttc	aaaccctatt	ctggcaacac	aaataagata	1128900
gatgttggtg	gatactatat	cataagagta	tactgtttcc	aatttcttca	aatccgtaag	1128960
cttttttctt	tccttacaca	cgactttatt	ttttgaaata	tcttatcaat	accttagaac	1129020
gaagtcttaa	ttaaaaataa	atcaggatgt	tatgcaggtc	tacgagttct	ctcgtaagt	1129080
tcaaccacaca	tttcaaaatt	tactcatgta	aaaattagat	gcctgctttt	tctttggagg	1129140
aaagcgggta	aaaatttatcg	gttttagatga	acctaattctg	gcttgaggaa	tagaagaaca	1129200
ggttgacta	tccattgcta	taaagatcct	taaaattatc	cttgcaactta	ttttgttccc	1129260
attagtttta	ctcgcttggg	tgattcgcta	tcaattgcac	gcaaatttcc	attgtagtgt	1129320
agtgccttcc	ccaggatttt	cggtaaacca	agcatacaaa	tgtagtggag	ctaagataga	1129380
agaaatgcta	gatcttctag	acttagaaac	cctggaatgg	tcatacaagt	gccttcgtca	1129440
agatatgaca	tttgcaaactc	ggctagagga	agagctgatt	caagaacttc	gtgtgtcaga	1129500
gaccgaggag	ttgattagtc	ttgggtggtaa	acgaaacctt	gtgcgtttac	ttctcacgca	1129560
ctctttttaa	tcctccaaaa	gagatcgctg	gtagagtctg	taggtcatga	ggttgtcttt	1129620
cctgtatttg	ataggctaaa	gagagaagag	gaaatcattg	gggatggacc	catcactcga	1129680
tccaatgagg	aactgtgggc	tcttctagat	catggaactg	ctcgcgggat	ccataagacc	1129740
ctttggtttt	cgattttttt	taagtatcta	acacaaatcg	aactgttcta	gaagcaggta	1129800
ttggagggga	gattttcaag	agacttaacg	ctatatccca	gacttctacc	ggctcaaacat	1129860
tgacttttagc	tccgaagctc	tcgaatcttt	gcttttctgt	tcatttctct	gggttgctgc	1129920
gttgggaaaa	cattcaagtt	gagtagagag	aaattgttna	ttttgtttct	tnncaaanat	1129980
tttatcttcc	cagtctcttc	tatttgtctg	agttacttga	gtgatgcgtg	aattttttaca	1130040
tgtgactttt	ggatcatgga	taactggaac	ttttataaaa	gatatcgagt	tcagaaaaaga	1130100
agaaaaaaac	ctctttttatt	taatgattta	ttttttaaag	tatataaata	attttataatt	1130160
ataaaataat	ttactttttta	ataattaaaa	tgtaaactgt	ttgcacttta	ataataatta	1130220
taattataga	ttttgatgct	tgtctattgt	tttgatccct	cgggtaccaac	ttcaccagaa	1130280
caccgcctga	tggcggcatt	agaccgttgg	tttttcttag	gaggacatcg	tgtaagaatt	1130340
ctcacgcttg	agggtaatca	ctatcgggct	tttcaagaaa	atatgtctat	ctcaacagta	1130400
gagaagatat	tgaaactaat	ttcctatcta	ctcatcccta	ttgtccttat	tgcttttgcta	1130460
atccgttggt	tctttacactc	taggttttaa	tgtaacttga	aatgcgattc	tctaagtgac	1130520
gcaagagctc	cccacgacgt	tcaacctttc	aatgatttcc	aacttttcaa	taatcaggag	1130580
aggctaaata	tatggaaaaa	tcggagatat	gtctctggaa	tagatgtgct	tatgggtgccg	1130640
gtcgattatc	tcagatctca	gtttcccggt	tttaaggaga	ttccagaagc	tatccgttgc	1130700
gaaaactatg	taagtgatgg	tcagttttct	gaagaaagta	aaacaagcta	tcttagagcg	1130760
atgctgaccg	acattgttgg	gtatatcttg	tcattagatg	agacctattg	gacgaatgtg	1130820
atcctcaaga	tccgtgcgat	gtgcatcacc	ttcgaaaagt	tccctggaaa	agaagcagac	1130880
cctaactatt	cccctcgctg	aactcaccac	tattttgatg	aatcttgga	ggcacttgcg	1130940
cgacatgtat	taggagaagg	taacatgggt	aatagactag	atgaggcgct	aattcgtaaca	1131000
gagaagccgg	gcaaagaagg	ggaatgtatt	acgaaacagt	ttttaaaaga	ttactgtaaa	1131060
aagcatctcg	aagttatgag	ttgtccagat	ttcattgaat	ctctggtaga	tgaaaaaatc	1131120
cgagagtttc	gttgtccaag	tatttttaaac	tcagcagtat	gtgatgtaat	agatcgcaaa	1131180
tgccaagaac	atttgttaaa	ggcaataata	aacgaagcaa	accgcaggct	ccctgggatg	1131240
aaaaatagct	cattcactat	gcgtggtaac	caagttttat	tttataccat	cttttctcca	1131300
ccaaaattgc	cacctgctgc	gagttccgta	tattttttaa	gaaaggagat	ctcttggtct	1131360
cctagtcttg	ctataagggtc	ttgatataca	tctttttgga	gtaatttcat	cttttatatt	1131420
attttattaa	aatctttata	attcgtttct	tttgaaatat	ttattgtatt	tcttaataac	1131480
tgtatataaa	ccaatttgct	aatattttta	aaagttagtt	tttgatggaa	gtttatagtt	1131540
tttccccctt	agtaagaact	tcgtttcagc	accgtgtaat	ggcggcacta	gataattgggt	1131600
tttttctagg	agggcgccgt	ttaaaagtag	tttctctaga	tagttgtaac	tcagggcagg	1131660
cttgatgaaga	atacgtgcct	atttcaacga	cagaaaaggt	cttaaagata	ctctcttacc	1131720
tactcatacc	gattgtcata	atagctctgt	taattcggtta	tcttttgcat	agcaatttta	1131780
cggcaaaaggt	atcacagaaa	ccttggttaa	agaccctgca	gttaggaatt	gatataaaaa	1131840
gcttcatact	tcccggttct	catgtaaaaca	cgatggattc	agctactttg	tttaaagcaa	1131900
ttcgtttgga	agggaagcgt	gttgatgtag	aatatcatag	gctacatagc	agcgataagg	1131960
tggtttttta	tatccctgct	cagaaacttc	cagatgatct	gcgtttgact	cattggcttc	1132020
cagaaaaaga	aacaagaaag	actgagtatg	tgagacatat	gctggcccat	gtcatgggtt	1132080



atctaacaatc	acagggtgaag	gaacggcttc	aacaggtagt	gcaagactct	cgaagcagta	1132140
cttccttggg	ggctgaaaaa	gtccttcaat	acagattcat	tgatcatcca	cagagtcaag	1132200
gagaatttca	acgtctgctt	aatgaaaata	taacgaccaa	agggtccgag	gataagggaag	1132260
ttgtacagag	tgattttattt	gacatggctt	ttcagtggtg	gtggccacag	tttattttcag	1132320
ttataacaatc	tccgaccttc	agtgaagaat	tagtacacga	aatgagtcag	aaacttgatt	1132380
tagattgtat	ataccagaa	gatgatgaat	ttgagcagaa	gttccttaat	acccttctga	1132440
aagcagtctt	gcaccacggg	tttgaaggaa	tcagtggtgc	gagtatgggt	ggtatcttcc	1132500
tgatttgtcc	ggactctctt	gcattacaga	ttcccttctt	aaggaatcaa	aaatgatgca	1132560
gggtgctgag	ttcttagttt	taaggtagta	agacctcccc	gcggtagaat	ataggatctt	1132620
caagctcaaa	gtctccggct	ttgagcgatg	ttccctcaa	actttaattc	tacatcatga	1132680
agtattctca	atctaaagat	aaaaaatcct	tttgtagtgc	tgtgttagtt	acatatgatt	1132740
tgttttttta	atatgcattg	tatttttcaa	taaataatga	taaacacttc	gcgaatgttt	1132800
tgaaaatatt	tttttatgga	agttttatagt	tttcacctgc	ggtaaggact	tcgtttcagc	1132860
accgtgtaat	ggcagcacta	gatgcttggg	tttttctagg	agggcaccgt	ttaaaagtag	1132920
tttctctaga	tagttgtaac	tcaggttggg	cgtatcaaga	acttgtgtct	atttcaacga	1132980
cagaaaaagt	cttgaaacta	ctctcttacc	tactcgtacc	gattgtcata	atagctctgt	1133040
taattcgttg	tcctttacat	agcaatttta	ggatagacgt	agagaaggaa	cgttgggttaa	1133100
aaataaggga	gtaggaatt	gatatagaaa	gctgcaaaact	ccccagttct	tatgtaaacc	1133160
aggtttcttc	gtttatttgg	tttgaaaaag	ataaatccaa	acggccacgt	attgatgtag	1133220
attatcatatc	gctacatagc	aaagactggg	tagttttccc	tatcgttttt	cagaaaaattc	1133280
caaagacctc	gcgtttcagt	tattgggtct	cacaaaaaga	aacaagggaag	agggattatg	1133340
tgagaaatat	gctggaccac	gtcattgggt	atctaactgc	agaagggtggg	gagtgggtgc	1133400
agtatatatc	gaaaacctct	tatcaaagcg	ctacttctct	ggatcctgaa	agagttcttc	1133460
aatattgctt	aactgataac	caggagctcc	agggagaagt	gcaacgtttg	cttaatgagg	1133520
agagtgcgac	caaaagctct	ggggataagg	aagttttggt	aagtcagtga	tctgacatta	1133580
tttgccagtg	ttgggtggcca	aagtttcttg	aagttataca	atctccggcc	tttattgaag	1133640
aattagtaga	agaagtgagt	ggtaaactta	atttagattt	tttatgccta	gaaaaggcta	1133700
atacattaga	tcaggagtgg	agaaacagtc	ttctaagagc	agtcgtacac	cacgggtctg	1133760
aaggagttaga	tattaagaaa	gttgggtgccg	gcctcattat	ttatacggaa	gctattcaat	1133820
tacagattcc	cttctcaagg	agttaaaaat	gatcgtagtg	tcgggggtgct	tagtttttaag	1133880
gtaacaagac	atcctcgcag	tagaagagag	gatcttcaag	ctcaaagtct	cgggatttga	1133940
gcgagtgttc	cctcaaaact	taattctaca	tcatgaagta	ttctcaatct	aaagatatata	1134000
aatccctttg	ttcgaatggt	ttcgtcacat	atgatttgtt	tttcgtaatt	actaggtagc	1134060
agaacctgtg	ttagctagta	tacgatggta	ttctgcttca	tcgaaagaca	accttcttga	1134120
gggatagata	tgataactaa	gcaattgcgt	tcgtggctag	ctgtacttgt	tggttcaagt	1134180
ctgctagctc	ttcctttatc	agggcaagct	gtcgggaaaa	aagaatctcg	agtttccgag	1134240
ctgcctcaag	acgttcttct	taaagagatc	tcgggagggt	tttctaagg	cgctaccaag	1134300
gcgactcccg	ctgttgtgta	catagaaaagt	ttcccaaaga	gccaggctgt	aacacatcct	1134360
tctcctggac	gccgtggggc	ttatgaaaaa	ccttttgatt	attttaatga	tgagtttttc	1134420
aatcggtttt	ttggtctacc	ttcacagagg	gaaaaaacctc	aaagtaaaga	ggcgggtcga	1134480
ggaacagggt	tctagtatc	tccagatggc	tattattgtga	ctaataacca	tggtgtcgaa	1134540
gatacaggta	agattcacgt	aactcttcat	gatgggcaaa	agtaccacgc	aactgtaatc	1134600
ggactcgatc	ctaaaacaga	ccttgacgtc	attaaaatta	aatcccaaaa	cctcccgtat	1134660
ctttcttttg	gaaactccga	ccacttaaaa	gtcggagatt	gggcaattgc	aattggaaat	1134720
cccttcgggtc	ttcaagctac	ggtcacccgta	gtgtcatcag	tgctaaagga	agaaatcaac	1134780
tccacattgc	agattttgaa	gattttattc	agacagatgc	tgcgattaat	ccaggcaact	1134840
ctggaggccc	tcttctaaat	attgatggac	aggtcatcgg	tggttaatact	gccattgtca	1134900
tggttagtgg	tggctatatt	ggaatcgggt	ttgcgattcc	tagccttatg	gcaaatagaa	1134960
tcatagatca	gctgattcgt	gatgggtcaag	ttacccgagg	attcttagga	gtgactttac	1135020
aacctataga	tgcggaactc	gctgcttgc	acaaactcga	aaaggtttat	ggcgctttag	1135080
tcacagatgt	tggttaaagga	tctccagcag	ataaagcagg	gctaaaacaa	gaagatgtga	1135140
tcattgctta	taatgggaaa	gaagtcgatt	cactgagtat	gttccgtaat	gctgtttctt	1135200
taatgaatcc	agatacacgt	attgttctaa	aggtagttcg	tgaaggaaag	gttatcgaaa	1135260
tacccgtgac	agtttctcaa	gctccaaaag	aagatggaat	gtcggcttta	cagcgtgtgg	1135320
gaatccgtgt	gcaaaaacct	actcctgaaa	ctgctaagaa	gctgggaatt	gctccagaga	1135380
ctaaaggcat	tttgattata	agtgttgaa	cagggtctgt	agcagcttct	tcaggaaattg	1135440
ctcctgggtca	gctgatcctt	gctgtgaata	gacaaaaagt	atcttcgatt	gaagatctga	1135500
atagaacgtt	aaaagattct	aacaatgaga	atattcttct	tatggtttct	caaggagatg	1135560
ttattcgctt	cattgccctg	aaacctgaag	aataaaaagc	ttggagtcac	acatttgatt	1135620
cataaagagg	aatgaagaga	gttctctctt	cactctttta	tttttaggaag	cttatcaaga	1135680
agctgacaaa	tagaaaggaa	tcccttttta	agttgggtcca	tcgagaaatg	ctcttctgca	1135740
gcgtgaatat	catcactaag	atacgaagtc	ccacaaatga	taggtgaggt	ttgtgctgct	1135800
tcccctaata	ggggacctat	cgggatcgta	gcaggcatca	ctaactctcag	gcattcttca	1135860
ttgtagagg	cactatagat	ctcttgaagc	actttgacta	ttgggagggt	cgcagaactt	1135920



ctccaacctc	gagatcctcc	tggaagaatt	tcataagaga	acctttaacg	aagaaggagc	1135980
ttgttgtttc	aagtgatgga	taacttggtg	agcagcttta	tcaggatctt	gattaggaac	1136040
aagtcggcag	gagaggtagg	cagtggtctc	ataggggatc	acagtcttaa	atcctgggtcc	1136100
cgtataacct	ccagaaattc	cattgatttc	tacagtagga	cgtaacgcag	attcttcagg	1136160
gctataagaa	gcttcgtaac	cctgaggtcg	aaaccctaag	ttttcttcgc	attcccgaag	1136220
ggtatccgac	ttcgggaagat	caggacgatc	gctatccgag	gggagagcaa	gatcatcata	1136280
aaatccttca	atagctatag	aattgtcagg	gtgatgcaga	gagctcagaa	tttctgataa	1136340
agcacgatcc	gtattgtagg	caattcctcc	taaaactcct	gagtgcatgt	ccttgttccc	1136400
ctcttcaagg	gagattttca	tggaacaacat	accccgagct	ccaatgctta	cgtaggggtg	1136460
tttttcagaa	aggaaacccc	catctacgat	cagaagatag	tccgcgcgta	aagcttcttt	1136520
tttcttttct	aaccaagtaa	ataatgcgag	actcccactc	tcttcttcac	cctcaattaa	1136580
ccaaataata	tttagaggga	agtttccttg	agattcgtaa	tagtgctgta	atgcctttta	1136640
ggtgtaaaaa	cattgtcctt	tgttatcaga	ggctcctcgg	gcatagagat	tgccattctc	1136700
ttctctaagg	ataaagggat	ctcccttcca	accatcagat	agctgtgctg	gctgcacatc	1136760
atagtgggta	tagagcataa	gagtagggct	aagaggatct	tcgcttttat	aggatgcata	1136820
gatgataggg	ggatgcccag	gcgtttccca	gagctctaca	tcgaaaatct	tattcacatg	1136880
atctactaaa	aaatgtgcac	aattttcaca	atcctgaaga	tgatcactat	ccgcagatat	1136940
cgaggggaag	cttataaatt	ttgcaaactc	ttccaggaaa	tttgactat	ttatatcaaa	1137000
atgtttcgaa	tctagattca	taggtttccc	agagcagttg	ttgaaaataa	tatcacagta	1137060
acttaacttg	tcttttgtcg	aaaagaaaat	aagaacatag	ggtttagcgt	gcttttttagc	1137120
atgattaagc	atgacaaatt	agggattcag	ccctaactaa	tcagatgagt	tacagaaagt	1137180
atgaaagctg	gtgatacgta	tagaaatttc	attattaagt	catgcaaaga	tcttctgaa	1137240
atagaaaagta	agctccttga	ggcggaaacat	aagccgcagag	gagcttctat	tatgatgatc	1137300
gtcaacaacg	atgaggaaaa	cgatttcaat	atttgcctta	gaacatgccc	acaaacttct	1137360
aacgggtgtg	cgcatgttct	agagcatatg	gtcctttgtg	gttccgagaa	ctaccccggtg	1137420
cgggatccct	tcttttcgat	gacacgtcgt	agtctgaata	ccttcatcaa	cgcgtttaca	1137480
ggtccagatt	ttacatgcta	tcttgcagct	tctcagattc	ctgaagattt	ttataattta	1137540
ctcagcgtgt	atattgacgc	cgtgtttcat	cctttgctta	ccaagcaaag	tttcttcaa	1137600
gaggcatgga	gatacgaatt	caattccgag	aatcatctct	gttatacagg	agtagttttc	1137660
aatgagatga	aaggtgcgat	gatgtcggga	gaggcacggc	tctctgaggc	gtctaatgca	1137720
gctatttttc	cttctgtgac	ctacggcgta	aactcaggag	gagaaccat	agagattgta	1137780
actctattct	atgaagacgt	ccgagcattc	catcaaagcc	agtatagtat	caatcgatgc	1137840
ttgttttact	ttttaggaaa	tatcaaacct	tcccgctcatt	tagatttctt	ggaagaaaag	1137900
ctactcagac	aagctacaaa	gctagaaaag	caggcagtat	ccgtaccttt	gcaaaagcgg	1137960
tttaagggaac	cagtaaggaa	catcttaacg	tatcctgtcg	atcatcaaga	agaagataag	1138020
gtcctttttcg	gaatttcttg	gcttacctgt	tccatttttag	aacaacaaga	acttcttgcg	1138080
ctgcatgtgt	tagaaaattat	cctcatgggt	acagatgcct	ctcctttaaa	atctcgattg	1138140
ctgaaatcag	ggttctgtaa	gcagacagaa	atgagcatcg	agaatgatat	ccgtgaaatc	1138200
cccatgacct	tggtatgtaa	aggatgttct	ccagcaggag	cccagaaatt	agaagctttg	1138260
attttgcgct	ctcttgaaga	aatcatccgc	gaagggatat	cagaaaaat	tgtagaggga	1138320
gcagttcatc	agtttagagtt	atctagaaaa	gagatcacag	gatatttctt	accctacggg	1138380
ctgtctctat	ttttccgctc	cggactattg	aaacagcacg	gaggctctgc	cgaagatggc	1138440
ctgagaatcc	ataacctctt	ttctgagctc	cgtaattcgt	taaaaaattc	tgatttatctt	1138500
gccaagtgtg	tccgcaagta	cttcttagat	aatccacatt	ttgcaagagt	gattttactt	1138560
cctgataccg	aacttggtgc	taaggacaat	aaagatgagc	agcagctttt	actcagtggt	1138620
agtgaaaaac	tcacagacga	gaataaagaa	aaaattcaac	aaaatgtacg	agaactcaca	1138680
gaatctcaag	aacaaaagga	agatctgaat	ggtattcttc	ctaaccctgc	tttggataaa	1138740
gtgcccacgt	ctgggaagga	atttccttta	attaaagagg	ggctgagtc	aggagaagtt	1138800
cttcatcacg	aatgcttcac	gaatgatatt	gtcttcatag	atgttgtctt	agatatccct	1138860
ccgctatctg	gagaagaact	tccttggttg	cgtttgctcg	tatttttaat	gttgcagctg	1138920
ggatgtggag	gcaggtctta	taaagaacat	ttagagtttt	tgtagaaca	tacaggtggc	1138980
gtggacgtct	cttatgattt	ctctcctcat	gcaaataaaa	atagtttctt	ctctccatcg	1139040
gtaagtatcc	gaggcaaagc	tctgtcatcg	aaatctgaga	agctctgtgg	tattgtcagc	1139100
gatatgttaa	caagcgtgga	tttcacggat	attcctagga	ttcgtgagtt	gctgatgcag	1139160
cataacgaag	ccttgacca	tagtgtgaga	aatagtccca	tgagctatgc	agtgagcatg	1139220
gcctgctctg	ggaattctat	aacaggggcg	atgtcttact	tgactacagg	gcttccctat	1139280
gtgaaaaaaa	ttcgcgaact	cacaaaaaac	tttgatcaga	atatagacga	agcgggtgtc	1139340
atcctacaac	gattatacac	caagtgtttc	tcagggaaac	ggcaaatgtt	cattagtggg	1139400
agcgctcata	actatcagca	attaaaagat	aataagtttt	acggtctttt	agactacctg	1139460
attgtgatcc	ccgaaccttg	ggaaaaatcca	agtataaact	tatatgtaac	ctctcggggg	1139520
ttgcatatcc	ctgcacgtgc	agcattcaat	gctcttgctt	tccctattgg	cgatatagct	1139580
tatgaccatc	ctgatgctgc	agctctaaca	gtagcagcag	agatcttaga	taatgtgggtc	1139640
ttgcatacta	agattcgaga	gcaaggagga	gcctatgggt	cgggagcagc	tgcaaaccta	1139700
tcacgaggat	ctttctattg	ctatagttat	cgagatccag	aaattgcaac	tacctacaaa	1139760

acgttttctaa	agggagtgtc	agagatttgc	tctggtaatt	tcactaaaga	agatatctat	1139820
gaaggagctc	ttggagtgtg	ccaaggtttg	gatatgcccg	tagcgccagg	aagccgtgct	1139880
tccgtagcgt	tttataggct	aaaaagtgg	aggattcccg	tgttgcgcca	agcattccgc	1139940
cgttctgtcc	ttgaagtgtc	taaagaacac	atgtgtatgg	ttatggataa	atatctagag	1140000
tcaacagttc	aggagacaac	tttgatatct	tttgcagggg	aagagatgct	tcgtaataat	1140060
gttcttactc	tagataaaga	tttccccata	gtaccagcaa	tttgagactt	agtcttgttt	1140120
ttctaaagac	tcaataacag	ctaagtctcg	atctatatca	catgtgtgtg	gaaacgaggt	1140180
ggctaagctt	tctatagggg	taggctcttc	aatctgatgg	gatgacgagg	tttccaagcc	1140240
ttcgaacttc	cttaatgtag	gcagtaacccg	gtattgaaag	ctagaggtca	tatcgttgta	1140300
actttgtacc	gtctgggtta	aatttttgcc	tatcttctga	aaatgtgtga	acactacctg	1140360
tagggcgacga	tggagctctt	tacctaaaag	actgacctct	tgaatttggt	tttgcagatt	1140420
ctcttgcttc	cacatgttaag	caatcgtctt	aagtagagca	agtaaagtca	aaggactgga	1140480
taagattacg	tttgaagaag	ctccaatctc	catcaattca	ggagctaacc	gaattgcatc	1140540
attgaataag	ctctccccag	gaagaaaaag	aatcacgtat	tctgggtgatt	gatgaaactt	1140600
ttcccagtaa	ctcttggtat	tcagagtctt	aatgtgctct	ttaattttat	caacaagatc	1140660
ccccctgtca	atctcctcta	cagaaaaata	ggagtctgaa	atcggagctt	tagcatcaat	1140720
aatataacag	cgatcttgag	gcagccgaat	aataatatcc	gcccgaatg	ctccttgggc	1140780
acttgtgggt	tgactgtcgt	agtcacagta	ttttaacatc	ccggcaagct	ctaaaattct	1140840
ctccagttgg	atttctcccc	aacgtcctcg	agatcctggg	tgctttaaaa	tgctcgtgag	1140900
aacatgagtt	tcagtctcca	attttttctc	tacagcaagt	aattgcgata	tctgttcttt	1140960
taaccttcca	cgatcttcgg	catgcttagt	ttcaaagtgc	tctaaacttt	gcttaaattgt	1141020
cgtgagtgtc	gttttgatag	gagaaagtat	agactgaaaa	gatttagacg	tatcaccaaa	1141080
ataattctga	gcctcttctt	tcatatcttt	gatgagtttg	tgagaagaaa	gtgctagacg	1141140
attgctgaaa	tcttcaatta	actgctcttg	atggcggcta	agatttaaa	aagtctgtag	1141200
cagttgggtt	tcattgttcta	atttctgaat	cttctctaga	aacgcacgct	tcttcttgc	1141260
atagagagaa	gacgatacga	agactcccag	aaaaaacaca	caccagata	aaagtaggca	1141320
cgctagggaa	acagggaggt	tcataacaga	tgctagctct	tttttctata	gatgattgaa	1141380
aagatcggaa	agcctactaa	agtatatagc	caagatacaa	ggaaaaagac	ttcaacaaaa	1141440
tgatctacaa	gtcctgaaaa	gaaaagacat	gctgctaaac	ctatagtcac	taccagcaga	1141500
aaagaagaaa	cattaaagcg	gaaatgcttc	actccaggaa	atttccatgg	agaaatcatc	1141560
agacccccaa	tgaaaagaag	ggcaaagtat	aatagacctt	cccgaagtgt	ggcagggagg	1141620
tctggaagaa	aatccgaagc	aagaaataaa	gctaaggaga	caataacttg	agcagcagca	1141680
ggaaatgggca	gaccaataaa	acaataaggc	tttgaacat	ctacagtctt	ttgagaaaag	1141740
aggttgtaac	gtaccaaccg	caacactcca	cacagagaat	aaataatcga	ggtgatgagt	1141800
agtagcgaag	agaaaaaatt	cccaacataa	atcccatcaa	gactttttat	agcaatcaaa	1141860
ggtggggcaa	tgccgaaagt	gaccgcatca	gaaagagaat	caaactgagc	acaaaaagcg	1141920
ctctcggctt	tcattgattcg	agcgatcgca	ccatcagaaa	aatcccgcat	catagcacta	1141980
ataagcaaga	gagataagcc	ctgcaaacga	tggaataact	ctacagagga	cgacgttctt	1142040
aatacgcttt	tgaaaataat	aaataatcca	caacaaagtc	caaaagcagt	aatagcggtta	1142100
gggtgcacta	cgcgacgctt	gcctcgtgct	tctagatcta	atcccgccat	gtcaatttgc	1142160
cagagttttct	tttgctcgta	gcataatgga	ttcttctaaa	atcaacaagt	ttttgcagtc	1142220
ctcttgtcta	ttaagatctc	tatctccaaa	agctcctaga	gtatgatatt	tttaccgaga	1142280
aagggagcat	ttttcaattg	caggaaacca	tgacaattcc	tatatatgg	agataagcgc	1142340
ataacgtttc	actacatatt	gggtttttta	aagaaaaatc	cttcttatgt	ttaaaggcgt	1142400
ttttctttct	actttttaat	tataacaaa	gaaaaagtac	tccaatattt	atgggttttg	1142460
agtcttgatt	ttctagtgcg	caaagaataa	nagaatctaa	tctttanata	tcattttagg	1142520
gaaaagttat	ggtcgaagtt	gaagaaaagc	attacaccat	cgtcaaacgt	aatggaatgt	1142580
ttgtccatt	taatcaagat	cggattttcc	aggctttgga	ggcagctttt	cgagatacgc	1142640
gtagcttaga	aactagttct	ccactaccta	aagacttaga	agaatctatt	gcgcaaatta	1142700
ctcataaagt	cgtgaaggaa	gtcctcgcta	aaatttcaga	aggctcagga	gtcactgtag	1142760
agagaatcca	ggatcttgta	gaaagtcagc	tctatattag	cgggttgtag	gatgtggctc	1142820
gcgattatat	tgtttacagg	gaccaacgca	aggcagagcg	cggtaactct	tcgtccataa	1142880
ttgccatcat	acgtagagac	gggggaagcg	ctaaatttaa	tcctatgaag	atctctgcag	1142940
ctctcgaaaa	agcattcaga	gcgacgtctc	aaattaatgg	gatgactcct	cctgcaacac	1143000
tatccgaaat	taattgacctt	acccttagga	tcgttgaa	tgctctaagc	cttcatgggt	1143060
aagaagctat	taattctggaa	gagatccaag	atattgttga	aaagcaactt	atgggtgccc	1143120
gctattatga	tggtggccaag	aattatattt	tatatagaga	agctcgtgca	cgagcccggt	1143180
ctaataaaga	tcaagatgga	caagaagagt	ttgtcccca	agaggaaacg	tacgttggtc	1143240
aaaaagaaga	cggcaccacc	taccttctga	gaaaaacaga	tttagaaaag	aggttttctt	1143300
gggcatgcaa	acgttttctt	aaaactacag	attctcaact	gcttgcatat	atggcattta	1143360
tgaatttgta	ttcaggaatc	aaagaagacg	aggtcaccac	agcatgcac	atggcggcac	1143420
gtgccaatat	cgagagagaa	cctgattacg	ctttatcgc	agcagaactc	ctcacagatt	1143480
ccttgatatga	agagacctta	ggatgcagct	ctcaagacc	gaatttatca	gaaatacata	1143540
aaaaacattt	taaagaatac	atcctcaatg	gagaagagta	tcgcttgaat	cctcaattaa	1143600

aggattatga	tctcgatgct	cttagtgaag	tcctagacct	ctctagagac	caacagtttt	1143660
cctatatggg	agtccaaaat	ctctacgata	gctattttta	tctgcatgaa	ggacgacgtt	1143720
tagagactgc	gcagatcttt	tggatgcggg	tttctatggg	cttagcctta	aatgaaggag	1143780
aacaaaagaa	tttttgggca	atcactttct	ataatctgtt	atccacattc	cgctataccc	1143840
cagcaactcc	tacattgttt	aactccggaa	tgcgtcattc	ccaactcagt	tcatgctatc	1143900
tttccacagt	aaaagatgac	ctaagtcaca	tttataaggt	gatttctgat	aatgctttgc	1143960
tttctaaatg	ggcaggggga	attggaaatg	attggacaga	tgcccggtct	acaggagctg	1144020
taattaaggg	aaccaatgga	aagagtcaag	gcgtcattcc	cttcattaag	gttgccaatg	1144080
atactgcaat	tgcagtgaat	caggggggca	aacgtaaagg	tgctatgtgc	gtatatttag	1144140
aaaactggca	cttggattac	gaagactttt	tagaattgct	gaagaatata	ggagatgagc	1144200
gtcgtagaac	tcacgatata	aatacagcaa	gctggattcc	tgatctcttc	tttaagagac	1144260
tagaaaaaaa	aggcatgtgg	acactcttta	gccccgatga	tgctccaggt	ttacacgaag	1144320
cctatgggtt	agagtttgaa	aagctttatg	aagaatatga	acgtaagggt	gaatctgggg	1144380
aaatccgtct	ttataaaaaa	gtagaagccg	aagtgtctgt	gcgtaaaatg	ttaagcatgc	1144440
tttacgaaac	agggcctcct	tggattacat	ttaaagatcc	ttcgaatatt	cgctcaaac	1144500
aagatcatgt	tggcgctcga	cgctgttcta	atctatgtac	agagatttta	ttgaactgtt	1144560
cggaatcaga	gactgcagtt	tgtaatttag	gttccataaa	cttggtagaa	catatccgta	1144620
atgacaagtt	agatgaagaa	aaattaaaag	aaactatctc	aatagccatc	cgtatttttg	1144680
ataacgttat	tgacctgaac	ttctacccta	caccagaggc	taaacaagcc	aacctaaact	1144740
acagagctgt	gggggtgggg	gttatgggat	tccaggatgt	tctttacgag	ttgaacatta	1144800
gctatgcctc	acaagaagct	gtcgaatttt	ctgacgagtg	ctcggagatc	atcgcatact	1144860
acgctattct	agcctcgagc	ttactcgaga	aagaacgagg	tcacatagct	tcttattcag	1144920
gatctaagtg	ggatcgtggg	tatctaccct	tagatactat	cagagcttct	aaagaaactc	1144980
gcggagagca	taatgttctt	gtagacacat	caagtaaaaa	agattggact	ccagttcgtg	1145040
atactatcca	gaaatacggg	atgagaaata	gccaggtcat	ggcaattgct	cctacagcaa	1145100
cgatctcgaa	tatcataggg	gtcacccaat	ctatagagcc	catgtataaa	catctctttg	1145160
taaagtccaa	cctttccgga	gagtttacga	tccccaacac	ctacctgatt	aaaaaactta	1145220
aggaattagg	actttgggat	gcagaaatgt	tagatgatct	aaaatatatt	gacggatctc	1145280
tattggaaat	tgaaaggatc	cctaatacct	tgaaaaagct	tttccttacg	gcattttgaa	1145340
tcgaacccga	gtggattata	gagtgtagct	ctagaagaca	gaaatggatt	gatattggag	1145400
tttctctaaa	tctgtatctt	gctgagccag	attgtaaaaa	actctccaat	atgtatctca	1145460
cggcttggaa	aaaaggatta	aagactacct	attattttaag	atctcaagct	gcaacatcag	1145520
tagagaaatc	atttatagat	atcaataaac	gcggcattca	gcctcggttg	atgaaaaata	1145580
aatcagcgtc	cacaagtatt	gtggtcgaaa	gaaaaacaac	ccccgtttgt	tcaatggaag	1145640
aagggtgcca	atcttgtcaa	taacggaaaa	aagaggagct	aaaatggaag	cagatatttt	1145700
agatggaaag	ctcaaacggg	ttgaggtaag	taaaaaagga	ttggtgaatt	gtaatcaagt	1145760
agatgtcaat	cagctagtc	ctatcaagta	taaattgggt	tggaacatt	acctcaatgg	1145820
atgtgcaaac	aactggcttc	ctactgaagt	tcctatggca	agagatatcg	agttgtggaa	1145880
atcagatgaa	ctgtctgaag	acgaacgcag	ggtcattttg	ttaaacctag	gattttctcag	1145940
taccgcgga	agcctagtcg	gaaataacat	cgttcttgct	atcttcaaac	atatcacaaa	1146000
ccctgaagca	agacagtatt	tactgcgtca	agcttttgag	gaagccgtac	atacacatac	1146060
atctctctat	atcttgcaat	ctttaggact	tgatgaaggc	gaagtattca	atgcctataa	1146120
tgaaagagcc	tcaattaggg	ctaaagatga	ttttcaaatt	acattaacag	tcgatgtcct	1146180
tgatcctaata	ttttctgtac	agtcttcaga	aggccttggg	cagttcatta	aaaacttagt	1146240
aggatactat	atcattatgg	aaggaaatct	cttctatagt	ggttttgtaa	tgattctctc	1146300
tttccataga	caaaaataaaa	tgacaggaat	tggaagacag	taccaatata	tcctcagaga	1146360
tgaaaccata	catttaaatt	ttggaatcga	tcttatcaat	ggaattaaag	aagaaaaccc	1146420
cgaagtgttg	actacggaac	tacaagaaga	aatcgctcgt	cttattgaaa	aagctgtaga	1146480
gcttgaaatt	gagtacgcta	aagattgctt	acctcgagga	atcttgggat	taagatcttc	1146540
gatgtttata	gattacgttc	gtcatattgc	agatcgctcg	ttagagagaa	ttgggttgaa	1146600
gcctatctat	cactccagaa	atcctttccc	ttggatgagc	gaaacatgg	atctgaataa	1146660
agaaaagaat	ttctttgaaa	ccgggtttac	cgaataccaa	accgctggta	atttaagttg	1146720
gtaatttcac	ctctttttca	agggagtttt	gagagatggg	cttagatcgt	ctctcaggat	1146780
ttttcagctt	tcccttccga	agaaagtcct	tagaaaaaac	ttcaagaagc	tttatacttt	1146840
cctaaagcaa	acagtctctg	atttctgctt	tttatgaaac	cccaagatct	atccccgcca	1146900
tttttatgga	aagaacgccg	tccttgattt	caagatggag	ttctctatgt	tcctagacat	1146960
tactttgaac	accgaatttt	ttcaacaagc	taccatcaag	aattttttca	aaatcatact	1147020
tctatagctt	gtgaactatg	ctctggtaat	ggggattggg	tagttgctca	agcgcaaaaa	1147080
gatcctcaag	tactttggat	cgctgtggaa	cagcggtttg	atagggtaag	gaaaatttgg	1147140
tctaaaatga	tcaaccacca	gatccaaaat	ttaaggattg	tctgtggtac	tgccgaaacc	1147200
tttttccagt	actatgttcc	tgatcagttt	ttgcaacgcc	ttgttggtga	ttttccagat	1147260
ccctggccaa	agatgcccga	tcgtaaacac	cgctctctcc	aacctcatt	cgttcaagaa	1147320
atctcccgtc	ctctccaaga	ttccgcagtt	tttgctttgg	ctaccgatga	taaaacatac	1147380
ctattggaat	ccatagaagc	gctgcaaaca	catttagctc	caagaatgga	aacaccatat	1147440

tatataaaaa	tgacagatac	ttatggaaat	tcttggtttg	aaaacctttg	gcggacaaa	1147500
ggacaggaaa	ttttttatac	agaatttata	aaaaaggctg	ggatatagct	gacttgaaca	1147560
gctgaccttc	acgatgtcaa	cgtgacgctc	taaccaactg	agctaatacc	ccgagttcag	1147620
ctactatcct	aactagaaaa	tggtatcttt	gcaataggct	tcttcatggt	tgcatatcgt	1147680
accctgctta	cacataatgt	agtccaggta	tcacacgaaa	tttttaaaac	cacagttggt	1147740
cccggagata	cagtcatgta	tgcgacctgc	ggaaacggta	acgacagcct	tttttttagcg	1147800
cgcttgcttc	aaggagaggg	aagacttggt	gtctacgata	tccaaaaaga	agcgttggtc	1147860
aatgctttac	tattgtttga	aacacacttg	tcagagcaag	aaagaagtgt	tatcgaaatg	1147920
aaagagcagt	cgcacgagca	tatttttagag	aaagatgtga	agctcattca	ctacaacttg	1147980
ggctatcttc	cgaaggga	taaagaaatc	accacattgg	caagaactac	agaaataagc	1148040
ttagaatatg	ctttaaacat	agtccgcccc	gatggactca	ttactgtcgt	atgctatcca	1148100
gggcatccag	aaggagaaaa	ggaaacacat	agtgtcgaga	gcctagcaca	acggttacat	1148160
cctaaggaaat	ggtgcgtgag	tcatttttatg	tagcgaatcg	gtgtcgagcc	cctagacttt	1148220
ttattttttca	gagacagggg	agtgaatctt	cggttgataa	gggataatgc	gaatctcgtg	1148280
ttccagatca	atgccttgcg	tttttaacgt	tgattggatg	atagctatga	gttgcttgac	1148340
ctcatcagaa	gtggccttgc	cagtattgat	aatgaagttt	gcatgcaacg	gagaaatttg	1148400
tgccccctcg	attgctaatac	ccttcaaccc	aggctgcgtc	aataagcttg	ccagcagaag	1148460
ttccttcagg	attacggaaa	atacagccag	cagaaggctg	cgtatagggc	tgcgtcatga	1148520
gccgatgttg	cagaatggat	ttcgagtggg	cggcagaaac	ttgctttttt	gaaagctgga	1148580
aggctcgtga	taaaataaac	tcttggtgtc	tatggaagcg	cgaggagcga	tagctcagct	1148640
ctaattcttc	tacagaatag	gaacaaagct	ctccttcaga	gttgattgtc	tcaacatttc	1148700
tcaccacgga	agatatgtcg	ctttcatttg	tacctgcatt	cataaaaatg	gccccgccaa	1148760
ccgacccagg	gatgcccgca	gcaaactcaa	gtcccgaata	tccattatag	gcagtcgctt	1148820
tacctaaagc	tgcaaaggaa	agaccggaat	acgctttaat	actagcatcc	tctaggaaact	1148880
gtttaccata	gattgcattg	tagagtacaa	agccatcaaa	accacgggtca	tcaaaataaac	1148940
aattagagcc	tttccctatg	atgaggaagg	gatagttgat	tgaatgtagg	aaacggataa	1149000
cttcacgagc	ctcctcaata	gtatggatgg	ctttaaagta	atgtgcaggt	cctccaatgc	1149060
ggaaagtgga	atacctattc	agccacacac	tacgacgaac	aggaaaaggga	aaatgcatag	1149120
gcgcagcttc	tttcattttt	agaatccctt	ggtctaaatt	aatcagattg	ataaagaatt	1149180
ttcattttaga	gatgaatctg	tgaaaatgtc	attcaaaatc	gcctgaatga	aaggacaggc	1149240
ttctgaataa	ctaaactttt	taactagacg	aattgcttct	gcaataagaa	tggccttggt	1149300
aatgggtggg	ctgtaaaaat	gctcaaagag	agtcaggcgt	aggacatttt	tttctacaag	1149360
atctaaacta	tcaaaagact	tatttttaag	agcattccca	ataattagat	ccaattcttg	1149420
tgatttttct	aaaatgcttt	tagtctgggt	taaagctacg	agtacgtgtt	tttgagacac	1149480
cgcagtttgt	gacataagca	aaggaactaa	actgtcctct	gctgaaggag	ccatatctag	1149540
ggcatacaac	atctgcaaga	tgatttctct	catcttttgc	tgagggaatt	ccttcgagat	1149600
cgaaataggg	gaccccgaga	attttttcagg	actcaatgtg	gccatgacaa	gcaacccaaa	1149660
aatagttaat	aatacacatt	taactgctaa	agaggtcctt	agctaaggag	ttgtgagaaa	1149720
gaaacaaggt	tatctattag	aaagttttaa	ttgcaacaaa	aacttcttag	ttgaaaaatg	1149780
tactttgttt	tcggaactca	cttattttct	gattcagaga	aagagttgct	ggagattttt	1149840
tatataaaaa	tttttaattt	ctaaagacga	caaggataat	tatgagaaag	ggatttccgt	1149900
tgcttttctt	ttcctaatac	cctaagatag	ccttcttctt	gtctagaacg	gataaaaagat	1149960
cggattgtct	tttctggaac	actcagtgtc	ttcagaccat	agcaattgtc	ttaacaggaa	1150020
attgagatag	agtgtggcat	taaattttta	gattaacagg	caaataagag	ctcctaagat	1150080
tcgtctcatt	ggttcagccg	gagaacagtt	aggaatactt	gctatcaaag	atgcttttga	1150140
tttagcccg	gaggcaggtc	ttgatttagt	tgaagttgct	tcaaatagcg	agcctcctgt	1150200
atgtaagatc	atggactacg	gtaaataaccg	ttatggtctg	acaaaaaagg	aaaaagatag	1150260
taaaaaagct	caacatcagg	tgcgcataaa	agaagtttaag	cttaagccta	acatagacga	1150320
aaatgatttt	tcgactaagt	taaagcaagc	gcgtacgttc	gttgaaaaag	gaaataaagt	1150380
caaaattaca	tgcatgttcc	gtggtagaga	attagcttat	ccagaacatg	gttttaagat	1150440
tgttcaaaaa	atgagtcagg	gttttagagga	tattggtttc	gttgaagctg	aacccaaact	1150500
agcaggctcg	tccttgattt	gtgttggtgc	tccaggaaca	gtaaaaacaa	agaaaaaaca	1150560
ggaaaagtct	catgcccaag	atgaaaacca	ataagtctgt	ttcagcacgt	tttaaatata	1150620
cagcctcagg	ccaattaaaa	agaactcgtc	caggggaagag	acataagttg	tctaaaaagt	1150680
cttcgcaaga	aaaacgcaac	ctatctaagc	agcctcttgt	agataaaggt	caggtaggta	1150740
tgtataagcg	aatgatgctt	gtttaaaggt	aaggaaagtt	agttatggta	agagcaacag	1150800
gttcggtagc	ttctagacgt	cgctcgtaaac	gtatatataa	acaagctaaa	ggtttctggg	1150860
gtgatagaaa	agggcattat	cgtcagagtc	gctctagtgt	catgcgcgct	atggcattca	1150920
attacatgca	caggaaagac	cgtaaagggg	atttccgtag	cctttggatt	gctcgtctta	1150980
atgtcgcttc	aagaattcat	agcctctctt	atagccgttt	aatcaacggc	ttgaaatgcg	1151040
cgaatatattc	tttaaacaga	aagatgcttt	cagaaatagc	tatccacaat	cctgaagggt	1151100
ttgcagaaat	tgcaaaccag	gctaaaaaag	ctttggaagc	cacagtttag	ggattagaat	1151160
ttctatggaa	atgaaagaag	agattgaagc	tgtaaagcag	caatttcact	ctgagttaga	1151220
tcagggtgaac	tcttctcagg	cacttgacga	tcttaaggte	cgctacttag	gaaaaaaagg	1151280

aatttttctcg	agtttctcag	aaaaattaaa	gcaatgtaca	gataaggcaa	aactaggttc	1151340
ccttatcaac	gactttaaaa	cttatgtaga	ggatctttta	caagaaaaaa	gccttggtgct	1151400
tcttgcttca	gaacaagccg	aagccttttc	taaagaaaaa	atagatagct	ctctccctgg	1151460
agattctcaa	ccttctgggg	gaagacacat	tttaaaaagt	atcctcgtatg	atgttgctga	1151520
tatttttggt	cacctaggat	ttgtgttcg	agaagccct	aacatcgaaa	gtgaagccaa	1151580
taattttacc	ttactcaact	tcactgaaga	tcactcgtct	agacagatgc	atgatacttt	1151640
ctatctaaat	gtacaacag	tactgcgaac	acacacatca	aacgtacagg	ctcgtgaact	1151700
aaagaaacaa	caacctccaa	tcaaagttgt	tgccccggc	ctatgttttc	gtaacgaaga	1151760
tatttctgca	cgttctcatg	tgctcttcca	tcaagtggaa	gctttttatg	tagatcacia	1151820
tgtaacgttt	ctggacttga	ctgcaatcct	cagtgcattc	taccattcct	tcttccaaag	1151880
gaaaacagag	ttacgtttta	gacatagcta	ctttcctttt	gttgagccag	gtatagaagt	1151940
agatgtctct	tgtgaatgtt	gtggcaaaag	atgtgcccct	tgcaaacata	caggttggct	1152000
ggaagttgag	ggagcgggaa	tgattcatcc	ccaagtacta	cgtaacggaa	atgttgatcc	1152060
tgaaatctat	tctgggtatg	ctgttggcat	gggaatcgaa	agattggcaa	tgttaaaata	1152120
tggcgtctcc	gatataccgac	tttttagtga	aaacgattta	aggtttttac	aacaattctc	1152180
ttaaggaaga	atggcagagc	ggtttaatgc	acctgtcttg	aaaacaggag	acctgaaagg	1152240
gtccgggggt	tcgaatccct	cttcttccgt	tctcttttta	ttcacgttta	ttccgataga	1152300
ggaactttgt	ggctaagagc	cacgagtttc	tggtattcaa	cgagttcttt	ctttttcttt	1152360
ttgatttctt	gccttttctag	gtttcatagt	ttttattaac	ttttaatttt	ctctttatta	1152420
attatttata	tctaaatcta	ttatttttat	ttttaaacta	attgatgggt	aattttgttt	1152480
tataataaat	tagaaagacg	atctcataaa	aaataatcta	acttttttgg	ttccatcgag	1152540
gaggtagaat	gaaaagggtct	cgacgtaact	tcgaacaggc	tttagaaaat	ttagaaaagc	1152600
tcaaagagat	ttcttttagct	acctcgaatg	attcctacct	aaataatcca	gcacgcttca	1152660
accagagaaa	acaaacaggc	tcttctgtca	tggaatgaa	agaggctctg	aaaaatgttg	1152720
aaaattatct	actcgaaatc	agctgtgttt	cgaaaagtca	tgagataaaa	gctcttaaag	1152780
aatcagattt	tttaattgca	ggtgtgcaaa	acgtcttttc	cttttttagag	aaccaagaag	1152840
acctctataa	gtctttacta	gacgaatatt	ctgaagttac	taaggcttat	gatgaggtaa	1152900
aaaagaatct	taaagaagtc	ccaacttatg	acctctcgac	agatgaagaa	accgaggaac	1152960
acaaagaacc	cgagtgtctt	ttaaataacc	ttgttgaagt	taagcgggac	cgttcctatg	1153020
agcttttcta	catgctagat	gagcaagaca	aacgctttta	taacgatgct	cttgctccaga	1153080
tcactataaa	gcaaaataaa	ctacacgaaa	ctgtaaaatga	agggtgaccc	ctaactaaaa	1153140
cactcctctg	gaatagtga	gaagttaaaa	acattgcctc	ttcgctgggt	atcgtaaatg	1153200
atatgcctct	gcgattgttt	tatcagcgtg	ctttaagcca	tttagacatc	gaagctgtgg	1153260
tcaaagttca	taacgcagtc	atggcgttgt	tcttctcaag	atacgaagct	acaatgggtct	1153320
tcaaaagccc	taagaagcat	aatatatggg	actttaatga	ctttttgctc	tttttgagag	1153380
aagcatggaa	agacttaaat	aataacgtga	ttgattctca	agagagaaaa	cagacgaaac	1153440
ttcttgcttc	cgctttaagt	ctcgggatct	ttgaaagcaa	actagtattt	gaagaggcat	1153500
ctcgttatct	ctacttcaat	attcaaacga	aattagaaaa	cgccaacggg	aagaagcctc	1153560
tttcaccagg	acaatatctt	acagacgctt	atgaagaact	tcactcgtct	atctctaaat	1153620
atcctaacgg	gcctcttttt	aaagctatgg	atagagtttt	agaacatgaa	tcccgtccct	1153680
atgatcctat	gatttttagga	atcctcccta	gccttgaagg	aacgttaaag	ctccacggga	1153740
aatctataga	tatcatacga	tctcccagtc	ctgtgaccca	aagctcgatt	ttgtatgcta	1153800
attgtaatga	ggaattctta	gggtttctta	atgctaaagc	acatcgagct	gaggtgactt	1153860
tagttctaaa	tattcagaat	cgtatatcaa	gaaaagaacg	tgccggaagc	cgtgttatcg	1153920
aagaagcttt	agaacaagaa	gaacacgccc	cctatgtcca	cgcttctctt	ttccctgaac	1153980
ccgaagaact	cctccagaat	ttggaaaagta	ttcatggaga	tattgaaact	tttgctgatt	1154040
tcttttctat	tctgcaagaa	gagtttcata	aacctcttct	tgcttcata	tttttcttaa	1154100
cgaaagaatt	aaaagagttc	gtaggtagct	tcttaaaaga	aaaactcacg	gcgttgaaag	1154160
acattttctt	tgctaagaaa	aaaattctat	tcagaaatga	taagcttttg	cttctacacc	1154220
tcctctcgta	cctaattgtc	tttaagttaa	tagaacgtac	caatcccaac	tctattgtcg	1154280
tcgtatctaa	agatgggctg	gattatgttt	ctgtctttat	tgccgggattt	gcgttctttt	1154340
ctaggggaagc	gttttgggat	gaacatagct	tgaaactatt	acttacgaat	gttttatctc	1154400
ctacactcgt	agctagagat	cgtctgggtc	tcgtatccca	tattgaactc	ttaagtaaat	1154460
ttgtaaactg	tctaaagaaa	aatcgtcagg	gattttctag	tctgaagtct	ttctcaag	1154520
atgacattga	aggttgggag	ttcaccgggt	acttgcatga	actcactgaa	gttttcgcata	1154580
agcataattt	gtaagtagaa	agagtactat	aagaggaaaa	gccatcacag	gaagtgtggg	1154640
aagaacgctg	ctactggcta	agacgattcc	cgcttttagg	aagacaaaga	aaatatattac	1154700
cgcccctaag	gggatcaaat	aggctagagt	gaccgttggt	gttctactaa	atctcaaaca	1154760
gagataggca	gataaaatga	tagccgccat	acaggcaagt	gggtgaaatta	agacgtaata	1154820
gaattgagcc	agaagagaaa	gaatcctttg	tggcacttgt	gtcgagagtc	ctaaacctgt	1154880
agcgttccaa	gggatggcct	tgaaaaatcc	tgaaagacgg	tttttattcc	ctgcagaaaa	1154940
tagcttggaa	aaaggatttt	catagaaaat	aaactcgatc	tcaggaaaact	ccttcatatc	1155000
gaaaaactcc	ttaagctcaa	gattttctga	atcattagcg	aaaaattgtg	tgacatttaa	1155060
accaatcgga	agagagaggg	tggtgaacgc	taacttttcc	atgggtgtaa	tggttttagg	1155120

atcttttgatc	cagaagacat	tatttaaagt	aagcgtctta	ggctcaatag	agaatataa	1155180
gagtactgtt	tgatctttga	ggtaaagagc	aggaattttt	ccctgctctt	tatctgtcgt	1155240
gcctctatcc	atattttctt	tagtaataga	gattttctcg	caaataggat	gcaaccactg	1155300
gaaattcgca	tagagcacca	tcatgatcac	agctcccgaa	aggagaagag	gatgcattag	1155360
agattttaag	gagagaccag	aagcttgtag	aagaataatt	tctcgcttat	tttgcatagc	1155420
aaaaagcgtg	cttgtttgtg	ctactgcaac	aagctgaggg	atgaggaact	ctgcttttaa	1155480
cgaaatctgt	gctaggtagt	acaatataga	gagcttgaca	gaagctccag	aagcagctgt	1155540
agaggcccc	ttaaggggtat	gcaaagagtg	atgaatggaa	gcatagaata	taagagcaag	1155600
taccaaagaa	gaggttaagt	caaaccacaaa	tctagttagt	aagtggcggt	tccaaatcaa	1155660
catacgttaa	gcataccctc	gactttccct	atacgcgcg	gcagcaaaga	caaccacaga	1155720
gaccaattgg	gggaagacaa	atagcatgaa	ggctaggggt	agattttttg	tatttttccc	1155780
aacgataagc	agaataaggt	ccaaaatagg	gaaaatgaaa	tataaagcta	tagattttcg	1155840
aatcttaggt	ttatgaattc	caaggatcat	gccagcatat	gtcagcggtg	tacagagaaa	1155900
accaatagca	actcttcgga	gcgtttcagg	aagatgagag	tgcttttagg	actgtttaac	1155960
aagctgcttc	caaggcagat	agtctgtccg	tgtctttaaa	taagattttc	ctgcaaacaa	1156020
tggtgaagta	atcttgggaa	ttagcaattc	atctaagggt	tcaatataga	atctttgaga	1156080
agatggtgag	gaagattctg	ttaacgagtc	tgggaagcttt	gagataaaga	ccacatcctt	1156140
agctttttaca	gtatcttttag	tagtgtcagg	gatgatactt	tttataattc	ccacatggga	1156200
gatctcatta	tttcttttta	gagctacaat	gacattgtca	aacttgcttt	tagcacaatg	1156260
atctacagcg	atgaaaatac	gattgttttc	ttttttctgt	agagtctgta	agagcagggc	1156320
tggtgatgtc	attgccatgt	ttgcaatttc	cttgcatgtt	tgatagcgac	aaattgaagc	1156380
aagctctgag	catgtgtaaa	agtttaaaca	gcaaattggct	ccagaaacca	tcaaacacag	1156440
aaacatgatg	atgcttttag	aagctccaga	cgctctttag	aacgtcatgt	ggttggtatc	1156500
tgataattta	cggaaaagag	agaatgctga	gacaaaacaa	gagccaggga	gaataaagg	1156560
aagaaggtag	gggatttggg	aagccattaa	acgtaagact	gtatcgtaag	gaacgtcttt	1156620
agcaatgtag	gcaacaattt	cctgtagaga	gctaattata	gaaatacaaa	ttaagcttaa	1156680
ggtacagaaa	gctgctgttt	ttaagtaacg	gaaaatgaga	actttccata	aaataggcat	1156740
ggcttacctg	gtaattacaa	tttcttagat	gccttgatag	agtgaagag	tcacgatctg	1156800
ttttgaaaaa	tccctagcaa	cactattctt	ttcaatgatt	tttatatagg	cgtataaaat	1156860
ggtactaagc	tcagattttac	tccgtgatga	taagcaatta	gatctttttt	ttgcttcttt	1156920
agatgtaaaa	aaaagatatt	tgcttgctct	ttctggagga	agcgactctc	ttttcttttt	1156980
ttatctactt	aaagagcgag	gggtttcctt	tactgcggta	catatagatc	atggttgag	1157040
gtctacctct	gctcaagaag	ctaagaggtt	agaggaaact	tgcgctcgtg	aaggtgttcc	1157100
cttcgttcta	tatactttga	ctgctgaaga	gcaaggagat	aaagatttag	agaatcaggc	1157160
aagaaagaaa	cgggtatgct	ttctttatga	atcctatcga	caattagatg	cgggaggaat	1157220
tttctctgct	catcatgcca	atgatcaagc	agaaacggtc	ttaaaacggt	tgtagaagag	1157280
cgcccatttg	actaatctca	aagctatggc	ggaaagatca	tacgttgaag	atgtgttact	1157340
tttacgacct	ttgttacata	ttcctaaaag	ctcgttgaaa	gaagctctag	acgctcgagg	1157400
tatttcttat	ttgcaagatc	cttcaaatga	agatgaaagg	tatttaagag	cgaggatgag	1157460
gaaaaaactt	ttcccttggc	ttgaagaggt	ctttggaaaa	aatattacct	ttcctttact	1157520
aacttttaggt	gaagaatcag	cagaactatc	cgagtatctt	gagaagcagg	cacaaccatt	1157580
tttttctgcc	gctacccatc	aagattctca	aggagagctt	ccctgtccag	actgcctcat	1157640
tcaacaagcg	tttttatgca	aatgggttat	gaagaaattt	tttaataatg	ctggaattgc	1157700
tgtttcaagg	cattttttgc	aaatggttta	tgatcattta	tctcgaggtt	cttgcgcaac	1157760
tttgcgcatg	aggaataaga	tagtaatcat	aaaacctgga	gtagtagtga	tagattagaa	1157820
agtatatact	cattatcttc	tctatatgtg	aaaaaaagag	agaacactag	gtcattgtat	1157880
tagtgccctg	tcataattttt	tatttggtcg	ttatagttta	aaatattttt	tctaaaacaa	1157940
aataataaaa	aatatgttat	attgaataat	tatccgtctg	attgattagc	ttagtgtgta	1158000
agttttatgtc	gaaagataag	aaaatgaaac	ctgaaccgaa	aaaaaatttc	cctacagtct	1158060
ttttttttct	tttgtttggc	gtgggtttttg	gtgtagtcgc	atttcaaaat	tttctagctg	1158120
gaaagaaggc	tagagtcggt	ttcagtcatc	aaatcgagca	ccttggttaac	ttacgtctga	1158180
ttgttccaga	agatagccat	aagatagctc	ttaatgacaa	ccttagtttct	tttggcgagc	1158240
gttttctgtg	tgtccaaact	caagaaggac	aactacgtta	tcattatcta	gagcttattg	1158300
atcagggcca	tcggttagac	cttgatcttc	aagagacgag	caagagtctt	acgaccttag	1158360
ggaaaagaggt	cacgaattcc	atactttggg	tttctgcaat	ttctggatcc	ccgattcctg	1158420
aacaagggtg	tgccatttct	tatccgagtg	aagtcagcgg	ctctgtattg	acagaaccctc	1158480
tcgttggttac	aggacctgca	actccacagc	taatcaatct	ccactctctg	caggagcggt	1158540
atcctacact	atcacgatct	ccagaagctt	tacgcacctt	tggatccgat	ctttatgagt	1158600
taataggaaa	atatctatct	cctgttttag	gaataggatc	tgagacgcta	aaaagagaa	1158660
ttaaagatct	ctaccagcaa	gtggaagtct	ccttaactca	ggagacggat	acggaagcag	1158720
cctacaccct	ttatgggcag	gttcttagta	ctttgaacag	gatctcttct	tcttttagtcg	1158780
tgtctgaggg	aggagaacgt	ttttctcaac	tccgttctgt	acgtctctat	cgggaggagt	1158840
ggaataagta	tcataaattg	gtggaagcgc	gcgatctgaa	tcaagcgcaa	ctagagaagc	1158900
tccgtggtga	attaagccag	acagtttggt	attttaataa	ccaagagctc	tcctccccta	1158960

gtttagagaa	acaagatcct	gaagtttttg	gccatttggt	tgccggggct	aaggaagagt	1159020
ggactgcctt	taaattttaac	cactccctat	catttaaagc	tccagaccaa	ccaagaaatc	1159080
tcgttttaga	gaaaacattt	aagagccaag	agccttcgcc	acatnattta	ggatatcttt	1159140
tcacantcct	acctatcatc	ttagttctac	tctttgtcta	cttggtgttc	tctcgtcaga	1159200
tgagaggcat	gagtgggtct	gcaatgtcct	tcgggaaatc	cccagcgcg	atgctcctta	1159260
agggacagaa	taaggttacc	tttgctgatg	ttgctgggat	cgaggaagct	aaagaagagc	1159320
tcacgcgagat	tggtgacttc	ttgaaaaatc	ctaataagtt	taccagttta	ggggggcgta	1159380
ttcctaaagg	agtcctcttg	ataggacctc	caggaacagg	aaagactttg	atagctaagg	1159440
ctgtatctgg	agagggcgac	cgcccccttt	tctccattgc	tggttctgat	tttggtgaga	1159500
tggttcggttg	agtcgggtgct	agccgtatcc	gtgatatggt	tgagcaagca	aaacgtaatg	1159560
ctccctgcat	tatctttatt	gatgaaattg	atgctgtagg	acgtcatcgt	ggtgcccgtta	1159620
ttggtgggtg	tcagtgatgaa	agagaacaga	cattaaacca	gcttcttgta	gaaatggatg	1159680
ggtttgccac	caatgaagg	gtcattctta	tggtgcaac	aaaccgtcct	gatgtccctag	1159740
ataaggctct	attgcgcccc	ggacgtttcg	atcgacgtgt	tgtaatgaac	cttcctgata	1159800
ttaagggacg	ttttgagatt	cttatggtag	atgccaaagg	aatcaagtta	gacccctactg	1159860
tagatcttat	ggcgtgggt	agaagtaccc	caggagcttc	tgagagcagat	ttagagaatt	1159920
tattaaatga	ggctgcctta	ttagcagcac	gtaaggatcg	aactgcagtg	actgctgttg	1159980
atgtcgctga	agctcgtgat	aaagtctctt	atggtaaaga	gcgtagaagc	ttagagatgg	1160040
atgccgaaga	gagaaaaact	acagcgtatc	atgagtctgg	tcagtcctgt	gtagggcttt	1160100
gtgtacagca	tgagatccct	gtagataaag	ttacaatcat	tccaagaggg	ctctcttttag	1160160
gagctactca	tttcctacca	gagaaaaaca	agctcagcta	ttggaaaaaa	gaactttacg	1160220
accagctcgc	agtgttgatg	ggaggtcgtg	ctgctgagga	gattttcctc	ggagacattt	1160280
ctagcgggtg	tcagcaagat	atatctcagg	ctacaaagtt	agtcgtagt	atggtttgtg	1160340
aatggggaa	gagtcctcag	ctaggaatg	tgacttatga	tgagcgttcc	gatggcttga	1160400
caggctacgg	tggttatcat	gaaaagagct	attcagaaga	aacagcaaaa	actatcgata	1160460
cagaattgag	aatgcttcta	gatgcggcat	accaacgtgc	gttagatatt	attaatgagc	1160520
ataaggcaga	aatagagctt	atgactcaga	tgctcattga	attcgaaact	cttgattcta	1160580
aagatgtgaa	agaaattatg	gaccatactt	gggatccctga	gaagaagaga	gcacgtctaa	1160640
aagaagaagg	gatgctattt	aaaaagtctt	ccgacgatct	tcctcctcct	cctcccaagg	1160700
aagacactct	acctggtttg	gggttttaag	ctacgtagg	aggaatacct	caagatgcac	1160760
tctgatccga	aaagaacctt	ggaaatcctc	ctaggttctt	ttttgtctc	aattgaaatca	1160820
gattagagtt	agatgtaatc	ataaaaaaag	ctagtctttc	taagaagact	agcttttcat	1160880
gttaagcgta	tagaatagaa	tgtatgtgaa	agattattct	agagttgctt	tatggctcaa	1160940
cttaagttga	cctttttcat	tgatgcttaa	gagttttaca	tcaatgatat	cgccttcctt	1161000
aacaacatca	cttatatttt	ctattcgtcg	tctagaacac	tcagagatgt	ggcagagtc	1161060
ttcttttccg	gggagaactt	caacaaaggc	tccaaacgca	actacggaag	ttacgcgacc	1161120
tctgtaggtt	tttccaaact	caacttctcc	aactaaacct	tcaatgattt	ctttagcttt	1161180
attgatagct	gatgctgagg	acgcagagat	gctaacaact	cctaagtcgt	taacatcaat	1161240
ttggacgcca	gtctcttcaa	tgatctgacg	gatttgcttg	cctcccggcc	caattactga	1161300
agcaattttt	gttggtttta	tttgcatgtg	ttcaatacga	ggcgctgatt	gagataggtc	1161360
tgctttggga	gctgaaagg	cttcgttcat	aatattttaa	atatcattac	acccttgctt	1161420
cgcttgggaa	agagctttct	tcagatagc	tggtgtgatt	ccttcaactt	tgatatccat	1161480
ttggaaggct	gtaattcctt	taccactccc	tgctatttta	aagtccatgt	ctccaagggtg	1161540
atcttcaaga	ccggaaatat	cagaaaggat	aatcgctcct	tgatcatcaa	ggatcaatcc	1161600
catagcaatt	cctgcaatat	gagaagaaat	agggacgcca	gcgtccataa	gagcgaggca	1161660
accgccacat	acagaagcca	tggtgaaga	accattagat	tctgtaatat	tagattctat	1161720
acggatggta	tagggaaatg	tagcgtatc	aggaagagca	tgacttaaa	gcttctctgc	1161780
caatttgcca	tgccaatttt	ctctccttcc	tgagagccg	attcttctta	cctctccaac	1161840
agagaaggga	gggaagaagt	attgtaagta	aaattttgaa	agtccttcac	cattcaaatc	1161900
ctcatagcgt	tgagccattg	cctcactgcc	taaagtacat	accgcaagt	tctgagtctc	1161960
tccacgagtg	aagaggcagc	ttccgtgagt	acgaggaagg	taagaagttt	caatagtaat	1162020
aggacggact	gtagttaaag	aacgtccatc	tgacggatc	tctctatctc	ttatgagagc	1162080
acgcatcgtg	tcagatttta	aagttttaca	tgccgctttg	atgttaaaa	aagagaaaag	1162140
atcatcatct	tcgcgctgta	atttttctaa	aatattttct	tcaatctcat	gcgcagtagc	1162200
tgcatgtact	tttttatctt	taatatttaa	gagttcagta	aacttgctct	gcgcagctc	1162260
tttcacagct	gttaaaactt	ctgcaggaag	aggatataca	gcacttagat	tttttagattt	1162320
tccaacttct	tcttgccaca	actgtaatct	tttacagatg	gtaacaatat	gcttggtgacc	1162380
aaattctatg	gcatcaagta	cttgctcttc	ggtaaagaaa	tcgcaatgac	cttctatcat	1162440
tagaatagcg	ttttctgttc	cagctaatac	aagatctaaa	gtagaggatg	ctaactcagt	1162500
ttttgtagga	ttgatgacct	attgggtatc	aatacatcca	atccgtactc	cagcaacaat	1162560
gttgctctgt	ggaatatctg	aaattgctaa	agcagcagat	ntgcgcagat	agcaagagga	1162620
tcaggtaaaa	cttgaccgtc	atacgaccat	acataagata	aaacttgac	atcttgcatg	1162680
agtcggtagg	ggaaggaagg	acgtagagac	cgatcaatca	atcgagaaac	taaaatttct	1162740
ttttcagagg	ggcgctcctc	tctttttata	aatccaccaa	gagttttccc	tggtggaagag	1162800



aatttttctt	ggtagtcac	tcgtaaagga	agaaagtcta	ctttgtcatc	aagatctaca	1162860
gcgcatgcac	ttgcaaaaac	acagggtttcc	cctgaacgga	caagaacagc	tccggttagct	1162920
tgacgagcaa	ttttccctgt	ttcaaacacc	aatatatttac	ttcggtcaga	ttaatagaaa	1162980
tagtttgaaa	attcatgaag	gtctcctgtt	agatatttgt	aaaggggaacg	aaaaaactac	1163040
ttacgtagat	tcaatcttgt	aattaaattt	ttgtaccttt	cgggtatctgt	agaattaaga	1163100
tactccaaga	gctttctcct	ttgaccaaca	agcttaagca	atgctaagcg	ggagtttttg	1163160
tcttttagggg	atcttttaag	atgttctttc	aattccttgc	ganatgttcc	gtgagaatag	1163220
caatttgtac	atctgccgat	cctgtatcct	tttcatgaag	ttgaaacttc	tttgtgattt	1163280
cttccttagt	tcctttatcc	aaagacatcg	gatgtctcct	taaaataatt	gccgcaaaag	1163340
ctgattatac	ttgagaacat	ggttaatgta	caccttttgg	tagggtaaga	cttttttttc	1163400
tataaacaaa	gaaaaaatta	ggggctgtgg	aaaggctctga	gattgcttca	taaaagcggt	1163460
ttattgatat	tgtatattgt	tatttttttt	gttttttagaa	ctcataatgg	aataaataat	1163520
attatttaga	attgggtgga	gagaagctta	tcaatatgga	aaaagatatt	ttttttatgc	1163580
aacaagcctt	caaagaagcg	cgtaaggcat	atgatcagga	tgaagttcct	gtgggctgtg	1163640
tgattgtcaa	agacgataag	atcattgtct	gtgcgcataa	ttcagtggag	aagcttaagg	1163700
atgctacagc	ccatgctgaa	attttatgta	tagggctctgc	ggcccaagat	ttagataatt	1163760
ggcgtttgg	ggataccgtc	ctttactgta	cgtagagcc	gtgtttgatg	tgtgcgggtg	1163820
cgattcaatt	ggctagaatt	cctagaattg	tctgggcagc	tccagacgtg	cgtttaggag	1163880
caggaggaag	ttgggtcaat	atctttactg	aagagcatcc	tttccatacg	gtttcttgta	1163940
ctgggggctg	gtgtagcgag	gaggcagagc	atctaatagaa	aaaatttttt	gtagaaaagc	1164000
gcagagagaa	aagtgaaaaa	taaaattggt	acattatttag	atcagctcta	cgaggatcag	1164060
gagtcacgac	ttcagaagtt	aggagaggaa	attgttcccta	acctcactcc	tgaagattta	1164120
ttgcaaccta	tggattttnc	tcaattggaa	gggaatccgg	catttcggtt	tgaagagggt	1164180
gtcttatcag	gaatttggtga	ggtgcgagct	gcgattttta	acggcgctct	ctcaagagaa	1164240
ctagaatctc	aaagaagtag	tataggggtt	ggggatcttt	tcttttttac	aaaataggat	1164300
agccagaacg	atcgcaagca	tcgatgagag	gagtagaagg	aaggcccttg	agaaaataag	1164360
aatgcaacag	tagaacccta	agacgaacaa	gaatccccac	tttattgaga	cggatagggg	1164420
agtgggtcct	atggttaaagc	gcttttctgg	atctaagaag	atctgtactg	tcaaacacc	1164480
acagataata	ctttccggac	cgaagaaaga	ttgggagctg	tgatgagagc	catgaatccc	1164540
cagagaacag	ctcctataat	gagtgcctgg	cctgagatta	caacgagaac	actgaaggct	1164600
cccaatttgc	ggatgagggtg	ttggatagct	ttatagaaaa	gaaaaaaatc	caagcatattg	1164660
cgcaaaagaa	gtctttgggt	gatttcgaag	ctttgatctt	tatttaggga	tagggaatct	1164720
gctgtgatta	gggggtagggt	gagaaactgc	caaaaatggt	gtttctgtat	ccctttaaca	1164780
gagagggcta	gaatttcgag	gagcccagga	attccaaaaa	atttatttat	gatataagag	1164840
aaaaacgggg	cgatacacga	agtaactaat	ataactgaag	gaagtttttt	taaaagcttg	1164900
gatagggttg	ggaagtatt	atgtttatcg	gggaaaatca	ccctcatgga	ggctttacct	1164960
gcaatctgac	ggtcaggccc	ccatagtaga	ggatgaattg	ttttattaga	agtctattgt	1165020
catagtttag	tcagaggggtg	agttcggttag	atttgccttg	attgttagtt	cctttagggt	1165080
agagagcatg	gagctgggtg	ctttagaagt	ttgcatggat	tctatgggtg	ttgagtttac	1165140
agacttttgg	tttgccctgtg	ctctttgttg	tgccgagag	agctcctgtt	gtatcatttg	1165200
acgatttgct	gagatctgtt	ggtttagact	ttggtaggct	tggatttcat	tttggttctt	1165260
atattcgtea	tcgcttccat	cttttttctg	tagatcgggt	actttaagta	aggggaggtt	1165320
aatgagctct	ttcactcttt	gctgttggtg	tattgtatta	tcttctagta	cggctaagat	1165380
tgatttgccg	tactctgttg	tggattcaga	gagccgaagc	atgacggaga	tgcaaaagta	1165440
gaatgcagac	tgtttgttaa	ttgtgatgga	gtcagaaatt	actttttag	aatcaggaat	1165500
cactttatcg	gcttttagttg	ttgtattaga	gacgggttgt	atcgacatga	gttcctctat	1165560
acttagatgt	tagcaattag	gcttacaatt	tgagagaagg	ctgggataag	agcctgtcct	1165620
acctgtaagg	attgttggat	gatgttatta	tttgtgttca	agttactgga	gattacctga	1165680
gccgcgtttc	ctaaactgga	aatttggttt	tggatagctt	gccgagaagc	tcctatcgct	1165740
tggttatcgg	attggatgtt	ttgtagatag	ctagaggagt	tatcgttcag	tttattttta	1165800
ggaataactga	cgtattggta	taaggcttct	tggttattta	ggtaggtttg	agctgaagag	1165860
tttgcttgga	gttcttgggc	aatgatggag	aggttatctt	gagcaactaa	tacggattga	1165920
tagacgtagt	aaacagtaac	aatcagaggg	tttgagtctt	tggagaattt	tgcaatgata	1165980
tcgtcagcag	ttgctgtatt	aggctcctct	gtaattggag	tgccaggaac	atttatggct	1166040
gcttcttagag	gtntttttgc	tgatagaggg	tcatatgcc	acataattcaa	cctaactgggt	1166100
tttcgatttt	aaaaatgttta	cggatgggtt	taattcctta	tcctagggggt	ttattcagtt	1166160
ggtttacgggt	gcttcctatg	gagtttggtg	ttttgataaa	tgaggagtct	tgtgaggatt	1166220
gctgttggat	gatgttaatg	ttttagagag	cgtgtgagag	gataatttga	ccgttttgct	1166280
ttgttggtac	gagttcgtct	tggatattag	atctttgtgc	tgagtagttt	tggttctgat	1166340
tttgactctt	agtgatctcg	tcttcttttg	ctccagcact	tactattgca	tacttgattt	1166400
gattagtttc	ttggtttaaat	tgttggtgaa	tatttagtatt	gtcgtttaat	tgttggtgatt	1166460
gagtcagaac	tgtttggtgt	cgaatttcaa	ttgcttgtaa	aagaagctcg	taaatgctaa	1166520
aaagcacagc	acctattttta	ggtgtattta	gaggctcaag	gggaggacga	gaactgttta	1166580
tagtattaac	tgtgggaaga	gtcccctaagg	tggttataga	cataataaaa	aaattcactt	1166640



ttgttttagtt	ttatttctaac	aagaagaaaa	acgttttatta	aaataaaaatt	tttatgatttt	1166700
ttcttttatta	gttggttatta	agtgttttgt	ttttttataa	ttaataagaa	atttttggcgg	1166760
cccagagaat	attgggtact	agattggagt	aagaagagct	taatatgggt	cctaattggag	1166820
gcattttag	actccctagt	tgtggtataa	atcttttagct	ggagaggaga	aggacgtgtc	1166880
tgggaatgag	tgcaatgact	atccagaagt	ttttaaagat	gacgtaagt	cttacgtatt	1166940
ggtaacttgt	ggtcagatgt	cttctgaagg	caaaatccag	gtggagatga	cttatgaagg	1167000
agatccagct	gtgatcagct	atttattaac	aaaagcacga	gactcttttag	atgagtcctta	1167060
aactattcat	ttattgggat	gttgaaaccg	atgtacgtgc	ttagcaaacg	tcttttatcga	1167120
tgggtaaatt	aactaattaa	attaggggat	ttggtaaaga	actcacgac	attttctgtg	1167180
gaatgggttt	ttatcagcgc	tctgttggtg	atttttggat	gtttaggctg	cgcactctgtt	1167240
gttaaagt	cttttagttcc	ctttctatta	ctattttcgt	tttttagcgtt	tcctctgatt	1167300
ttatgttttc	gtgggaagg	ctatgctttg	cttctggggg	tttttgtaac	tctttatgtc	1167360
gctaagtatg	ttgttggaga	gacctatat	gtctcttttt	ggttatcttg	cttaggagtc	1167420
tccttttttgc	ttgcttttgg	gcttttcttc	caaggagtgt	ggcttgctca	agaagaagag	1167480
atggtaaagg	ggaaggagca	actcaggctt	tctgaggatt	tggatgcaca	acgtagtgtc	1167540
tatgaagatt	tgctgctgac	aaagagtcag	gagaaggagt	ttttagatgc	tcgtgctcag	1167600
ggtttagatc	gggaacttac	tgagtgtcag	gagcttttga	aagcggctta	tcagaaacaa	1167660
gagtatttaa	ctatagattt	gaaaattcta	gcggaccaaa	agaacagttg	gttagaggat	1167720
tacgcggaac	tccataataa	gtatatcag	ttggtttcca	agaatgggga	tggtgtattt	1167780
ccttgggtag	cagagccttc	agtaggtgaa	agtcagggtc	cagagagggt	ggatgtttct	1167840
agatgggtag	cggctttaca	ggagaaggaa	gagagttag	agcgtctacg	aaatgagatt	1167900
ttagtagaga	agcagcgttg	ttctgattat	gaacaccgtt	gtcaagagtt	gggccttttg	1167960
ttgcaaaatt	tactgctct	tgaaaggaga	tgtgaggagc	ttcaaaacct	tttaaatcag	1168020
aaagaaacgc	agataaatga	gctccaccaa	ttggtctgta	aatctgaaga	gaagggtctct	1168080
gtggaacctt	ctgcacatgc	tgaaacgagt	tgtgtggaag	aaaaacagta	taaagggttg	1168140
tattctcagc	ttcaggagca	gtttctagaa	aagagtgaga	ctctttcttt	agtaagaaag	1168200
aagctttttg	cgggttcagga	gaagtatttg	actttgaaga	agaaggaga	actcacaaag	1168260
caagacatat	cttttgatga	tatctctatg	attcaagggtc	tcttagagcg	catagagatt	1168320
ttggaagaag	aagtcagtc	tttagaagag	ttagtatctc	gtagcctgtc	tctgtaattg	1168380
ctatagtgtg	ttcccattgt	gcgctgggtt	gattatcgca	tgtgcgtgct	tcccattgat	1168440
ttttgggggtc	tacaacgcct	tctttttttc	ctacattaat	cataggctct	atagtgaaga	1168500
tcaccccttg	tgctagagga	atcatggagc	ggtttctata	atgtggcacg	taggggtttt	1168560
cgtgaaactc	aattccaacg	ccatgtccta	caaattgggtc	tactacagaa	aatccatagg	1168620
tgtctgcacg	tgcttctata	gcttctccaa	tttcacagag	gggaatacca	ggttttaaaa	1168680
tggctataga	atcgtttaaga	cattccaaag	ctgcttgga	tatcttcttt	ttaatctctg	1168740
gcacctctcc	gatcatgacc	atgcggttac	agtctccata	gtagccatcc	acaatgcagg	1168800
acacatctat	attcatgata	tcaccgtctt	ttagtgggat	atcgtagga	atcccgtgac	1168860
agatcacttc	gtttaatgat	gtgcagattg	tttttggaaa	tggtggtgag	cgtaatgga	1168920
atggagcggc	aatcgctga	tatttcttat	ggagctcttg	ggagagctca	tccaactcat	1168980
ttgtagttag	gcccttttga	gatgctttgc	atagctcatc	tagaattctt	gctgtaattt	1169040
ggcaggcgtt	atagattttt	gctttctgtt	ctgggggtttt	gagtaggata	ttatattgcg	1169100
aggcgtagt	ttgttttaag	gcttctggag	acatttttgg	gggttgaggg	tagtggcact	1169160
gtttccattt	acgtccactg	ccgcaccagc	aagggtcgtt	tcttttcata	aggatcaccc	1169220
gatgtaaaag	cctatatata	acgctattga	gatccctttc	aacataaggt	ttaccgacat	1169280
aagtagtaaa	gcaataaccga	agagtctctc	gagtgcgagg	agtccgaaat	ttccagaaag	1169340
gcggtcaaa	aagctagagc	atagcagagt	aaataaaaga	aatgccagg	cgataatcat	1169400
agcagtaaaa	ataatttccc	tagagttagt	tccctcttcc	atgtagctaa	ggagtgtgt	1169460
aatcacagca	gggcctgtga	ttactgggaa	agctaagggg	aaaaatatag	gttctgtttt	1169520
ggaagtatca	tcttttagctt	tttctggcat	gggtgccagc	atcattttta	tagagactgt	1169580
aaagaggaga	aagccgccta	tgatctgaaa	agcgtagaga	gaaatatcca	agaattggaa	1169640
gaagcttctt	ccaaaagtaa	cgaagaggat	gagggctccg	agagcaaaaa	ggcattctct	1169700
taggatcacc	cgttgttggt	tctttctaga	aaagtttttg	agcaaagcaa	caaagacagg	1169760
aatggagcct	ggagaatcga	acaggacata	aaatagttag	ctaagattga	gtaagattga	1169820
cataacttat	tctataaaaa	tgcttgttgt	aatcctgaga	ctaggagtgt	ggtaccacaa	1169880
attgttacaa	aaagtcctaa	aacggtttgt	gtagctagga	gtactttgtt	ccctttgcag	1169940
aagatctgaa	gagaaaaggt	ggctagggta	atagtagacc	agctgagaat	taggatttgg	1170000
aaattgatca	gagtattgtg	atttctcgct	atgagtgtac	agcaagctgc	taaccagagg	1170060
gtccaaacat	taaagggaga	gctattggag	aatgacacgg	agaatatgag	ggggacatat	1170120
tgaatttata	agggatccag	gattcttctt	ttcccaatcg	caaaacagct	cggactcctg	1170180
ctagtgttac	cgcaattcct	ccgacaactt	ctatagcgca	tacgggggta	ttcaataactt	1170240
tcaggcctcc	gagagcgagt	ccgtaaagag	caaacatagc	gatgaatgag	aagaagcttt	1170300
ctctcagtag	aacaagcatt	cgctgtttta	ctgaataatg	cgcgaggaga	tggtgtagcg	1170360
ctaggatatt	agttaaagag	tctgaggcta	gcagcagaat	gcatgtttgg	ggcaagaaaa	1170420
aagaaaactg	tatcatgggg	taatttttta	acctcatttc	ctattatttt	caagggaatc	1170480

ctctagagga	tacttcggaa	ttgggagagt	ttatcgaggt	ttgtataaat	tttattttata	1170540
ggtaatat	tttagaacag	ggtgtgagtt	acacactctg	ttcttctggt	agtacggat	1170600
tgtagaggtc	gttttagagaa	aacttcgcga	cttctgaagc	aagttcggga	taccgtttaa	1170660
tgattgtttc	gaggagtttg	tctacaaggt	ctttgcttaa	gggatcttgg	gactgagcta	1170720
ggagggggaa	agtttcctcc	cattggagat	actcctgata	gagattttta	ggtatgcttt	1170780
tagtttcttt	agcgtagagt	ttaaaagcat	cttcgggggtg	gtctttttgag	aatatgatgc	1170840
tttcttgaag	agcttttttg	aaagcttcaa	caatttcggg	ttcgctagct	ttcgttcctt	1170900
tttttagtaaa	gacaatcaac	tgggggcctg	tgggaagatc	acaggatatcg	gagagaaagc	1170960
atttcacggg	catgcctaaa	gtttgttaatt	ttactccttc	aatattgtag	aaagcgccgt	1171020
agaggaaatc	aattttgttt	aataacatcg	gagagatgag	atcagaactt	acattttttga	1171080
cttcagaggg	aaccacaccg	ttacgattta	aggtttcaag	tagacgattt	agatctctgg	1171140
agttgtttaa	gcagaaacct	aagactttgc	catttagggtc	ttcaaatttg	tagatggggt	1171200
cctgacttct	gtagagaaat	cttgcaggga	actgtctatc	aatctcccta	cgattttgtat	1171260
tggcatgcct	tttatggagg	tcttcatgat	gccgagagca	tggtaaaggg	ccatatctac	1171320
ttgttcaaat	agaacgtggg	gaacagcaga	acctgagctt	gtattttttt	gaagtgtgag	1171380
atccaaaccg	tgttgtttga	agtatccttt	ggctactcct	gcatagaggg	gaatatgggt	1171440
aggattgggg	gtccaatcga	gtaaaagtgt	tagtgaagta	agattttttt	tgctcaggagg	1171500
agatttagag	tttccttttc	agggaaataag	cattatagga	attaaggcga	gtacggataa	1171560
agctttttta	gctacggatt	tgtgcttaag	gctcatccgt	tttactcgga	atagtgaana	1171620
aatcaatttt	tcaattaaca	aggtgatttg	gaagaggctg	agggtgagaa	ttgagagagt	1171680
cgcgagtcct	gcgaatgcta	attccatttc	ataattttctg	cggttttcga	gcataaggat	1171740
gccgagaccc	gattggggagg	ctacccattc	tcctgcaatg	gcagcaaate	ctgcagatcc	1171800
tatagcaatt	tttaatcccg	agaatatgtg	ggggagagcg	tggggaatcc	ggagtttgat	1171860
caggagttgg	aattttgtac	tccgcaaagg	acgaattgct	ctataagttc	ttctggtgtt	1171920
gataagatgc	cctgatagat	agtcagggtg	agcggaaaga	atatggtgag	tgctgtaggg	1171980
acgattacag	caccgattcc	ccagccaaac	caaagtacaa	tcagtggagc	cagagcaaac	1172040
ataggagtgc	actgtagcag	gatgaaaaga	ggttgtagga	gatcttttagc	tgattttataa	1172100
gacaacataa	ttgttgctag	aacaatggag	agagtaatcg	caaggaagaa	ccctcctaga	1172160
atcgctttta	aggtgtgcca	agcagatgtt	aacaagagtg	gaagggattg	gagagtacta	1172220
gaggcaatgc	tcgagggggg	agggcagaaa	aaggaaaacg	tgggtcgggtg	gcgtgacgtc	1172280
atctcccaaa	gaaatagcag	ggaaaaaacg	ataacaaagt	agaaaaataa	tttttttttc	1172340
atttttgaag	taattaacga	gaaaatagcc	taaatcaatg	gggaaatata	gatatgcgac	1172400
aagaaaagga	tagtttagga	atcgtagaag	ttcctgagga	taagttatat	ggagctcaaa	1172460
ctatgcgttc	taggaatttt	ttttcttggg	gacctgagtt	gatgccttat	gaggtaatac	1172520
gagctctcgt	atggattaaa	aaatgtgctg	ctcaggcgaa	tcaagattta	ggattttttg	1172580
attccaagca	ttgcgatatg	attgttgctg	ctgccgatga	gatttttagag	ggagggtttg	1172640
aagagcattt	cccttttaaaa	gtttggcaga	cagggagcgg	cacacaatct	aatatgaatg	1172700
tgaatgaggt	gattgcgaat	cttgccattc	gtcatcacgg	aggggtgtta	ggcagtaagg	1172760
atcctatcca	tcctaatgat	catgtgaata	agtcctcaatc	gtccaatgat	gttttcctta	1172820
cagcaatgca	tgctgctgct	gtgattgatt	taaaaaataa	gttaattcca	gcttttagatc	1172880
atatgattcg	ggtgttagat	gctaaagtgg	aagaattttcg	tcattgatgta	aagataggac	1172940
ggacccatct	tatggatgcg	gtgcctatga	cggtgggtca	ggaattttct	ggttatagca	1173000
gtcaattgcg	tcactgctta	gagagtatag	cattttcttt	agctcattta	tatgaacttg	1173060
cgattggagc	tactgctgta	gggactgggt	tgaatgttcc	tgaagggttc	gtggaaaaga	1173120
tcattccatta	tttaagggaag	ganacagatg	aaccgtttat	tccagctncc	aattattttt	1173180
cagcactgtc	ttgtcacgat	gcttttagtag	atgcccatgg	gtcttttagca	acttttagcat	1173240
gtgcttttaac	taagatagct	acggatttga	gcttttttagg	ttcaggacc	aggtgtgggt	1173300
tgggtgaggt	atttttccct	gaaaatgaac	caggatcttc	tatcatgcct	ggttaaagtca	1173360
atcctacgca	gtgtgaagct	ctccaaatgg	tttgtgtctca	agttcttggg	aataatcaaa	1173420
cagtgattat	tggaggaagt	cgaggaaatt	ttgagcttaa	tgtgatgaag	cctgtgatca	1173480
tctataaatt	cctgcagtct	gtggatctcc	tttctgaggg	gatgagggct	ttctctgaat	1173540
tctttgtgaa	aggattaaaa	gtaaaataaag	ctcgtttaca	agataaatatc	aataattctt	1173600
tgatgttggt	tacagcttta	gctcctgtat	taggttacga	caagtgttcg	aaagcagcac	1173660
tgaagcatt	tcattgaatct	atatctttga	aggaggcgtg	tctagctttg	ggatattctt	1173720
ctgagaagga	atgtgatcgt	ttagtgggtc	ctgagaatat	ggtgggaaac	cattagaatt	1173780
ttttaagag	agcgaacgct	gagtgtattg	taaagtaccg	tagcgtacgt	tttctcttcc	1173840
cttgttatga	aaatctttta	ggttgctttt	ctaggattta	gactaaatga	cgagttgaag	1173900
ttttgctctc	tagatttggt	agagcttggg	caaataaggag	agcactttta	atatttgaga	1173960
agatatgggtc	cacccaatc	agttcatcta	gatgataacg	tttcagggtca	gcaaggggag	1174020
ttttcttaac	tccagcgagg	agaagtaggg	tcccttgacg	atcacattcc	aagaaaaatt	1174080
cttcgagagc	atgcatagct	gaggcatcta	ttgtggggac	tcgcgtcatg	catagaataa	1174140
agatttttagg	gggtttttct	ataticattaa	gaagattctt	taatctatct	gcaattccga	1174200
agaagaaagg	accattaatt	tcgtagatct	ctgtgttttg	aggaacttca	gctttgctta	1174260
aaaagtctga	atccttatcg	aagtatttgg	ctgtggagat	cacatcgga	agatcactca	1174320

tttgtttcat	aaataagaat	gccgctagca	tcattccac	ttgtacagct	gctgtaatcg	1174380
ttgtcattac	cgtgaggatg	aagacagtga	ggagaaccac	aatatctttt	ttaggagcgg	1174440
taaagagatg	gataaagtgg	tggatttcgc	tcatattcca	tgcaatcaaa	atcaaaacgg	1174500
cagcgaggca	ggtgagagga	attttgacag	tgagtggggc	cagaagaagt	aaaataaagc	1174560
aaataaagat	ggagtgaacg	attcctgcta	tgggagttgt	tgcttcagac	ttgatgctgg	1174620
ctgctgtgcy	agatagcgac	cctgtgacgg	ggattcctga	aaataatgag	gttccgtagt	1174680
ttgctacccc	ttgggcgaca	agctgacagt	tggattgggtg	acgccatcct	gtcattcccg	1174740
ccgcgaccac	ggcagatagt	aaagtctcca	atcccataaa	gactgcaatg	gtcagagcgt	1174800
ctggcatcag	ttgaagaatt	ttggtgatgc	tcagttgtgg	gatttttaggt	aaaggaatcg	1174860
cggtaggtag	agttccgtaa	cgactgccga	tggtaggaat	atcgatttta	agtaaccaaa	1174920
cgagggtggg	cgccgttaca	attgcaatca	tgactccagg	atagcgaggc	ttgtagtttc	1174980
ggaagtagat	catgatcaat	agggtaaaga	gacccaccgc	gaaggactta	ctgtcccaag	1175040
tccataaatg	atcccagtaa	gctatccatt	tagggaggaa	atctgcagga	atattagctc	1175100
ccatttgtag	acccaggaaa	tctttaattt	gcgaggagaa	tataatgatc	gcaagctctg	1175160
tgggtgagtc	ctgtgacaac	gggatagggc	atgtatttaa	tgaacgtgcc	taagccagtg	1175220
agtcgaagg	cgataagaaa	gacgccggcc	agcaatgtga	cggtaaaaaag	cgctcagccc	1175280
ccgtattttg	cagataagca	gtataaaata	gaaataaagg	cactggatgg	ccctgaaatc	1175340
agaacgttac	ttcctcccat	agccgaagcg	agaaggcctc	cgataataga	agctaacagt	1175400
ccctgaattg	gggagactcc	gacaccaatg	gctatggcaa	tagcaaaaagg	aaaggctagg	1175460
attcctacag	taattcctgc	ttggaaatcc	tttttaaaag	tattaaacga	atagccttct	1175520
ttgatacttg	tgtagagttt	agggatgaag	tttttaaagt	cccaagggac	tttcacgatg	1175580
caataaccta	aagtagaagc	cagtgcctac	catttttttc	attcctttga	atctttgtca	1175640
aatggttcgt	gcaatttttt	aatctttttt	cttcataatc	ttctgtctagg	gatccgtaaa	1175700
agaataattt	caaaaatttt	tccttcttta	cctctgtaag	agttaggagt	aaagtagatc	1175760
acgaaatcat	tttagagggtg	accatgctga	aactacaatt	gtgtgcgcta	tttttatctg	1175820
gatatctcgc	aattgtcttt	gaacatattg	ttagagtga	taaatctgca	attgccttag	1175880
ctatgggagg	actgatgtgg	ttagtatgct	tctccacat	tcccatggcg	gatcatatga	1175940
ttttagtcga	agaaattgcy	gacatgtccc	aagtcattct	cttcttggtc	tcagcaatgg	1176000
ctattgtcga	gcttattgat	gcgcataaag	gattttctgt	gatcggttaag	ttctgtcgta	1176060
ttcagtcgcy	aaccctgctt	ctctgggctc	ttatcgggct	ttctttcttc	ttatccgcyg	1176120
ccttagacaa	tcttacatct	atcattatca	ttatctcgat	tttgaagcgt	ttagtgaagg	1176180
ctagggaaga	tcgcttggtta	ttaggagcta	tttgtgtcat	tgcaagtaaat	gcagggtggg	1176240
catggactcc	tctaggtgat	gtaactacaa	caatgttatg	gattaacaac	aagattactt	1176300
cttggggcat	tatacgtgct	ttatttggtc	cgagtttggt	ctgtgtgttg	gtcgtggtt	1176360
tttgtggtca	atttttcctt	cgtaaaccgag	ggagtactct	cattgccaaag	gatgtagagt	1176420
tacaatctgc	gcctcctaag	agtcctttgga	ttatttttat	aggttttaggt	tccttactca	1176480
tgggttcctgt	gtggaaggca	tgtttaggat	tgccctcctt	tatgggagcg	ttggttaggt	1176540
taggtcttgt	ctgggttaacc	agtgactgga	ttcactctcc	tcatgggtgag	gatcggtacc	1176600
atttgcagct	tcctcatatt	ttgactaaaa	tcgatattct	ttcgattacg	ttctttattg	1176660
gaattttgct	tgctgttaac	gcgctatctt	ttgccaattt	gcttacagat	ttttctctat	1176720
ggatggataa	gatcttttct	aggaacgtgg	ttgcaatcgt	tatcggattg	ctctctagcg	1176780
tattagataa	cgtaccttta	gtagctgnta	ccatggggat	gtacactctt	cctcttgatg	1176840
atactttgtg	gaaattgatt	gcttatgctg	cagnaaccgg	aggaagcatt	ctgatcattg	1176900
gttctgcagc	tgggtgtgcc	tttatggggc	tcgagaaagt	agacttttta	tggtacttca	1176960
aaaggatttc	ttggattgct	ttagccagtt	atttcggcgg	attgttttct	tattttgttt	1177020
tagagagcct	caattttttc	atttaatttt	ttatagggaa	acaacagaga	ctgtgcgttc	1177080
gggtttttcta	tgattttgtg	tattttttca	gataatgttt	ttaaaaaaat	gttttaaaac	1177140
cctaaaaatcc	tacctccttg	taaccattct	cggtagaaaa	gagaggtatt	tatgaaaaaa	1177200
gggaaattag	gagccatagt	ttttggcctt	ctattttaca	gtagtgttgc	tggtttttct	1177260
aaggatttga	ctaaagacaa	cgcttatcaa	gatttaaatg	tcataagagca	tttaatatcg	1177320
ttaaaaatag	ctcctttacc	atggaaggaa	ctattatttg	gttgggattt	atctcagcaa	1177380
acacagcaag	ctcgtttgca	actggtctta	gaagaaaaac	caacaacca	ctactgccag	1177440
aaggtagctt	ctaactacgt	gagatcatta	aacgattatc	atgcagggat	tacgttttat	1177500
cgtactgaaa	gtgcgtatat	cccttacgta	ttgaagttaa	gtgaagatgg	tcagtctctt	1177560
gtagtcgacg	tacagactag	ccaaggggat	atttacttag	gggatgaaat	ccttgaagta	1177620
gatggaatgg	ggattcgtga	ggctatcgaa	agccttcgct	ttggacgagg	gagtgccaca	1177680
gactattctg	ctgcagttcg	ttccttgaca	tcgcgttccg	ccgcttttgg	agatgcggtt	1177740
ccttcaggaa	ttgccatgtt	gaaacttcgc	cgacccagtg	gtttgatccg	ttcgacaccg	1177800
gtccgttggc	gttatactcc	agagcatatc	ggagattttt	cttttagttgc	tccttttgatt	1177860
cctgaacata	aacctcaatt	acctacacaa	agttgtgtgc	tattccgttc	cggggtaaat	1177920
tcacagtctt	ctagtagctc	tttattcagt	tcctacatgg	tgcccttattt	ctgggaagaa	1177980
ttgctgggttc	aaaataagca	gcgttttgac	agtaaccacc	atatagggag	ccgtaatgga	1178040
tttttaccta	cgtttggtcc	tattctttgg	gaacaagaca	aggggccccta	tcgttcctat	1178100
atcttttaag	caaaagattc	tcagggcaat	ccccatcgca	taggattttt	aagaatttct	1178160

tcttatgttt	ggactgattt	agaaggactt	gaagaggatc	ataaggatag	tccttgggag	1178220
ctcttttgag	agatcatcga	tcattttgaa	aaagagactg	atgctttgat	tattgatcag	1178280
acccataatc	ctggaggcag	tgttttctat	ctctattcgt	tactatctat	gttaacagat	1178340
catccttttag	atactcctaa	acatagaatg	atcttctactc	aggatgaagt	cagctcggct	1178400
ttgcactggc	aagatctact	agaagatgtc	ttcacagatg	agcaggcagt	tgccgtgcta	1178460
ggggaaacta	tgggaaggata	ttgcatggat	atgcatgctg	tagcctctct	tcaaaacttc	1178520
tctcagagt	tcctttcttc	ctgggtttca	ggtgatatta	acctttcaaa	acctatgcct	1178580
ttgctaggat	ttgcacagg	tcgacctcat	cctaaacatc	aataactaa	acctttgttt	1178640
atgttgatag	acgaggatga	cttctcttgt	ggagatttag	cgcttgcaat	tttgaaggat	1178700
aatggccg	ctactctcat	tggaaagcca	acagcaggag	ctggagggtt	tgtattccaa	1178760
gtcactttcc	ctaaccgttc	tggaaataaa	ggtctttctt	taacaggatc	tttagctgtt	1178820
aggaaagatg	gtgagtttat	tgaaaactta	ggagtggctc	ctcatattga	tttaggattt	1178880
acctccagg	atgttgcaaac	ttccagggtt	actgattacg	ttgaggcagt	gaaaactata	1178940
gttttaactt	ctttgtctga	gaacgctaag	aagagtgaag	agcagacttc	tccgcaagag	1179000
acgcctgaag	ttattcgagt	ctcttatccc	acaacgactt	ctgctttgta	aacgggacgt	1179060
aatagaataa	tttttattat	tgcttttaata	tgcgcgcttc	caatataagc	attgtgaagc	1179120
gcgtttcata	tgtcttttat	ctttaggtaa	ttattatgag	aaaacttatt	ttatgcaatc	1179180
ctagaggatt	ttgctctgga	gttgtgctgc	ctattcaagt	tgtagagggt	gcttttagaaa	1179240
agtggggagc	tcctatctat	gtaaaacatg	agattgttca	caatcgccat	gttgttaatg	1179300
ctttacgagc	caagggagcg	atctttgttg	aagaacttgt	tgatgttcct	gaagggtgaga	1179360
gagtcattta	ttcagctcat	ggaattcctc	cttcagtttag	agctgaagca	aaagcccgtta	1179420
agcttattga	tattgatgct	acctgtgggt	tggttactaa	ggtgcattct	gctgcgaagt	1179480
tatacgcaag	taaaggatac	aaaatcatat	tgatcgccca	taagaagcac	gttgaggtga	1179540
ttggtattgt	tggagaagtt	cctgaacaca	ttactgttgt	cgagaagggt	gctgacgtcg	1179600
aggccttacc	tttttagttc	gatacacctt	tattttatat	tactcaaagc	acgttgagtt	1179660
tggatgatgt	tcaggagatc	tcacgcgctt	tgctaaagcg	atatccctct	atcattactc	1179720
tgccatgttc	ttcgatttgt	tatgcaacca	cgaaccgtca	aaaagcattg	cgttctgttt	1179780
tatctcgcgt	gaattacgtc	tatgtggttg	gagatgtcaa	cagctcgaat	tccaatcgct	1179840
ttcgcggaag	ggctttgaga	aggggagttc	ccgctgattt	gatcaacaat	cccaggagata	1179900
ttgatacgaa	catcgtaaat	cattctggag	atatagcaat	gactgcagga	gcctcaactc	1179960
ccgaagacgt	agttcaagct	tgcattcgaa	agctatcatc	acttatccct	ggtttacaa	1180020
tggaaaaatga	tatatattgt	gtagaggatg	tcgtatttca	attaccaaaa	gaactccgtt	1180080
gttcttaggt	cttttaggctt	acttgccaag	tttttctcga	gattgcttta	tagagtcttc	1180140
ttctcgttca	gagagggtat	ttaccttttt	agttctctgt	atttgaaata	tcctagatta	1180200
tttttttatg	atcttggtaa	gtatgtctat	tctttaaggc	attgccctta	tgcaaagctc	1180260
ggtcgcttgc	caggagcctc	tttattgaaa	gaaggaaaacg	tctacggaga	gactccatgg	1180320
tctgttcttg	caaagatctg	tcaggctttt	gatattactt	ctcaagacat	tctctatgat	1180380
ttgggatg	gcctaggaaa	ggtatgtttt	tggttctctc	atgttgtg	gtgccaagtt	1180440
atagggatg	ataatcaacc	ccacttcatt	cggttttctt	caaacatgca	ccgcaagctc	1180500
tcttcaggat	tcgcgttatt	cgatactgaa	gagtttaaga	acgtagtctt	ctcacaagct	1180560
tcttatgtct	atttttatgg	ttcttcgttt	tcacgacgcc	tgttaaatga	gatcattctt	1180620
aaattatcgg	agatggctcc	aggaagtgt	gtcattagta	tttcttccc	tttagactct	1180680
ttctcaagg	ggaaggatg	tttctttact	gaaaagagct	gctcggtg	cttcccttgg	1180740
ggaaagacaa	tagcatataa	aaatattcga	aaaggctctt	aattctactg	atacagactg	1180800
cgagcagcgt	catgttctgt	ttggagaatg	ttcagaagga	aattgtccat	acttttccag	1180860
ttgtctttga	cttccctcaat	ggtacgtgtg	acttcatcct	gtctcattct	gaagacttct	1180920
tttctgtact	cagcaacagc	tcgtacagca	ctctctgata	actcatgtac	tttagaagcg	1180980
gcttcagtaa	gttgtgatag	agaggtgaaa	acttttcccta	ttccttttaa	gaaggttttc	1181040
gcagtcgcat	ctttgaatct	ttcagaaatc	ctttggacaa	accctaaaat	gctatctccg	1181100
gaaattttct	caaccatagg	agcaatcgct	cctaaaatac	ctaacgttgc	tgctcgcatc	1181160
cctagccagc	gggcgtattt	agcttgacgt	gaataactcg	ccgccaattc	atgagcttcc	1181220
ctttccatga	gctctctttc	ttcaagacgt	gtcattgtgt	cgttagctct	acttttgagc	1181280
atcaacttca	ttagctctgt	acatattcta	aggacatcaa	ggttggtcac	acgctttcct	1181340
gcaagcacgc	ttagctgtga	ttcagacaaa	gcaaaactca	caataggatc	aggaataata	1181400
ggagtataag	actcgtacac	ctgggttcgaa	cttgaaagct	gtttagagag	ttccacagt	1181460
caccatgggt	tctttttctt	gccttctctt	tgctcttggt	cttgctcgta	tccttcttgt	1181520
tgcttttgat	ctcgatgttc	ttcatctttt	tggttggttt	ttgtagagga	tagtgcttga	1181580
ggtacttctt	tatgtaaggt	gctatagagt	gacatcggtc	taagagtcgc	atcagactta	1181640
gtttgtgtgt	gtttttgtgt	ctctgccgac	ttggtgcttt	gtgagacttt	ttcttttagca	1181700
ctatgttctt	ttatgggtgt	gctagaatag	gaccttacat	gaaattgtgc	ttggctttga	1181760
gaagcgcttg	cttcttgttg	ctcttgtgct	tttgggtgtt	ggacagacac	tgtgaacgtt	1181820
ttgtccacac	tggagtctcc	ttcaggagct	ttgcatgaga	aaaacggaaa	ggaagacgag	1181880
gttgtttctg	ttgatgcttt	ccctgtggaa	ttcgaagatg	tggtattctgc	gtaaggggat	1181940
ttctatgtga	agctaagcta	gtctgctg	attgtcctgg	ttttaggttc	ggcagagatg	1182000

tégatecgc	taatatgcc	ttttttacta	gaaattgctc	ttcttgtaat	ggttttttcc	1182060
ttgggaggca	gtgcttggt	caaagcacat	tccgattgtg	tnaaaatccc	aaaacatagc	1182120
tcggaagttg	ctctcagcat	cgcataattg	tctcctgcag	ggagagctac	ttgtacttct	1182180
gcagcaacaa	cagcttcttc	agtggcattt	ccatctacaa	aaatatcaaa	ctctccttca	1182240
ggaggaggag	tcgatatgga	ttggtaagat	acagtcataa	tatntcttct	gtggatttat	1182300
cctcttaagg	agtggagata	cacttgatct	agttcacgca	tgtaattdaa	gattcttgaa	1182360
agggtctcga	aagaactctc	catgttatct	aaaagttctt	gagaacgttc	gtaatgatcg	1182420
tccttatcaa	aacttttcaa	ttcaatgtcg	agttggattt	tagtgagttt	tcctttgagt	1182480
ttatagattt	ctgcttgaga	aaacagtata	gcgcattctt	aagcagccat	cgtagattct	1182540
atcgcggtt	ggatttcctt	aatagctcct	tctataatag	gggaaaaacc	taaattttct	1182600
acttttaatg	tgcataatga	gagaatgaca	gggtttaa	agacgacca	ctggattatg	1182660
gttataat	ttcgtcttag	ttcttcatta	tttataggca	gatgtttttc	tagccaatcc	1182720
cagaacttta	gtttctctaa	acacttgata	acaagagaaa	ttagccctgc	aaaaaaacct	1182780
gcaaaagcaa	agataaccgc	tccactcaag	atagcaacaa	tgccgatccc	tatagaaaca	1182840
aacggagcta	gccaaccgat	aatgtcagaa	agagatcccc	ataatctttc	tcgtttttct	1182900
ttctcgatgc	agctctcgat	ctcttttcat	gtagagcatc	gagctctcgt	1182960	
tggtgcgact	ccacggaatc	tttgtggcat	ccatacgaag	aaaagtctga	aagaatccct	1183020
tgttttgtga	gtagatagct	caatgtaaac	actcctatgc	ttggaggagg	aattacagga	1183080
acagcttggt	ctgctttggc	tattctat	ttacgtgatg	tatcttggtg	gaaaggggat	1183140
ttcttttgtt	tttgattgga	atcctgatcc	tgagaaaaga	ggtctttaca	gagatctttt	1183200
atctgaactt	tggtttctat	ttttttctca	gaactctgct	ggtttgcata	ggtttctactg	1183260
cgctcttctc	ttcgtgattg	gaggagtctt	tgctgttcac	tatctaggct	ttgagaaat	1183320
agcgagtcaa	cgtttccaaa	caacttgaga	tggtgttgta	ggtgcagcgt	atcaaaat	1183380
ttgcaagagc	cttcttggtt	agaactcagg	tttttatcta	gagccttctc	tgaagttttc	1183440
tccggagatt	ttggcatagt	cagttcttgc	atcagagctt	tacttgcttc	tggtctat	1183500
ttttgagaaa	aaagattcca	aggagatgaa	gtttgagctt	gcatgtgtgt	gtgaagtga	1183560
gattcgaaag	agctgccgaa	acgcaagatt	ctctctcttg	gtgttgcaat	aatgaatgtt	1183620
ttatgatggg	tgataggagg	ctcagactta	cattgtgact	gaaatctctg	agtgaanaac	1183680
ttgggaagag	acttttgagc	ttcttgaggc	gctacagtga	tagaatagct	aatcttagga	1183740
accgaagatt	cttgtgacct	aggagcatca	gggatataag	gatcttgatt	gagaagaacc	1183800
tcacttgctt	gagataacca	agaggacata	gttgagtttc	cacattat	atgttttcga	1183860
atatctagaa	tttcttctt	caattcatta	tagaggggct	tggtgtgtgc	acgtaccac	1183920
gccatttcta	aaagcttttc	agcttcttca	tggtcatttg	taagagtata	gcataatgtg	1183980
gcataagta	gaggataggg	atctttatct	cgaaggactg	cagtgcactcc	ataggcatgc	1184040
aaagcttggt	aatattgttc	ggacatatgt	agagaggcac	ctaaagaaaa	ccaaaactta	1184100
gagacaaaag	gattgaagaa	aactaaccag	cgaanaacgg	tgatgctttt	agcatagtct	1184160
ttgtcgagat	aggcgtgata	accctcttta	tatacttttt	caagatcttc	ggaggatctc	1184220
ttgaagatct	tttggttaggt	atctaaagct	atatttttat	ccgggacata	tccttccaaa	1184280
tagctttcca	aatcatctgg	gaaagggag	tcttctctgg	aagatgcagc	gattttttct	1184340
agtaataaat	ttaaatgtga	cattaggggc	gtagggtgta	aatgaagggtg	tccataagtt	1184400
ctttcaataa	cttcaataca	ttagagcgcg	cttgatgaca	ttgagaaatc	tcttgagggt	1184460
gcctttgcat	gtccgtcctt	tccatttgag	tgattttctc	catattctct	ttgcgcattt	1184520
ggacattctc	ttttagaagt	cttttttctt	cttctgtcca	agtatatatt	tctttgtcta	1184580
tagtgactcc	aatctcttta	gctcgattta	aaagagcttt	catctcttca	ttttcactcc	1184640
aatcaatgtc	tttcttttca	ttattgatct	tagagataag	gactgtgagt	gtgtctacat	1184700
catcggtacg	ttgtttgact	cgcagttaga	gttcattagc	ttcggcttcg	gcttgcccta	1184760
agattccttg	catgagcttc	atgaacctta	agaacacatt	ttctactttt	ggagtgtgta	1184820
taggcncgtg	tattgaagag	cctacagata	acggattctt	actagggatg	aatctgctaa	1184880
acacagacat	tgagagaagg	agcttctttt	tgaatgtcgt	ttctttntta	gaagtctctt	1184940
cagcaggagg	tcgcatttga	tctgagaaga	ttaaagcggc	aatatctaga	ttttctccgg	1185000
gttctctcag	gactgcctct	acaccgagac	cacgtttctt	ctttttcttt	ttagattcag	1185060
cgtcttcttc	ctgatcgtgc	tttctgtcgt	gctgctctct	ttgttggcga	tcttgatcgc	1185120
gttctttata	gagttcatga	gattttgagg	tcgtcagggc	ctctttttgt	ttctctgcag	1185180
agaactggga	tagaggagag	aaggagcttg	ctttttgttg	ttctaatagt	gttctttctg	1185240
gcgcactttc	ttgcggagggt	aaggatctct	gagaacttga	gcttgcttga	gataaggaag	1185300
cgcgagcttg	tgtctcagggt	gacggtcttc	gctgtgtttt	cttacagcag	agtcttttgg	1185360
tgtttgaaga	gcttgctgtt	gtttagaatc	agaaatttca	ggtttttaagg	agcgtgggga	1185420
gagagcagat	tgtttactgc	tgctttgttg	agggagggtc	tgctcactcc	tactttgcgt	1185480
ttgtgtttct	tggtgttcac	ttgtgattgt	ctctgcatgt	tccaattgca	ctagcaagtc	1185540
aacaacttgg	atttctaatt	ctacaacttc	aggagggagg	aagaggagtt	gatgaacatt	1185600
tgtgctttgt	aagagcagtt	cttgttgggt	cgcaagaatg	atttgcctta	aagctaacgt	1185660
aattaaagca	tctgtagaag	agcttctctc	tagcgtgta	caagagacta	agacttcacc	1185720
tggtgcagtc	tttaaatattc	cagaggctgt	ggaaactgtt	gagctgtctt	cttttagagt	1185780
tatatttgca	gaggggaactg	cagaaggaac	aggcatattc	atgatttgta	atttgagtgc	1185840

gtagaaaaaa	aaggaaaaatt	agctaaaaaca	tcatttttcct	gcaagtttga	ttgtaagcgg	1185900
tttagaggga	aagagaaaaat	aaaacaaaaa	tccaaggggt	tttgtttgca	aaaaacactc	1185960
taactataga	gaataaatgg	gtcagtttca	tgtctttgac	aaagatgctc	tgcccagggtg	1186020
gtgaaattgg	tagacacgct	ggatttttaga	tccagtgctt	tcgggcatgt	aggttcaagt	1186080
cctatcctgg	gcatctcctt	ttctaattctc	tttaaatcca	cctaaaattt	gctattcgta	1186140
gtaaaataaa	atctaaggggt	tagattttttt	tagagatctt	tattatgaag	aaagtcgtaa	1186200
cactatccat	tatatTTTTT	gcaacgtatt	gtgcatcaga	gcttagtgct	gtaactgtag	1186260
tggctgtgoc	tttatcagag	gctccagggg	agattcaagt	tcgtcccgtc	gttggtctgc	1186320
aatttcaaga	agaacaggggt	tctgtgcctt	atagtttttta	ttatccttat	gactatgggt	1186380
attactatcc	agagacttat	ggctatacta	aaaatacagg	tcaagaaagt	cgcgaaatgtt	1186440
atacccgatt	tgaagatggc	acaattttttt	atgaatgcga	ttagagattc	ctgggggtgat	1186500
gggcaagaaa	cttctcgatt	agagaatccg	cggctacgtg	agtatacact	tctgtagagg	1186560
cgatgcgtgc	gtgacctaac	atctcttgaa	tgacgcgtag	gtctgcctta	ttgtctaata	1186620
gatgtgtagc	aaaggcgtgt	cgtaaggagt	ggggagatac	gggctttgag	gtcacttgct	1186680
ttgcgtaatt	gtgaatacgg	cgccacacac	agagcgttcc	gagcttggtg	ccccgggtag	1186740
agaggaaaag	atgatcttctg	tgaggattctt	ttttctggta	ttggtctcgg	aaaggacaaa	1186800
ggtagcgatc	gatagcttctt	cttgctcgag	atcccagagg	caccagtcgg	gttttagaac	1186860
ctttcccggt	gacgcgggatg	caatcatcag	agacatggcc	taaacgtagg	tcacaaagtt	1186920
cagaaacccg	gacaccagtt	gaatatagtg	tgtggagaat	ggctgtatca	cgaaaggcta	1186980
ggtgtcgggg	gtttttctctc	atltggagag	gaaccgcaag	tagagcatcg	acttcttgag	1187040
gagtcagtag	tgaaggaaag	cgtttccata	tttttggtg	ctctattatt	gggggatagg	1187100
gaagaagttg	ctgatctttt	aagaagagaa	aaaatacttt	taaagcaatg	agcctacgag	1187160
ctaacgtagt	ctctgcttct	ttacgtctat	atagttcttc	agcaaagata	tatacgctgt	1187220
tttgtagaat	atcttggggg	gagctaattg	cacttatggt	aaggaaggaa	gagatgtctt	1187280
ggcggttaagc	cgctatagat	tggtggcaaa	ggccgcgac	tacagataaa	aacaatgaga	1187340
attgttctag	aatcgttgtg	tgaaactgag	tcgagggcat	agtcatactc	gctaacgaat	1187400
gtaacttttag	tataggggagc	ggagaattttt	caagctacag	agagaaaacc	atggaaagaa	1187460
aaagattttat	agattgcat	tcaacaaaga	tactccaaga	gcttgcttta	aatcccctag	1187520
acctaacagc	tcccgggggt	ttatctgcag	agaggatcaa	gaagttttct	ttgctaggag	1187580
ggggattttac	ctttagcttt	gctaccgagc	ggttggagca	tgctatttta	gctgcattga	1187640
tctcattagc	agaagaaagg	ggattgcatg	agctctatgt	agcgatgcag	caggggcagg	1187700
tcgtgaacta	tattgaagg	tttccaaggt	aaatgcgacc	tgctctgcac	actgcaactc	1187760
gggcatgggt	aaccgcaggt	tcatttacag	gagaagctga	agatatcgcc	gtaagatctc	1187820
gggtggaggc	gcaacggctt	aaggattttt	taaccaaagt	gcgcagccag	ttcacgacca	1187880
tagtgcatag	aggaatcgga	gggtcggagc	taggccctaa	ggcactctat	cgggcccttc	1187940
gtgcgtactg	ccctacagat	aagcacgtac	atttcatatc	caatatagat	cctgacaatg	1188000
gcgccgaggt	gttagatacc	atagattgtg	ctaaggcttt	ggtagttgta	gtatcgaagt	1188060
cagggactac	aatagagact	gcagtgaatg	aggccttttt	tgcaagattat	ttcgcgaaga	1188120
agggctgtgc	atttaaggat	catttttatag	cagtcacttg	tgaaggcagt	cctatggatg	1188180
atacgggtaa	gtctctagag	gtctttcacc	tttgggagag	catcgaggga	agatttttct	1188240
ctacctctat	ggttggagggt	gttgttttag	gttttgctta	tggttttgag	gtttttttgc	1188300
aattacttca	aggagcctca	gctatggatc	aaattgcttt	gcaaccgaac	gctagggaga	1188360
atctccctat	gctttcagct	ttgattagca	tttggaatcg	aaatttctta	ggctatccca	1188420
cagaagctgt	cattccttat	tcttcagggt	tggagttttt	cccagcgcac	ttgcagcagt	1188480
gttgcatgga	atctaaccggg	aaaagcattg	tccaagatgg	tagaagggtg	ggatttttcta	1188540
cgagccctgt	catttgggggt	gagccgggaa	ccaacgggca	gcattctttt	ttccaatgccc	1188600
ttcatcagg	tacagacatt	attcctgtag	agtttatagg	ttttgaaaag	agccaaaagg	1188660
gtgaggatat	ctcatttcaa	ggaactacat	cttcacaaaa	gctttttgcc	aatatgattg	1188720
ctcaggcgat	tgcccttagca	tgtggctctg	aaaatacaaa	tccgaataag	aattttgatg	1188780
gaaaccgtcc	ttcttcgggt	ttagtgtcta	gccagctgaa	tccgtattct	cttgggggaat	1188840
tactttctta	ctatgagaat	aaaatcgat	ttcaaggggt	ctgttggggg	attaattctt	1188900
ttgatcagga	aggggtctcc	ttgggttaagg	cattggcaaa	ccgtgtttta	gagttgcttg	1188960
agggggcgga	tgcttccaat	ttccctgaag	ctgcatcggt	gttaacgctt	tttaacatca	1189020
agtttaggta	aaaattacac	tatcctttca	taagtctacc	tcagagagag	gtttttctta	1189080
aggttcttta	ttgtccgtct	gtgatataat	gtcccttttg	atttggaata	atttggagg	1189140
ataggatgtt	tttcattgca	gtacgctctc	gtggattttt	agatattcat	ggatattttag	1189200
ccgctcgtaa	gggtaagcaa	gtagtgaat	ctactgcggg	cgcatggata	gggtctcggtg	1189260
gcgccgtatt	ctacagcctg	gtttcgtaat	tttaataaaa	atattccgta	tctttgttga	1189320
aatatgccag	gttctgtgtc	atcacctcct	ttgtctcctg	taattgtccg	tgaaaggggtc	1189380
ccatcctctt	caggatccga	cctcatacag	cctcatgctg	ttttaaagat	ctccatccta	1189440
atttttgcgc	ttgtgacaat	tttaggaatt	gttctttagt	tgtctagtgc	tttaggagct	1189500
cttcttagtt	tagttttgac	ggtttctggt	tgtattgcaa	tagctgtagg	cctgattgggt	1189560
ttagggattc	ttgtgacacg	gctgattctc	ctacgatca	gaaaagtaga	tgccatgggt	1189620
tatgatgctg	cgggtcaagaa	agagcagtat	ttgtcacgta	tcagagaatt	agagtctgaa	1189680

aatagagaga	ttagagatag	aaatcgtgct	gtcgaagatc	agtgtgcccc	tttatccgaa	1189740
gagaacaagg	accttaggga	tcccgaatat	ctacatggaa	tgactgaaag	gtcatttgcg	1189800
agcttagaaa	tagagaatca	agctctcgta	gctgagaaca	ttcttctcaa	agactggaat	1189860
gcaagcctat	ctagagattt	ccgcgcata	aagcaaaaat	ttcttcttgg	ggcatttagaa	1189920
ccctggaaa	aagatattgc	atgtatcatg	gaacaaaatc	tcttttttaa	accggaatgt	1189980
atcgcgatgg	ttaagtctct	tccattagag	acgcaacggc	tgtttttata	tccaaaagga	1190040
tttcagtctt	tagttaatcg	atttgcctcg	cggctctcgct	ttttccagac	tccaaagtat	1190100
gaatataaca	gtaggaatga	aaatgaggac	ggaaaggtag	ccgcagtggt	cgcccggttg	1190160
aaaaaagaat	tcttcagtgc	tgttttagga	gcctgtagtt	acgaagaact	agggggcatt	1190220
tgtgaaagag	cagtagcact	taaagagacg	ttgccattgc	ctgaagctgt	ctatgatacc	1190280
ctagttcagg	agttcccaaa	tcttcttact	gctgagagtt	tatggaaaga	atgggtgcttc	1190340
tattcctatc	cctaccttcg	tccctatctt	tctgtggatt	actgtaagag	gttatttgta	1190400
caactttttg	aggaactctg	cctaaagctt	tttacaacgg	gatctccaga	agaccaagct	1190460
ttgggttcg	ttttctctta	ctataggaat	catattcccg	cagctctggc	ctcatttggt	1190520
ttgccccgcg	ctgagacagg	ggggctctga	tttgtattgc	tacaaaaaca	agaaaaacct	1190580
ctttggagtc	aaattgaggt	gctggctaca	aggatatctca	aagataacct	cgtgagaaac	1190640
tcagaatgga	cgggctcttt	cgagatgatg	ttttcttata	acgagatgtg	taaggagatc	1190700
tccgaaggaa	ggattcgttt	tgtgaagac	tatgaaacga	ggcattccga	agaattccct	1190760
ccttcccttc	tctctgaaga	aggagagggc	gaagaattcc	ttctcctctg	ctctgaagaa	1190820
gaggtttcgg	ttcttgagcg	cccagatcta	gatgtagact	ctatgtgggt	ctggcatccg	1190880
tccggctcct	aagggacctc	tttaatcacc	tagagttcta	ttttcagaat	cttcatagta	1190940
gtaattttcc	taagatataa	ggtcttaaat	gagttctaga	ggtttttaga	tcttttttaga	1191000
gagcttgntg	tgggttttaa	atcttgataa	gaagatatcc	tagtgtttag	aaacccaaaa	1191060
atttagggtt	tgaatgaattg	gagtcctcga	acgacttttt	tttcaatttc	ttgttttggt	1191120
tctacttaaa	gactatagtg	attttttttg	aaggggtgct	gtatggcatt	caaagaggtc	1191180
gttcgtgttg	ctgtcacagg	aggcaaaggg	cagattgcgt	ataatttttt	atttgcatta	1191240
gccccatggag	atgttttttg	agtggatcgt	ggtgtagatt	tacggatcta	tgatgtgccg	1191300
ggtacagaga	gagctctctc	aggggtgctg	atggagctcg	atgacgggtg	atctcctctt	1191360
tnacatcgtc	tgcgtgtgac	gacatcggtt	aacgacgctt	ttgatgggtat	cgatggcgcg	1191420
tttctgatag	gtgctgtgcc	tgcgtggacc	ggtatggagc	gaggagatct	tttaagagca	1191480
aatggtcaga	tcttttcgtt	acagggggcg	gcttttaata	cagcagcaaa	aagagatgct	1191540
aagatttttg	ttgtagggaa	ccctgtcaat	acgaattgct	ggattgctat	gaaacatgct	1191600
cccagattgc	atcggaaaaa	tttccatgct	atgttacgct	tggatcagaa	tgcgatgcat	1191660
agcatgctcg	ctcatcgctg	tgaggttcct	ctagaggagg	tctcccgtgt	tgtcatctgg	1191720
ggaaatcatt	ctgcaaagca	ggttcctgac	ttcacacaag	cacgtatctc	agggaaacct	1191780
gcagccgagg	ttatcggaga	tgcagattgg	ttggaaaaaca	ttttagtaca	ctccgtgcag	1191840
aatcgtggaa	gcgctgtaat	tgaagcaaga	gggaaatctt	cggcagcatc	cgcactctga	1191900
gcacttgccg	aggccgcgcg	atctattttt	tgtcctaaaa	gtgacgagtg	gttttcttct	1191960
ggagtgtgtt	cggatcataa	tccttatggt	attcctgaag	acttgatttt	tggttttcca	1192020
tgtcgtatgt	tgccttctgg	agattatgaa	atcattcctg	gattgccttg	ggagcctttt	1192080
atcagaaaata	agattcaaat	ttccctggat	gaaattgctc	aggaaaaagc	tagcgtgtct	1192140
tcgttataag	cacaatgttg	tggggagtaa	gtatgagaca	atcattcgat	gaattaaagtc	1192200
aaaatgcatt	taaaaatatt	tttaataaac	agaggttctg	ctttattttc	tgcagtctct	1192260
gttgcttttg	ttttgtgttt	gcattgtttc	tgaagctctg	ctcacggctg	gctcctgaaa	1192320
tttctttgtc	gacattaggt	ttgggagctt	ttttctgtgc	ctttagtgtg	atttgcgctt	1192380
cagcgattat	cgtgcaattt	ttattgcata	aggagtctca	aggagaaacg	agtaagctct	1192440
gctgtgctat	taagaacacc	tggctcttct	tatggctttc	tcttcttgta	tccatgcccgt	1192500
tcttcattgc	tatggctgcc	gtagtcactg	tagctatgct	ctcttctttt	ttaggatctc	1192560
ttccttgggt	gggtaagtta	ttccatacag	tgttgatttt	cattccttat	ctatcgccaa	1192620
cggcactgat	tttacttttt	ttaggttctt	ttagctgttt	gtttttctgc	attccgggtc	1192680
tccataatca	agagtctata	gactatagga	aattgcctag	agtgttttct	tgggaatatc	1192740
cttcggcagt	ttataggggt	ggtgattgct	ttgggtccnt	tagccctatg	cagttgggtta	1192800
gcttttagatt	ctttttattt	gatgacacat	cttggtgaaa	ttgcagatat	acatacctgg	1192860
tcatttctag	ctcagatggt	tgtgcttatt	gttccctatt	ctttgatttt	aactcctgcg	1192920
gtttctctct	tcttttaact	ttcttttagc	ttttaccttg	caaagcaaga	agaagagaaa	1192980
gcccttggtta	aatagtaaat	agaaattctt	tagcaatata	agctgtagat	tttcgtagaa	1193040
ctgcctgagc	gagcatgtct	cctgtaatcc	cgtgatacag	gagtcctttc	gacccgagtc	1193100
ctcctaagaa	ccagagtttt	tccttaatcc	tagagatgac	aggaagacgt	gatttgctag	1193160
aagagcgcat	gccagcataa	cagtgcagga	cttgagcatc	tttaagtcct	ggaaatagcg	1193220
agagcacagg	aggcatgatt	tcctgatagg	caatagcggg	atcaggagtc	tcttcgggtt	1193280
ggttggtgtc	gaaagtcgcc	cctaaaatgc	aggatttctt	ttgtgtattg	gcgaccatat	1193340
atztatgagc	attgatactg	aatgagagca	tggcaagatc	tttaggccaa	ctgatctcca	1193400
gcaactgtcc	tttacttta	tttaccggca	tgtcttttaag	ttcaggaaga	atcgaggcgt	1193460
tggctcctgg	agtcactatg	atatgatcat	agaactcttc	aatatcggca	aggctctcaa	1193520



tgagctcatc	atagaattgt	gtccctaatt	tcatgcaggc	gtcagccaat	ccctgaatat	1193580
agagatcatt	atttagagtt	acccactct	ttatgaatag	tgctccgaga	tttgggggga	1193640
tgaccatact	gggaatggag	atttcgcaac	gagcctctc	ccaccattcg	acttcttttg	1193700
ggaattcttc	aacacgctcc	gtgaatagct	gagcttgatc	ctcgtcaatt	gccggtctta	1193760
agatcccttg	agaaatcaca	ataggtacgt	tgaggggctt	actagcgcan	tgtgattaac	1193820
gcgtgtgtag	cattgattcc	ttgatccctac	caggggaggg	ttgagagctt	ttttcctcgt	1193880
gaaagcatgg	aggagtccctg	aagacattcc	agaggctcct	tctcctaagg	gaataggatc	1193940
aaagagatcg	atagttgcag	tccctgggga	gtggagaagc	agatgccaa	ttacagagag	1194000
tctgcataat	cctgctccta	aaacggctat	acgcataaag	tgtaccttaa	atcaagtatc	1194060
gttacataga	ccttgtcttg	agaataagag	aataagggat	aaaagaacag	gggggaatct	1194120
ctctgattgg	gagataaaaa	tgtagaagat	gaaaacctga	ttcttaaggg	tgaatttttt	1194180
actatagaga	agagaattag	ggagaccccc	acggcataag	ccgtggggaa	ggatgaaagt	1194240
ttaattaaat	tttgattctt	cctgttgaga	ataggaagat	cgctgtcagt	gcaagaaggg	1194300
ctatgaaagt	cattcctaca	atttcttttt	tagcaaagaa	tgtcttagca	ttttcttctt	1194360
ttttccctgc	gtctatatag	aaggggatgc	caagagctaa	aagaactaag	gccataagaa	1194420
ggtatttttg	acctcctgca	tagataagcc	atagagagta	aaccactccc	aggataccag	1194480
ttatcattgc	caaaggggct	ttaatagacc	cttttttagg	atatgttttg	cttttgctaa	1194540
gtttaaagag	aaaggcagca	ctcgctagat	acgcagggag	aaccatgacc	cccgatgatc	1194600
tgagcatagt	attccaagca	ttcgaagaaa	agtaaacaa	gagcatggcg	agctgcatca	1194660
cagagctcgt	aatgtatagg	gagacgctgg	gagatttctc	tttattttct	atagtgaaga	1194720
tctcagggaa	ggtgccattt	ttagctgctg	agaaggggat	ttctgcaacg	atgatcgtcc	1194780
aggataacca	gctagataaa	acagcaataa	tcaggccgac	attcatgagc	acttctcccc	1194840
atttccctac	gaggatgtcg	aggacaccag	ctgtagaggg	attgggggatg	ttcgtagatt	1194900
gatgttggaa	gagcgagcca	aaaggtaata	aagaaaataa	gatgtagatt	gttaggcaac	1194960
ctaaaaatcc	taagactgta	gcttgcccta	cagagagagg	attttttgct	cgtccagaca	1195020
tcaccacggc	accttcgatt	cctataaatg	cccatagggg	gaccaacata	gtccctttta	1195080
gttgtgaact	tacggatcct	aaactcgggt	gggcttttgt	tacggcatgt	ccccaaaaat	1195140
ctgttttgaa	aacagcgagc	ttgaagaaga	acgcagtcag	gataatgaag	atgattagag	1195200
ggatgatttt	aaatatagtt	ccgatgacgt	tgattatcga	tgcttgacgg	attcctttca	1195260
gaactatgaa	gttgaacacc	cagataagaa	tgagccctcc	taaaatagca	ggtaggggat	1195320
ttctcctctg	gaagtaggga	gggaagaagt	agtttagagc	atccatagta	attacggcat	1195380
atccccattt	accgaagatt	tgacaaagcc	aatatcccca	gccgatgggtg	aatcctatgt	1195440
agggggccgaa	accttctcta	ctgtacatgt	agatcccttc	cttaagggtcg	ggacgtattg	1195500
tagagaggat	cctaaacgta	tttgcgataa	agaacatgcc	gaagccagtg	agtatccaa	1195560
ataggattac	ggcaccagct	cctgctgtcg	ctgccatgtt	ttgggggagg	ctgaaaatcc	1195620
ctcccccaat	tatggaactg	actaccatac	ccgcaagggc	tatggctcct	aaattttttg	1195680
aggatttagt	ccttgaggtc	atgaaagtct	ccttaattta	ccttagctgg	ttcagcattt	1195740
tcgaaattta	ggaatcctaa	tgcagttaag	caaaaaccga	atttttggtt	gatgttgatg	1195800
taattatgga	agaattggaa	ttcgctatgc	tttgctatag	agcgtaggtc	aagttcgtgt	1195860
tgtagggatt	ttttcaacca	catttttagca	tgggtttctg	caatttcgtc	atttatccat	1195920
gtaggggaaga	attcaacata	ttctgctgcc	catccgccaa	taagctctcc	atttttatct	1195980
ttaccccagc	aatgccgat	tccgggtggcg	atcgcatggg	ttccgctcaga	gagagcagca	1196040
ccacgacccg	ccatgattac	ttcaaggaca	gcgccgtgtt	tgaaagattt	tacacaggta	1196100
tctacaggaa	cgatattccc	aaagagctct	ttaggaagta	cagatgtata	agggacgata	1196160
ttaaaatttt	cgattttttg	ttgtagaaga	gcagaatcgt	agcagaaagt	ttcaaagggg	1196220
tgtggggggc	taccgtcatc	agatttcacca	atgccccctg	tatggaaatg	tagcgtggga	1196280
taacgagttc	cgtaagccat	aagttactcc	taataaatat	tggtgtgggt	ttgttataag	1196340
gaaagatttg	cacgcaggcc	atacacttga	gaggttctcc	tctctggggc	taacgctggg	1196400
tggatataga	gttggaatc	tggagttaga	gatataata	gtccaaagcc	aatagtagcg	1196460
aaagcttcca	taacagactc	ataacgtcgt	agcttggtca	cattggaaat	cgcttttagca	1196520
tttaccttat	ttgtagcaaa	tcctatgcca	agaagatctt	gagagtggcg	gtttaaggga	1196580
ttctcagaga	caagacctaa	aacatacgaa	cggttttatg	ggagtgtctg	tcccgtagct	1196640
ccgttgattc	ttccgaatag	atagagcttt	tcatgaatat	gttgagcagc	attcaggggc	1196700
catcctgtga	cctgggaggt	ttgctcagga	actttgcgtg	tgctatagag	caatacagag	1196760
tactgtccat	ctccacacga	aggtttttga	gtccagggag	cgtagccgta	aaagttgtat	1196820
gttgcttttt	gtcagattat	aaatcgaaaa	gttggttcca	tcaatattat	aggaatcttg	1196880
aaaacctagt	tgaaccttga	tttcagaatt	tggagtgaac	tgagataaag	cacctgtact	1196940
tcccaatgag	taggttagcac	ttgcgttttg	tgataagggc	tagctaataa	acccagagta	1197000
ctgatcatta	tcgtaaagcg	tgccgtctat	agcatagagg	ctgtattgtc	ctatagctag	1197060
ggtcaaaaag	tctccagggg	aagtctgaga	gaaggtaagc	tgtgctaggt	tattttctct	1197120
attagagtaa	tcattcatat	tggaaagcgg	tcccgcggct	tgattggcgt	caacaccgtt	1197180
agtttgccag	taatgtatca	acgtatagct	aaagtctacg	attccttgac	ctgtgttggt	1197240
agaatcataa	agagtccagg	tagtgctagg	actgaaagtag	aactgccacg	aaggaatctc	1197300
tagggcttgc	gtttggccaa	gagcttttgt	agggtaaaa	cactggggaa	gaatactgaa	1197360



gtccaaggat	atctgagtat	ttgtcgtttt	ttctacagat	gttaaataggt	tggatacggg	1197420
aatgccatcc	ttccaaggat	gtgaacagaa	gatattagta	actggagaga	gaaggctgtt	1197480
atgatgtgga	gtttccgaag	gggcgctttc	ttttatggac	tccggatgtt	ttttttgaat	1197540
tcttgcttta	taacgatggt	agtgcccgt	cgtttcttta	ggagtttcgg	cataagagga	1197600
aattccaaga	gcgcagagtc	ctgaaagtaa	aagaaancga	aaggntatca	tgaattcccc	1197660
gtagaagaag	gcatagtgtt	tttttttgac	tctaaaaaaa	agaattgttt	ttatgtagca	1197720
aaaattttct	tctgaggaga	ggaatgctat	ggaatccaca	gtatcagtcg	ttaagaattc	1197780
tcttgagtag	tcttttttct	tattattcta	aaattatttt	ttattgagat	cgagaaccca	1197840
caaaagtaaa	cgtcaggag	tgcttatctt	taagaaggat	tattcgtgca	tttgggtggcg	1197900
cagaagaaga	gccgccgctt	cattgctgag	taatttttta	gagtagttgt	actgtacttg	1197960
tgcaatgtta	tcaaaataga	tccgggggtg	aagtccctga	gctttatagg	tgattccgaa	1198020
ataagcaatt	ccatattttt	ggcatagatc	accgatgcga	aggacatttt	cttttttggtt	1198080
atcaatatag	ataatcttag	cgggtaaggg	ggtgcatatt	tccaagaaga	gatcgagtcc	1198140
cggtcctttg	tggtagtctc	cagaaaaaag	aattcccgat	gtgtagagaa	ggttcttggt	1198200
taggggagct	tgaggttggt	gagcagtatc	ttctaaggag	acgttgagca	tatgaagttg	1198260
ctttagggta	agatcttttag	ctgttttagg	acgttccgtg	tagacaaagg	ttgtctttcc	1198320
ttgcttctgg	attttctcaa	tgagtagaaa	aatagcagat	tctataggct	gaacggttcc	1198380
catttcttga	atttcaatcc	agaaaggaac	tacagcctcc	caagcttctt	gttctggggt	1198440
tccctgtttc	tgtaaccctt	ggattgcttt	gcttttccat	atagaatgag	agagagcctc	1198500
tcttcttga	agaagcgtat	catcaagatc	taagatcagc	cagaagttct	cttcatcata	1198560
gaggatatca	ccagcaactt	catgaatgga	cctgacctcg	gcataacgac	aagaagcata	1198620
gaacgacgag	caggagaata	agaaagtga	gaacaaccag	gttttcataa	cgtaccttgc	1198680
aatcttttgg	acaaggatag	agtaagacaa	gtatttttta	tacttttgcc	atgaagtttt	1198740
ttacatagtt	tccgaaagag	tcacaagact	ctggagttag	gaaatctggg	aaccaaagag	1198800
caaattgtag	cagggttgt	tctatgaaca	tttcgtagcc	atggataatg	agagagccat	1198860
gtttttgagc	acgttcaagg	tagggagagg	gatgcggttt	ggtattgatg	tccatgacta	1198920
taggagggaa	tctccaaggg	aaggtcactt	ccggaggagg	acagttgatg	attatgtcta	1198980
tagtttttaa	attctctaa	gagcctaagg	gataggcttt	gcctttacag	caagtagcta	1199040
aagcagctgc	tgaagaaaga	gttctattga	agatgtggag	attagcacct	tgcatcgcca	1199100
gtgttgagc	gattgcttta	gcagcacctc	cagcacctac	aatggcaatg	tgttgttgt	1199160
taacagagat	attcttttgt	tttaggagtt	tggctactcc	ctcacctctc	gtattgtaac	1199220
ctagaatttt	ctgatttcgg	aagaccaggg	tgtttataga	ctcgcagagt	tgccgccgatg	1199280
catcaagagc	atcgacatgg	tcgaagattg	cggtttttag	tggcatagt	acactaagtc	1199340
ctgaaaaagg	aagatctcgg	atcgacagag	aaaagggtgac	gacttcccct	atagtaacag	1199400
ggaatttgat	atatgttgca	ttgagagaaa	gcttagagag	taagaagttg	tgggagaggt	1199460
gactgatgct	acggtctaca	ggatctccga	tgagtccgta	aatgtgtgat	ttttcagata	1199520
gcttcgagta	gttataggag	agcagctcct	caagtttagg	ttgtcccggg	gctacttgag	1199580
gcgcactgat	tccagcagcg	taattcatag	cggtgctgat	cagtggggag	agaactctag	1199640
aggggagccc	atgggttccc	atacaaagga	ctgtagatgg	ttttggtaac	agggcagctt	1199700
tttttatata	atcagagct	tactggagt	tctctgggga	gagtacgatt	ttgtagatct	1199760
cagcgggagt	tgcaagcatc	tattataga	ttgcatcgag	gtcttcattt	ttgtctgtat	1199820
gataggaaag	gatgagcttt	atttttaggt	ggctcttgcg	gatggtttga	agggcggtct	1199880
taggaagact	cacatcgata	tccatccact	tgggttcaag	ttttgctagg	gaatatagtt	1199940
tttgaatcca	tagcgtgtc	gacatctctt	tgtgtgtct	aaagggtgag	atggggtttt	1200000
gggctgtggt	aatgagggta	tgagttctt	gatcatcaag	ttcgtttatg	agatcgagtc	1200060
gtagttctat	aatatctaca	aggtgtagag	actttagaat	ttgttgtttt	gttccacaaa	1200120
atgagggacc	gctaacagt	gcgcataaca	tgacactcac	tccatagtat	atcatagaga	1200180
atctccatat	ttggagatgc	acaataggta	ccattaaagg	gagctgcacg	acctagatgc	1200240
tctatcatga	tcatttttag	ttcgtgttga	gaaagatttt	ttttatcgta	tcctaaagtg	1200300
tagatgatat	tttcaggact	atacaagctg	ttgtggagat	gttccggaac	aatagattgt	1200360
aaatctttca	aagtagaagg	gagattaaat	cgtttttagga	gtctttcaag	ttggtctatg	1200420
agttgtgggg	ttttcataac	tccttcagca	agagatattc	ttgtttctat	catcataaccg	1200480
acacttacgg	cttggccatg	atttaccgtt	ccttttgcca	gggtttctat	agcgtgggct	1200540
atggagtgc	cgaagtttag	gatttttctc	agacttcggt	catagggatc	ttcagcgaca	1200600
atcgccgctt	tgatttgga	gtttcttttg	atgaactcgt	ggaggatctg	cgatgaagaa	1200660
aatagcattt	tactatggct	atttagaaat	tcccagagat	aagcatccgc	gatgaatcca	1200720
tgtttttattg	cttctgcaat	tccatgatac	cattcttctc	ttgggagtgt	agagaggaac	1200780
tgaggacaca	tccatacttc	cttgggtaag	tagaatgtcc	ccagtcgatt	tttgattcct	1200840
cgtaagttga	ttccattttt	ccccccgata	ctcgtatcta	ccattgctggt	gatcgtcgtg	1200900
ggaattagat	atagaggggag	ccctcgacaa	tatgtagcag	ctaaaaatcc	tgtcatactc	1200960
aaaacagtc	cccctccaat	tccaataa	gaagatttcg	gagagatatt	ctgatctaca	1201020
agctgatatt	gtagagatat	gaatgtttcc	caggttttgt	taggttctcc	aggaggaaa	1201080
gttaggacaa	tgacttgata	tcctaacatt	ttaatatggt	ctaagatagg	acctaggaga	1201140
tgctgttgta	ctgaaacgtc	tgtaataatg	actaagggat	acgctgtgga	tatagaagag	1201200

aacaacttct	tctggaagaa	gttggatatg	agtttccacta	catgggggagt	cgtaattatt	1201260
gtctctgaca	tgatagtttg	gagcatcggt	ggtataatac	aagatctgca	agaacaaggt	1201320
ttatcatagc	ctcaacaaca	gggacagcgc	gtatggcgac	acaaggatca	tgacgtcctg	1201380
tttgaggtgt	cctataggta	gtttcttttt	ttgtctttgt	cactgtagca	cagggtcgct	1201440
ttatcgaaga	ggtaggttta	aatgctatgc	gcccttctat	aggaactcct	atagttatgc	1201500
ctcctagtgt	gcctccacag	ttgtagagct	tcaaggtaat	gttttctcct	tccatgacga	1201560
agggatcagt	atattgtgaa	cctctcattt	gagcagaggg	aaaccctttt	cctatttcga	1201620
atccttttagc	ggcggggatg	ctcattaaag	cacttgctaa	gagggcggtg	actttcccaa	1201680
agaggggttc	ccctagaaa	tcgtggattg	gagacgttat	gaaagaaatc	acccacaccta	1201740
gagaatcaga	gtcgtcgtgt	agagaagtaa	ggatctcttg	gattttctca	ttaggtaacg	1201800
gtgaatagaa	tgccgaggtg	tgaatcttgt	ggatgagctc	gggggagatc	ttcaggtagt	1201860
gagggagggg	tagagatcct	aacgaggaga	ggtaggctaa	agtaaaaaatg	ttttgattcg	1201920
cgaggaattt	ctctgcaact	acgccagcag	cgacgcgaca	tgccgtctct	cgagctgagg	1201980
agcgacctcc	tccgttagga	tctacaattc	cgaatttctt	ttcataggtg	tattgggagt	1202040
ggccaggacg	gtagagcctt	tactgttttt	cataagggga	gctatctacg	tcagtagtga	1202100
ggatttgacg	ggataggggg	gtgcctgtgg	tctttccttt	ataaactcca	gagaggattt	1202160
gcacgatatc	gttttctttg	cgcgatgagg	ttcctggatt	tcctggacga	cggcgcttca	1202220
tggcaggaac	aaaatctgat	tcatggagct	cgagtcctgc	gggacaacca	tcgattacaa	1202280
ctccgattga	gggaccgtgg	gattctcccc	atgttgtaaa	agaaaaacaaa	gagccaaagc	1202340
tatttttcat	gactttaaca	aggtaatgag	atcttgagac	gcttggttcta	aggagctctt	1202400
cgaggaatga	tctacgtgat	ccacgggaaa	aatgtaatca	gcaatttctt	tcattctgtc	1202460
gatgcgctca	gttaaaatct	cgcttagagg	ttttgttttc	atggccttct	tcagccgttc	1202520
tggtaacctc	cgtttctcga	gtctttcata	aattaaaggt	agttctacag	agagaaatc	1202580
aagagctccc	ctagtttgaa	tcgctcggtg	agaggcttca	tacatcaagg	tcctccacc	1202640
aaggagatc	aaggcatctt	ctggaggtaa	agtttcaaga	atacgagctt	cacattcact	1202700
gaatttctga	tccccataag	ctttatagat	ctctgcagat	gaggagtata	gtgcactgct	1202760
gtagttgctt	acaattaaat	catcaagatc	ataaaaagga	aggtttagaa	atttagccaa	1202820
agctttcccg	agcgaagact	ttccgcttgt	gggtagacca	catagaataa	ttgtcatgac	1202880
attcctcaat	tcgagcttcc	atttatattt	gagtctgaac	gaagtttaga	aagggttttcc	1202940
taacgcacgc	agtgttgtga	atacgactat	cgccagaagc	atatagagct	gctatgggtca	1203000
aggccatggc	aattctatga	tcacgtgtag	agtccaaaac	agcaccgtag	aggggactgg	1203060
gattcaccag	taagccatca	tgagttggct	gtatgcagtc	tccatttttc	tgtagtctct	1203120
cggtgattgc	aagaatgcga	tcgctttcct	tgtcttttaga	actgcgtgca	ttgtagaggt	1203180
gcgaagggga	atctgcaaaa	caacaaagga	ctgtgagaat	gggaagagca	tcgatacaac	1203240
catccatata	tatagagcca	ccagagaacg	acgaagggaa	tactaagatc	tcttcgttgt	1203300
cgtactgtat	agaggctcct	aagttttgca	tgagagaaaa	aaagattttg	tctccttgga	1203360
tatctaagat	gtccaagtta	cgaagacgta	tcggttgagg	tgattttgaa	agtagagcag	1203420
ctgcagcaat	gaaagctgcg	ctgctgaaat	caccagttac	gtggtaagag	aaaccttgag	1203480
gatgtgaact	taaccgggaa	gaataggtag	tatcagaaca	agaataggga	agatggagtt	1203540
tctctaacca	ccagagacta	agatcaaaac	atggagcttc	tttcggttct	atgatagtaa	1203600
aggaacaggg	accttcggct	aacgaacatg	ctacggctag	tgctgaggca	aattgagaat	1203660
cactaccttc	aacatcgcta	taagcagagc	gtaacggctc	tgacattgtg	aaaggtagaa	1203720
cgcttttatc	tgaagagaaa	tgaaacgaag	ctccaaagtt	tctcaaggct	tgaagtagag	1203780
gggccatagg	acgccgttgc	aactgtgacg	atcctgtgac	ggtgatttct	ttagagaaga	1203840
cacaggcaag	ggcagtcata	aaacgcaaca	cgataccaga	atttccagcg	tctatgagag	1203900
tatatatttg	aaatatagcc	aagggtattg	ccacaatttc	caaaatttga	gggaatttct	1203960
ttatagaagc	tcccatctgc	ttgcaagcac	aaatcatagc	ctcagtatca	ggagaattcta	1204020
aataattata	aattgtagat	tttccctcgg	caacagaagc	ccatagaatg	gctcttagag	1204080
tatgggactt	tgaggaagga	atgaaggcgt	tcccatacac	agaagaaggt	gaaactttat	1204140
aagtaagcat	tgtaaagcaa	acttatctct	tttttttttag	gtaatttgcc	tgacttctga	1204200
tttgctgctc	aagaaaaatt	ctagaacttt	gtaaaagtcg	aggaaggatc	gaagatcatt	1204260
tggttctaata	tctctacaaa	ctgcaagcaa	agctccccct	cgaattggca	agcatagcct	1204320
aagagttccc	tccccgtggg	ggagatcttt	aagttcacgt	tccatctctt	gcagatggcc	1204380
ttgctcttct	aagataatgg	attttaccgt	tatttttact	tgagcttctt	tcagaatatc	1204440
gtgatacaga	ggataaagtt	cagaagcacg	aagttcgatt	cggtaggtaa	ctaaaatata	1204500
cgctgcagtt	tttaacgttt	gtcccgatag	ggagtattca	ttttccagta	ctcggcacgt	1204560
ccttaaatct	agaagatgga	ggtaatat	tgtaaagtaag	cctcccagaa	gatttttaga	1204620
tgtatagtca	gggagagaag	tctctgagat	tctagaaatc	tgagttttta	gatagtgacc	1204680
atgacgaaat	tcttcagcag	catgttttaa	aacttcttcc	tttacctccg	taggatgttc	1204740
acttgccggg	attttttttg	ctccactatt	ttctaaaaaag	gacaggggtat	ttatccattg	1204800
tgcatgccaa	tagttggaag	ctacgatctc	tttgagaacg	ggctcccaac	gagaggctgt	1204860
gtggataaag	tgttttactg	tggttgtaga	catagggcag	cctgtaggtg	agaataaata	1204920
atccggagat	cttcttcttg	gatacagtag	gggggcagca	catacagtgt	gttccctaaa	1204980
ggacgaagaa	ggactccacg	ttctaagaaa	aagcgattga	gatgggtctt	atattgtgaa	1205040

aaatatacctg	tagcttctgc	agggtaaatct	agagcgagta	ccgtgcccag	aacctcacac	1205100
cgttgccata	gggaaccatg	agcttcttga	aactcttgat	gacaccgttc	tatcatttgc	1205160
ctttgttgta	ggcattctgg	agataggggtg	agatccaaag	aagcgagggc	agcactacag	1205220
cctaaaggat	ttcctgtgaa	ggataggcca	tgaagcagtg	ccttcatccg	atcttgggag	1205280
acaaaggcat	catgaatttc	tttagtgggt	actgtcaagg	ctagagggag	atagcctcct	1205340
gtaagacctt	tagaaagaca	gataatgtca	ggaggaatgt	ctgtaaattc	agaagcaaac	1205400
agtggaccgg	tacggccaaa	gccagtaaga	atttcatcag	caatacacag	aaccccgtaa	1205460
tgcttgccaa	gcttgagaat	ctcctttagg	ccttcgggat	tatacattaa	catccctcca	1205520
gcaccttgca	atagcggctc	atagataaac	gctgcgatat	tgctttcaga	aaagactgtt	1205580
tttgcttggg	caatggcaag	ctcttccttg	ccataatagg	gagcagcaat	tgtactggaa	1205640
ggaagaaaaa	gatcatgaaa	gggaactgta	gtagggctcg	tgccagctat	cgacatagct	1205700
ccaaatgtat	ctccgtgata	ggcattgctg	agtccaacaa	aatggctctt	agccttgttt	1205760
tgattgtagt	aatattgcac	agcaattttc	attgctattt	cgatagacgt	tgatccgttg	1205820
tcagagaaaa	agaaacgttc	tagaccttca	ggaaggaggg	gagcgagttt	cgatacgagc	1205880
tctagagccg	gttcatgggt	gaaatttgcg	aagatcacat	gttctaactt	ctgtgcttgc	1205940
tcacataaatt	tttttgtaat	gtagggatgc	ccatgaccgt	ggaggttgca	ccaccatgaa	1206000
gatatcgcat	caagatatct	tgttcctgat	tccgcataga	ggtaagcacc	ttctccctt	1206060
acaatcttta	tggtgttaga	atctaatagca	gattgagtga	aggggtgcca	gatacaccct	1206120
gaattccctg	atgattgctt	gtccatactt	ccttccattg	ttcggcataa	cagcttatga	1206180
ttgtctttgt	gatttctttt	tccttgccaa	gagtcctgat	tataggaagc	ttgatttctt	1206240
gagttagcca	gtgctcttcg	tcctctggat	acccatttac	caccatacct	aagatatgga	1206300
ggtttcgtga	gcgcattgct	tctaccgtta	aacaggtgtg	attgatactt	ccgagatag	1206360
cttggtctac	taaaatccaa	gaacatgacc	aagaagaaaa	cacatctccc	tgaagtcttt	1206420
ttgatgtgca	gggggataaa	aatcctcctg	aagtctcaat	aatcagattc	gaagttgttt	1206480
ttggcgca	aatatgactc	tcttcgatac	ttacattatc	gatttgcgct	gccttggtg	1206540
gagacaaggg	cttatgcaat	cgataagctt	cgggatgaca	gtaggctccc	gatagctcat	1206600
gaacaatatt	gctatctgaa	ttttctagat	tccctgcttg	tataggtttc	cagtattctg	1206660
cgtttaagtgc	tctagcaagg	atagcactga	caatggtttt	tcctacgcca	gtgtcgattc	1206720
ctacaatgat	gatacgttgc	ataaaaaaat	ttgctctaaa	gtatgtaaaa	gggtatctat	1206780
ttcatttttt	gtattgaagg	catgaaggca	aatacgttaac	agttcttctc	tttggtttac	1206840
tggtgggctc	acgtaggggc	gaacatcgta	ccctgagttt	tgtatttgca	atgagggttg	1206900
ccgagcacga	tggctccctg	aaacacaaat	agattgtata	ggtgtagtag	tattgtcttt	1206960
cattagctga	agtcccaagt	tttgagcttt	ttcgcgaaaa	tgatgaatga	gagcagaaaag	1207020
atgttcacgt	tgattaaaag	cacgttgggt	atgctcataa	gcgagctcta	tagctgtgag	1207080
cgcatgggga	ggttgggctg	tggtgtatat	gaaaggtcta	caaaaattaa	ttaggtagtc	1207140
tttgagtata	gaacttcctg	caatagcagc	gccatgagtg	cctagagctt	ttccaaaagt	1207200
atagacggtg	gctaggactt	tatcttgaag	acctaatagc	gagacaaggc	cttcgccttg	1207260
atctccaaaa	actccgactg	catgggcttc	gtcaacgatc	aggtaagcgg	aatatctttc	1207320
acagagttca	ctgatagctt	gtaaaaggagc	cacggagcca	tgaagcgagt	atacggattc	1207380
cacgcaaaaca	aagggtcttc	ctagatggga	gcttgctaaa	cgtttttcta	agtgattcag	1207440
atcattgtga	ttaaaggga	agctttgagc	tttgcttaat	cggtatgcat	cataaataga	1207500
agcatggata	taaaggctcg	gaagaatacg	atcctggctg	gtggcaagag	catagagcaa	1207560
gcctaagttt	gctgtgtaac	ctgtattgaa	gatcaaacag	ctttcaaaat	tatgataagc	1207620
ggctagtgtg	tcttctatac	gctgacagag	ttgcgagtg	cctgtgagaa	gccgagacct	1207680
tgtagctcca	agcgattcta	tcgcatggag	cttggttaag	tattctttcc	ttaattcttg	1207740
agaagaggca	aatccaagat	aatcattaga	ggtaaaaatca	atgagatgag	agtttaagct	1207800
tagcgagcgg	taggtatggt	tggacttacg	tcttgccaaa	gcctcaatta	ggaattgttg	1207860
gcataacatg	ggttacctct	ttctattcca	aatgaagggc	gagggattaa	gcctaaaagt	1207920
ttgatcattt	cagcatcttc	atctatatca	ttgttttcta	cagtcaacag	tttatctcca	1207980
tagaatatgg	agttggcacc	ggctagaaaa	cataagggtt	gttggtctac	tgtgaggaaa	1208040
gcgcgtcctg	cagcaagtcg	taccatggat	ctggggaaaa	caacccgtgc	cgttgctatg	1208100
gttcgcaaga	cttcccagaa	agaaatcgga	ggctgggtct	gcaaaggcgt	gccgtcaatc	1208160
ggccaaagta	aatttacagg	tacggattct	gggatattgat	ctcttggtgc	aagaacatga	1208220
agaagcttta	tacgggtctc	ttcagattct	ccataacccta	caataaccacc	gcagcatgta	1208280
ctaagtcagg	atttattttac	tacatcaaga	gtgttgaggc	gatcttcata	agaacgtgtt	1208340
gtgattatag	tttcatagaa	ttccggagaa	gagtctaaat	tatgattgta	ggcataaagt	1208400
cctgcatcat	acagtttttt	agcttgctct	tcggagagca	tgcttaaagc	acaacaaaacc	1208460
tcggctccga	gatctgtgat	acttttcacc	atagcgagga	ctctatcaaa	gtatcgatcg	1208520
tccttagcat	tgcgccaggc	agccccaaga	cacacacgag	tggcgccctag	ctctacagca	1208580
cgttttgccc	tttccacaac	gtctacaatt	ttcatcatag	gttctgggtg	gacgtgggta	1208640
tgatagcggg	aagattgggc	acagtagggc	caatcttcaa	cgcattccacc	agttttaatc	1208700
gaaatcagat	agcaagtcg	cagttctgaa	tggaggaaat	tactacgcaa	tatggcattg	1208760
gctttgtgaa	tacggtcaaa	tacgggagtg	tgataaattt	cgcgagtgct	ttctaattgac	1208820
caggatacag	tttcttcacg	catgtgtttt	gcctaggggg	taaattcaac	gaccgagcct	1208880

aagatatatta	catggaatttt	agagaaagtc	aataggaacc	aattttttggt	tcctatnttt	1208940
tatggtatga	tttgagaatt	attctaataa	aataagagaa	attacgtttt	ttaataaagc	1209000
agctctat	ttaaaaaatt	agaaataatc	atgaattatt	tcttggtgtc	taagggtgat	1209060
ttatcagagg	aactgtat	gcaatttttag	tagaaggcat	ccctaaaaac	ttgcggttg	1209120
tattcacagc	gagataaaaag	agcgggtgtcg	tgagaacaca	aaaagtaatt	ttataaatgt	1209180
aagagtagaa	cataatattt	aggggtttggg	ggaaagaaaag	ccccatgccg	aaatataaaa	1209240
tacaggtgtc	gacaatgaaa	gtatctggna	tttgtgagat	ccatgtagac	ccattgctac	1209300
gtagccatag	agatgaattg	ggagttcgat	ttttaaaaaa	agtgtaaagg	acgatgtcta	1209360
attgctgaga	gacaatgaaa	gcnagtagtg	aagctagaaa	acggagagga	cttaaatcaa	1209420
acaagcagtg	ccaggcagtt	tgcattctcag	gagaggctac	tgggaagaac	ataaaaaattt	1209480
gtacaattga	agaagctaag	aggttggcga	taaaagctga	aaatatcatg	acacgagctt	1209540
ttttagggcc	aaagatttcg	ttacaacagt	ctgagatgag	aaacgtcagg	ggataaagaa	1209600
tgagtcccc	aggaataatg	aagttaaaaa	aagtcgttgg	aatgagcttc	gaagagagga	1209660
caagattgga	gagaacaaga	agcaaagtaa	aggttgaaga	caagtaggaa	aataactaatg	1209720
tttttctgtg	ggatgtattc	attggcaagg	tacctcaaaa	ccagaaagat	atcttctctg	1209780
attgtaaagg	ggaattgatt	ctaacagacc	ttggctcgagc	atccattcta	attttgaagt	1209840
gagttctacc	agttcatcaa	aatgtcttat	tgaaaataaa	gtctcttggtg	gagttgatgt	1209900
attgaaggga	agacgaataa	tctgatccaa	ttctaaaggg	agaacacgta	cgttatcaat	1209960
gaaagcgtgt	ccaagttcct	gaggagaact	gataagaacg	gctccatattg	cttttcttcc	1210020
ttcatgggtt	tcaataagtc	cgctttcaac	agtaaaccac	aagcagcgta	caatagcgat	1210080
cagattgctt	tgtagggttt	gtatgcgttg	ttttttacta	ggaagagctt	gtactttttc	1210140
tatgacttta	gtgaagagtc	ttcccatggt	tatgaaaaat	tcagaaaaatg	agggatgtag	1210200
aagccaaggc	acgtgccccta	aaaggtcatg	gatgagatca	ggagtttaagg	agaaattatc	1210260
tttatcgaga	gttcgcatta	cagaggcaat	gggaaagtaa	cggtcctgca	acagagacaa	1210320
gtattgatgg	ggagctacaa	atcctgaaac	gggataatag	gaaaaatgtg	tttctaattc	1210380
gaagaattta	atgactgctt	gatggtctaa	gaaatcagaa	aggagaccga	aagcttctaa	1210440
gtaatcaaga	aaaatcttgg	acaatagctt	ttccatagag	aaaaccgtga	ggaaaggagt	1210500
cgataccata	aattccgatt	aaaaaaggga	gtgcttacaa	cagccatatac	agtggagcaa	1210560
ccttcccttt	gattcttttga	taatgacaga	agatgaacaa	agagtaagtt	tttgaaaaaat	1210620
tctaaaaatag	aaatgcattt	gtgtcgagct	aaagcttgct	tctctttatt	ttccttttgt	1210680
agaatgattc	ggtagtagga	atatgggggtc	gagtagtcac	tttggagtga	ttggctgttc	1210740
tggagaagaa	gggaaagtga	ttgtctcagc	tttagagcaa	tcttcagaat	atactttggg	1210800
tccagggttc	tctcgcagta	gtgcactcac	tctttttcaa	gtgattgcac	ataacgatgt	1210860
tcttggtgat	ttttccacc	ccttactaac	taaagaagtc	gttgcccatc	tcttaatctc	1210920
tcctaaaccc	ctcattatcg	gaactacagg	gttccctggg	aagtgtaaaag	aagctcatga	1210980
cagtctcgaa	gagctgactc	acatcgttcc	tgtagtgggt	tgtccaaatg	caagtctagg	1211040
agcttatata	cacaagcggc	ttgtaatggt	gctatcgcaa	ttatgtaacc	cacagtttga	1211100
tattcgcatt	cgcgagactc	atcatagata	taagaaggac	tctctctcag	gaacagctca	1211160
agatttactt	gatactatac	agcaagtaaa	acaagaggat	tggggagagg	agtatgaggt	1211220
aggccagcga	gattcttcta	agaagacgat	agaagtgcac	tcttcacgag	ttggagatat	1211280
ccctggagaa	catgaggtcg	cttttatcag	ttctggagag	caaatttttg	ttcgccacac	1211340
agtattttct	cgcaatgttt	ttggctcggg	aatcctttct	attttagatt	ggctaaaaac	1211400
attgaatccc	caacctggtt	tgtatagtct	tggggatact	ttggagctag	tcttacgaaa	1211460
tgaacattgc	ttgcttaaaa	agacaacgga	tcattaatat	gcagatataa	agatcttttg	1211520
cgctcgtaaaa	tcctgatctt	caaattagga	atgtagggtg	ccgcaattac	acaacttcgt	1211580
gtacaaaatt	ttaagcgagg	actgttttga	tttttagcat	cgataggacc	atcggttaaa	1211640
ttaggaagtg	ttgacaggca	attcaaaagg	aatcattgca	tgtctgtaaa	cactagagat	1211700
agggttatcg	tgcattccaa	tctgaagtaa	ataattgaga	tggagaaaagg	aaaggaatgc	1211760
gaatcgctgt	tttaggcgtt	actggacttg	ttggccagaa	attcgtagct	ttgcttcata	1211820
agtggtatcg	tgattgggtc	attgctgaag	tcgtagcttc	aaatagtaaa	tatgggcaat	1211880
cgataggaga	tgcctgtatt	tggcaggagc	aatcgccct	atgcctgaga	tggtagctga	1211940
tttgccctata	cgtaagatcg	aggaagtgc	gtccgacatc	gttggtttctt	ttttgccttc	1212000
tagtgctgag	tccatggagg	cgtattgcct	ctctcaagga	aaagttgtct	tttctaattgc	1212060
ctcaacatat	cgcatgcatt	cttcagttcc	tattatcatc	cctgaagtca	actcagatca	1212120
ttttcaactt	ttagaagagc	aaccttatcc	tgggaaaaata	atcacaaagtc	ccaattgttg	1212180
tgtctctgga	attactttgg	ctctagcacc	cttaagaaag	ttctccttag	atcacgtaca	1212240
cattgtcacc	ttacaatcag	caagtgggtg	aggctatcca	ggagtcccg	cgctagatct	1212300
tcttgccaat	acagttcttc	atatcggttg	agaagaagaa	aaaattctta	gagagactgt	1212360
gaagatttta	ggaagttcta	agcaaccttt	accttgtaag	ctctctgtga	cagtcctatcg	1212420
agttcccgta	gcctacggtc	atacgtcttc	tctgcatggt	accttttcta	aagatgtaga	1212480
tcttgacgag	attctgtact	cttaccaga	aaaaaataaa	gaattcccca	atacctacca	1212540
actctatgat	aaccttgggt	ctcctcaggc	tcgaaagcat	ctttctcacg	acgatatgcg	1212600
cgtacaccta	ggacccatta	cctacggagg	agatttttcgc	accataaaga	tgaagtgttt	1212660
aatacataat	ttgggtgcgag	gtgctgcagg	gactttactc	gcaagtatgg	agaattattt	1212720

tttcgactat	cttaagaggg	aatgtgtct	aagatagttt	ataaatttgg	tggcactagc	1212780
ttagcaactg	ctgagaatat	ctgtttgggt	tgtgatatca	tttgcaaaga	taagccttct	1212840
tttggtgttg	taagcgcaat	cgccggtgtg	acggacctcc	ttgtagactt	ctgctcgtct	1212900
tctttaagag	aacgagagga	ggtcttaaga	aaaatagagg	gaaaacatga	ggagattgta	1212960
aaaaacctag	cgattccttt	tcctgtctct	acatggacgt	ctcgactcct	tccttatcta	1213020
caacatctgg	agatctcaga	tctcgatttt	gctcgtattt	tgtctttagg	agaagatatt	1213080
tcagcttccc	tagttcgtgc	tgtttgtagc	accgtgggt	gggatttagg	atttctcgag	1213140
gcacgtagtg	tcattctaac	agacgatagc	taccgacgtg	cctctccaaa	cctagatcct	1213200
atgaaagcac	attggcatca	gctcgaacta	aatcagcctt	cgtatattat	ccaggggttc	1213260
atcggtatcta	atggtttggg	agaaacagtt	cttcttgggc	gcgagggcag	tgattattca	1213320
gcaactttga	tcgcagagct	tgcaagagca	acagaagtgc	gtattttatac	cgatgttaat	1213380
gggatctata	ccatggatcc	taaagtgatt	tccgatgcac	agcgcatctc	tgagctcagt	1213440
ttcgaagaga	tgcaagaattt	agcaagtfff	ggtgctaaag	tcctttatcc	tcctatgctc	1213500
tttcttgtga	tgctgctggg	aattcctatt	tttgtgacat	caacatttga	ccctgaaaaa	1213560
ggaggaacat	gggtctatgc	tgctgataag	tctgtgagtt	atgaaccaag	aataaaaagct	1213620
ttatccttaa	gtcaatacca	aagcttctgt	tctgtagact	atactgtcct	aggatgtggg	1213680
ggattagaag	agatttttagg	catttttagaa	tcccatggga	tagatcctga	attgatgata	1213740
gcacaaaaca	acgtcgttgg	atttgtaatg	gatgatgata	tcatttctca	agaagctcaa	1213800
gagcaccttg	tagatgtttt	atcgctatct	agtgtcacac	gcttgcatca	tagtgttgca	1213860
ttgattacca	tgatcggaga	taatctttct	tctccaaaag	ttgtctcaac	aattacggag	1213920
aaactcagag	gttttcaagg	acctgtatct	tgtttttgcc	aaagtccaat	ggcattaagc	1213980
tttgttgttg	cctcagagtt	ggcagagggg	attatagaag	aattacataa	tgattatgta	1214040
aaacaaaaag	ctatagtcgc	cacgtaggga	gaatcatgca	tttacttaca	gcaactgtta	1214100
cacctttttt	ccctaattggc	actatagatt	ttgctagctt	agaacgtctt	ttatcttttc	1214160
aagatgcagt	tgggaatgga	gtgggtcttt	tagggagcac	tggagaaggc	ctttcgctaa	1214220
caaaaaagga	aaaacaagca	ctgatttgct	ttgcttgtga	tctacagctt	aaagtccctc	1214280
tttttgttgg	gacttcggga	acccttctag	aggaagtctt	agattggatt	catttttgca	1214340
atgacttgcc	tatctcggga	ttcttaatga	caactcccat	ctatacgaag	cctaaactat	1214400
gcggtcaaat	cttatgggtc	gaagcagtac	tcaatgctgc	aaaacatccc	gcgattcttt	1214460
ataacattcc	atctcgtgca	gccacgccct	tatatattaga	tactgtaaaa	gcttggctc	1214520
atcatccaca	atctttggga	atcaaagatt	ctggaggctc	tgtagaagag	ttccagagtt	1214580
ataagagcat	cgctcctcat	atccaaactt	attgtggaga	cgatgttttt	tggagcgaga	1214640
tggcggcatg	tggagcccat	ggtttaatct	ctgtcttatc	gaatgcttgg	cctgaagaag	1214700
cccagagagta	tgtgctgaac	cctcaagaac	aagactatcg	ttctttatgg	atggagacgt	1214760
gtcgggtgggt	atataccaca	acaaatccta	ttggaattaa	agcgatcctt	gcctacaaaa	1214820
aagctattac	tcacgctcac	tgcgcttgcc	cttgtctata	gaagattttg	atttggagaa	1214880
tgtatctcct	gctgtagaaa	gtatgcttgc	ctggccgaag	ttacgtacct	ctgtgtctc	1214940
ctattcttaa	tgcaagaaaa	ccttatcttc	tgcatctaac	ttgttctaac	ttattacttt	1215000
acaaataaaa	tttttgcaaa	ggttttttct	agagaatagt	gcttttgctc	tggattttta	1215060
acaagatgag	tcgcattttt	ttcttctttt	tacatcgctt	atgatttttt	atgactccga	1215120
aatcgattca	acaattgcac	ttaataaaga	ctattgatcc	agtaagaaaa	atttctcctg	1215180
taacaacaaa	aaaatcttcg	ttcttttagac	agtctcttct	tagattttta	gaactatttt	1215240
ggatgtttct	ttactgtata	cgctctatta	gattccattg	tgttcatatc	gccaccttta	1215300
tctgtcgagg	tcttattctt	tttctgacta	ccttgttctt	atctatgata	tgcatcttgc	1215360
atttcattac	tcttccttgg	atctgtaagg	aagaccctcg	gattataaga	aaaaataaat	1215420
aatcttgttt	catcaccaag	aatcaggtca	tttgtctctc	atagtttctg	attttttttc	1215480
catttttgtc	gccatattca	agattttcaa	aatcgtgctt	cagctatact	gaggagttta	1215540
ttttgaataa	tttttcattc	aaaaaatgaa	atataattca	agagaaaaaa	taaaaagcgc	1215600
tttacggatt	tgctcttcat	attgtatcac	tgtctttcga	aataatttca	gtttaagttg	1215660
ttatgataaa	attttctatt	cgttgtcttg	ttatgttttc	aatggcccaa	acagtattgg	1215720
gcgctgccga	agtttttggt	tcttcagagg	aaaaaaaaact	gaagtagaaa	ctaaagaagt	1215780
gaaaatcaaa	gatgagattc	gtccttcatt	ggaaggaaat	gatcctgtaa	aagttgcgga	1215840
gtcattccct	aaaagaagag	cagctcttga	gtctttaagt	tctcaaagtt	ccatcgccaa	1215900
tctttgtgca	attagtaatt	tcttagattc	tcaaattgta	tctagaaatt	tctcaaaaga	1215960
gatctgggga	tctacaatct	tcacacgac	taaatctaca	tgtgatgccg	aaggatctga	1216020
gcctttccgt	tatactgcat	gtggatacct	agctggtctt	agatctaaac	tagcagggttc	1216080
ttatgaatta	ggtgtaactg	caggattgct	acagggacgc	cttaaagatg	tttcagatag	1216140
ccatagaact	cgtgcgacat	cttcaatatt	gtccgtgcat	ggtagtatgg	ttacaagacc	1216200
gttgagttgt	acgaagtata	tcgtaggaaa	agcgcgtcct	ttacttttct	tcttcagatt	1216260
aacatcgga	gtaagaagag	atttgaaaaa	aaagttcaga	cttgaatttt	gcaaagattg	1216320
atcacaatca	tctctacctt	acatgtttgg	gagatcttgg	tgtagcttgt	cctatacttt	1216380
ctacagattg	tctaccta	tatagcgaga	aagcatctca	tgagggttctt	gtttatagta	1216440
aatttagatg	catctctgga	gagccatctc	gacttgcaac	ttcaggaaat	gacacatatt	1216500
attctatagt	aagtttacct	ataggactcc	gttacgagtg	acttcaccat	caggacgtca	1216560

tgatttcaat	attgatatgc	atgtagctcc	aaagataggt	gcagtactct	ctcatggaac	1216620
acgagaggct	aaagagatcc	caggatcttc	aaaagactat	gcatttttta	gcttgactgc	1216680
tagagaaagt	ttaatgattt	ctgaaaagct	tgcatgact	ttccaagtta	gcgaagttat	1216740
tcagaattgt	tattcacaat	gtactaaagt	aacgaaaact	aattttaaag	aacagtatag	1216800
gcacttatcc	cacaatacag	ggtttgagtt	aagcgtcaag	tctgcattct	aaaaatagtt	1216860
cttgttctct	tggacttgaa	aaagccattc	ctatttgaaa	aaatgggaat	ggcttttttt	1216920
ataataggtc	gaaccaaaga	ggaacttggt	tcattaaaa	tacttaaaaa	gtgatatcgt	1216980
tttcttaata	caaagataaa	aatactcacc	aatatactcg	cacaaccttg	acaaaggaag	1217040
tttcttgtaa	gatctttttc	ggtttttata	agaaaattct	tctttagaag	gaagatgaat	1217100
ctctttgaat	aaaatactat	atattagtag	cttagtggtt	ttaattttatg	tgtttgatcg	1217160
cgatggcacc	acagattcat	aatgcaagta	cttctatctc	cgcagctacc	cccccccca	1217220
acactctgta	gggtcgattt	cttctccatc	taaacttcgc	gttttagcga	ttactttttt	1217280
agtttttggt	atgctcttac	tgatttcagg	agctctcttt	ctgacgttag	ggattccagg	1217340
attgagtgc	gcaatttctt	ttggattagg	catcggtctc	tccgcattag	gaggagtgt	1217400
gatgatttcg	ggactactat	gtcttttagt	aaaacgagag	attccgacag	tacgaccaga	1217460
agaaattcct	gaaggggttt	cgctggctcc	ttctgaggag	ccagctctac	aggcagctca	1217520
gaagacttta	gctcagctgc	ctaagggaat	ggatcagtta	gatacagata	ttcaggaagt	1217580
gttcgcatgt	ttaagaaagc	tgaaagattc	taagtatgaa	agtcgaagtt	ttttaaacga	1217640
tgctaagaag	gagcttcgag	tttttgactt	tgtggttgag	gataccctct	cggagatttt	1217700
cgagttgcgg	cagattgtgg	ctcaagaggg	atgggattta	aactttttga	tcaatggggg	1217760
acgaagcctc	atgatgactg	cagaatctga	atcgcttgat	ttgtttcatg	tatcgaagcg	1217820
gctaggggat	ttaccttctg	gggatgttcg	aggggagggg	ttaaagaaat	ctgcgaagga	1217880
gatagtgcgt	cgtttgatga	gcttgcatct	cgagattcac	aaggtggcgg	tagcgtttga	1217940
taggaattcc	tatgcatgg	cagaaaaggc	gtttgcgaaa	gcgttgggag	ctttagaaga	1218000
gagtgtgtat	cggagtctga	cgcagagtta	tagagataaa	tttttgagga	gtgagagggc	1218060
gaagatccca	tggaaatggc	atataacctg	gttaagagat	gatgccaaag	gtgggtgtgc	1218120
tgaaaagaag	cttcgggatg	ccgaggaacg	ttggaagaaa	tttaggaaag	cagtcttttg	1218180
ggtagaagaa	gacgggggct	ttgacatcaa	taatctcctt	ggagactggg	ggacagtgt	1218240
tgatccttat	agacaagaga	gaatggacga	gataacgttc	catgagttgt	atgaaaaaac	1218300
tacgtttttg	aaaagactgc	acagaaagtg	tgcgtttagcg	aaaacaacct	ttgaaaagaa	1218360
nagatctaaa	aagaatttgc	aggcagtcna	ggaggcgaat	gcacgtaggt	tgaaatatgt	1218420
aagggattgg	tatgatacag	antttcagaa	agcggggag	agattagaga	aactgcagtc	1218480
tttgtatcct	gaggtttcag	tctctataag	agagaacaaa	atacaagaga	cgcgctctaa	1218540
tttanagaaa	gcctatgagg	ctatcgana	gaactatcgt	tgctgtgtcc	gagagcaaga	1218600
ggactactgg	aaagaagaag	agaaaaggga	agcgganttt	agggagaggg	gaaacnagat	1218660
tctttctcct	gaggagctgg	aaanttcttt	ggagcaattc	gaccatgggt	tgaaaaattt	1218720
ttctgagaaa	ttaatggaat	tggaagggca	tatcttaaaa	cttcagaaaag	aagccacagc	1218780
agaggtggag	aataaaatac	tttcagatgc	agagagccgc	cttgagattg	tatttgaaag	1218840
tgtaaggag	atgccctgtc	gaattgagga	gatagagaag	acgctgcgta	tggcgganct	1218900
gcccctaggc	cctacgaaga	aggcgtttga	gaaggcctgc	tcacaatata	atagctgcgc	1218960
agagatgttg	gagaagggtga	agccttactg	caaggagagc	ctcgcctatg	tgactagcaa	1219020
agagcgttta	gtgagcttgg	atgaagattt	acgacgagcc	tacacagagt	gtcagaagag	1219080
attccagggg	gattcgggtt	tggagtcgga	agtaagagcc	tgctgagagc	aactgcgaga	1219140
gcggatccaa	gagtttgaaa	ctcaagggct	ggacttggtg	gaaaaagagt	tgctttgtgt	1219200
gagtagtaga	ttaagaaata	cagagtgcga	ttgtgtatct	ggtgttaaga	aagaagcacc	1219260
tcctggtaag	aagttttatg	cccagtatta	tgatgagatt	tatcgagtta	gagttcaatc	1219320
ccgatggatg	acgatgtctg	agagattgag	agagggagtt	caagcatgca	acaagatgtt	1219380
gaaggcaggc	ctaagcgaag	aagataagggt	tcttaagaaa	gaagagtatt	ggttgtatcg	1219440
agaggagaga	aagaataaag	agaaacgttt	ggttggtact	aagatagtag	caacgcagca	1219500
gcgagttgca	gcatttgaat	ccatagaagt	tcctgagatt	cctgaggccc	cagaggagaa	1219560
accgagtttg	ctggataaag	cgcgttcttt	atttactcgc	gaggaccata	cctagcataa	1219620
ctccaagagt	tgtgtttctt	taaaaattct	ttgaataaaa	tactatatgt	tagtagctta	1219680
gtgggtttta	cttatgtgtt	tgagcatgat	ggcgccacag	attcataatg	caagtacctc	1219740
tatcaccaca	gctaccccc	ccccccccag	accactctgt	aggggctttt	ttttgtctgt	1219800
ctaaattctg	tgtttttagca	atcacttttt	tagttcttgg	tgctgctttt	ttgattctcag	1219860
gagctctctt	tctgacgttg	gggatttctag	gattgagtgc	agcaatttct	tttggattag	1219920
gcataaggtct	ctctgcgtta	ggaggagtgc	ttgtgtctc	aggacttcta	tgtcttttag	1219980
caaaacgaga	ggttccgaca	gtacgaccag	aagaaattcc	tgaaggggtt	tctgtggctc	1220040
cttctgaaga	gccagctcta	caggcaactc	agaagacttt	agctcagctg	cctaaggaat	1220100
tggatcagtt	agatagggtat	attcaggaag	tggtctcatg	tttaggaaag	ctaaaagatc	1220160
ttaggtgtga	agatcaagggt	cttttaaaag	atgctaagga	gaaacttcaa	gtttttgact	1220220
ttgtctggaa	agacatgatg	accgagtttg	tagagctaca	acagatcatg	gatcaagagg	1220280
ggtggtatct	aaagtgcctg	attcaggaga	tgcgggatat	aggaagcaca	ctttttatga	1220340
gtcagggttag	tttatttaaa	ttatgggaat	ggcttgggta	tttaccttct	ggggatgttc	1220400

gaggggagcg	gttaaagaaa	tctgctcgtg	aggttggtga	tgcgtttatg	agaaggattt	1220460
gcgatacgcg	gaaggtggcc	atgacttttg	ataggaatgc	ctatggagtg	gcgaagacgg	1220520
cctttgaaaa	ggcttttgga	gctctggaaa	cgtgtgtata	taagagtatg	acagagagtt	1220580
atagagaggg	cttttgtgag	tataagaaga	cgaagatcct	tagggatgag	gagaagatat	1220640
taaggatatg	ttatctcgag	ttgaggagat	agagatgatg	cttcgtgtca	tagagcttcc	1220700
actacttcct	ataaagcaag	cgttggagaa	ggcttttgta	caatataata	gctacaaagc	1220760
gaagttaacc	aaggtagaac	cttgcttttag	agagagccct	gcctatataa	ctagcgaaga	1220820
gcgactcnag	agtttggatc	agacttttaga	acgtgcgtac	aaagagtacc	agaagagatt	1220880
ccaggagcct	tcacgtttgg	aatcggaagt	aagtggatgt	agagagcatc	ttagagagca	1220940
ggtaaaacaa	tttgaaactc	aaggactaga	cttgatcaaa	gaagagctta	tttttgttag	1221000
tgatgtgtta	ttccgaaaaa	tggtcagttg	tctagtgtcg	acagtgcattg	ttccctttat	1221060
ggagttttat	tatgagtatt	ttgagttgca	tagattgagg	ttgcgggccc	aatggatggc	1221120
gaatgccgag	atttatagca	aagtttagaaa	agcattccca	gagatgttga	aggagacctt	1221180
agaaaaagct	aaggctccca	gagaagaaga	gtattgggtta	ctttgcgagg	agagaaagag	1221240
taaggagaag	cgtttgattc	tcaacaagat	agaggcagct	cagcagcggg	taaaagattt	1221300
agaacctcct	cctattaaag	agacagggaa	acagaaaacg	aagaaagaat	attcgttttt	1221360
cattcgatta	aaatcgtgat	tcgaggcaac	cctgcattct	atagattttt	tctcagagtt	1221420
ctagtgtatc	aagtacgaag	aggaagaaa	acttttgtat	tttttgcatt	ctagaatttt	1221480
ttgttttgca	tagtattcgt	tatagaagt	ttttaattat	tactaactat	tttatttata	1221540
aaatgggttag	ctcttctgtt	catcataaga	attgtaaaat	gtgtattaaa	agacgagaat	1221600
tttattttaa	ataaattata	cacttttact	tttttaattt	tgctatgcct	gagcctctat	1221660
atacgaataa	gctaatacaca	gagaaatctc	catatttgct	tctttatgct	cataccctctg	1221720
ttaattggta	tccttgggga	gctgaggcat	ttcatattgc	agctatcgag	aataagcccc	1221780
tcttcttgct	tataggatgc	aagcattctc	gatgggtgca	gggtatgttg	caggagagct	1221840
acacgaatcc	tgaaattgct	gctatgctca	atgaatactt	cgtgaatgta	aaagtagata	1221900
aggaagaact	tccttatgta	gccaagctgt	atgggtgatc	tgctcagatg	cttgccggtt	1221960
ccggagatca	ccaagaaact	gtctcctggc	ctttaaacgt	ctttcttact	cccgatctcg	1222020
ttcctttttt	ctctgtaaac	tatttgggga	acgagggaaa	actcgggtct	ccctcattcc	1222080
cacaaattat	tgataagctt	cattttatgt	gggaggatgc	tgaggaaaaga	gaagctctcg	1222140
tcgaacaggc	aatgagattt	ctggaaatcg	cgtcgttttt	agaggggtgt	gtaagaaaag	1222200
agatctttaga	cgagagctct	ctaaagcgaa	ccgtagccgc	gttataccga	gatatcgatc	1222260
cccattatgg	aggagtgaag	gcatttctta	aacgattgcc	aggtttgctc	ttacaatttt	1222320
tcctccgata	cagcctcgaa	tatcaggaga	gccgaggctt	attttttgta	gatcgctctt	1222380
tgagtatggt	ggctttggga	ggagtctgag	atcacattgg	cgggggagtt	tattcataca	1222440
ctatcgacga	taagtgggtg	atccccgctt	ttgaaaaacg	gctgattgat	aatgccttaa	1222500
tggcttttaa	ttatttagaa	gcttgggcat	gtctgggcaa	agaagaatac	cgtggtatag	1222560
gaaaacagat	actttcctat	atcttgagtg	aattatactc	tccagaggtg	ggtgcctttt	1222620
atagctctga	gcaagcagaa	aattggggag	caggaggaca	aaatttttat	acatggctctg	1222680
tcgaagaaat	ctccaatgct	ttgggagaag	atgctgagat	ttctgtgat	tactacggga	1222740
tttctagggg	gggcttcttc	aatggcagga	atatactcca	tattcctgta	catagagaaa	1222800
tagaagagct	gtcagaaaaa	tatcatcggt	ctatagaggc	tattgaagat	atcgtagata	1222860
gatctcgaga	tatttttaag	gggattagag	cccaacgttc	ccatcggtct	aaagatgatc	1222920
tatctttaac	ttttaacaat	ggctggatga	tttatacttt	tgcttacgca	ggccgacttc	1222980
ttggagaggt	tgagtatatt	gagattgaga	aaaagtgtgg	ggaatttgct	cgaaattccc	1223040
tctataaaca	ccatgaactt	taccggagat	ggagagaggg	agaggcaaaa	tatcgagcga	1223100
gtttagaaga	ttatgggtgt	cttatttttag	gggtgctagc	tctttatgaa	tcaggatgtg	1223160
gatctttctg	gttaagcttt	gctgaagagc	tgatgcaaga	agtcgtcctt	tccttcggtt	1223220
cagaagaagg	aggtttttat	agtgatgatg	gtcgggatag	caccttgctg	atcaagcaat	1223280
ctcccccttc	tgatggagag	acgatctcag	gaaacgctct	aatctgtcaa	tgcttgctct	1223340
cactgcacct	aatcacagaa	aaaaaacact	acctgactta	tgctgaagac	atcttgcaga	1223400
tagctcaagc	atgtgctcat	accataaagt	tctcttcctt	aggattgctg	attgcacac	1223460
agaactattt	ttctagaaaa	catgtaaaag	ttttaatccc	tttaggggat	caagaagatc	1223520
gcagtcctgt	tttgaaatgt	ctctcaggtt	tattccttcc	ttatctatct	ctaatttgga	1223580
tgactcagga	gaaccaagaa	catttagaga	ctgtgcttcc	agaatatgag	cactgtctta	1223640
tccctaaaag	ggggattgca	cagctacgac	aaatttatgt	ttagaagtgc	atcaatgcaa	1223700
aagattttaa	gacttagaat	tgtttcgtcg	ttatctaatt	tctctataga	acgctatact	1223760
agttattgat	aaagtgtttt	ttactaatta	aaatttatct	tttttaggaa	agaaaacacc	1223820
ttctctcagt	ggtcaaaatt	accacaattc	cttatagtaa	agtcctctgg	gcagggtcaa	1223880
atctataggg	taggaagtca	tgaaattata	tcagaccttg	cgagggtattg	tttttagtaag	1223940
tacgggatgc	atattcttag	gaatgcacgg	aggatatgcc	gctgagggtc	cagtgcattc	1224000
atctgggtat	gagaatcttt	tagaatctaa	ggaacaggat	ccttcagggtc	tagcgatcca	1224060
cgatcgcatt	ttgtttaagg	tagatgaaga	gaatgtagtg	actgccttag	atgtgatcca	1224120
taaattaaac	ttactatttt	ataattcgta	tcctcatctt	atagattctt	tccttcgcacg	1224180
atcccagtag	tatactgcga	tgtggcctgt	ggttcttgaa	tctgtgattg	atgagttttt	1224240



gatggtggca	gatgccaaagg	caaagagaat	cgctacagat	cccaccgcag	tgaatcaaga	1224300
aatcgaagag	atgttcggaa	gagatctctc	tcctttgtat	gcgcattttg	aaatgagtc	1224360
caacgatatt	tttaatgtga	tcgatcgcac	tttgacagca	caaaggggtga	tgggtatgat	1224420
ggtgcgctct	aaggtaatgt	tgaaggtgac	tccagggaaa	attcgagaat	attaccgaaa	1224480
gctagaagaa	gaagcctcta	ggaaagtcac	ctggaagtat	cgtgtgttga	cgattaaagc	1224540
caacacagaa	tccttggcta	gccagattgc	tgataaagtg	cgtgctcgtc	taaatgaagc	1224600
gaaaacctgg	gataaagatc	gtttaactgc	tcttgtgac	tctcagggag	ggcaactcgt	1224660
ctgctccgaa	gagttttctc	gagagaatag	tgagctctcc	caaagccata	agcaagagct	1224720
ggacttgatt	ggctatccta	aagagctctg	tgggttgcc	aaggcacata	agtcaggata	1224780
taaactctat	atgttgttag	acaaaacctc	aggttctata	gagcctttag	atgttatgga	1224840
gtccaagatc	aaacagcatc	tttttgcctt	agaagctgag	agtgtagaga	aacaatataa	1224900
agacagatta	cgcaagcgct	acggctatga	tgcttctatg	attgcgaaac	ttctttctga	1224960
agaagctcca	cctctatttt	ccttattata	ggggattgag	tgacaagaag	ttctcctgca	1225020
caactctccc	ggtttctttc	tgaaattcaa	aataagccga	agaaaagcct	ctctcaaaat	1225080
ttcttagtgg	atcagaatat	tgtcaaaaaa	attgtggcaa	cctctgaggt	gattcctcaa	1225140
gattgggtgt	tggagatcgg	cccaggattt	ggagccctta	cagaagaact	catagctgca	1225200
ggagctcagg	tcattgctat	tgaaaaagac	ccgatgtttg	cgccatcttt	agaagagctc	1225260
cctatccgct	tagaaattat	cgatgcctgt	aaatacccg	tagatcagct	tcagggaatat	1225320
aagacttttg	gaaaaggctc	agtagtagca	aatcttccct	accatattac	cactccattg	1225380
cttaccaagt	tgtttctgga	agccccagat	ttctggaaaa	cagtgcaggt	tatgggtccaa	1225440
gatgaagtgg	cccggcgctat	tgtagccag	ccagggggta	gggattatgg	gtctctaacg	1225500
atctttttgc	agttttttgc	tgatatacac	tatgctttta	aagtttctgc	ttcatgcttc	1225560
tatccaaaac	cgcaagtgc	atctgcagtc	attcatatga	aagtcaaaga	aacacttcc	1225620
ctatcagacg	aggagattcc	tgtatttttt	actttaacaa	gaactgcatt	tcaacagcgt	1225680
cgaaaagtac	tcgctaatac	tctaaaaggc	ctctatccta	aagagcaagt	ggaacaagct	1225740
ttgaaggaat	taggattact	tctaaatgtg	cgctctgaag	tattgagctc	taatgattat	1225800
cttgcctctc	tccataagat	gcaagcgggt	taaaggctact	ttcccttcta	aggaaattac	1225860
aatctctagg	gataattaaa	ctctgacgct	tccaacagtc	tgcttttttg	atctgaagtt	1225920
gaaatgagtg	agaatgcggt	tggtcatact	actctcatca	aggcctatag	attttgtgag	1225980
ggcttcctta	ctcccatggg	ataggaatgt	atcggggatt	gcaaaaattta	agataticgac	1226040
cttaaaattg	aacgtagcta	caaaaattatt	aaactcggac	gctaattcctc	ctcgaattgga	1226100
gtgctcttct	atggtaatac	ccttagagtg	actcatcagt	aaaagactga	aaagatcggt	1226160
atcaaaaggt	tttataaaga	tcgggtctac	aacagttgctg	gagatgccat	aagcaagcaa	1226220
ctgatgtttt	atagataggg	ccgtgaagca	gaggggtcca	agagctatga	tgagaacgct	1226280
ctcaccttgt	gagaggggtc	cagcattgcc	tggggatctt	aggaaatttg	gatctccagt	1226340
gagtgggtct	ccatgaggag	ctgggatatt	ggggtagcgg	atagcagaag	gagaggacca	1226400
gtgtagagaa	gaatacagta	gctgttgga	taccacctgg	ctacgtggct	gacagataat	1226460
catctggggc	atcgcacgta	ggaaactcat	atcatagatg	ccgtgatgac	tacgtccatc	1226520
accataggga	agtcctgcac	gatctatagc	aaaaatcacg	ggaagatctt	gcatgcaaac	1226580
atcgtggaaa	acattatcga	gagcacggtg	taaaaatgta	gaatatatag	aacagatcac	1226640
aggattgccg	gcttttgcaa	tgcttgcact	gaaagtcact	gcatggcctt	cagcaatccc	1226700
tacatcaaag	aagcgtttctg	ggaacttctg	tttgaaacct	tccaaacgag	atcctataga	1226760
cattgcagga	gtcaccacat	ggagacgtga	ggaaacctct	ccaagttcac	atagcgtttg	1226820
gccaaatata	tcaggggaaag	aaggcttagg	cttaatcgca	ggaagatgtt	ttgcggattc	1226880
tcgcttattg	aagtttgctc	tgactccgtg	atactttgca	gggttatttt	gggcttggtc	1226940
taggcccttc	cccttagttg	tacagacgtg	gacaagaata	gaaaaaggga	ggttacgaac	1227000
ggactgaagg	atggggatca	gttttttaac	attatgaccg	tctatagggc	cgacatcacg	1227060
taatccgaat	tgttcaaata	aaggagtggg	acagaagaga	tttttaacac	attgtgaaag	1227120
tctccgactg	tgctttgcta	agctatcccc	atagcgtgga	attttagcga	gccatttttc	1227180
cacttgctta	gtgagtttat	tgggtgcagg	gtggtgtagc	catcgggaaa	agattcgaga	1227240
catggctcct	acgttttttag	agatcgacat	attgttgtca	ttcaaaaata	caacaaactt	1227300
cgataaatct	gttgaaatat	tgttcaacgc	ttctaaggta	agaccacaag	agaatgcagc	1227360
atctccaagg	atgggaatga	cgtgtgtgctg	tgattctaaa	gggggtgttt	gagccattcc	1227420
tagagctaaa	gacaatgccg	tccttgcattg	tccagagaaa	aataaatcgt	ggtcactctc	1227480
cgtagggttg	gtaaaaccac	tgaggccgtt	gtcattgcgt	atatgggtcaa	atccttcatt	1227540
atctcttctc	gtcagtagtt	tatgaggata	ggcttagtgt	ctcatatcaa	aaataaattt	1227600
atctttttggg	gaagagaaca	cgtaatgtaa	ggctatagta	agctctacga	ttccaagatt	1227660
tgaagataag	tggcctcctg	tttgtgataa	tacagagatg	atgcgataac	ggatttcttc	1227720
agctaaacca	ggaagctgag	aaatagagag	tttcttttaa	tctgcaggag	acaatatcag	1227780
gtctaaaagg	gggcaagaag	acgaagtcac	gaccttagtg	atgtggatgt	ataggaaaacg	1227840
tttggtactat	agggctctcca	gaaggacttt	tgaggagtgc	tcctttggag	ttaacagaaa	1227900
gaagataaca	tagttgatct	tttcttaatg	ctttatttaa	tccttcatag	atcaaaagaaa	1227960
acatggcctc	atatgtagct	acaatatcac	tcaaagagtt	taaggtttct	aaagattgtt	1228020
gtaaggcgaa	taactttttt	aatgaggggt	ctttgtgatg	gatttctacc	ataagactac	1228080



```

cgaactacag cttgttcctc aaagagagaa ctttcatgac gcttttctgc caactcacgg 1228140
actcttttgct ctacttgctg aatacgagat tcacaaatac gcattaaggc atcagcttct 1228200
tcatataggg ctagagatgc atccaaagaa gtcgtgggtt gattcataag gtcaacaatt 1228260
tcttctagtc gttgcattgc attttcgaag gggacctctt ccatgattta gccttttata 1228320
agtttacaaa tttcaatatt tgtgacagtt aaaatggcct cgccatcttg caactgaatc 1228380
cttacacgag cattttcttg taagctgtct acggaaatca tagcggaatt ttcattaaag 1228440
tcaaagagca ttgcataccc gcgttttaaa acatttttcg gatttaaaga gtgaagtgtg 1228500
tcttttagcg cagagtagcg ggcaacagaa ttttcgtaac gacgttctag aattgttgct 1228560
aaagtttctt tgacatttgc ataggcgatt ttttggtttt gtagatttag ctgcctcct 1228620
ctcgatagac gtctgcctaa tagttccagt ttctgcacat ggctacggag ctgttgctct 1228680
aagacattgt gagcatgctt gagtcgtgtg tgtttatgaa aatattcttc tttttggtag 1228740
tgaggcgctc gtgaaattag ggtgtctagc tgttgacgcc aaggggataa tttctgtgat 1228800
gcctgttgga tttggcgagg ataggtaagg cttttcttta gttggtggca acgtacttgg 1228860
agagaaaagt ctttatggga tagggcttgt gaaagcattt ttttcaaact ttgcagtcgg 1228920
caggtcatgc gggaacaag atctccttgg agccaccgag agatgttgct atagcgttgt 1228980
ttgctttcgt gaattttccc ttggacacct ttttgaatag cgatctcaat agagtcgagt 1229040
tgctgttggt cgttagtata gaattctgcg cgatctaaaa agcgtctcca gggaagcaat 1229100
tgctgttttt ttgatgtgag gagttggcga gagtgtgaga gtagatggcg gaggtatccc 1229160
tcgaacacct gaacttgctc ttcgctactt ttacagacga tctctgcggc tgcagaagga 1229220
gtgggagcac gcacatcaga agcaaagtca cataaagtgt aatcagtttc atggccgaca 1229280
gcagagacaa tagggattgt gcttgcatga atggctttaa ctaagatttc ttcgttaaag 1229340
gcccagagat cttcaatact tctcctctcc cgagcaataa taagaacgtc agcgaggttc 1229400
tcagcgttca tcacttcaat agccttggag atttcatgag ctgcagagtt cccttggaca 1229460
gtgacgggat aaactaaaa tttatagtgt cgagcacgcc gggagagtag acgtaagata 1229520
tcttggatca cagctcctgt tgggctagta atgacgccaa tgcattgagg agcaaagggg 1229580
aggggcttct ttttttcagt tgcgaaatac ccttcagcag tcagacgtct ttttgtttct 1229640
tcaaattttt gtaggagatc gccctctcca gcgtaaacca aagcatgggc tacaatttgg 1229700
tactgtcctc taggagcata gaccgcaagc ttcccatgaa taataactgc atccccatct 1229760
ttgggtttgc ggtcatagta cttactttta aaatgaaaaa aggcaccatt aagaaacgct 1229820
tggctatcct taatcccaaa atagagatga ccacttggtt gtaggagac gttgctaagc 1229880
tcgcccttca ctatgatctg acaaaaattg gactcaagaa gagtcttaat gcgttcagtt 1229940
agggatgcaa cagcctgtgg aggcgatgac ataacaggaa agcctctcta gagaattcag 1230000
tgactttaga gtaagtgatt ttctg 1230025

```

&lt;210&gt;2

&lt;211&gt;251

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;2

```

Met Arg Ile Lys Phe Arg Glu Asn Lys Glu Arg Lys Met Thr Arg Gln
 1           5           10           15
Ser Tyr Val Leu Gly Asn Trp Lys Met His Lys Thr Ile Gln Glu Ala
          20          25          30
Lys Glu Tyr Val Gln Thr Leu Ala Ser Xaa Leu Gln Gly Glu Pro Leu
          35          40          45
Ser Cys Thr Ile Gly Ile Ala Ser Pro Phe Thr Ser Leu Arg Ala Ile
          50          55          60
His Glu Met Ile Asn Thr Thr Gly Ala Phe Leu Trp Leu Gly Ala Gln
          65          70          75          80
Asn Val His Pro Glu Leu Ser Gly Ala Phe Thr Gly Glu Ile Ser Leu
          85          90          95
Pro Met Leu Lys Glu Val Gly Val Glu Phe Val Leu Val Gly His Ser
          100         105         110
Glu Arg Arg His Ile Phe Gly Glu Ser Asp Ala Phe Ile Ala Ser Lys
          115         120         125
Val Lys Ser Val Ala Gln Ala Gly Leu Val Pro Val Leu Cys Val Gly
          130         135         140
Glu Ser Leu Glu Val Arg Glu Glu Gly Lys Ala His Gln Val Ile Lys
          145         150         155         160
Lys Gln Leu Leu Leu Gly Leu Glu Gln Met Asp Asn Gly Ser Glu Phe
          165         170         175
Leu Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys Val Ala
          180         185         190
Glu Ala Ser Asp Val Gln Asp Ile His Met Phe Cys Arg Glu Val Val
          195         200         205

```

Ala Glu Arg Phe Ser Glu Ala Thr Ala Glu Glu Ile Ser Ile Leu Tyr  
 210 215 220  
 Gly Gly Ser Val Lys Val Asp Asn Ala Gln Arg Phe Gly Gln Cys Ser  
 225 230 235 240  
 Asp Val Asp Gly Leu Leu Val Gly Gly Xaa Leu  
 245 250

&lt;210&gt;3

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;3

Ser Met Ser Leu Asn Lys Glu Ile Gly Met Thr Val Leu Phe Tyr Ala  
 1 5 10 15  
 Phe Leu Phe Ile Phe Leu Phe Leu Cys Val Ile Leu Cys Gly Leu Ile  
 20 25 30  
 Leu Val Gln Glu Ser Lys Ser Met Gly Leu Gly Ser Ser Phe Gly Val  
 35 40 45  
 Asp Ser Gly Asp Ser Val Phe Gly Val Ser Thr Pro Asp Ile Leu Lys  
 50 55 60  
 Lys Val Thr Ser Xaa Cys Ala Val Ala Phe Cys Ile Gly Cys Leu Leu  
 65 70 75 80  
 Leu Ser Phe Ser Thr Asn Leu Leu Gly Lys Lys Leu Asp Ala Lys Glu  
 85 90 95  
 Phe Leu Leu Pro Ala Ala Glu Glu Ser Asp Thr Gln Ala Ser Ser Glu  
 100 105 110  
 Ser Val Glu Ala Asp Glu Ser  
 115

&lt;210&gt;4

&lt;211&gt;204

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;4

Val Leu Val Val Arg Asp Phe Phe Thr Glu Leu Cys Gln Ala His Val  
 1 5 10 15  
 Gln Thr Met Ile Arg Arg Leu Glu Tyr Tyr Gly Ser Pro Ile Leu Arg  
 20 25 30  
 Lys Lys Ser Ser Pro Ile Ala Glu Ile Thr Asp Glu Ile Arg Asn Leu  
 35 40 45  
 Val Ser Asp Met Cys Asp Thr Met Glu Ala His Arg Gly Val Gly Leu  
 50 55 60  
 Ala Ala Pro Gln Val Gly Lys Asn Val Ser Leu Phe Val Met Cys Val  
 65 70 75 80  
 Asp Arg Glu Thr Glu Asp Gly Glu Leu Ile Phe Ser Glu Ser Pro Arg  
 85 90 95  
 Val Phe Ile Asn Pro Val Leu Ser Asp Pro Ser Glu Thr Pro Ile Ile  
 100 105 110  
 Gly Lys Glu Gly Cys Leu Ser Ile Pro Gly Leu Arg Gly Glu Val Phe  
 115 120 125  
 Arg Pro Gln Lys Ile Thr Val Thr Ala Met Asp Leu Asn Gly Lys Ile  
 130 135 140  
 Phe Thr Glu His Leu Glu Gly Phe Thr Ala Arg Ile Ile Met His Glu  
 145 150 155 160  
 Thr Asp His Leu Asn Gly Val Leu Tyr Ile Asp Leu Met Glu Glu Pro  
 165 170 175  
 Lys Asp Pro Lys Lys Phe Lys Ala Ser Leu Glu Lys Ile Lys Arg Arg  
 180 185 190  
 Tyr Asn Thr His Leu Ser Lys Glu Glu Leu Val Ser  
 195 200

&lt;210&gt;5

&lt;211&gt;301

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;5

Met Ser Cys Met Pro Pro Pro Phe Val Val Thr Leu Thr Thr Ser Ala

1 5 10 15  
 Gln Asn Asn Leu Arg Asp Gln Leu Lys Glu Lys Asn Phe Ile Phe Ser  
 20 25 30  
 Gln Pro Gln Asn Thr Val Phe Gln Ala Arg Ser Asn Thr Val Thr Cys  
 35 40 45  
 Thr Leu Tyr Pro Ser Gly Lys Leu Val Ile Gln Gly Lys Gly Ser Glu  
 50 55 60  
 Glu Phe Ile Glu Phe Phe Leu Glu Pro Glu Ile Leu His Thr Phe Thr  
 65 70 75 80  
 His Ala Arg Val Glu Gln Asp Leu Arg Pro Arg Leu Gly Val Asp Glu  
 85 90 95  
 Ser Gly Lys Gly Asp Phe Phe Gly Pro Leu Cys Ile Ala Ala Val Tyr  
 100 105 110  
 Ala Ser Asn Ala Glu Ile Leu Lys Lys Leu Tyr Glu Asn Lys Val Gln  
 115 120 125  
 Asp Ser Lys Asn Leu Lys Asp Thr Lys Ile Ala Ser Leu Ala Arg Ile  
 130 135 140  
 Ile Arg Ser Leu Cys Val Cys Asp Val Ile Ile Leu Tyr Pro Glu Lys  
 145 150 155 160  
 Tyr Asn Glu Leu Tyr Gly Lys Phe Gln Asn Leu Asn Thr Leu Leu Ala  
 165 170 175  
 Trp Ala His Ala Thr Val Ile Asn Asn Leu Ala Pro Lys Pro Ala Gly  
 180 185 190  
 Asp Val Phe Ala Ile Ser Asp Gln Phe Ala Ala Ser Glu Tyr Thr Leu  
 195 200 205  
 Leu Lys Ala Leu Gln Lys Lys Glu Thr Asp Ile Thr Leu Ile Gln Lys  
 210 215 220  
 Pro Arg Ala Glu Gln Asp Val Val Val Ala Ala Ala Ser Ile Leu Ala  
 225 230 235 240  
 Arg Asp Ala Phe Val Gln Ser Ile Gln Lys Leu Glu Glu Gln Tyr Gln  
 245 250 255  
 Val Gln Leu Pro Lys Gly Ala Gly Phe Asn Val Lys Ala Ala Gly Arg  
 260 265 270  
 Glu Ile Ala Lys Gln Arg Gly Lys Glu Leu Leu Ala Lys Ile Ser Lys  
 275 280 285  
 Thr His Phe Lys Thr Phe Asp Glu Ile Cys Ser Gly Lys  
 290 295 300  
 <210>6  
 <211>143  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>6  
 Met Gln Glu His Ile His Lys Glu Leu Leu His Leu Gly Glu Ile Phe  
 1 5 10 15  
 Arg Ser Ser Arg Glu Ser Gln Ser Leu Ser Leu Lys Asp Val Glu Ala  
 20 25 30  
 Ala Thr Ser Ile Arg Tyr Ser Cys Leu Glu Ala Ile Glu Gln Gly Cys  
 35 40 45  
 Leu Gly Lys Leu Ile Ser Pro Val Tyr Ala Gln Gly Phe Ile Lys Lys  
 50 55 60  
 Tyr Ala Thr Tyr Leu Gly Leu Asp Gly Asp Ser Ile Leu Gln Glu His  
 65 70 75 80  
 Pro Tyr Val Met Lys Ile Phe Lys Glu Phe Ser Asp His Asn Met Glu  
 85 90 95  
 Met Leu Leu Asp Leu Glu Ser Met Gly Gly Arg Asn Ser Pro Glu Arg  
 100 105 110  
 Ala Ile His Ser Trp Ser Asn Leu Trp Trp Ala Gly Leu Ile Ile Ile  
 115 120 125  
 Gly Gly Ile Met Val Trp Trp Leu Gly Ser Leu Phe Ser Ile Phe  
 130 135 140  
 <210>7  
 <211>460  
 <212>PRT  
 <213>Chlamydia pneumoniae

<400>7  
 Arg Arg Ser Leu Met Thr Phe Pro Cys Gly Asn Cys Asn Cys Tyr Tyr  
           1                  5                  10                  15  
 Arg Glu Thr Pro Pro Pro Asn Pro Gly Gly Glu Asp Ile Pro Leu Gln  
                   20                  25                  30  
 Glu Gly Gly Gln Ser Gly Ser Gln Gly Gly Arg Val Ile Thr Gln Gln  
           35                  40                  45  
 Pro Gly Thr Gly Gly Arg Glu Met Gly Ile Ser Leu Gly Ser Asp Asn  
           50                  55                  60  
 Val Leu Gly Met Val Glu Gln Ala Gly Ser Leu Leu Asn Asn Leu Leu  
           65                  70                  75                  80  
 Asp Ser Ala Arg Met Gln Arg Leu Gly His Tyr Cys Tyr Arg Thr Gly  
                   85                  90                  95  
 Thr Pro Trp Cys Arg Glu His Cys Pro Gly Phe Leu Gln Trp Ile Trp  
                   100                  105                  110  
 Gly Gly Cys Cys Ala Cys Cys Leu Glu Thr Val Asp Asp Pro Asp Asn  
           115                  120                  125  
 Pro Ser Ala Gln Phe Leu Gln Gln Leu Ile Gln Gln Tyr Gly Pro Ile  
           130                  135                  140  
 Cys Val Gly Met Ser Phe Gln Gln Leu Pro His Cys Thr Gln Lys Ile  
           145                  150                  155                  160  
 Glu Gln Gly Glu Pro Leu Gly Asp Gly Asp Lys Gln Glu Val Glu Asn  
                   165                  170                  175  
 Gly Cys Lys Leu His Arg Glu Leu Leu Lys Ala Ala Gln Pro Arg Cys  
           180                  185                  190  
 Met Gly Glu Ser Leu Val Lys Leu Leu Gln Asn Asn Gly Leu Gly Glu  
           195                  200                  205  
 Asp Met Gln Gln Thr Pro Pro Trp Ser Leu Ile Leu Gln Ala Val Ser  
           210                  215                  220  
 Glu Gly Ala Leu Ser Phe Val Thr Ser Ser Asp Asn Pro Pro Thr Cys  
           225                  230                  235                  240  
 Trp Ile Leu Gln Pro Glu Gln Gln Pro Cys Pro Pro Pro Pro Thr Asp  
                   245                  250                  255  
 Glu Glu Gln Leu Gln Gly Ala Val Gly Gly Ala Pro Ala Pro Gln Gln  
           260                  265                  270  
 Lys Lys His Pro Ala Gln Glu Cys Arg Val Thr Cys Lys Leu Asn Phe  
           275                  280                  285  
 Arg Thr Leu Leu Gln Lys Leu Ser Arg Leu Glu Val Leu Ser Leu Glu  
           290                  295                  300  
 Ser Gly Tyr Lys Gly Pro Leu Gly Gln Ala Ala Lys Gln Ile Val Asp  
           305                  310                  315                  320  
 Leu Ile Lys Lys Ser Leu Lys Arg Leu Val Ala Ser Asp Leu Ala Thr  
                   325                  330                  335  
 Phe Leu Gly Pro Gly Ile Gly Leu Ser Leu Glu Ser Gln Val Phe Glu  
           340                  345                  350  
 Val Leu Val Leu Leu Cys Leu Leu Ser Lys Gly Tyr Leu Pro Leu Asp  
           355                  360                  365  
 Pro Leu His Pro Glu Gln Thr Val Leu Asp Pro Arg Val Gln Gly Pro  
           370                  375                  380  
 Trp Gln Arg Ile Leu Arg Lys Val Leu Val Thr Thr Thr Ala Gly Glu  
           385                  390                  395                  400  
 Asn Ile Trp Arg Gln Thr Gln Gly Glu Ala Pro Arg Gln Ala Pro Pro  
                   405                  410                  415  
 Pro Pro Asp Pro Trp Asp Asp Asp Glu Ile Glu Arg Asp Gly Ile Val  
           420                  425                  430  
 Thr Gly Gly Gly Phe Gly Ile Pro Cys Gln Cys Leu Arg Cys Trp Arg  
           435                  440                  445  
 Lys Leu Pro Thr Glu Lys Arg Pro Asn Arg Trp Leu  
           450                  455                  460

&lt;210&gt;8

&lt;211&gt;484

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;8

Lys Gly Thr Thr Met Val Cys Pro Asn Asn Ser Trp Phe Arg Met Cys  
 1 5 10 15  
 Gly Asn Phe Asn Cys Glu Trp Val Glu Val Thr Thr Thr Glu Glu Thr  
 20 25 30  
 Thr Arg Gln Ser Ala Ser Asp Ile Ser Glu Glu Ala Gly Ser Ser Gly  
 35 40 45  
 Gly Ala Ala Pro Ile Thr Thr Glu Pro Thr Lys Ile Thr Lys Val Glu  
 50 55 60  
 Lys Arg Val Gln Phe Asn Thr Ala Gln Gly Asp Glu Ser Thr Ile His  
 65 70 75 80  
 Met Ile Gln Glu Ala Gly Glu Leu Val Asp Ser Ile Leu Ser His Arg  
 85 90 95  
 Arg Thr Gln Gly Cys Thr Glu Tyr Cys Tyr Asp Ser Tyr Ala Thr Gly  
 100 105 110  
 Cys Gly Gln Arg Cys Gly Ser Phe Gly Arg Leu Ile Cys Gly Thr Tyr  
 115 120 125  
 Lys Ala Cys Cys Leu Asp Arg Glu Asp Asn Gln Val Ala Gly Leu Val  
 130 135 140  
 His Glu Cys Glu Gln Thr His Gly Pro Ile Ala Val Ala Leu Ala Ala  
 145 150 155 160  
 Lys Thr Met Gly Leu Asn Leu Met Glu Leu Val Glu Lys Asn Thr Ile  
 165 170 175  
 Leu Ser Glu Glu Gln Lys Asn Glu Phe Arg Gln His Cys Ser Glu Ala  
 180 185 190  
 Lys Thr Gln Leu Tyr Gly Thr Met Gln Ser Leu Ser Gln Asn Phe Phe  
 195 200 205  
 Leu Glu Gly Val Asn Ser Ile Arg Glu Arg Gly Leu Asp Asp Ser Leu  
 210 215 220  
 Val Gln Ala Val Leu Ser Phe Ile Ala Thr Arg Ser Trp Glu Lys Thr  
 225 230 235 240  
 Ile Glu Ser Glu Glu Ala Ser Gly Thr Ser Ser Ala Ser Asn Ser Thr  
 245 250 255  
 Arg Ile Pro Ala Cys Tyr Ile Leu Asn Thr Ser Pro Leu Thr Thr Ser  
 260 265 270  
 Arg Leu Ser Cys Gly Ser Arg Asp Ala Arg Arg Pro Ser Ser Val Gly  
 275 280 285  
 Ala Glu Pro Gln Tyr Val Ala Lys Lys Tyr Asn Asp Asn Gly Met Ala  
 290 295 300  
 Arg Gln Leu Gly Lys Ile Gln Val Thr Asn Leu Lys Thr Gly Asp Phe  
 305 310 315 320  
 Ser Ala Leu Gly Pro Phe Gly Leu Leu Ile Val Lys Met Leu Asn Ser  
 325 330 335  
 Phe Leu Leu Ser Ala Ser Gln Ser Thr Ser Ser Ile Leu Lys His Thr  
 340 345 350  
 Gly Gly Glu Ile Cys Tyr Thr Cys Pro Asn Phe Arg Asp Ile Val Val  
 355 360 365  
 Leu Leu Met Leu Ala Ile Gly Tyr Cys Pro Ala Asn Thr Asp Glu Thr  
 370 375 380  
 Ser Val Val Asp Ile His Met Ile Asp Asp Pro Ile Met Thr Ile Phe  
 385 390 395 400  
 Tyr Arg Leu Gln Tyr Ser Tyr Arg Thr Gly Lys Thr Ser Ala Ser Phe  
 405 410 415  
 Leu Lys Lys Lys Pro Ser Leu Val Arg Gln Glu Ser Leu Asp Cys Pro  
 420 425 430  
 Thr Pro Ala Glu Ser Val Pro Leu Met Ser Ser Leu Glu Glu Glu Asp  
 435 440 445  
 Glu Asn Glu Asp Asp Asp Glu Asp Gly Asn Leu Ala Tyr Gln Gln Arg  
 450 455 460  
 Ile Leu Glu Cys Ser Gly His Leu Gln Thr Leu Phe Leu Gly Ile Lys  
 465 470 475 480  
 Ile Asn Lys Glu

&lt;210&gt;9

&lt;211&gt;304

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;9

Lys Lys Asp Tyr Ile Leu His Ala Asn Trp Cys Cys Trp Lys Gln Met  
 1 5 10 15  
 Leu Lys Ile Gln Lys Lys Arg Met Cys Val Ser Val Val Ile Thr Val  
 20 25 30  
 Gly Ala Ile Val Gly Phe Phe Asn Ser Ala Asp Ala Ala Pro Lys Lys  
 35 40 45  
 Lys Lys Ile Pro Ile Gln Ile Leu Tyr Ser Phe Thr Lys Val Ser Ser  
 50 55 60  
 Tyr Leu Lys Asn Glu Asp Ala Ser Thr Ile Phe Cys Val Asp Val Asp  
 65 70 75 80  
 Arg Gly Leu Leu Gln His Arg Tyr Leu Gly Ser Pro Gly Trp Gln Glu  
 85 90 95  
 Thr Arg Arg Arg Gln Leu Phe Lys Ser Leu Glu Asn Gln Ser Tyr Gly  
 100 105 110  
 Asn Glu Arg Leu Gly Glu Glu Thr Leu Ala Ile Asp Ile Phe Arg Asn  
 115 120 125  
 Lys Glu Cys Leu Glu Ser Glu Ile Pro Glu Gln Met Glu Ala Ile Leu  
 130 135 140  
 Ala Asn Ser Ser Ala Leu Val Leu Gly Ile Ser Ser Phe Gly Ile Thr  
 145 150 155 160  
 Gly Ile Pro Ala Thr Leu His Ser Leu Leu Arg Gln Asn Leu Ser Phe  
 165 170 175  
 Gln Lys Arg Ser Ile Ala Ser Glu Ser Phe Leu Leu Lys Ile Asp Ser  
 180 185 190  
 Ala Pro Ser Asp Ala Ser Val Phe Tyr Lys Gly Val Leu Phe Arg Gly  
 195 200 205  
 Glu Thr Ala Ile Val Asp Ala Leu Ser Gln Leu Phe Ala Gln Leu Asp  
 210 215 220  
 Leu Ser Pro Lys Lys Ile Phe Leu Gly Glu Asp Pro Glu Val Val  
 225 230 235 240  
 Gln Ala Val Gly Ser Ala Cys Ile Gly Trp Gly Met Asn Phe Leu Gly  
 245 250 255  
 Leu Val Tyr Tyr Pro Ala Gln Glu Ser Leu Phe Ser Tyr Val His Pro  
 260 265 270  
 Tyr Ser Thr Ala Thr Glu Leu Gln Glu Ala Gln Gly Leu Gln Val Ile  
 275 280 285  
 Ser Asp Glu Val Ala Gln Leu Thr Leu Asn Ala Leu Pro Lys Met Asn  
 290 295 300

&lt;210&gt;10

&lt;211&gt;277

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;10

Arg Ile Phe Met Arg Arg Tyr Leu Phe Met Val Leu Ala Leu Cys Leu  
 1 5 10 15  
 Tyr Arg Ala Ala Pro Leu Glu Ala Val Val Ile Lys Ile Thr Asp Ala  
 20 25 30  
 Gln Ala Val Leu Lys Phe Ala Arg Glu Lys Thr Leu Val Cys Phe Asn  
 35 40 45  
 Ile Glu Asp Thr Val Val Phe Pro Lys Gln Met Val Gly Gln Ser Ala  
 50 55 60  
 Trp Leu Tyr Asn Arg Glu Leu Asp Leu Lys Thr Thr Leu Ser Glu Glu  
 65 70 75 80  
 Gln Ala Arg Glu Gln Ala Phe Leu Glu Trp Met Gly Ile Ser Phe Leu  
 85 90 95  
 Val Asp Tyr Glu Leu Val Ser Ala Asn Leu Arg Asn Val Leu Thr Gly  
 100 105 110  
 Leu Ser Leu Lys Arg Ser Trp Val Leu Gly Ile Ser Gln Arg Pro Val  
 115 120 125  
 His Leu Ile Lys Asn Thr Leu Arg Ile Leu Arg Ser Phe Asn Ile Asp  
 130 135 140

Phe Thr Ser Cys Pro Ala Ile Cys Glu Asp Gly Trp Leu Ser His Pro  
 145 150 155 160  
 Thr Lys Asp Thr Thr Phe Asp Gln Ala Met Ala Ile Glu Lys Asn Ile  
 165 170 175  
 Leu Phe Val Gly Ser Leu Lys Asn Gly Gln Pro Met Asp Ala Ala Leu  
 180 185 190  
 Glu Val Leu Leu Ser Gly Ile Ser Ser Pro Pro Ser Gln Ile Ile Tyr  
 195 200 205  
 Val Asp Gln Asp Ala Glu Arg Leu Arg Ser Ile Gly Ala Phe Cys Lys  
 210 215 220  
 Lys Ala Asn Ile Tyr Phe Ile Gly Met Leu Tyr Thr Pro Ala Lys Gln  
 225 230 235 240  
 Arg Val Glu Ser Tyr Asn Pro Lys Leu Thr Ala Ile Gln Trp Ser Gln  
 245 250 255  
 Ile Arg Lys Asn Leu Ser Asp Glu Tyr Tyr Glu Ser Leu Leu Ser Tyr  
 260 265 270  
 Val Lys Ser Lys Gly  
 275

&lt;210&gt;11

&lt;211&gt;109

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;11

Lys Arg Leu Lys Asp Glu Ile Lys Tyr Thr Ser Leu Arg Arg Lys Ala  
 1 5 10 15  
 Met Leu Gly Lys Ile Ile Arg Gly Leu Ser Ser Leu Ile Val Ile Leu  
 20 25 30  
 Cys Ala Leu Asn Val Gly Leu Ile Gly Ile Thr His Asn Lys Leu Asn  
 35 40 45  
 Ile Ile Ala Lys Leu Cys Gly Gly Val Ser Thr Pro Ala Thr Gln Ile  
 50 55 60  
 Thr Tyr Ile Ile Ile Gly Ile Ala Gly Val Ile Cys Leu Leu Ser Phe  
 65 70 75 80  
 Cys Pro Phe Cys Ser Lys Lys Ser Arg His Ser His Gly Asp Ser Cys  
 85 90 95  
 Ser Ser Gly Gly Cys His Ser His His Ser Asp Lys Asn  
 100 105

&lt;210&gt;12

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;12

His Met Glu Gln Phe His Leu Asp Arg Glu Glu Ile Leu Leu Leu Ala  
 1 5 10 15  
 Lys Ala Ser Ala Leu Gln Leu Ser Glu Leu Ile Gln Glu Tyr Gln  
 20 25 30  
 Thr Ser Leu Ser Ala Val Ile Thr Ser Met Lys Glu Ala Leu Ala Ile  
 35 40 45  
 Glu Ile Asp Asp Ala Asp Ser Cys Glu Ser Leu Phe Met His Val Val  
 50 55 60  
 Asn Val Glu Asp Leu Arg Glu Asp Ser Val Thr Ser Asp Phe Asn Arg  
 65 70 75 80  
 Glu Glu Phe Leu Arg Asn Val Pro Glu Ser Leu Gly Gly Leu Val Lys  
 85 90 95  
 Val Pro Ala Val Ile Lys  
 100

&lt;210&gt;13

&lt;211&gt;494

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;13

Lys Ile Met Tyr Arg Tyr Ser Ala Leu Glu Leu Ala Lys Ala Val Thr  
 1 5 10 15  
 Leu Gly Glu Leu Thr Ala Thr Gly Val Thr Gln His Phe Phe His Arg

```

      20      25      30
Ile Glu Glu Ala Glu Gly Gln Val Gly Ala Phe Ile Ser Leu Cys Lys
      35      40      45
Glu Gln Ala Leu Glu Gln Ala Glu Leu Ile Asp Lys Lys Arg Ser Arg
      50      55      60
Gly Glu Pro Leu Gly Lys Leu Ala Gly Val Pro Val Gly Ile Lys Asp
      65      70      75      80
Asn Ile His Val Thr Gly Leu Lys Thr Thr Cys Ala Ser Arg Val Leu
      85      90      95
Glu Asn Tyr Gln Pro Pro Phe Asp Ala Thr Val Val Glu Arg Ile Lys
      100      105      110
Lys Glu Asp Gly Ile Ile Leu Gly Lys Leu Asn Met Asp Glu Phe Ala
      115      120      125
Met Gly Ser Thr Thr Leu Tyr Ser Ala Phe His Pro Thr His Asn Pro
      130      135      140
Trp Asp Leu Ser Arg Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala
      145      150      155      160
Ala Val Ser Ala Arg Phe Cys Pro Val Ala Leu Gly Ser Asp Thr Gly
      165      170      175
Gly Ser Ile Arg Gln Pro Ala Ala Phe Cys Gly Val Val Gly Phe Lys
      180      185      190
Pro Ser Tyr Gly Ala Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser
      195      200      205
Ser Leu Asp Gln Ile Gly Pro Leu Ala Asn Thr Val Glu Asp Val Ala
      210      215      220
Leu Met Met Asp Val Phe Ser Gly Arg Asp Pro Lys Asp Ala Thr Ser
      225      230      235      240
Arg Glu Phe Phe Arg Asp Ser Phe Met Ser Lys Leu Ser Thr Glu Val
      245      250      255
Pro Lys Val Ile Gly Val Pro Arg Thr Phe Leu Glu Gly Leu Arg Asp
      260      265      270
Asp Ile Arg Glu Asn Phe Phe Ser Ser Leu Ala Ile Phe Glu Gly Glu
      275      280      285
Gly Thr His Leu Val Asp Val Glu Leu Asp Ile Leu Ser His Ala Val
      290      295      300
Ser Ile Tyr Tyr Ile Leu Ala Ser Ala Glu Ala Ala Thr Asn Leu Ala
      305      310      315
Arg Phe Asp Gly Val Arg Tyr Gly Tyr Arg Ser Pro Gln Ala His Thr
      325      330      335
Ile Ser Gln Leu Tyr Asp Leu Ser Arg Gly Glu Gly Phe Gly Lys Glu
      340      345      350
Val Met Arg Arg Ile Leu Leu Gly Asn Tyr Val Leu Ser Ala Glu Arg
      355      360      365
Gln Asn Val Tyr Tyr Lys Lys Ala Thr Ala Val Arg Ala Lys Ile Val
      370      375      380
Lys Ala Phe Arg Thr Ala Phe Glu Lys Cys Glu Ile Leu Ala Met Pro
      385      390      395
Val Cys Ser Ser Pro Ala Phe Glu Ile Gly Glu Ile Leu Asp Pro Val
      405      410      415
Thr Leu Tyr Leu Gln Asp Ile Tyr Thr Val Ala Met Asn Leu Ala Tyr
      420      425      430
Leu Pro Ala Ile Ala Val Pro Ser Gly Phe Ser Lys Glu Gly Leu Pro
      435      440      445
Leu Gly Leu Gln Ile Ile Gly Gln Gln Gly Gln Asp Gln Gln Val Cys
      450      455      460
Gln Val Gly Tyr Ser Phe Gln Glu His Ala Gln Ile Lys Gln Leu Phe
      465      470      475      480
Ser Lys Arg Tyr Ala Lys Ser Val Val Leu Gly Gly Gln Ser
      485      490

```

&lt;210&gt;14

&lt;211&gt;500

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;14



Glu Ile Cys Gln Lys Cys Cys Ser Arg Arg Ser Ile Met Ser Ala Val  
 1 5 10 15  
 Tyr Ala Asp Trp Glu Ser Val Ile Gly Leu Glu Val His Val Glu Leu  
 20 25 30  
 Asn Thr Ala Ser Lys Leu Phe Ser Ser Ala Leu Asn Arg Phe Gly Asp  
 35 40 45  
 Glu Pro Asn Thr Asn Ile Ser Thr Val Cys Thr Gly Leu Pro Gly Ser  
 50 55 60  
 Leu Pro Val Leu Asn Gln Ser Ala Val Glu Lys Ala Val Leu Phe Gly  
 65 70 75 80  
 Cys Ala Val Glu Gly Glu Ile Ser Leu Leu Ser Arg Phe Asp Arg Lys  
 85 90 95  
 Ser Tyr Phe Tyr Pro Asp Ser Pro Arg Asn Phe Gln Ile Thr Gln Phe  
 100 105 110  
 Glu His Pro Ile Ile Arg Gly Gly Arg Ile Lys Ala Ile Val Gln Gly  
 115 120 125  
 Glu Glu Arg Tyr Phe Glu Leu Ala Gln Thr His Ile Glu Asp Asp Ala  
 130 135 140  
 Gly Met Leu Lys His Phe Gly Glu Phe Ala Gly Val Asp Tyr Asn Arg  
 145 150 155 160  
 Ala Gly Val Pro Leu Ile Glu Ile Val Ser Lys Pro Cys Met Phe Cys  
 165 170 175  
 Pro Glu Asp Gly Cys Cys Tyr Ala Thr Ser Leu Val Ser Leu Leu Asp  
 180 185 190  
 Tyr Ile Gly Ile Ser Asp Cys Asn Met Glu Glu Gly Ser Ile Arg Phe  
 195 200 205  
 Asp Val Asn Val Ser Val Arg Pro Lys Gly Ser Pro Glu Leu Arg Asn  
 210 215 220  
 Lys Val Glu Ile Lys Asn Met Asn Ser Phe Ala Phe Met Ala Gln Ala  
 225 230 235 240  
 Leu Glu Ala Glu Lys Gln Arg Gln Ile Asp Glu Tyr Leu Asn Gln Pro  
 245 250 255  
 Asn Lys Asp Pro Lys Leu Val Ile Pro Ala Ala Thr Tyr Arg Trp Asp  
 260 265 270  
 Pro Glu Lys Lys Lys Thr Val Leu Met Arg Leu Lys Glu Ser Ala Glu  
 275 280 285  
 Asp Tyr Lys Tyr Phe Pro Glu Pro Asp Leu Pro Thr Leu Gln Leu Thr  
 290 295 300  
 Glu Ser Tyr Ile Glu Arg Ile Arg Lys Thr Leu Pro Glu Leu Pro Tyr  
 305 310 315 320  
 Asp Lys Tyr His Arg Tyr Ile Gln Glu Tyr Gly Leu Ser Glu Asp Ile  
 325 330 335  
 Ala Ser Ile Leu Ile Ser Asp Lys Asn Ile Ala Thr Phe Phe Glu Val  
 340 345 350  
 Ala Cys Lys Asp Cys Lys Asn Phe Arg Ser Leu Ser Asn Trp Val Thr  
 355 360 365  
 Val Glu Phe Gly Gly Arg Cys Lys Thr Leu Gly Val Lys Leu Pro Ser  
 370 375 380  
 Ser Gly Ile Phe Pro Glu Gly Val Ala Gln Leu Val Asn Ala Ile Asp  
 385 390 395 400  
 Gln Gly Val Ile Thr Gly Lys Ile Ala Lys Glu Ile Ala Asp Leu Met  
 405 410 415  
 Met Glu Ser Pro Gly Lys Asn Pro Glu Glu Ile Leu Lys Glu Lys Pro  
 420 425 430  
 Glu Leu Leu Pro Met Ser Asp Glu Gly Glu Leu Gln Lys Ile Ile Ala  
 435 440 445  
 Glu Val Val Leu Ala Asn Pro Glu Ser Ile Val Asp Tyr Lys Asn Gly  
 450 455 460  
 Lys Thr Lys Ala Leu Gly Phe Leu Val Gly Gln Ile Met Lys Arg Thr  
 465 470 475 480  
 Ala Gly Lys Ala Pro Pro Lys Arg Val Asn Glu Leu Leu Leu Leu Glu  
 485 490 495  
 Leu Asp Lys Gly  
 500

&lt;210&gt;15

&lt;211&gt;922

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;15

```

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu
 1          5          10          15
Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
          20          25          30
Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
          35          40          45
Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
          50          55          60
Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Xaa Val Thr
          65          70          75          80
Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Xaa Tyr Phe Asn
          85          90          95
Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
          100          105          110
Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
          115          120          125
Asn Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
          130          135          140
Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
          145          150          155          160
Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
          165          170          175
Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
          180          185          190
Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
          195          200          205
Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
          210          215          220
Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
          225          230          235          240
Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
          245          250          255
Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
          260          265          270
Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
          275          280          285
Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
          290          295          300
Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
          305          310          315          320
Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
          325          330          335
Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
          340          345          350
Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
          355          360          365
Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr
          370          375          380
Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
          385          390          395          400
Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
          405          410          415
Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
          420          425          430
Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
          435          440          445
Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
          450          455          460
Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala

```

465 470 475 480  
 Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys  
 485 490 495  
 Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu  
 500 505 510  
 Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser  
 515 520 525  
 Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val  
 530 535 540  
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe  
 545 550 555 560  
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly  
 565 570 575  
 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu  
 580 585 590  
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg  
 595 600 605  
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp  
 610 615 620  
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Leu Phe His Val Ser Ala  
 625 630 635 640  
 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu  
 645 650 655  
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe  
 660 665 670  
 Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu  
 675 680 685  
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu  
 690 695 700  
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly  
 705 710 715 720  
 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe  
 725 730 735  
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala  
 740 745 750  
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile  
 755 760 765  
 Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu  
 770 775 780  
 Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr  
 785 790 795 800  
 Gln Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn  
 805 810 815  
 Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys  
 820 825 830  
 Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile  
 835 840 845  
 Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile  
 850 855 860  
 Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala  
 865 870 875 880  
 Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu  
 885 890 895  
 Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr  
 900 905 910  
 Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe  
 915 920

&lt;210&gt;16

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;16

Ala Leu Pro Val Gly Glu Ile Ser Ser Ile Glu Ser Val Thr Asp Ile  
 1 5 10 15

Cys Leu Phe Ala Val Phe Ala Leu Ile Thr Ala Ala Val Glu Asp Glu  
                   20                                  25                  30  
 Leu Lys Leu Ser Ile Ser Ile Ala Arg Pro Val Met Ala Met Ser Ser  
                   35                                  40                  45  
 Leu Glu Ala Ile Ser Leu Val Pro Lys Ser Lys Thr Lys Cys Asp Pro  
                   50                                  55                  60  
 Gly Asp Cys Val Asn Phe Glu Thr Val Thr Ser Ala Pro Ser Leu Ile  
                   65                                  70                  75                  80  
 Thr Lys Tyr Pro Ala Asp Arg Leu Thr Phe  
                                   85                                  90

&lt;210&gt;17

&lt;211&gt;1003

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;17

Lys Ser Phe Arg Tyr Asn Leu Ser Leu Ile Phe Ser Phe Leu Val Val  
   1                                  5                                  10                                  15  
 Ile Pro Leu Thr Asp Ser Thr Thr Ser Ser Leu Ser Thr Ser Leu Leu  
                   20                                  25                                  30  
 Asp Glu Gly Asn Pro Gln Ser Met Arg Lys Leu Arg Ile Leu Ala Ile  
                   35                                  40                                  45  
 Val Leu Ile Ala Leu Ser Ile Ile Leu Ile Ala Gly Gly Val Val Leu  
                   50                                  55                                  60  
 Leu Thr Val Ala Ile Pro Gly Leu Ser Ser Val Ile Ser Ser Pro Ala  
                   65                                  70                                  75                                  80  
 Gly Met Gly Ala Cys Ala Leu Gly Cys Val Met Leu Ala Leu Gly Ile  
                                   85                                  90                                  95  
 Asp Val Leu Leu Lys Lys Arg Glu Val Pro Ile Val Leu Ala Ser Val  
                   100                                  105                                  110  
 Thr Thr Thr Pro Gly Thr Gly Ser Pro Arg Ser Gly Ile Ser Ile Ser  
                   115                                  120                                  125  
 Gly Ala Asp Ser Thr Ile Arg Ser Leu Pro Thr Tyr Leu Leu Asp Glu  
                   130                                  135                                  140  
 Gly His Pro Gln Ser Met Arg Lys Leu Arg Ile Leu Ala Ile Val Leu  
                   145                                  150                                  155                                  160  
 Ile Val Phe Ser Ile Ile Leu Ile Ala Ser Gly Val Val Leu Leu Thr  
                                   165                                  170                                  175  
 Val Ala Ile Pro Gly Leu Ser Ser Val Ile Ser Ser Pro Ala Gly Met  
                   180                                  185                                  190  
 Gly Ala Cys Ala Leu Gly Cys Val Met Leu Ala Leu Gly Ile Asp Val  
                   195                                  200                                  205  
 Leu Leu Lys Lys Arg Glu Val Pro Ile Val Leu Ala Ser Val Thr Thr  
                   210                                  215                                  220  
 Thr Pro Gly Thr Gly Ser Pro Arg Ser Gly Ile Ser Ile Ser Gly Ala  
                   225                                  230                                  235                                  240  
 Asp Ser Thr Ile Arg Ser Leu Pro Thr Tyr Pro Leu Asp Glu Gly His  
                                   245                                  250                                  255  
 Pro Gln Ser Met Arg Lys Leu Arg Ile Leu Ala Ile Val Leu Ile Val  
                   260                                  265                                  270  
 Phe Ser Ile Ile Leu Ile Ala Ser Gly Val Val Leu Leu Thr Val Ala  
                   275                                  280                                  285  
 Ile Pro Gly Leu Ser Ser Ile Ile Ser Ser Pro Ala Glu Met Gly Ala  
                   290                                  295                                  300  
 Cys Ala Leu Gly Cys Val Met Leu Ala Leu Gly Ile Asp Val Leu Leu  
                   305                                  310                                  315                                  320  
 Lys Lys Arg Glu Val Pro Ile Val Val Pro Ala Pro Ile Pro Glu Glu  
                                   325                                  330                                  335  
 Val Val Ile Asp Asp Ile Asp Glu Glu Ser Ile Arg Leu Gln Gln Glu  
                   340                                  345                                  350  
 Ala Glu Ala Ala Leu Ala Arg Leu Pro Glu Glu Met Ser Ala Phe Glu  
                   355                                  360                                  365  
 Gly Tyr Ile Lys Val Val Glu Ser His Leu Glu Asn Met Lys Ser Leu  
                   370                                  375                                  380  
 Pro Tyr Asp Gly His Gly Leu Glu Glu Lys Thr Lys His Gln Ile Arg

```

385          390          395          400
Val Val Arg Ser Ser Leu Lys Ala Met Val Pro Glu Phe Leu Asp Ile
          405          410          415
Arg Arg Ile Phe Glu Glu Glu Glu Phe Phe Leu Ser Ala Arg Lys
          420          425          430
Arg Leu Ile Asp Leu Ala Thr Thr Leu Val Glu Arg Lys Ile Leu Thr
          435          440          445
Glu Gln Leu Glu Arg Asn Asn Leu Arg Lys Ala Phe Ser Tyr Leu Tyr
          450          455          460
Gln Asp Ser Ile Phe Lys Lys Ile Ile Asp Asn Phe Glu Lys Leu Ala
465          470          475
Trp Lys Phe Met Ile Leu Ser Lys Ser Ile Cys Arg Phe Thr Ile Ile
          485          490          495
Phe Glu Asn His Glu His Gly Val Ala Lys Ser Leu Leu His Lys Asn
          500          505          510
Ala Val Leu Leu Glu Lys Val Ile Tyr Arg Ser Leu Gln Lys Ser Tyr
          515          520          525
Arg Asp Ile Gly Met Ser Ser Ala Lys Met Lys Ile Leu His Gly Asn
530          535          540
Pro Phe Phe Ser Leu Glu Asp Asn Lys Lys Thr Ile Met Lys Glu His
545          550          555
Ala Glu Met Leu Glu Ser Leu Ser Ser Tyr Arg Lys Val Phe Leu Ala
          565          570          575
Leu Ser Asp Glu Asn Val Val Asp Thr Pro Ser Asp Pro Lys Lys Trp
          580          585          590
Asp Leu Ser Gly Ile Pro Cys Arg Asp Ala Leu Ser Glu Ile Ser Arg
          595          600          605
Asp Glu Gln Trp Gln Lys Lys Ala His Leu Lys His Gln Glu Ser Leu
          610          615          620
Tyr Thr Gln Ala Arg Asp Arg Leu Thr Asp Gln Ser Ser Lys Glu Asn
625          630          635
Gln Lys Glu Leu Glu Lys Ala Glu Gln Glu Tyr Ile Ser Ser Trp Glu
          645          650          655
Arg Val Lys Lys Phe Glu Ile Glu Arg Val Gln Glu Arg Ile Gln Ala
          660          665          670
Ile Gln Lys Leu Tyr Pro Asn Ile Leu Glu Arg Glu Glu Glu Thr Thr
          675          680          685
Gly Gln Glu Thr Val Thr Pro Thr Val Gln Gly Thr Thr Ala Ser Ser
          690          695          700
Asp Leu Thr Asp Ile Leu Gly Arg Ile Glu Val Ser Ser Arg Glu Asp
705          710          715
Asn Gln Asn Gln Glu Ser Cys Val Lys Val Leu Arg Ser His Glu Val
          725          730          735
Glu Met Ser Trp Glu Val Lys Gln Glu Tyr Gly Pro Lys Lys Lys Glu
          740          745          750
Phe Gln Asp Gln Met Gly Ser Leu Glu Arg Phe Phe Thr Glu His Ile
          755          760          765
Glu Glu Leu Glu Val Leu Gln Lys Asp Tyr Ser Lys His Leu Ser Tyr
          770          775          780
Phe Lys Lys Val Asn Asn Lys Lys Glu Val Gln Tyr Ala Lys Phe Arg
785          790          795
Leu Lys Val Leu Glu Ser Asp Leu Glu Gly Ile Leu Ala Gln Thr Glu
          805          810          815
Ser Ala Glu Ser Leu Leu Thr Gln Glu Leu Leu Pro Ile Leu Ala Thr
          820          825          830
Arg Gly Ala Leu Glu Lys Ala Val Phe Lys Gly Ser Leu Cys Cys Ala
          835          840          845
Leu Ala Ser Lys Ala Lys Pro Tyr Phe Glu Glu Asp Pro Arg Phe Gln
          850          855          860
Asp Ser Asp Thr Gln Leu Arg Ala Leu Thr Leu Arg Leu Gln Glu Ala
865          870          875
Lys Ala Ser Leu Glu Glu Glu Ile Lys Arg Phe Ser Asn Leu Glu Asn
          885          890          895
Asp Ile Ala Glu Glu Arg Arg Leu Leu Lys Glu Ser Lys Gln Thr Phe

```

900 905 910  
 Glu Arg Ala Gly Leu Gly Val Leu Arg Glu Ile Ala Val Glu Ser Thr  
 915 920 925  
 Tyr Asp Leu Arg Ser Leu Thr Asn Thr Trp Glu Gly Thr Pro Glu Ser  
 930 935 940  
 Glu Lys Val Tyr Phe Ser Met Tyr Leu Asn Tyr Tyr Asn Glu Glu Lys  
 945 950 955 960  
 Arg Arg Xaa Lys Thr Arg Leu Val Glu Met Thr Gln Arg Tyr Arg Asp  
 965 970 975  
 Phe Lys Met Ala Leu Glu Ala Met Gln Phe Asn Glu Glu Ala Leu Leu  
 980 985 990  
 Gln Glu Glu Leu Ser Ile Gln Ala Pro Ser Glu  
 995 1000

&lt;210&gt;18

&lt;211&gt;302

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;18

Cys Lys Tyr Ser Tyr Leu Leu Asn Tyr Pro Pro Pro Pro Arg Arg Ser  
 1 5 10 15  
 Leu Gly Val Ser Cys Ser Lys Leu Arg Ser Leu Ser Ile Thr Leu Leu  
 20 25 30  
 Val Leu Gly Val Leu Leu Leu Thr Leu Gly Ile Pro Gly Leu Thr Ala  
 35 40 45  
 Gly Ile Ser Phe Gly Ala Gly Leu Gly Phe Ser Ala Leu Gly Gly Val  
 50 55 60  
 Leu Val Ile Ser Gly Leu Leu Phe Leu Leu Val Arg Arg Glu Val Pro  
 65 70 75 80  
 Thr Val Arg Ser Glu Glu Ile Pro Arg Gly Val Ser Val Thr Pro Ser  
 85 90 95  
 Glu Glu Pro Ala Leu Glu Lys Ala Gln Lys Glu Pro Glu Thr Lys Lys  
 100 105 110  
 Ile Leu Asp Arg Leu Pro Lys Glu Leu Asp Gln Leu Asp Thr Tyr Ile  
 115 120 125  
 Gln Glu Val Phe Ala Cys Leu Glu Arg Leu Lys Asp Pro Lys Tyr Glu  
 130 135 140  
 Asp Arg Gly Leu Leu Thr Glu Ala Lys Glu Lys Leu Arg Val Phe Asp  
 145 150 155 160  
 Val Val Glu Lys Asp Met Met Ser Glu Phe Leu Asp Ile Gln Arg Val  
 165 170 175  
 Leu Asn Glu Glu Ala Tyr Tyr Val Glu His Cys Gln Asp Pro Leu Glu  
 180 185 190  
 Asn Ile Ala Tyr Glu Ile Phe Ser Ser Gln Glu Leu Arg Asp Tyr Tyr  
 195 200 205  
 Cys Ala Gly Val Cys Gly Tyr Leu Pro Ser Gly Asp Ala Arg Ala Asp  
 210 215 220  
 Arg Leu Lys Arg Ser Val Lys Glu Val Met Asp Arg Phe Met Arg Val  
 225 230 235 240  
 Thr Trp Lys Ser Trp Glu Ala Ser Val Met Leu Asp His Ser Tyr Gly  
 245 250 255  
 Val Ala Arg Glu Leu Phe Lys Lys Ala Val Gly Val Leu Glu Glu Ser  
 260 265 270  
 Val Tyr Lys Ile Leu Phe Lys Ser Tyr Arg Asp Ala Phe Tyr Glu Cys  
 275 280 285  
 Glu Lys Ala Lys Ile Gln Arg Asp Gly Arg Phe Lys Trp Leu  
 290 295 300

&lt;210&gt;19

&lt;211&gt;477

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;19

Asp Thr Ser Ala His Ala Glu Gln Arg Phe Arg Asp Ile Asn Gly Cys  
 1 5 10 15  
 Trp Glu Asp Leu Lys Gln Thr Ile Phe Trp Val Gly Glu His Asp Cys

335

Gly Ser Ile Ser Ser Pro Ser Lys Leu Arg Val Leu Ala Ile Thr Phe  
                     20                    25                    30  
 Leu Val Phe Gly Met Leu Leu Leu Ile Ser Gly Ala Leu Phe Leu Thr  
                     35                    40                    45  
 Leu Gly Ile Pro Gly Leu Ser Ala Ala Ile Ser Phe Gly Leu Gly Ile  
                     50                    55                    60  
 Gly Leu Ser Ala Leu Gly Gly Val Leu Met Ile Ser Gly Leu Leu Cys  
                     65                    70                    75                    80  
 Leu Leu Val Lys Arg Glu Ile Pro Thr Val Arg Pro Glu Glu Ile Pro  
                     85                    90                    95  
 Glu Gly Val Ser Leu Ala Pro Ser Glu Glu Pro Ala Leu Gln Ala Ala  
                     100                    105                    110  
 Gln Lys Thr Leu Ala Gln Leu Pro Lys Glu Leu Asp Gln Leu Asp Thr  
                     115                    120                    125  
 Asp Ile Gln Glu Val Phe Ala Cys Leu Arg Lys Leu Lys Asp Ser Lys  
                     130                    135                    140  
 Tyr Glu Ser Arg Ser Phe Leu Asn Asp Ala Lys Lys Glu Leu Arg Val  
                     145                    150                    155                    160  
 Phe Asp Phe Val Val Glu Asp Thr Leu Ser Glu Ile Phe Glu Leu Arg  
                     165                    170                    175  
 Gln Ile Val Ala Gln Glu Gly Trp Asp Leu Asn Phe Leu Ile Asn Gly  
                     180                    185                    190  
 Gly Arg Ser Leu Met Met Thr Ala Glu Ser Glu Ser Leu Asp Leu Phe  
                     195                    200                    205  
 His Val Ser Lys Arg Leu Gly Tyr Leu Pro Ser Gly Asp Val Arg Gly  
                     210                    215                    220  
 Glu Gly Leu Lys Lys Ser Ala Lys Glu Ile Val Ala Arg Leu Met Ser  
                     225                    230                    235                    240  
 Leu His Cys Glu Ile His Lys Val Ala Val Ala Phe Asp Arg Asn Ser  
                     245                    250                    255  
 Tyr Ala Met Ala Glu Lys Ala Phe Ala Lys Ala Leu Gly Ala Leu Glu  
                     260                    265                    270  
 Glu Ser Val Tyr Arg Ser Leu Thr Gln Ser Tyr Arg Asp Lys Phe Leu  
                     275                    280                    285  
 Glu Ser Glu Arg Ala Lys Ile Pro Trp Asn Gly His Ile Thr Trp Leu  
                     290                    295                    300  
 Arg Asp Asp Ala Lys Ser Gly Cys Ala Glu Lys Lys Leu Arg Asp Ala  
                     305                    310                    315                    320  
 Glu Glu Arg Trp Lys Lys Phe Arg Lys Ala Val Phe Trp Val Glu Glu  
                     325                    330                    335  
 Asp Gly Gly Phe Asp Ile Asn Asn Leu Leu Gly Asp Trp Gly Thr Val  
                     340                    345                    350  
 Leu Asp Pro Tyr Arg Gln Glu Arg Met Asp Glu Ile Thr Phe His Glu  
                     355                    360                    365  
 Leu Tyr Glu Lys Thr Thr Phe Leu Lys Arg Leu His Arg Lys Cys Ala  
                     370                    375                    380  
 Leu Ala Lys Thr Thr Phe Glu Lys Lys Arg Ser Lys Lys Asn Leu Gln  
                     385                    390                    395                    400  
 Ala Val Glu Glu Ala Asn Ala Arg Arg Leu Lys Tyr Val Arg Asp Trp  
                     405                    410                    415  
 Tyr Asp Gln Glu Phe Gln Lys Ala Gly Glu Arg Leu Glu Lys Leu His  
                     420                    425                    430  
 Ala Leu Tyr Pro Glu Val Ser Val Ser Ile Arg Glu Asn Lys Ile Gln  
                     435                    440                    445  
 Glu Thr Arg Ser Asn Leu Glu Lys Ala Tyr Glu Ala Ile Glu Glu Asn  
                     450                    455                    460  
 Tyr Arg Cys Cys Val Arg Glu Gln Glu Asp Tyr Trp Lys Glu Glu Glu  
                     465                    470                    475                    480  
 Lys Arg Glu Ala Glu Phe Arg Glu Arg Gly Asn Lys Ile Leu Ser Pro  
                     485                    490                    495  
 Glu Glu Leu Glu Ser Ser Leu Glu Gln Phe Asp His Gly Leu Lys Asn  
                     500                    505                    510  
 Phe Ser Glu Lys Leu Met Glu Leu Glu Gly His Ile Leu Lys Leu Gln  
                     515                    520                    525



Lys Glu Ala Thr Ala Glu Val Glu Asn Lys Ile Leu Ser Asp Ala Glu  
 530 535 540  
 Ser Arg Leu Glu Ile Val Phe Glu Asp Val Lys Glu Met Pro Cys Arg  
 545 550 555 560  
 Ile Glu Glu Ile Glu Lys Thr Leu Arg Met Ala Glu Leu Pro Leu Leu  
 565 570 575  
 Pro Thr Lys Lys Ala Phe Glu Lys Ala Cys Ser Gln Tyr Asn Ser Cys  
 580 585 590  
 Ala Glu Met Leu Glu Lys Val Lys Pro Tyr Cys Lys Glu Ser Leu Ala  
 595 600 605  
 Tyr Val Thr Ser Lys Glu Arg Leu Val Ser Leu Asp Glu Asp Leu Arg  
 610 615 620  
 Arg Ala Tyr Thr Glu Cys Gln Lys Arg Phe Gln Gly Asp Ser Gly Leu  
 625 630 635 640  
 Glu Ser Glu Val Arg Ala Cys Arg Glu Gln Leu Arg Glu Arg Ile Gln  
 645 650 655  
 Glu Phe Glu Thr Gln Gly Leu Asp Leu Val Glu Lys Glu Leu Leu Cys  
 660 665 670  
 Val Ser Ser Arg Leu Arg Asn Thr Glu Cys Asp Cys Val Ser Gly Val  
 675 680 685  
 Lys Lys Glu Ala Pro Pro Gly Lys Lys Phe Tyr Ala Gln Tyr Tyr Asp  
 690 695 700  
 Glu Ile Tyr Arg Val Arg Val Gln Ser Arg Trp Met Thr Met Ser Glu  
 705 710 715 720  
 Arg Leu Arg Glu Gly Val Gln Ala Cys Asn Lys Met Leu Lys Ala Gly  
 725 730 735  
 Leu Ser Glu Glu Asp Lys Val Leu Lys Glu Glu Glu Tyr Trp Leu Tyr  
 740 745 750  
 Arg Glu Glu Arg Lys Asn Lys Glu Lys Arg Leu Val Gly Thr Lys Ile  
 755 760 765  
 Val Ala Thr Gln Gln Arg Val Ala Ala Phe Glu Ser Ile Glu Val Pro  
 770 775 780  
 Glu Ile Pro Glu Ala Pro Glu Glu Lys Pro Ser Leu Leu Asp Lys Ala  
 785 790 795 800  
 Arg Ser Leu Phe Thr Arg Glu Asp His Ser  
 805 810

&lt;210&gt;21

&lt;211&gt;83

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;21

Glu Trp Ser Ser Arg Val Asn Lys Glu Arg Ala Leu Ser Ser Lys Leu  
 1 5 10 15  
 Gly Phe Ser Ser Gly Ala Ser Gly Ile Ser Gly Thr Ser Met Asp Ser  
 20 25 30  
 Asn Ala Ala Thr Arg Cys Cys Val Ala Thr Ile Leu Val Pro Thr Lys  
 35 40 45  
 Arg Phe Ser Leu Phe Phe Leu Ser Ser Arg Tyr Asn Gln Tyr Ser Ser  
 50 55 60  
 Ser Leu Arg Thr Leu Ser Ser Ser Leu Arg Pro Ala Phe Asn Ile Leu  
 65 70 75 80  
 Leu His Ala

&lt;210&gt;22

&lt;211&gt;246

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;22

Phe Trp Tyr Ser Ile Met Thr Ala Ala Pro Ala Ile Leu His Val Ser  
 1 5 10 15  
 Pro Thr Pro Pro Glu Glu Thr Lys Phe Val Ile Pro Lys Asp Ser Lys  
 20 25 30  
 Ser Arg Ala Leu Gly Ile Thr Leu Leu Val Val Gly Ile Leu Leu Val  
 35 40 45

Val Cys Gly Ala Ile Val Leu Ser Gly Val Ile Ser Gly Leu Ser Ala  
 50 55 60  
 Leu Ile Val Cys Gly Leu Gly Ile Ser Thr Ile Ser Leu Gly Val Val  
 65 70 75 80  
 Leu Phe Val Leu Gly Leu Ile Leu Leu Arg Lys Arg Glu Leu Thr  
 85 90 95  
 Leu Glu Gln Ile Glu Ala Lys Gln Ile Ala Glu Thr Phe Ala Asp Glu  
 100 105 110  
 Leu Lys Glu Leu Glu Met Tyr Ile Gln Ser Thr Glu Lys Ser Leu Glu  
 115 120 125  
 Lys Ile Glu Gly Ser Arg Tyr Ser Asp Gln Gly Phe Leu Asn Arg Ala  
 130 135 140  
 Thr Gln Lys Ile Leu Asp Leu Glu Ser Ser Leu Ser Ser Ile Thr Ser  
 145 150 155 160  
 Glu Phe Arg Asp Leu Arg Gln Leu Phe Asp Glu Glu Lys Ile Glu Leu  
 165 170 175  
 Leu Ser Gly Glu Arg Leu Leu Glu Phe Ile Ala Ala Asn Leu Phe Lys  
 180 185 190  
 Gln Gly Arg Asp Val Tyr Leu Asn Leu Gly Asn Leu Ala Asp Ile Arg  
 195 200 205  
 Ala Tyr Met Gly Pro Asn Asn Tyr Lys Val Ala Met Val Ile Glu Lys  
 210 215 220  
 Ala Lys Ala Val Val His Glu Phe Ile Val Leu Thr Thr Met Ala Arg  
 225 230 235 240  
 Glu Leu Glu Phe Phe Phe  
 245

&lt;210&gt;23

&lt;211&gt;265

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;23

Gly Ile Arg Val Phe Phe Leu Lys Asn Lys Tyr Gly Leu Leu Lys Gly  
 1 5 10 15  
 Met Tyr Gln Glu Asn Leu Arg Leu Leu Glu Arg Leu Leu Tyr Asn Ser  
 20 25 30  
 Val Gln Lys Ser Tyr Ala Asp Arg Leu Phe Ser Tyr Glu Lys Thr Lys  
 35 40 45  
 Met Val His Asp Thr Pro Leu Ile Pro Trp Glu Glu Asp Lys Glu Lys  
 50 55 60  
 Cys Ala Glu Ala Glu Lys Ala Phe Leu Glu Gln Gln Lys Ile Leu Leu  
 65 70 75 80  
 Asp Tyr Gly Lys Ser Ile Phe Trp Leu Asn Glu Asn Asp Glu Ile Asn  
 85 90 95  
 Leu Asn Asp Pro Trp Ser Trp Gly Leu Asn Thr Val Arg Thr Arg Lys  
 100 105 110  
 Val Phe Gln Glu Val Asp Asp Ser Glu Arg Trp Asn His Lys Val Leu  
 115 120 125  
 Ile Gln Lys Leu Glu Asp Asp Tyr Glu Lys Leu Leu Glu Glu Ser Ser  
 130 135 140  
 Lys Glu Ser Thr Glu Ala Asn Lys Lys Leu Leu Ser Asp Leu Val Asp  
 145 150 155 160  
 Arg Leu Glu Asp Ala Lys Thr Lys Phe Phe Leu Lys Lys Gln Glu Glu  
 165 170 175  
 Val Glu Thr Arg Val Lys Asp Leu Arg Ala Arg Tyr Gly Gly Thr Val  
 180 185 190  
 Asp Pro Lys Gln Asp Thr Glu Ala Lys Lys Lys Val Glu Leu Glu Ala  
 195 200 205  
 Ser Leu Glu Thr Phe Leu Asp Ser Ile Glu Ser Glu Leu Val Gln Cys  
 210 215 220  
 Leu Glu Asp Gln Asp Ile Tyr Trp Lys Glu Gln Asp Val Lys Asp Leu  
 225 230 235 240  
 Ala Arg Thr Gln Glu Leu Glu Glu Gln Asp Ile Glu Ala Lys Arg Glu  
 245 250 255  
 Glu Ala Ala Glu Asp Leu Arg Lys Ser

260 265

<210>24  
 <211>277  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>24

Glu Ser Leu Asn Glu Arg Leu Lys Lys Ser Lys Thr Met Leu Asp Arg  
 1 5 10 15  
 Ala Lys Trp His Ile Glu Asn Ala Glu Asp Ser Ile Thr Trp Trp Thr  
 20 25 30  
 Ser Gln Ile Glu Met Lys Asp Met Lys Ala Arg Leu Lys Ile Leu Lys  
 35 40 45  
 Glu Asp Ile Thr Ser Val Leu Pro Glu Ile Asp Glu Ile Glu Thr Cys  
 50 55 60  
 Leu Ser Leu Glu Glu Leu Pro Leu Leu Thr Thr Arg Glu Leu Leu Thr  
 65 70 75 80  
 Lys Ser Tyr Leu Lys Phe Lys Ile Cys Ser Glu Thr Leu Leu Lys Met  
 85 90 95  
 Thr Ser Val Phe Glu Asn Asn Ile Tyr Val Gln Glu Tyr Glu Val Gln  
 100 105 110  
 Leu Gln Asn Leu Gly Phe Lys Leu Gln Gly Ile Ser Gln Arg Phe Gly  
 115 120 125  
 Lys Lys Gln Asp Asp Phe Ala Asn Leu Glu Glu Gln Val Ala Leu Gln  
 130 135 140  
 Lys Lys Arg Leu Arg Glu Leu Thr Gln Asn Phe Glu Ile Gln Gly Phe  
 145 150 155 160  
 Asn Phe Met Lys Glu Asp Phe Lys Ala Ala Ala Lys Asp Leu Tyr Ile  
 165 170 175  
 Arg Ser Thr Ala Glu Gln Lys Met Asn Phe Asp Val Pro Cys Met Glu  
 180 185 190  
 Leu Phe Arg Arg Tyr His Glu Glu Val Asn Lys Pro Leu Leu Glu Leu  
 195 200 205  
 Met Tyr Asn Cys Ala Asp Ser Tyr Arg Asp Ala Lys Lys Lys Leu Cys  
 210 215 220  
 Ser Leu Arg Leu Asp Glu Lys Glu Leu Leu Gln Lys Glu Ile Lys Lys  
 225 230 235 240  
 Glu Glu Phe Tyr Gln Lys Lys Gln Gln Arg His Ala Asp Arg Ser Arg  
 245 250 255  
 His Thr Arg Tyr Gln Lys Leu Arg Ile Ala Glu Glu Leu Ala Leu Glu  
 260 265 270  
 Leu Lys Lys Lys Ile  
 275

<210>25  
 <211>202  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>25

Leu Leu Ser Leu Ser Asn Leu Leu Tyr Trp Lys Glu Ser Pro Leu Arg  
 1 5 10 15  
 Glu Lys Lys Val Val Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser  
 20 25 30  
 Leu Val Pro Thr Leu Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr  
 35 40 45  
 Glu Glu Leu Ser Ala Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr  
 50 55 60  
 Ser Phe Ser Ser Lys Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val  
 65 70 75 80  
 Phe Lys Asp Ser Val Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr  
 85 90 95  
 Gln Ser Thr Ser Cys Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn  
 100 105 110  
 Phe Leu Gly Gly Gly Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr  
 115 120 125  
 Thr Ala Ser Gly Ala Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val

130 135 140  
 Thr Leu Ser Gly Phe Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser  
 145 150 155 160  
 Thr Val Thr Asn Gly Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser  
 165 170 175  
 Leu Leu Asp Asn Asp Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly  
 180 185 190  
 Asp Gly Gly Gln Leu Ile Val Gln Ala Pro  
 195 200

&lt;210&gt;26

&lt;211&gt;199

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;26

Gly Ile Asp Ser Gly Gln Phe Leu Asn Arg Arg Trp Arg Thr Ile Asn  
 1 5 10 15  
 Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe Ile  
 20 25 30  
 Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn Leu  
 35 40 45  
 Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala Pro  
 50 55 60  
 Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Thr  
 65 70 75 80  
 Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn Thr  
 85 90 95  
 Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly Thr  
 100 105 110  
 Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile Tyr  
 115 120 125  
 Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp Ala  
 130 135 140  
 Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr Gly  
 145 150 155 160  
 Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys Asp  
 165 170 175  
 Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys Asn  
 180 185 190  
 Gly Thr Val Val Leu Lys Arg  
 195

&lt;210&gt;27

&lt;211&gt;483

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;27

Lys Gly Asp Val Val Leu Ser Ala Asn Gly Phe Ser Gln Asp Ala Asn  
 1 5 10 15  
 Ser Lys Leu Ile Met Asp Leu Gly Thr Ser Leu Val Ala Asn Thr Glu  
 20 25 30  
 Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn Ile Asp Ser Leu Arg Asn  
 35 40 45  
 Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr Ala Gln Lys Asp Ile Arg  
 50 55 60  
 Ile Asp Arg Pro Val Val Leu Ala Ile Ser Asp Glu Ser Phe Tyr Gln  
 65 70 75 80  
 Asn Gly Phe Leu Asn Glu Asp His Ser Tyr Asp Gly Ile Leu Glu Leu  
 85 90 95  
 Asp Ala Gly Lys Asp Ile Val Ile Ser Ala Asp Ser Arg Ser Ile Asp  
 100 105 110  
 Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly Lys Trp Thr Ile Asn Trp  
 115 120 125  
 Ser Thr Asp Asp Lys Lys Ala Thr Val Ser Trp Ala Lys Gln Ser Phe  
 130 135 140  
 Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu Val Pro Asn Leu Leu Trp

145                      150                      155                      160  
 Gly Ser Phe Ile Asp Val Arg Ser Phe Gln Asn Phe Ile Glu Leu Gly  
                                  165                      170                      175  
 Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe Trp Val Ala Gly Ile Ser  
                                  180                      185                      190  
 Asn Val Leu His Arg Ser Gly Arg Glu Asn Gln Arg Lys Phe Arg His  
                                  195                      200                      205  
 Val Ser Gly Gly Ala Val Val Gly Ala Ser Thr Arg Met Pro Gly Gly  
                                  210                      215                      220  
 Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu Phe Ala Arg Asp Lys Asp  
 225                                   230                      235                      240  
 Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr Tyr Ala Gly Ser Leu Arg  
                                  245                      250                      255  
 Leu Gln His Asp Ala Ser Leu Tyr Ser Val Val Ser Ile Leu Leu Gly  
                                  260                      265                      270  
 Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro Tyr Val Ser Lys Thr Leu  
                                  275                      280                      285  
 Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr Gly His Thr Asp His Arg  
 290                                   295                      300  
 Met Lys Thr Glu Ser Leu Pro Pro Pro Pro Pro Thr Leu Ser Thr Asp  
 305                                   310                      315                      320  
 His Thr Ser Trp Gly Gly Tyr Val Trp Ala Gly Glu Leu Gly Thr Arg  
                                  325                      330                      335  
 Val Ala Val Glu Asn Thr Ser Gly Arg Gly Phe Phe Gln Glu Tyr Thr  
                                  340                      345                      350  
 Pro Phe Val Lys Val Gln Ala Val Tyr Ala Arg Gln Asp Ser Phe Val  
                                  355                      360                      365  
 Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser Asp Ser His Leu Tyr Asn  
 370                                   375                      380  
 Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu Lys Arg Phe Ala Glu Gln  
 385                                   390                      395  
 Tyr Tyr His Val Val Ala Met Tyr Ser Pro Asp Val Cys Arg Ser Asn  
                                  405                      410                      415  
 Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn Gln Gly Ser Trp Lys Thr  
                                  420                      425                      430  
 Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly Ile Val Gln Ala Ser Gly  
                                  435                      440                      445  
 Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu Phe Gly Asn Phe Gly Phe  
 450                                   455                      460  
 Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn Val Asp Ala Gly Ser Lys  
 465                                   470                      475                      480  
 Ile Lys Phe

&lt;210&gt;28

&lt;211&gt;177

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;28

Met Lys Ser Ser Phe Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe  
   1                                  5                                  10                                  15  
 Pro Leu Ser Met Ile Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser  
                                   20                                  25                                  30  
 Phe Asp Gly Asn Lys Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu  
                                   35                                  40                                  45  
 Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn  
                                   50                                  55                                  60  
 Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr  
 65                                   70                                   75                                   80  
 Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln  
                                   85                                   90                                   95  
 Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val  
                                   100                                   105                                   110  
 Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile  
                                   115                                   120                                   125

Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys  
 130 135 140  
 Ser Thr Gly Ser Leu Ser Leu Thr Lys Met Ser Val Cys Ser Ser Ala  
 145 150 155 160  
 Lys Thr Phe Gln Arg Ile Met Ala Val Leu Ser Pro Gln Lys Leu Phe  
 165 170 175

His

<210>29

<211>597

<212>PRT

<213>Chlamydia pneumoniae

<400>29

Leu Glu Phe Asp Lys Asn Val Ser Leu Leu Phe Ser Lys Asn Phe Ser  
 1 5 10 15  
 Thr Asp Asn Gly Ala Ile Thr Ala Lys Thr Leu Ser Leu Thr Gly  
 20 25 30  
 Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser Ser Lys Lys Gly  
 35 40 45  
 Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr Gly Asn Gln Gly  
 50 55 60  
 Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser Gly Ala Ala Ile  
 65 70 75 80  
 Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala Lys Val Ser Phe  
 85 90 95  
 Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr Thr Gly Asp Met  
 100 105 110  
 Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr Asp Thr Lys Val  
 115 120 125  
 Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn Asn Thr Ser Thr  
 130 135 140  
 Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu Leu Ala Ser Gly  
 145 150 155 160  
 Gly Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly Gly Thr Ala Pro  
 165 170 175  
 Lys Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu Leu Ser Leu Ser  
 180 185 190  
 Ala Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr Val Thr Ser Thr  
 195 200 205  
 Thr Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly Thr Ser Ala Lys  
 210 215 220  
 Met Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile Tyr Phe Tyr Asp  
 225 230 235 240  
 Pro Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp Val Leu Lys Val  
 245 250 255  
 Asn Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr Gly Asn Ile Ile  
 260 265 270  
 Phe Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala Asp Ser Lys Asn  
 275 280 285  
 Leu Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser Gly Gly Thr Leu  
 290 295 300  
 Ser Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala Phe Thr Gln Gln  
 305 310 315 320  
 Ala Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr Leu Glu Pro Ala  
 325 330 335  
 Asp Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile Ser Ser Ile Asp  
 340 345 350  
 Gly Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr Ser Lys Asn Leu  
 355 360 365  
 Thr Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr Gly Thr Phe Tyr  
 370 375 380  
 Glu Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp Ile Leu Glu Leu  
 385 390 395 400  
 Lys Ala Ser Gly Thr Val Thr Ser Thr Ala Val Thr Pro Asp Pro Ile

405 410 415  
 Met Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr Trp Gly Pro Ile  
 420 425 430  
 Val Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe Asn Trp Thr Lys  
 435 440 445  
 Thr Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser Leu Val Pro Asn  
 450 455 460  
 Ser Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu His Tyr Leu Met  
 465 470 475 480  
 Glu Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala Phe Trp Cys Ala  
 485 490 495  
 Gly Leu Ser Asn Phe Phe His Lys Asp Ser Thr Lys Thr Arg Arg Gly  
 500 505 510  
 Phe Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly Asn Leu His Thr  
 515 520 525  
 Cys Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln Leu Phe Gly Arg  
 530 535 540  
 Asp Arg Asp Tyr Phe Val Ala Lys Asn Gln Arg Tyr Ser Leu Arg Arg  
 545 550 555 560  
 Asn Ser Leu Leu Pro Ala Gln Arg Asn Leu Tyr Leu Ser Ser Leu Gln  
 565 570 575  
 Thr Thr Ala Leu Phe Val Val Leu Cys Ser Tyr Arg Asp Ser Cys Ser  
 580 585 590  
 Leu Phe Arg Lys Pro  
 595

&lt;210&gt;30

&lt;211&gt;230

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;30

Leu Arg Ile Lys Gly Thr Val Tyr Gly Gly Thr Leu Tyr Tyr Gln His  
 1 5 10 15  
 Asn Glu Thr Tyr Ile Ser Leu Pro Cys Lys Leu Arg Pro Cys Ser Leu  
 20 25 30  
 Ser Tyr Val Pro Thr Glu Ile Pro Val Leu Phe Ser Gly Asn Leu Ser  
 35 40 45  
 Tyr Thr His Thr Asp Asn Asp Leu Lys Thr Lys Tyr Thr Tyr Pro  
 50 55 60  
 Thr Val Lys Gly Ser Trp Gly Asn Asp Ser Phe Ala Leu Glu Phe Gly  
 65 70 75 80  
 Gly Arg Ala Pro Ile Cys Leu Asp Glu Ser Ala Leu Phe Glu Gln Tyr  
 85 90 95  
 Met Pro Phe Met Lys Leu Gln Phe Val Tyr Ala His Gln Glu Gly Phe  
 100 105 110  
 Lys Glu Gln Gly Thr Glu Ala Arg Glu Phe Gly Ser Ser Arg Leu Val  
 115 120 125  
 Asn Leu Ala Leu Pro Ile Gly Ile Arg Phe Asp Lys Glu Ser Asp Cys  
 130 135 140  
 Gln Asp Ala Thr Tyr Asn Leu Thr Leu Gly Tyr Thr Val Asp Leu Val  
 145 150 155 160  
 Arg Ser Asn Pro Asp Cys Thr Thr Thr Leu Arg Ile Ser Gly Asp Ser  
 165 170 175  
 Trp Lys Thr Phe Gly Thr Asn Leu Ala Arg Gln Ala Leu Val Leu Arg  
 180 185 190  
 Ala Gly Asn His Phe Cys Phe Asn Ser Asn Phe Glu Ala Phe Ser Gln  
 195 200 205  
 Phe Ser Phe Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp Leu  
 210 215 220  
 Gly Ala Lys Tyr Gln Phe  
 225 230

&lt;210&gt;31

&lt;211&gt;427

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;31

```

Met Arg Ser Ser Phe Ser Leu Leu Leu Ile Ser Ser Ser Leu Ala Phe
 1          5          10          15
Pro Leu Leu Met Ser Val Ser Ala Asp Ala Ala Asp Leu Thr Leu Gly
          20          25          30
Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr Thr Glu Phe Thr Pro
          35          40          45
Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr Tyr Ile Leu Asp Gly
          50          55          60
Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr Ser Leu Thr Thr Ser
          65          70          75          80
Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe Leu Gly Asn Gly Phe
          85          90          95
Ser Leu His Phe Asp Asn Ile Ile Ser Thr Val Ala Gly Val Val
          100          105          110
Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys Phe Ser Gly Phe Ser
          115          120          125
Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr Gly Lys Gly Ala Ile
          130          135          140
Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile Gly Asn Leu Asp Leu
          145          150          155          160
Asn Glu Asn Ala Ser Ser Glu Asn Gly Gly Ala Ile Asn Thr Lys Thr
          165          170          175
Leu Ser Leu Thr Gly Ser Thr Arg Phe Val Ala Phe Leu Gly Asn Ser
          180          185          190
Ser Ser Gln Gln Gly Gly Ala Ile Tyr Ala Ser Gly Asp Ser Val Ile
          195          200          205
Ser Glu Asn Ala Gly Ile Leu Ser Phe Gly Asn Asn Ser Ala Thr Thr
          210          215          220
Ser Gly Gly Ala Ile Ser Ala Glu Gly Asn Leu Val Ile Ser Asn Asn
          225          230          235          240
Gln Asn Ile Phe Phe Asp Gly Cys Lys Ala Thr Thr Asn Gly Gly Ala
          245          250          255
Ile Asp Cys Asn Lys Ala Gly Ala Asn Pro Asp Pro Ile Leu Thr Leu
          260          265          270
Ser Gly Asn Glu Ser Leu His Phe Leu Asn Asn Thr Ala Gly Asn Ser
          275          280          285
Gly Gly Ala Ile Tyr Thr Lys Lys Leu Val Leu Ser Ser Gly Arg Gly
          290          295          300
Gly Val Leu Phe Ser Asn Asn Lys Ala Ala Asn Ala Thr Pro Lys Gly
          305          310          315          320
Gly Ala Ile Ala Ile Leu Asp Ser Gly Glu Ile Ser Ile Ser Ala Asp
          325          330          335
Leu Gly Asn Ile Ile Phe Glu Gly Asn Thr Thr Ser Thr Thr Gly Ser
          340          345          350
Pro Ala Ser Val Thr Arg Asn Ala Ile Asp Leu Ala Ser Asn Ala Lys
          355          360          365
Phe Leu Asn Leu Arg Ala Thr Arg Gly Asn Lys Val Ile Phe Tyr Asp
          370          375          380
Pro Ile Thr Ser Ser Gly Ala Thr Asp Lys Leu Ser Leu Asn Lys Ala
          385          390          395          400
Asp Ala Gly Ser Gly Asn Thr Tyr Glu Gly Tyr Ile Val Phe Ser Gly
          405          410          415
Glu Lys Leu Ser Glu Val Arg Asn Leu Thr Ile
          420          425

```

&lt;210&gt;32

&lt;211&gt;507

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;32

```

Arg Leu His Arg Phe Leu Trp Arg Glu Thr Leu Arg Ser Lys Lys Pro
 1          5          10          15
Asp Asn Leu Lys Ser Thr Phe Thr Gln Ala Val Glu Leu Ala Ala Gly
          20          25          30

```



Ala Leu Val Leu Lys Asp Gly Val Thr Val Val Ala Asn Thr Ile Thr  
 35 40 45  
 Gln Val Glu Gly Ser Lys Val Val Met Asp Gly Gly Thr Thr Phe Glu  
 50 55 60  
 Ala Ser Ala Glu Gly Val Thr Leu Asn Gly Leu Ala Ile Asn Ile Asp  
 65 70 75 80  
 Ser Leu Asp Gly Thr Asn Lys Ala Ile Ile Lys Ala Thr Ala Ala Ser  
 85 90 95  
 Lys Asp Val Ala Leu Ser Gly Pro Ile Met Leu Val Asp Ala Gln Gly  
 100 105 110  
 Asn Tyr Tyr Glu His His Asn Leu Ser Gln Gln Gln Val Phe Ala Leu  
 115 120 125  
 Ile Glu Leu Ser Ala Gln Gly Thr Met Thr Thr Thr Asp Ile Pro Asp  
 130 135 140  
 Thr Pro Ile Leu Asn Thr Thr Asn His Tyr Gly Ile Lys Gly Thr Gly  
 145 150 155 160  
 Ile Ile Val Trp Val Asp Asp Ala Thr Ala Lys Thr Lys Asn Ala Thr  
 165 170 175  
 Leu Thr Trp Thr Lys Thr Gly Tyr Lys Pro Asn Pro Glu Arg Gln Gly  
 180 185 190  
 Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp Val Arg Ser  
 195 200 205  
 Ile Gln Ser Leu Met Asp Arg Ser Thr Ser Ser Leu Ser Ser Ser Thr  
 210 215 220  
 Asn Leu Trp Val Ser Gly Ile Ala Asp Phe Leu His Glu Asp Gln Lys  
 225 230 235 240  
 Gly Asn Gln Arg Ser Tyr Arg His Ser Ser Ala Gly Tyr Ala Leu Gly  
 245 250 255  
 Gly Gly Phe Phe Thr Ala Ser Glu Asn Phe Phe Asn Phe Ala Phe Cys  
 260 265 270  
 Gln Leu Phe Gly Tyr Asp Lys Asp His Leu Val Ala Lys Asn His Thr  
 275 280 285  
 His Val Tyr Ala Gly Ala Met Ser Tyr Arg His Leu Gly Glu Ser Lys  
 290 295 300  
 Thr Leu Ala Lys Ile Leu Ser Gly Asn Ser Asp Ser Leu Pro Phe Val  
 305 310 315 320  
 Phe Asn Ala Arg Phe Ala Tyr Gly His Thr Asp Asn Asn Met Thr Thr  
 325 330 335  
 Lys Tyr Thr Gly Tyr Ser Pro Val Lys Gly Ser Trp Gly Asn Asp Ala  
 340 345 350  
 Phe Gly Ile Glu Cys Gly Gly Ala Ile Pro Val Val Ala Ser Gly Arg  
 355 360 365  
 Arg Ser Trp Val Asp Thr His Thr Pro Phe Leu Asn Leu Glu Met Ile  
 370 375 380  
 Tyr Ala His Gln Asn Asp Phe Lys Glu Asn Gly Thr Glu Gly Arg Ser  
 385 390 395 400  
 Phe Gln Ser Glu Asp Leu Phe Asn Leu Ala Val Pro Val Gly Ile Lys  
 405 410 415  
 Phe Glu Lys Phe Ser Asp Lys Ser Thr Tyr Asp Leu Ser Ile Ala Tyr  
 420 425 430  
 Val Pro Asp Val Ile Arg Asn Asp Pro Gly Cys Thr Thr Thr Leu Met  
 435 440 445  
 Val Ser Gly Asp Ser Trp Ser Thr Cys Gly Thr Ser Leu Ser Arg Gln  
 450 455 460  
 Ala Leu Leu Val Arg Ala Gly Asn His His Ala Phe Ala Ser Asn Phe  
 465 470 475 480  
 Glu Val Phe Ser Gln Phe Glu Val Glu Leu Arg Gly Ser Ser Arg Ser  
 485 490 495  
 Tyr Ala Ile Asp Leu Gly Gly Arg Phe Gly Phe  
 500 505

&lt;210&gt;33

&lt;211&gt;494

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;33

```

Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala
 1          5          10          15
Ser Ser Ile Val Leu His Ala Ala Thr Pro Leu Asn Pro Glu Asp
          20          25          30
Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr
          35          40          45
Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Tyr
          50          55          60
Ile Asp Pro Gly Lys Gly Gly Ser Ile Thr Gly Thr Cys Phe Val Glu
          65          70          75          80
Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe
          85          90          95
Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly
          100          105          110
Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu
          115          120          125
Ser Pro Lys Ser Ala Val Thr Thr Gly Lys Gly Ser Leu Val Ser Leu
          130          135          140
Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn
          145          150          155          160
Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile
          165          170          175
Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys
          180          185          190
Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn
          195          200          205
Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly
          210          215          220
Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu
          225          230          235          240
Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
          245          250          255
Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu
          260          265          270
Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr
          275          280          285
Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn
          290          295          300
Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile
          305          310          315          320
Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
          325          330          335
Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
          340          345          350
Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
          355          360          365
Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
          370          375          380
Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
          385          390          395          400
Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
          405          410          415
Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
          420          425          430
Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
          435          440          445
Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
          450          455          460
Leu Val Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
          465          470          475          480
Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu
          485          490

```

&lt;210&gt;34

&lt;211&gt;86

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;34

```

Met Val Ser Ala Phe Ile Asp Lys Phe Val Met Thr Ile Ser Ser Val
 1           5           10           15
Glu Ala Tyr Asn Glu Val Pro Arg Ser Lys Arg Ser Val Asp Ser Gly
           20           25           30
Ser Cys Glu Asn Pro Cys Val Ile Lys Val Thr Pro Cys Leu Ser Thr
           35           40           45
Lys Leu Pro Ser Thr Lys Val Thr Gly Trp Leu Ile Leu Glu Val Arg
           50           55           60
Phe Ser Ala Ile Ala Ser Ala Val Asp Asn Leu Ser Pro Glu Asn Thr
           65           70           75           80
Ile Asp Pro Glu Ser Phe
                   85

```

&lt;210&gt;35

&lt;211&gt;450

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;35

```

Ala Ser Thr Glu Asp Ile Val Ile Thr Asn Leu Ser Ile Asn Ala Asp
 1           5           10           15
Thr Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn
           20           25           30
Lys Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly
           35           40           45
Ala Phe Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe
           50           55           60
Val Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala
           65           70           75           80
Ser Gln Lys Pro Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr
           85           90           95
Gln Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro
           100          105          110
Ser Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro
           115          120          125
Glu Arg Gln Gly Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val
           130          135          140
Asp Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu
           145          150          155          160
Cys Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His
           165          170          175
Arg Asp Lys Ile Asn Glu His Arg Tyr Arg His Ser Gly Val Gly Tyr
           180          185          190
Leu Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala
           195          200          205
Ala Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys
           210          215          220
Asn His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu
           225          230          235          240
Glu Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Ser Glu Ala
           245          250          255
Cys Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser Tyr Ser His
           260          265          270
Arg Asn Asn Asp Met Lys Thr Lys Tyr Thr Thr Tyr Pro Glu Ala Gln
           275          280          285
Gly Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr
           290          295          300
Tyr Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe
           305          310          315          320
Leu Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr
           325          330          335
Gly Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala

```

```

340          345          350
Val Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly
355          360          365
Ser Tyr Glu Leu Thr Phe Ala Tyr Val Pro Asp Val Ile Arg Lys Asp
370          375          380
Pro Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His
385          390          395          400
Gly Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His
405          410          415
Cys Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu
420          425          430
Leu Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr
435          440          445
Arg Phe
450
<210>36
<211>661
<212>PRT
<213>Chlamydia pneumoniae
<400>36
Lys Leu Trp Ser Asn Pro Asn Leu Arg Leu Met Lys Arg Cys Phe Leu
1          5          10          15
Phe Leu Ala Ser Phe Val Leu Met Gly Ser Ser Ala Asp Ala Leu Thr
20          25          30
His Gln Glu Ala Val Lys Lys Lys Asn Ser Tyr Leu Ser His Phe Lys
35          40          45
Ser Val Ser Gly Ile Val Thr Ile Glu Asp Gly Val Leu Asn Ile His
50          55          60
Asn Asn Leu Arg Ile Gln Ala Asn Lys Val Tyr Val Glu Asn Thr Val
65          70          75          80
Gly Gln Ser Leu Lys Leu Val Ala His Gly Asn Val Met Val Asn Tyr
85          90          95
Arg Ala Lys Thr Leu Val Cys Asp Tyr Leu Glu Tyr Tyr Glu Asp Thr
100          105          110
Asp Ser Cys Leu Leu Thr Asn Gly Arg Phe Ala Met Tyr Pro Trp Phe
115          120          125
Leu Gly Gly Ser Met Ile Thr Leu Thr Pro Glu Thr Ile Val Ile Arg
130          135          140
Lys Gly Tyr Ile Ser Thr Ser Glu Gly Pro Lys Lys Asp Leu Cys Leu
145          150          155          160
Ser Gly Asp Tyr Leu Glu Tyr Ser Ser Asp Ser Leu Leu Ser Ile Gly
165          170          175
Lys Thr Thr Leu Arg Val Cys Arg Ile Pro Ile Leu Phe Leu Pro Pro
180          185          190
Phe Ser Ile Met Pro Met Glu Ile Pro Lys Pro Pro Ile Asn Phe Arg
195          200          205
Gly Gly Thr Gly Gly Phe Leu Gly Ser Tyr Leu Gly Met Ser Tyr Ser
210          215          220
Pro Ile Ser Arg Lys His Phe Ser Ser Thr Phe Phe Leu Asp Ser Phe
225          230          235          240
Phe Lys His Gly Val Gly Met Gly Phe Asn Leu His Cys Ser Gln Lys
245          250          255
Gln Val Pro Glu Asn Val Phe Asn Met Lys Ser Tyr Tyr Ala His Arg
260          265          270
Leu Ala Ile Asp Met Ala Glu Ala His Asp Arg Tyr Arg Leu His Gly
275          280          285
Asp Phe Cys Phe Thr His Lys His Val Asn Phe Ser Gly Glu Tyr His
290          295          300
Leu Ser Asp Ser Trp Glu Thr Val Ala Asp Ile Phe Pro Asn Asn Phe
305          310          315          320
Met Leu Lys Asn Thr Gly Pro Thr Arg Val Asp Cys Thr Trp Asn Asp
325          330          335
Asn Tyr Phe Glu Gly Tyr Leu Thr Ser Ser Val Lys Val Asn Ser Phe
340          345          350

```

Gln Asn Ala Asn Gln Glu Leu Pro Tyr Leu Thr Leu Arg Gln Tyr Pro  
 355 360 365  
 Ile Ser Ile Tyr Asn Thr Gly Val Tyr Leu Glu Asn Ile Val Glu Cys  
 370 375 380  
 Gly Tyr Leu Asn Phe Ala Phe Ser Asp His Ile Val Gly Glu Asn Phe  
 385 390 395 400  
 Ser Ser Leu Arg Leu Ala Ala Arg Pro Lys Leu His Lys Thr Val Pro  
 405 410 415  
 Leu Pro Ile Gly Thr Leu Ser Ser Thr Leu Gly Ser Ser Leu Ile Tyr  
 420 425 430  
 Tyr Ser Asp Val Pro Glu Ile Ser Ser Arg His Ser Gln Leu Ser Ala  
 435 440 445  
 Lys Leu Gln Leu Asp Tyr Arg Phe Leu Leu His Lys Ser Tyr Ile Gln  
 450 455 460  
 Arg Arg His Ile Ile Glu Pro Phe Val Thr Phe Ile Thr Glu Thr Arg  
 465 470 475 480  
 Pro Leu Ala Lys Asn Glu Asp His Tyr Ile Phe Ser Ile Gln Asp Ala  
 485 490 495  
 Phe His Ser Leu Asn Leu Leu Lys Ala Gly Ile Asp Thr Ser Val Leu  
 500 505 510  
 Ser Lys Thr Asn Pro Arg Phe Pro Arg Ile His Ala Lys Leu Trp Thr  
 515 520 525  
 Thr His Ile Leu Ser Asn Thr Glu Ser Lys Pro Thr Phe Pro Lys Thr  
 530 535 540  
 Ala Cys Glu Leu Ser Leu Pro Phe Gly Lys Lys Asn Thr Val Ser Leu  
 545 550 555 560  
 Asp Ala Glu Trp Ile Trp Lys Lys His Cys Trp Asp His Met Asn Ile  
 565 570 575  
 Arg Trp Glu Trp Ile Gly Asn Asp Asn Val Ala Met Thr Leu Glu Ser  
 580 585 590  
 Leu His Arg Ser Lys Tyr Ser Leu Ile Lys Cys Asp Arg Glu Asn Phe  
 595 600 605  
 Ile Leu Asp Val Ser Arg Pro Ile Asp Gln Leu Leu Asp Ser Pro Leu  
 610 615 620  
 Ser Asp His Arg Asn Leu Ile Leu Gly Lys Leu Phe Val Arg Pro His  
 625 630 635 640  
 Pro Cys Trp Asn Tyr Arg Leu Ser Leu Arg Tyr Gly Trp His Arg Arg  
 645 650 655  
 Thr Leu Arg Thr Thr  
 660

&lt;210&gt;37

&lt;211&gt;245

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;37

Glu Gln Arg Ser Lys Leu Asn Val Ala Leu Ala Leu Leu Glu Leu Gly  
 1 5 10 15  
 Cys Asp Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg Leu Val Gln  
 20 25 30  
 Pro His Tyr Asn Glu Thr Leu Ala Leu Ser Phe Ser Lys Gly Arg Thr  
 35 40 45  
 Leu Gln Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln Asp Pro Gln  
 50 55 60  
 Glu Arg Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu Glu Gln Ile  
 65 70 75 80  
 Leu Thr Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu Pro Cys Ile  
 85 90 95  
 Tyr Lys Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr Thr Ala Ile  
 100 105 110  
 Ser Phe Leu Ser His Thr Ser His Gln Glu Ala Leu Asp Leu Leu Phe  
 115 120 125  
 Gln Ala Ala Lys Leu Pro Gly Glu Pro Ile Ile Arg Ala Tyr Ala Asp  
 130 135 140  
 Leu Ala Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys Arg Ser Leu

145 150 155 160  
 His Asp Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu Phe Val Asp  
 165 170 175  
 Thr Glu Asn Gln Arg Pro His Pro Ser Met Pro Tyr Leu Arg Tyr Gln  
 180 185 190  
 Val Thr Pro Glu Ser Arg Thr Lys Leu Met Leu Asp Ile Leu Glu Thr  
 195 200 205  
 Leu Ala Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu Ile Gln Leu  
 210 215 220  
 Met Thr Glu Gly Asp Ala Lys Asn Phe Pro Val Leu Ala Gly Leu Leu  
 225 230 235 240  
 Ile Lys Ile Val Glu  
 245  
 <210>38  
 <211>348  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>38  
 Cys Ser Arg Ser Pro Tyr Pro Asn Ile Glu Ile Leu Ala Arg Gly Val  
 1 5 10 15  
 Glu His Arg Ser Met Gly Leu Phe His Leu Thr Leu Phe Gly Leu Leu  
 20 25 30  
 Leu Cys Ser Leu Pro Ile Ser Leu Val Ala Lys Phe Pro Glu Ser Val  
 35 40 45  
 Gly His Lys Ile Leu Tyr Ile Ser Thr Gln Ser Thr Gln Gln Ala Leu  
 50 55 60  
 Ala Thr Tyr Leu Glu Ala Leu Asp Ala Tyr Gly Asp His Asp Phe Phe  
 65 70 75 80  
 Val Leu Arg Lys Ile Gly Glu Asp Tyr Leu Lys Gln Ser Ile His Ser  
 85 90 95  
 Ser Asp Pro Gln Thr Arg Lys Ser Thr Ile Ile Gly Ala Gly Leu Ala  
 100 105 110  
 Gly Ser Ser Glu Ala Leu Asp Val Leu Ser Gln Ala Met Glu Thr Ala  
 115 120 125  
 Asp Pro Leu Gln Gln Leu Leu Val Leu Ser Ala Val Ser Gly His Leu  
 130 135 140  
 Gly Lys Thr Ser Asp Asp Leu Leu Phe Lys Ala Leu Ala Ser Pro Tyr  
 145 150 155 160  
 Pro Val Ile Arg Leu Glu Ala Ala Tyr Arg Leu Ala Asn Leu Lys Asn  
 165 170 175  
 Thr Lys Val Ile Asp His Leu His Ser Phe Ile His Lys Leu Pro Glu  
 180 185 190  
 Glu Ile Gln Cys Leu Ser Ala Ala Ile Phe Leu Arg Leu Glu Thr Glu  
 195 200 205  
 Glu Ser Asp Ala Tyr Ile Arg Asp Leu Leu Ala Ala Lys Lys Ser Ala  
 210 215 220  
 Ile Arg Ser Ala Thr Ala Leu Gln Ile Gly Glu Tyr Gln Gln Lys Arg  
 225 230 235 240  
 Phe Leu Pro Thr Leu Arg Asn Leu Leu Thr Ser Ala Ser Pro Gln Asp  
 245 250 255  
 Gln Glu Ala Ile Leu Tyr Ala Leu Gly Lys Leu Lys Asp Gly Gln Ser  
 260 265 270  
 Tyr Tyr Asn Ile Lys Lys Gln Leu Gln Lys Pro Asp Val Asp Val Thr  
 275 280 285  
 Leu Ala Ala Ala Gln Ala Leu Ile Ala Leu Gly Lys Glu Glu Asp Ala  
 290 295 300  
 Leu Pro Val Ile Lys Lys Gln Ala Leu Glu Glu Arg Pro Arg Ala Leu  
 305 310 315 320  
 Tyr Ala Leu Arg His Leu Pro Ser Glu Ile Gly Ile Pro Ile Ala Leu  
 325 330 335  
 Pro Ile Phe Leu Lys Thr Lys Asn Ser Glu Ala Ser  
 340 345  
 <210>39  
 <211>196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;39

```

Met Ser Leu Pro Leu Val Leu Gly Ser Ser Ser Pro Arg Arg Lys Phe
 1           5           10           15
Ile Leu Glu Lys Phe Arg Val Pro Phe Thr Val Ile Pro Ser Asn Phe
           20           25           30
Asp Glu Ser Lys Val Ser Tyr Ser Gly Asp Pro Ile Ala Tyr Thr Gln
           35           40           45
Glu Leu Ala Ala Gln Lys Ala Tyr Ala Val Ser Glu Leu His Ser Pro
           50           55           60
Cys Asp Cys Ile Ile Leu Thr Gly Asp Thr Ile Val Ser Tyr Asp Gly
65           70           75           80
Arg Ile Phe Thr Lys Pro Gln Xaa Lys Ala Xaa Ala Ile Gln Met Leu
           85           90           95
Lys Thr Leu Arg Asn Gln Thr His Asp Val Val Thr Ser Ile Ala Val
           100          105          110
Leu His Lys Gly Lys Leu Leu Thr Gly Ser Glu Thr Ser Gln Ile Ser
           115          120          125
Leu Thr Met Ile Pro Asp His Arg Ile Glu Ser Tyr Ile Asp Thr Val
130          135          140
Gly Thr Leu Asn Asn Cys Gly Ala Tyr Asp Val Cys His Gly Gly Leu
145          150          155          160
Ile Leu Lys Lys Val His Gly Cys Val Tyr Asn Val Gln Gly Leu Pro
           165          170          175
Ile Gln Thr Leu Lys Tyr Leu Leu Glu Glu Leu Asn Ile Asp Leu Trp
           180          185          190
Asp Tyr Ser Ile
           195

```

&lt;210&gt;40

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;40

```

Val Xaa Arg Asn Arg Lys Thr Gly Ile Asn Asp Gln Glu Ile Arg Ser
 1           5           10           15
Val Leu Gly Lys Met Leu Phe Gly Gly Asp Asp Ala Phe Lys Gln Ile
           20           25           30
Gln Ala Leu Ser Gly Gly Glu Thr Ala Arg Leu Leu Met Ala Gly Met
           35           40           45
Met Leu Glu Asn His Asn Val Leu Ile Leu Asp Glu Ala Asn Asn His
           50           55           60
Leu Asp Leu Glu Ser Val Ser Ala Leu Ser Trp Ala Ile Asn Asp Tyr
65           70           75           80
Lys Gly Thr Ala Ile Phe Val Ser His Asp Arg Gly Leu Ile Gln Asp
           85           90           95
Cys Ala Thr Lys Leu Leu Ile Phe Asp Lys Asp Lys Ile Thr Phe Phe
           100          105          110
Asp Gly Thr Met Val Asp Tyr Thr Ala Gly His Lys Gln Leu Leu
           115          120          125

```

&lt;210&gt;41

&lt;211&gt;432

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;41

```

Leu Tyr Ser Lys Gln His Phe Val Met Leu Ser Ala Met Ser Ile Val
 1           5           10           15
Leu Asp Lys Ile Gly Lys Ser Leu Gly Thr Arg Ile Leu Phe Asp Asp
           20           25           30
Val Ser Val Val Phe Asn Pro Gly Asn Cys Tyr Gly Leu Thr Gly Pro
           35           40           45
Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ile Ile Met Gly Met Ile
           50           55           60
Glu Pro Thr Arg Gly Ser Ile Ser Leu Pro Lys Lys Val Gly Ile Leu

```

```

65          70          75          80
Arg Gln Asn Ile Asp Ser Phe His Asp Thr Thr Val Leu Asp Cys Val
      85          90          95
Ile Met Gly Asn Thr Arg Leu Trp Glu Ala Leu Gln Arg Arg Asp Asn
      100          105          110
Leu Tyr Leu Gln Glu Phe Thr Asp Ala Ile Gly Met Glu Leu Gly Glu
      115          120          125
Ile Glu Glu Ile Ile Gly Glu Glu Asn Gly Tyr Arg Ala Asp Ser Glu
      130          135          140
Ala Glu Glu Leu Leu Thr Gly Ile Gly Ile Pro Asn Glu Met Phe Asp
145          150          155          160
Lys Lys Met Ala Met Ile Pro Ile Asp Leu Gln Phe Arg Val Leu Leu
      165          170          175
Cys Gln Ala Leu Phe Gly His Pro Glu Ala Leu Leu Leu Asp Glu Pro
      180          185          190
Thr Asn His Leu Asp Leu Tyr Ser Ile Asn Trp Leu Gly Asn Phe Leu
      195          200          205
Lys Asp Tyr Glu Gly Thr Val Ile Val Val Ser His Asp Arg His Phe
210          215          220
Leu Asn Thr Ile Thr Thr His Ile Ala Asp Ile Asp Tyr Asp Thr Ile
225          230          235          240
Ile Ile Tyr Pro Gly Asn Tyr Asp Asp Met Val Glu Met Lys Thr Ala
      245          250          255
Ser Arg Glu Gln Glu Lys Ala Asp Ile Lys Ser Lys Glu Lys Lys Ile
      260          265          270
Ser Gln Leu Lys Glu Phe Val Ala Lys Phe Gly Ala Gly Ser Arg Ala
275          280          285
Ser Gln Val Gln Ser Arg Leu Arg Glu Ile Lys Lys Leu Gln Pro Gln
290          295          300
Glu Leu Lys Lys Ser Asn Ile Gln Arg Pro Tyr Ile Arg Phe Pro Leu
305          310          315          320
Ser Asp Lys Ser Ser Gly Lys Val Val Leu Ser Leu Glu Ala Ile Thr
      325          330          335
Lys Asp Tyr Gly Asp His Gln Val Ile His Pro Phe Ser Leu Glu Ile
      340          345          350
Tyr Gln Gly Asp Lys Leu Gly Ile Ile Gly Asn Asn Gly Leu Gly Lys
355          360          365
Thr Thr Leu Met Lys Leu Leu Ala Gly Val Glu Ala Pro Ser Ser Gly
370          375          380
Ser Ile Lys Leu Gly His Gln Ala Ile Cys Ser Tyr Phe Pro Gln Asn
385          390          395          400
His Ser Asp Val Leu Ala Asp Cys Gly Gln Glu Thr Leu Phe Glu Xaa
      405          410          415
Tyr Ala Ile Ala Lys Pro Glu Leu Thr Ile Lys Lys Ser Ala Val Cys
      420          425          430

```

&lt;210&gt;42

&lt;211&gt;131

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;42

```

Arg Glu Val Met Ile Ala Ser Ile Tyr Ser Phe Leu Asp Tyr Leu Lys
1          5          10          15
Met Val Lys Ser Ala Ser Pro His Thr Leu Arg Asn Tyr Cys Leu Asp
20          25          30
Leu Asn Gly Leu Lys Ile Phe Leu Xaa Glu Arg Gly Asn Leu Ala Pro
35          40          45
Ser Ser Pro Leu Gln Leu Ala Thr Glu Lys Arg Lys Val Ser Glu Leu
50          55          60
Pro Phe Ser Leu Phe Thr Lys Glu His Val Arg Met Tyr Ile Ala Lys
65          70          75          80
Leu Ile Glu Asn Gly Lys Ala Lys Arg Thr Ile Lys Arg Cys Leu Ser
85          90          95
Ser Ile Lys Ser Phe Ala His Tyr Cys Val Ile Gln Lys Ile Leu Leu
100          105          110

```



Glu Asn Leu Arg Lys Leu Ser Thr Asp Leu Val Phe Leu Arg Ser Cys  
           115                                  120                                  125  
 Leu Pro Arg  
           130  
 <210>43  
 <211>307  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>43  
 Met Ser Ser Arg Glu Leu Ile Ile Leu Gly Cys Ser Ser Gln Gln Pro  
       1                                  5                                  10                                  15  
 Thr Arg Thr Arg Asn Gln Gly Ala Tyr Leu Phe Arg Trp Asn Gly Glu  
                                   20                                  25                                  30  
 Gly Leu Leu Phe Asp Pro Gly Glu Gly Thr Gln Arg Gln Phe Ile Phe  
                                   35                                  40                                  45  
 Ala Asn Ile Ala Pro Thr Thr Val Asn Arg Ile Phe Val Ser His Phe  
           50                                  55                                  60  
 His Gly Asp His Cys Leu Gly Leu Gly Ser Met Leu Met Arg Leu Asn  
       65                                  70                                  75                                  80  
 Leu Asp Lys Val Ser His Pro Ile His Cys Tyr Tyr Pro Ala Ser Gly  
                                   85                                  90                                  95  
 Lys Lys Tyr Phe Asp Arg Leu Arg Tyr Gly Thr Ile Tyr His Glu Thr  
                                   100                                  105                                  110  
 Ile Gln Val Val Glu His Pro Ile Ser Glu Glu Gly Ile Val Glu Asp  
           115                                  120                                  125  
 Phe Gly Ser Phe Arg Ile Glu Ala Gln Arg Leu Gln His Gln Val Asp  
       130                                  135                                  140  
 Thr Leu Gly Trp Arg Ile Thr Glu Pro Asp Thr Ile Lys Phe Leu Pro  
       145                                  150                                  155                                  160  
 Lys Glu Leu Glu Ser Arg Gly Ile Arg Gly Leu Ile Ile Gln Asp Leu  
                                   165                                  170                                  175  
 Ile Arg Asp Gln Glu Ile Ser Ile Gly Gly Ser Thr Val Tyr Leu Ser  
                                   180                                  185                                  190  
 Asp Val Ser Tyr Val Arg Lys Gly Asp Ser Ile Ala Ile Ile Ala Asp  
       195                                  200                                  205  
 Thr Leu Pro Cys Gln Ala Ala Ile Asp Leu Ala Lys Asn Ser Cys Met  
       210                                  215                                  220  
 Met Leu Cys Glu Ser Thr Tyr Leu Glu Gln His Arg His Leu Ala Glu  
       225                                  230                                  235                                  240  
 Ser His Phe His Met Thr Ala Lys Gln Ala Ala Thr Leu Ala Lys Arg  
                                   245                                  250                                  255  
 Ala Ala Thr Gln Lys Leu Ile Leu Thr His Phe Ser Ala Arg Tyr Leu  
                                   260                                  265                                  270  
 Asn Leu Asp Asp Phe Tyr Lys Glu Ala Ser Ala Val Phe Pro Asn Val  
       275                                  280                                  285  
 Ser Val Ala Gln Glu Tyr Arg Ser Tyr Pro Phe Pro Lys Asn Pro Leu  
       290                                  295                                  300  
 Leu Asn Lys  
       305  
 <210>44  
 <211>440  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>44  
 Ala Phe Gln Arg Ile Lys Arg Lys Tyr His Leu Ser Cys Arg Pro Ser  
       1                                  5                                  10                                  15  
 Arg Ser Trp Glu Asn Lys His Arg Ala His Ile Ala Lys Val Leu His  
                                   20                                  25                                  30  
 Arg Lys Phe Phe Arg Phe Ser Val Gly Gly Met Arg Asp Glu Ala Glu  
                                   35                                  40                                  45  
 Ile Lys Gly His Arg Arg Thr Tyr Ile Gly Ala Met Pro Gly Lys Met  
           50                                  55                                  60  
 Val Gln Ala Leu Lys Gln Ser Gln Ala Met Asn Pro Val Ile Met Ile  
       65                                  70                                  75                                  80

Asp Glu Val Asp Lys Ile Gly Ala Ser Tyr His Gly Asp Pro Ala Ser  
 85 90 95  
 Ala Leu Leu Glu Val Leu Asp Pro Glu Gln Asn Lys Asp Phe Leu Asp  
 100 105 110  
 His Tyr Leu Asp Val Arg Val Asp Leu Ser Asn Val Leu Phe Ile Leu  
 115 120 125  
 Thr Ala Asn Val Leu Asp Thr Ile Pro Asp Pro Leu Leu Asp Arg Met  
 130 135 140  
 Glu Ile Leu Arg Leu Ser Gly Tyr Ile Leu Glu Glu Lys Leu Gln Ile  
 145 150 155 160  
 Ala Lys Lys Tyr Leu Val Pro Lys Ala Arg Lys Glu Ile Gly Leu Thr  
 165 170 175  
 Ala Ser Glu Val Asn Phe Gln Pro Glu Ala Leu Lys Tyr Met Ile Asn  
 180 185 190  
 Asn Tyr Ala Arg Glu Ala Gly Val Arg Thr Leu Asn Gly Asn Ile Lys  
 195 200 205  
 Lys Val Leu Arg Lys Val Ala Leu Lys Ile Val Gln Asn Gln Glu Lys  
 210 215 220  
 Pro Lys Ser Lys Lys Ile Thr Phe Lys Ile Ser Ser Lys Asn Leu Gln  
 225 230 235 240  
 Thr Tyr Leu Gly Lys Pro Ile Phe Ser Ser Asp Arg Phe Tyr Glu Ser  
 245 250 255  
 Thr Pro Val Gly Val Ala Thr Gly Leu Ala Trp Thr Ser Leu Gly Gly  
 260 265 270  
 Ala Thr Leu Tyr Ile Glu Ser Val Gln Val Ser Ser Leu Lys Thr Asp  
 275 280 285  
 Met His Leu Thr Gly Gln Ala Gly Glu Val Met Lys Glu Ser Ser Gln  
 290 295 300  
 Ile Ala Trp Thr Tyr Leu His Ser Ala Leu His Arg Tyr Ala Pro Gly  
 305 310 315 320  
 Tyr Thr Phe Phe Pro Lys Ser Gln Val His Ile His Ile Pro Glu Gly  
 325 330 335  
 Ala Thr Pro Lys Asp Gly Pro Ser Ala Gly Ile Thr Met Val Thr Ser  
 340 345 350  
 Leu Leu Ser Leu Leu Leu Glu Thr Pro Val Val Asn Asn Leu Gly Met  
 355 360 365  
 Thr Gly Glu Ile Thr Leu Thr Gly Arg Val Leu Gly Val Gly Gly Ile  
 370 375 380  
 Arg Glu Lys Leu Ile Ala Ala Arg Arg Ser Arg Leu Asn Ile Leu Ile  
 385 390 395 400  
 Phe Pro Glu Asp Asn Arg Arg Asp Tyr Glu Glu Leu Pro Ala Tyr Leu  
 405 410 415  
 Lys Thr Gly Leu Lys Ile His Phe Val Ser His Tyr Asp Asp Val Leu  
 420 425 430  
 Lys Val Ala Phe Pro Lys Leu Lys  
 435 440  
 <210>45  
 <211>424  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>45  
 Pro Ser Ile Arg Thr Ile Val Asp Ser Thr Thr Asn Ser Asp Ser Pro  
 1 5 10 15  
 Ile Leu Asp Pro Asn Pro Glu Asp Val Glu Lys Leu Leu Asp Glu Ser  
 20 25 30  
 Glu Glu Glu Ser Glu Asp Gln Ser Thr Glu Arg Leu Leu Pro Ser Glu  
 35 40 45  
 Leu Phe Ile Leu Pro Leu Asn Lys Arg Pro Phe Phe Pro Gly Met Ala  
 50 55 60  
 Ala Pro Ile Leu Ile Glu Ser Gly Pro Tyr Tyr Glu Val Leu Lys Val  
 65 70 75 80  
 Leu Ala Lys Ser Ser Gln Lys Tyr Ile Gly Leu Val Leu Thr Lys Lys  
 85 90 95  
 Glu Asn Ala Asp Ile Leu Lys Val Ser Phe Asn Gln Leu His Lys Thr

100 105 110  
 Gly Val Ala Ala Arg Ile Leu Arg Ile Met Pro Ile Glu Gly Gly Ser  
 115 120 125  
 Ala Gln Val Leu Leu Ser Ile Glu Glu Arg Ile Arg Ile Ile Glu Pro  
 130 135 140  
 Ile Lys Asp Lys Tyr Leu Lys Ala Arg Val Ser Tyr His Ala Asp Asn  
 145 150 155 160  
 Lys Glu Leu Thr Glu Glu Leu Lys Ala Tyr Ser Ile Ser Ile Val Ser  
 165 170 175  
 Val Ile Lys Asp Leu Leu Lys Leu Asn Pro Leu Phe Lys Glu Glu Leu  
 180 185 190  
 Gln Ile Phe Leu Gly His Ser Asp Phe Thr Glu Pro Gly Lys Leu Ala  
 195 200 205  
 Asp Phe Ser Val Ala Leu Thr Thr Ala Thr Arg Glu Glu Leu Gln Glu  
 210 215 220  
 Val Leu Glu Thr Thr Asn Met His Asp Arg Ile Asp Lys Ala Leu Ile  
 225 230 235 240  
 Leu Leu Lys Lys Glu Leu Asp Leu Ser Arg Leu Gln Ser Ser Ile Asn  
 245 250 255  
 Gln Lys Ile Glu Ala Thr Ile Thr Lys Ser Gln Lys Glu Phe Phe Leu  
 260 265 270  
 Lys Glu Gln Leu Lys Thr Xaa Lys Lys Glu Leu Gly Leu Glu Lys Glu  
 275 280 285  
 Asp Arg Ala Ile Asp Ile Glu Lys Phe Ser Glu Arg Leu Arg Lys Arg  
 290 295 300  
 His Val Pro Asp Tyr Ala Met Glu Val Ile Gln Asp Glu Ile Glu Lys  
 305 310 315 320  
 Leu Gln Thr Leu Glu Thr Ser Ser Ala Glu Tyr Thr Val Cys Arg Asn  
 325 330 335  
 Tyr Leu Asp Trp Leu Thr Ile Ile Pro Trp Gly Ile Gln Ser Lys Glu  
 340 345 350  
 Tyr His Asp Leu Lys Lys Ala Glu Ile Val Leu Asn Lys Asp His Tyr  
 355 360 365  
 Gly Leu Asp Glu Ile Lys Gln Arg Ile Leu Glu Leu Ile Ser Val Gly  
 370 375 380  
 Lys Leu Ser Lys Gly Leu Lys Gly Ser Ile Ile Cys Leu Val Gly Pro  
 385 390 395 400  
 Pro Gly Val Gly Lys Thr Ser Ile Gly Arg Thr Leu Leu Lys Ser Cys  
 405 410 415  
 Ile Glu Ser Ser Ser Val Ser Gln  
 420

&lt;210&gt;46

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;46

Arg Met Phe Leu Gln Phe Phe His Pro Ile Val Phe Ser Asp Gln Ser  
 1 5 10 15  
 Leu Ser Phe Leu Pro Tyr Leu Gly Lys Ser Ser Gly Ile Ile Glu Lys  
 20 25 30  
 Cys Ser Asn Ile Val Glu His Tyr Leu His Leu Gly Gly Asp Thr Ser  
 35 40 45  
 Val Ile Ile Thr Gly Val Ser Gly Ala Thr Phe Leu Ser Val Asp His  
 50 55 60  
 Ala Leu Pro Ile Ser Lys Ser Glu Lys Ile Ile Lys Ile Leu Ser Tyr  
 65 70 75 80  
 Ile Leu Ile Leu Pro Leu Ile Leu Ala Leu Phe Ile Lys Ile Val Leu  
 85 90 95  
 Arg Ile Ile Leu Phe Xaa Lys Tyr Arg Gly Leu Ile Xaa Asp Val Lys  
 100 105 110  
 Lys Glu Asp Leu Glu Lys Asn Thr Tyr Thr  
 115 120

&lt;210&gt;47

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;47

```

Ser Asn Lys Asn Glu Arg Asn Glu Asn Ile Tyr Cys Phe Asn Leu Phe
 1          5          10          15
Arg Tyr Ile Arg Phe Phe Ala Ala Leu Asn Ile Arg Thr Asn Asp Gly
          20          25          30
Leu Arg Phe Cys Tyr Ser Tyr Ile Leu Leu Arg Pro Met Leu Leu Asp
          35          40          45
Ser Ser Leu Leu Arg Lys Gly Gly Gln Glu Leu Leu Lys Lys Phe Gln
          50          55          60
Ile Lys Leu Arg Thr Thr Ser Ile Lys Ser Ser Leu Ile Ser Leu Arg
          65          70          75          80
Gln Gln Leu Gly Lys Arg Glu Ala Thr Gln Ser Asp Ile Leu Tyr Gly
          85          90          95
Thr Ser Arg Phe Gln Tyr Leu Asn Ser Phe Glu Ile Glu Asp Pro Arg
          100          105          110
Ile Pro Pro Thr Met Ala Ala Gln Leu Gln Glu Ile Ile Trp Ser Arg
          115          120          125
Ser Val Met Glu Leu Lys Ile Lys Phe Tyr Val Tyr Leu Asn Ser Glu
          130          135          140
Arg Asn Lys Thr Lys Pro
          145          150

```

&lt;210&gt;48

&lt;211&gt;392

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;48

```

Met Asp Tyr Tyr Ser Ile Leu Gly Ile Ser Lys Thr Ala Ser Ala Glu
 1          5          10          15
Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Val Lys Tyr His Pro Asp
          20          25          30
Lys Asn Pro Gly Asp Ala Ala Ala Glu Lys Arg Phe Lys Glu Val Ser
          35          40          45
Glu Ala Tyr Glu Val Leu Ser Asp Pro Gln Lys Arg Asp Ser Tyr Asp
          50          55          60
Arg Phe Gly Lys Asp Gly Pro Phe Ala Gly Ala Gly Phe Gly Gly
          65          70          75          80
Ala Gly Gly Met Gly Asn Met Glu Asp Ala Leu Arg Thr Phe Met Gly
          85          90          95
Ala Phe Gly Gly Glu Phe Gly Gly Gly Ser Phe Phe Asp Gly Leu Phe
          100          105          110
Gly Gly Leu Gly Glu Ala Phe Gly Met Arg Ser Asp Pro Ala Gly Ala
          115          120          125
Arg Gln Gly Ala Ser Lys Lys Val His Ile Asn Leu Thr Phe Glu Glu
          130          135          140
Ala Ala His Gly Val Glu Lys Glu Leu Val Val Ser Gly Tyr Lys Ser
          145          150          155          160
Cys Glu Thr Cys Ser Gly Gln Gly Ala Val Asn Pro Gln Gly Ile Lys
          165          170          175
Ser Cys Glu Arg Cys Lys Gly Ser Gly Gln Val Val Gln Ser Arg Gly
          180          185          190
Phe Phe Ser Met Ala Ser Thr Cys Pro Glu Cys Gly Gly Glu Gly Arg
          195          200          205
Ile Ile Thr Asp Pro Cys Ser Ser Cys Arg Gly Gln Gly Arg Val Lys
          210          215          220
Asp Lys Arg Ser Val His Val His Ile Pro Ala Gly Val Asp Ser Gly
          225          230          235          240
Met Arg Leu Lys Met Glu Gly Tyr Gly Asp Ala Gly Gln Asn Gly Ala
          245          250          255
Pro Ser Gly Asp Leu Tyr Val Phe Ile Asp Val Glu Ser His Pro Val
          260          265          270
Phe Glu Arg Arg Gly Asp Asp Leu Ile Leu Glu Leu Pro Ile Gly Phe
          275          280          285

```

Val Asp Ala Ala Leu Gly Met Lys Lys Glu Ile Pro Thr Leu Leu Lys  
 290 295 300  
 Thr Glu Gly Ser Cys Arg Leu Thr Val Pro Glu Gly Ile Gln Ser Gly  
 305 310 315 320  
 Thr Ile Leu Lys Val Arg Asn Gln Gly Phe Pro Asn Val His Gly Lys  
 325 330 335  
 Gly Arg Gly Asp Leu Leu Val Arg Ile Ser Val Glu Thr Pro Gln Asn  
 340 345 350  
 Leu Ser Glu Glu Gln Lys Glu Leu Leu Arg Thr Phe Ala Ser Thr Glu  
 355 360 365  
 Lys Ala Glu Asn Phe Pro Lys Lys Arg Ser Phe Leu Asp Lys Ile Lys  
 370 375 380  
 Gly Phe Phe Ser Asp Phe Thr Val  
 385 390

&lt;210&gt;49

&lt;211&gt;258

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;49

Met Gly Val Val Gln Asn Gln Val Ile Ser Ser Ile Arg Asp Val Leu  
 1 5 10 15  
 Lys Leu Val Trp Glu Leu Arg Phe Ala Glu His Lys Met Leu Leu  
 20 25 30  
 Ser Arg Gln Ser Gly Ser Gly Gly Thr Phe Gln Leu Ser Cys Ala Gly  
 35 40 45  
 His Glu Leu Ala Gly Val Leu Ala Gly Lys Ser Leu Ile Pro Gly Lys  
 50 55 60  
 Asp Trp Ser Phe Pro Tyr Tyr Arg Asp Gln Gly Phe Pro Ile Gly Leu  
 65 70 75 80  
 Gly Cys Asp Leu Ser Glu Ile Phe Ala Ser Phe Leu Ala Arg Thr Thr  
 85 90 95  
 Pro Asn His Ser Ser Ala Arg Met Met Pro Tyr His Tyr Ser His Lys  
 100 105 110  
 Lys Leu Arg Ile Cys Cys Gln Ser Ser Val Val Gly Thr Gln Phe Leu  
 115 120 125  
 Gln Ala Ala Gly Arg Ala Trp Ala Val Lys His Ser Ser Ala Asp Glu  
 130 135 140  
 Val Val Tyr Val Ser Gly Gly Asp Gly Ala Thr Ser Gln Gly Glu Phe  
 145 150 155 160  
 His Glu Met Leu Asn Phe Val Ala Leu His Gln Leu Pro Leu Ile Thr  
 165 170 175  
 Val Ile Gln Asn Asn His Trp Ala Ile Ser Val Pro Phe Glu Asp Gln  
 180 185 190  
 Cys Gly Ala Asp Leu Ala Ser Leu Gly Arg Cys His Gln Gly Leu Ala  
 195 200 205  
 Val Tyr Glu Val Asp Gly Gly Asn Tyr Thr Ser Leu Thr Glu Thr Phe  
 210 215 220  
 Ser His Ala Val Asp Gln Ala Arg Gln His Ser Val Pro Ala Leu Ile  
 225 230 235 240  
 Leu Ile Asp Val Val Arg Leu Ser Ser His Ser Asn Ser Asp Asn Gln  
 245 250 255  
 Glu Lys

&lt;210&gt;50

&lt;211&gt;410

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;50

Met Asp Lys Asp Pro Leu Ile Leu Leu Glu Lys Glu Ala Ile Asn Val  
 1 5 10 15  
 Phe Gly Leu Ser Pro Phe Glu Ile Glu Glu Ile Lys Ala Glu Ala Gln  
 20 25 30  
 Glu Glu Val Arg Lys Ser Cys Glu Ile Ala Glu Ala Leu Pro Phe Pro  
 35 40 45

Ser Lys Gly Ser Thr Ser His Glu Val Phe Ser Pro Tyr Thr Glu Thr  
 50 55 60  
 Leu Ile Asp Tyr Glu Asn Ser Glu Ser Ala Gln Asn Leu Arg Asn Ser  
 65 70 75 80  
 Glu Pro Lys Val Met Arg Asp Ala Ile Ser Glu Ala Leu Val Glu Glu  
 85 90 95  
 Met Thr Arg Asp Ser Gly Val Ile Val Phe Gly Glu Asp Val Ala Gly  
 100 105 110  
 Asp Lys Gly Gly Val Phe Gly Val Thr Arg Asn Leu Thr Glu Lys Phe  
 115 120 125  
 Gly Pro Gln Arg Cys Phe Asn Ser Pro Leu Ala Glu Ala Thr Ile Ile  
 130 135 140  
 Gly Thr Ala Ile Gly Met Ala Leu Asp Gly Ile His Lys Pro Val Val  
 145 150 155 160  
 Glu Ile Gln Phe Ala Asp Tyr Ile Trp Pro Gly Ile Asn Gln Leu Phe  
 165 170 175  
 Ser Glu Ala Ser Ser Ile Tyr Tyr Arg Ser Ala Gly Glu Trp Glu Val  
 180 185 190  
 Pro Leu Val Ile Arg Ala Pro Ser Gly Gly Tyr Ile Gln Gly Gly Pro  
 195 200 205  
 Tyr His Ser Gln Ser Ile Glu Gly Phe Leu Ala His Cys Pro Gly Ile  
 210 215 220  
 Lys Val Ala Tyr Pro Ser Asn Ala Ala Asp Ala Lys Ala Leu Leu Lys  
 225 230 235 240  
 Ala Ala Ile Arg Asp Pro Asn Pro Val Val Phe Leu Glu His Lys Ala  
 245 250 255  
 Leu Tyr Gln Arg Arg Ile Phe Ser Ala Cys Pro Val Phe Ser His Asp  
 260 265 270  
 Tyr Val Leu Pro Phe Arg Lys Ala Ala Ile Val His Pro Gly Lys Asp  
 275 280 285  
 Leu Thr Ile Val Ser Trp Gly Met Pro Leu Val Leu Ser Leu Glu Val  
 290 295 300  
 Ala Gln Glu Leu Ala Ser Arg Gly Ile Ser Ile Glu Val Ile Asp Leu  
 305 310 315 320  
 Arg Thr Met Val Pro Cys Asp Phe Ala Thr Val Leu Lys Ser Leu Glu  
 325 330 335  
 Lys Thr Gly Arg Leu Leu Val Ile His Glu Ala Ser Glu Phe Cys Gly  
 340 345 350  
 Phe Gly Ser Glu Leu Val Ala Thr Met Ser Glu Gln Gly Tyr Ala Tyr  
 355 360 365  
 Leu Asp Ala Pro Ile Arg Arg Leu Gly Gly Leu His Ala Pro Val Pro  
 370 375 380  
 Tyr Ser Lys Val Leu Glu Asn Glu Val Leu Pro His Lys Glu Ser Ile  
 385 390 395 400  
 Leu Gln Ala Ala Lys Ser Leu Ala Glu Phe  
 405 410

&lt;210&gt;51

&lt;211&gt;429

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;51

Val Asn Phe Leu Leu Pro Thr Thr Cys Arg Gly Ile Leu Met Ala Glu  
 1 5 10 15  
 Ile Ser Thr Pro Ser Leu Pro Asp Ser Ser Ile Val Ser Gln Lys Thr  
 20 25 30  
 Pro Pro Val Pro Asp Pro Asp Ser Ser Pro Asp His Ile Pro Thr Ile  
 35 40 45  
 Pro Thr Gln Ala Pro Phe Lys Pro Gln Arg Lys Lys Glu Thr Pro Ser  
 50 55 60  
 Ser Ile Val Asn Ala Ile Ala Phe Ala Ile Leu Ala Phe Leu Ser Cys  
 65 70 75 80  
 Leu Gly Gly Val Phe Ala Ile Cys Leu Gly Cys Ser Leu Glu Ile Thr  
 85 90 95  
 Met Pro Leu Phe Ile Leu Thr Ala Val Phe Ile Ala Phe Thr Leu Leu

100 105 110  
 Tyr Phe Ile His Tyr Leu Glu Lys Pro Lys Ile Pro Glu Pro Leu Pro  
 115 120 125  
 Thr Pro Pro Pro Ser Pro Thr Leu Arg Ala Pro Thr Leu Thr Pro Glu  
 130 135 140  
 Ile Pro Ala Pro Ala Pro Gly Ile Pro Leu Pro Pro Thr Leu Pro Lys  
 145 150 155 160  
 Val Asp Arg Thr Lys Leu Thr Cys Asn Pro Asp Ile His Tyr Pro Ser  
 165 170 175  
 Thr Tyr Asp Pro Lys Ala Cys Phe Ser Leu Leu Lys Gln Leu Phe Ser  
 180 185 190  
 Leu Asp Pro Glu Thr Arg Pro Glu Asp Arg Lys Tyr Ser Asn Lys Leu  
 195 200 205  
 Ala Ser Ile Leu Leu Arg Ser Lys Glu Lys Ser Gly Phe Arg Phe His  
 210 215 220  
 Cys Phe Lys Gly His Phe Ser His Asp Lys Ile Leu Asn Lys Lys Ser  
 225 230 235 240  
 Gly Ala Val Val Ile Ser Ser His Ser Ser Met Asp Phe Ser Thr Thr  
 245 250 255  
 Leu Gly Arg Ala Phe Ala Val Thr Thr Cys Leu Gln Arg Ser Cys Trp  
 260 265 270  
 Glu Lys Ile Lys Asn Asn Ile Pro Thr Pro Glu Lys His Leu Pro Ile  
 275 280 285  
 Gly Ser Cys Val Ser Gly Pro Trp Asp Val Glu Glu Gly Ala Gln Leu  
 290 295 300  
 Tyr Thr Ser His Leu Ile Val Ile Asn Pro Pro Thr Leu Glu Thr Leu  
 305 310 315 320  
 Ile Lys Glu Lys Met Arg Arg Ala Ile Thr Leu Lys Asp Phe Ser Met  
 325 330 335  
 Lys Glu Ala Phe Thr Asn Leu Val Leu Ala Tyr Leu Gln Cys Phe Asp  
 340 345 350  
 Ile Cys Ile Glu His Asn Leu Glu Ser Val Gln Leu Glu Val Phe Gly  
 355 360 365  
 Leu Asn Asn Leu Ser Ala Asp Gln Glu Glu Phe Thr Thr Trp Glu Ser  
 370 375 380  
 Cys Cys His Leu Ala Leu Glu Ser Val Arg Ile Leu Leu Ala Ser  
 385 390 395 400  
 Lys Glu Glu Tyr Ala Leu Ser Asn Val Ser Val Asn Ser Ile Ser Gln  
 405 410 415  
 Val Pro Leu Gln Thr Ala Cys Arg Ala Leu Phe Leu Asn  
 420 425

&lt;210&gt;52

&lt;211&gt;524

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;52

Thr Thr Leu Glu Glu Asp Ala Gly Ser Ser Leu Lys Pro Leu Pro Lys  
 1 5 10 15  
 Thr Phe Pro Cys Ala Thr Ala Leu Tyr Ile Thr His Arg Arg Glu Arg  
 20 25 30  
 Lys Ser Glu His Gln Met Trp Asn Arg Cys Gln Val Phe Ser Ser Phe  
 35 40 45  
 Phe Phe Arg Tyr Pro Ile Ser Ser Trp Leu Ile Arg Leu Arg Ala Ser  
 50 55 60  
 Cys Glu Cys Phe Gln Gln Arg His Pro Ile Phe Leu Cys Gly Leu Tyr  
 65 70 75 80  
 Trp Leu Ala Gly Ile Thr Ser Arg Gly Tyr Pro Glu Cys Ser Ala Leu  
 85 90 95  
 Ile Leu Ile Phe Leu Gly Met Phe Leu Pro Arg Asn Pro Lys Gln Trp  
 100 105 110  
 Leu Pro Leu Ala Ser Ala Trp Ile Ile Ser Leu Met Leu Thr Pro Ala  
 115 120 125  
 Pro Phe Leu His Asp Gly Pro Ile Ser Gly Thr Phe Val Ile His His  
 130 135 140

Ala Gly Gly Gln Gly Xaa Thr Thr Glu Lys Leu Phe Val Phe Arg Arg  
 145 150 155 160  
 Pro Val Gly Lys Arg Ala His His Leu Xaa Cys Gln Ile Leu Ser Glu  
 165 170 175  
 Ser Arg Leu Glu Leu Lys Lys Val Tyr Glu Leu Glu Gly Thr Leu His  
 180 185 190  
 His Thr Ser Gln Ile Val Phe Lys Ser Asn Ala Cys Tyr Lys Glu Ile  
 195 200 205  
 Pro Arg Ser Arg Phe Tyr Ile Met Lys Glu Lys Cys Arg Glu Ser Ser  
 210 215 220  
 Cys His Phe Leu Asn His Arg Phe Pro Ser Ser Glu Val Gly Pro Phe  
 225 230 235 240  
 Ala Ser Ser Leu Leu Gly Thr Pro Leu Pro Gln Asn Leu Arg Asp  
 245 250 255  
 Leu Phe Arg Gln Lys Gly Leu Ser His Leu Phe Ala Ile Ser Gly Trp  
 260 265 270  
 His Phe Ser Leu Cys Ala Thr Thr Leu Trp Met Leu Cys Ala Leu Leu  
 275 280 285  
 Pro Leu Lys Ile Lys Lys Ile Leu Ser Phe Ile Val Leu Thr Ser Leu  
 290 295 300  
 Ser Cys Ile Phe Pro Met Ser Leu Ser Val Trp Arg Ser Trp Ile Ser  
 305 310 315 320  
 Val Thr Leu Leu Cys Phe Ser Trp Cys Phe Ser Gly Ser Cys Ser Gly  
 325 330 335  
 Leu Asn Arg Leu Gly Ala Gly Phe Ile Leu Cys Ser Ile Phe Phe Ser  
 340 345 350  
 Arg Phe Ser Pro Thr Phe Val Leu Ser Phe Leu Ala Thr Leu Gly Ile  
 355 360 365  
 Leu Leu Phe Phe Pro Lys Ile Phe Ser Phe Leu Tyr Thr Pro Trp Thr  
 370 375 380  
 Gln Phe Leu Ser Pro Phe Trp Leu Tyr Pro Ile Arg Tyr Leu Ala Met  
 385 390 395 400  
 Thr Leu Ala Ile Ser Leu Ser Ala Gln Leu Phe Ile Val Leu Pro Ile  
 405 410 415  
 Met Gln Tyr Phe Gly Ser Leu Pro Leu Glu Gly Leu Leu Tyr Asn Leu  
 420 425 430  
 Ile Val Pro Phe Thr Ile Leu Pro Ile Ile Val Phe Leu Ile Ala Thr  
 435 440 445  
 Ile Ile Leu Pro Cys Cys Ser Pro Ile Thr Glu Ala Leu Ile Gln Gly  
 450 455 460  
 Phe Leu Ser His Pro Trp Leu His Asn Pro Asn Ile Leu Lys Thr Leu  
 465 470 475 480  
 Ser Phe Ala Pro Val Pro Pro Trp Met Leu Thr Leu Ala Ser Leu Ile  
 485 490 495  
 Leu Phe Phe Ile Gly Ile Leu Arg Thr Asn Val Ser Pro Tyr Ala Ser  
 500 505 510  
 Thr Ser Ala Thr Ser Tyr Arg Phe Ile Glu Thr Leu  
 515 520  
 <210>53  
 <211>276  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>53  
 Ala Lys Ser Leu Trp Asp Ser Glu Arg Lys Lys Met Lys Lys Pro Asp  
 1 5 10 15  
 Asn Asp Ser Thr Phe Asp Val Arg Ser Phe Phe Pro Phe Asp Val Leu  
 20 25 30  
 Cys Ile Glu Gln Leu Arg Lys Glu Met Ser Trp Glu Val Val Ser Ala  
 35 40 45  
 Lys Ile Pro Arg Leu Pro Arg Gly Trp Tyr Glu Leu Met Gly Leu Ser  
 50 55 60  
 Lys Glu Asp Arg Ile Asp Phe Cys Leu Asp Phe Trp Cys Ser Val Leu  
 65 70 75 80  
 Gly Ile Glu His Lys Glu Ser Pro Ser Ile Cys Arg Phe Phe Ser Leu



85 90 95  
 Leu Glu Thr Ile Glu Val Tyr Ile Tyr Arg Leu Glu Lys Glu Pro Tyr  
 100 105 110  
 Gln Leu Lys Met Phe Tyr Val Phe Arg Asp Gly Arg Cys Gly Phe Gln  
 115 120 125  
 Gly Glu Pro Pro Leu Leu Asp Phe Leu Gly His His Arg Leu Pro Pro  
 130 135 140  
 Leu Gly Asp Arg His Tyr Glu Lys Phe Phe Ser Ile His Asn Gly Phe  
 145 150 155 160  
 Gly Lys Trp Glu Asp Glu Gly Ile Phe Pro Met Arg Ser Leu Ala Lys  
 165 170 175  
 Val Gln Gln Lys Leu Arg Gln Gln Leu Val Val Met Asn Lys Met Gln  
 180 185 190  
 Ala Glu Asp Asn Cys Tyr Ser Leu Gly Ile Phe Pro Phe Tyr Gly Tyr  
 195 200 205  
 Glu Glu Pro Phe Ala Tyr Gln Ser Phe Phe Phe Asp Pro Glu Ile Arg  
 210 215 220  
 Arg Asp Leu Pro Ser Pro Asn Val Leu Leu Asn Glu Glu Ser Leu Glu  
 225 230 235 240  
 His Arg Ser Leu Glu Thr Ile Glu Leu Leu His Leu Ser Lys Ser Tyr  
 245 250 255  
 Tyr Pro Ser Phe Leu Ser Trp Leu Glu Asn Tyr Leu His Ser Glu Glu  
 260 265 270  
 Val Tyr Asn Glu  
 275

&lt;210&gt;54

&lt;211&gt;113

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;54

Val Arg Arg Cys Ile Met Asn Glu Pro Thr Arg Thr Tyr Leu Glu Ser  
 1 5 10 15  
 Glu Lys Asp Thr Gln Asp Gln Ile Glu Glu Leu Gln Ala Thr Cys Ile  
 20 25 30  
 Val Lys Asn Ala Ala Gly Ile His Val Arg Pro Ala Gly Val Ile Val  
 35 40 45  
 Arg Leu Phe Asp Gly Glu Pro Cys Asp Val His Phe Thr Tyr Ala Gly  
 50 55 60  
 Lys Thr Ile Asn Ala Lys Ser Ile Met Ser Ile Leu Met Leu Gly Ala  
 65 70 75 80  
 Pro Gln Gly Gly Glu Ile Leu Val Thr Ile Arg Ser Lys Glu Ala His  
 85 90 95  
 Arg Ile Leu Gln Lys Ile Gln Asp Ala Phe Ser Ser Gly Phe Gly Glu  
 100 105 110  
 Leu

&lt;210&gt;55

&lt;211&gt;420

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;55

Met Asp Thr Gln Ser Ser Ile Gly Asn Glu Glu Trp Arg Ile Ala Gly  
 1 5 10 15  
 Thr Ser Val Val Ser Gly Met Ala Leu Gly Lys Val Phe Phe Leu Gly  
 20 25 30  
 Thr Ser Pro Leu His Val Arg Glu Leu Thr Leu Pro Gln Glu Glu Val  
 35 40 45  
 Glu His Glu Ile His Arg Tyr Tyr Lys Ala Leu Asn Arg Ser Lys Ser  
 50 55 60  
 Asp Ile Val Ala Leu Glu Gln Glu Val Thr Gly Gln Gln Gly Leu Gln  
 65 70 75 80  
 Glu Val Ser Ser Ile Leu Gln Ala His Leu Glu Ile Met Lys Asp Pro  
 85 90 95  
 Leu Leu Thr Glu Glu Val Val Asn Thr Ile Arg Lys Asp Arg Lys Asn

100	105	110
Ala Glu Tyr Val Phe Ser Ser	Val Met Gly Lys Ile Glu Glu Ser Leu	
115	120	125
Thr Ala Val Arg Gly Met Pro	Ser Val Val Asp Arg Val Gln Asp Ile	
130	135	140
His Asp Ile Ser Asn Arg Val	Ile Gly His Leu Cys Cys Gln His Lys	
145	150	155
Ser Ser Leu Gly Glu Ser Asp	Gln Asn Leu Ile Ile Phe Ser Glu Glu	
165	170	175
Leu Thr Pro Ser Glu Val Ala	Ser Ala Asn Ser Ala Tyr Ile Arg Gly	
180	185	190
Phe Val Ser Leu Val Gly Ala	Ala Thr Ser His Thr Ala Ile Val Ser	
195	200	205
Arg Ala Lys Ser Ile Pro Tyr	Leu Ala Asn Ile Ser Glu Glu Leu Trp	
210	215	220
Asn Ile Ala Lys Arg Tyr Asn	Gly Lys Leu Val Leu Ile Asp Gly Tyr	
225	230	235
Arg Gly Glu Leu Ile Phe Asn	Pro Lys Pro Ala Thr Leu Gln Ser Cys	
245	250	255
Tyr Lys Lys Glu Leu Ser Val	Val Ala His Thr Ser Gln Arg Leu Val	
260	265	270
Arg Lys Ser Leu His Pro Ile	Val Ser Ser His Ala Gly Ser Asp Lys	
275	280	285
Asp Val Glu Asp Leu Leu Glu	Asn Phe Pro Gln Thr Ser Ile Gly Leu	
290	295	300
Phe Arg Ser Glu Phe Leu Ala	Val Ile Leu Gly Arg Leu Pro Thr Leu	
305	310	315
Arg Glu Gln Val Asp Leu Tyr	Glu Lys Leu Ala Arg Phe Pro Gly Asp	
325	330	335
Ser Pro Ser Val Leu Arg Leu	Phe Asp Phe Gly Glu Asp Lys Pro Cys	
340	345	350
Pro Gly Ile Lys Asn Lys Lys	Glu Arg Ser Ile Arg Trp Leu Leu Asp	
355	360	365
Tyr Ser Val Ile Leu Glu Asp	Gln Leu Gln Ala Ile Ala Lys Ala Ser	
370	375	380
Leu Gln Gly Ser Ile Lys Val	Leu Ile Pro Gly Val Ser Asp Val Ser	
385	390	395
Glu Ile Ile Glu Val Lys Lys	Lys Trp Glu Thr Ile Gln Thr Arg Phe	
405	410	415
Pro Lys Arg Pro		
420		

&lt;210&gt;56

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;56

Thr Ser Lys Cys Asn Phe Ala Pro Ser Ser Asp Pro His Asp Ser Pro	
1	5
Cys Thr Ser Ser Cys Glu Gln Asn Gln Val Pro Val Ser Ile Cys Gly	
20	25
Glu Ala Ala Gly Gln Leu Ser Leu Thr Pro Leu Phe Ile Gly Leu Gly	
35	40
Val Gln Glu Leu Ser Val Ala Met Pro Val Ile Asn Arg Leu Arg Asn	
50	55
His Ile Ala Leu Leu Glu Leu Asn Ser Cys Leu Glu Ile Thr Glu Ala	
65	70
Leu Leu Gln Ala Lys Thr Cys Ser Glu Val Glu Glu Leu Leu Asn Arg	
85	90
Asn Asn Lys Ile Thr Ser	
100	

&lt;210&gt;57

&lt;211&gt;98

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;57

Ile Ser Met Gly Ser Gly Tyr Ala Lys Lys Lys Lys Glu Ala Lys Ile  
 1 5 10 15  
 Met Glu Gln Gln Phe Leu Glu Met Glu Ala Ser Leu Leu Glu Lys Arg  
 20 25 30  
 Tyr Glu Gly Gln Ala Gly Asn Gly Leu Val Ser Val Val Ile Asn Gly  
 35 40 45  
 Lys Cys Asp Leu Ile Ser Val Lys Val Gln Pro Thr Cys Leu Asp Pro  
 50 55 60  
 Glu Asp Pro Glu Val Ile Glu Asp Leu Phe Arg Ala Ala Phe Lys Leu  
 65 70 75 80  
 Ala Lys Glu Gln Met Asp Gln Glu Met Ser Leu Met Arg Ser Thr Met  
 85 90 95  
 Pro Phe

&lt;210&gt;58

&lt;211&gt;271

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;58

Val Val Val Lys Lys Cys Ile Phe Lys Gly Phe Leu Lys Lys Arg Ser  
 1 5 10 15  
 Trp Arg Ser Tyr Arg Leu Trp Leu Lys Met Thr Ile Leu Arg Arg Arg  
 20 25 30  
 Lys Lys His Trp Arg Arg Ser Pro Val Gln His Lys Glu Ala Cys Val  
 35 40 45  
 Met Gln Asn Leu Phe Met Thr Tyr Val Ile Ser Leu Phe Pro Lys Ser  
 50 55 60  
 Leu Ser Pro Asp Thr Val Ala Gln Ala Leu Gly Phe Ala Ser Gln Asp  
 65 70 75 80  
 Ser Leu Arg Thr Leu Asp Asn Ala Ile Leu Gln Arg Asp Tyr Ala Thr  
 85 90 95  
 Ala Leu Gly Ile Val Thr Asp Phe Leu Asn Ser Gly Val Ala Pro Val  
 100 105 110  
 Thr Phe Leu His Asp Leu Thr Leu Phe Tyr Arg Asn Leu Leu Leu Thr  
 115 120 125  
 Asn Ser Thr Thr Ser Lys Phe Ser Ser Gln Tyr Lys Thr Glu Gln Leu  
 130 135 140  
 Leu Glu Ile Ile Asp Phe Leu Gly Glu Ser Ala Lys His Leu Gln Asn  
 145 150 155 160  
 Thr Ile Phe Glu Gln Thr Phe Leu Glu Thr Val Ile Ile His Ile Ile  
 165 170 175  
 Arg Ile Tyr Gln Arg Pro Val Leu Ser Glu Leu Ile Ser Ser Ile Lys  
 180 185 190  
 Ser Arg Gln Phe Glu Gly Leu Arg Asn Ile Lys Glu Pro Thr Leu Thr  
 195 200 205  
 Gln Gln Val Ser Ala Pro Gln Pro Gln Pro Thr Tyr Lys Glu Gln Ser  
 210 215 220  
 Phe Leu Glu Lys Lys Asn Gln Pro Ala Ala Glu Gly Lys Ile Ile Ser  
 225 230 235 240  
 Val Glu Val Lys Ser Ser Ala Ser Ile Lys Ser Ala Ala Val Asp Thr  
 245 250 255  
 Leu Leu Gln Phe Ala Val Val Glu Phe Ser Gly Ile Leu Arg Gln  
 260 265 270

&lt;210&gt;59

&lt;211&gt;233

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;59

Met Thr Leu Gln Pro Tyr Gln Ala Ser Ser Arg Lys Tyr Arg Pro Gln  
 1 5 10 15  
 Ile Phe Arg Glu Ile Leu Gly Gln Ser Ser Val Val Ala Val Leu Lys  
 20 25 30  
 Asn Ala Leu Val Phe Asn Arg Ala Ala His Ala Tyr Leu Phe Ser Gly

```

      35              40              45
Ile Arg Gly Thr Gly Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ala
      50              55              60
Leu Asn Cys Val His Leu Ser Glu Asp Gly Glu Pro Cys Asn Gln Cys
      65              70              75              80
Phe Ser Cys Lys Glu Ile Ala Ser Gly Ser Ser Leu Asp Val Leu Glu
      85              90              95
Ile Asp Gly Ala Ser His Arg Gly Ile Glu Asp Ile Arg Gln Ile Asn
      100              105              110
Glu Thr Val Leu Phe Thr Pro Val Lys Ala Lys Phe Lys Ile Tyr Ile
      115              120              125
Ile Asp Glu Val His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu
      130              135              140
Lys Thr Leu Glu Glu Pro Gln His Val Lys Phe Phe Phe Ala Thr
      145              150              155              160
Thr Glu Ile His Lys Ile Pro Gly Thr Ile Leu Ser Arg Cys Gln Lys
      165              170              175
Met His Leu Gln Arg Ile Pro Glu Lys Thr Ile Leu Glu Lys Leu Ser
      180              185              190
Leu Met Ala Gln Asp Asp His Ile Glu Ala Ser Gln Glu Ala Leu Ala
      195              200              205
Pro Ile Ala Arg Ala Ala Gln Gly Ser Leu Arg Asp Ala Glu Ser Leu
      210              215              220
Tyr Asp Leu Arg Asn Ile Phe Ile Ser
      225              230
<210>60
<211>346
<212>PRT
<213>Chlamydia pneumoniae
<400>60
Cys Lys Tyr Leu Tyr His His Ser Tyr Pro Pro Pro Gln His Ser Val
      1              5              10              15
Gly Ser Ile Ser Ser Arg Tyr Lys Leu Arg Val Leu Ala Ile Thr Phe
      20              25              30
Leu Val Leu Gly Val Leu Leu Leu Ile Ser Gly Ala Leu Phe Leu Thr
      35              40              45
Leu Gly Ile Pro Gly Leu Thr Ala Gly Val Ser Phe Gly Leu Gly Ile
      50              55              60
Gly Leu Ser Ala Leu Gly Gly Val Leu Val Val Ser Gly Leu Leu Cys
      65              70              75              80
Leu Leu Val Lys Arg Glu Val Ser Lys Val Cys Pro Glu Glu Ile Pro
      85              90              95
Ala Val Gln Pro Glu Glu Thr Pro Glu Gly Val Pro Val Thr Pro Phe
      100              105              110
Glu Lys Pro Ala Leu Asp Glu Ala Gln Lys Glu Gln Lys Thr Gln Lys
      115              120              125
Ile Leu Asp Gln Leu Pro Gln Glu Leu Asp Gln Leu Asp Arg Tyr Ile
      130              135              140
Gln Glu Val Phe Ala Cys Leu Gly Pro Leu Lys Asp Leu Lys Tyr Glu
      145              150              155              160
Asp Gln Gly Phe Leu Gln Asp Val Lys Glu Glu Phe Gln Val Phe Asp
      165              170              175
Phe Val Gln Lys Asp Met Ile Ala Glu Phe Val Glu Leu Gln Gln Ile
      180              185              190
Leu Cys Gln Glu Gly Arg Leu Leu Glu Phe Val Ile Asn Gln Thr Arg
      195              200              205
Tyr Ile Gly Arg Asp Leu Phe Lys Arg Glu Asp Ser Leu Tyr Lys Leu
      210              215              220
Trp Glu Trp Leu Gly Tyr Leu Pro Ser Gly Asp Val Arg Gly Glu Arg
      225              230              235              240
Leu Lys Lys Ser Ala Arg Glu Val Val Asp Arg Phe Met Arg Thr Thr
      245              250              255
Cys Asn Ile Arg Lys Ile Ala Met Thr Phe Asp Arg His Val Tyr Ser
      260              265              270

```

Val Ala Lys Thr Ala Phe Glu Lys Ala Phe Gly Ala Leu Glu Thr Cys  
 275 280 285  
 Val Tyr Glu Ser Met Arg Glu Ser Tyr Arg Glu Ala Phe Cys Glu Tyr  
 290 295 300  
 Glu Lys Ala Lys Leu Leu Gly Asp Glu Glu Lys Ser Ala His Ala Glu  
 305 310 315 320  
 Gln Arg Phe Gln Asp Ile Lys Asn Arg Trp Glu Asp Val Lys Asp Ala  
 325 330 335  
 Phe Phe Trp Val Lys Glu Asp Gly Glu Asp  
 340 345

&lt;210&gt;61

&lt;211&gt;145

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;61

Lys Lys Met Gly Lys Ile Glu Ile Asp Asp Ala Ile Gly Asn Ser Cys  
 1 5 10 15  
 Lys Trp Ser Glu Arg Tyr Glu Glu His Arg Ile Thr Arg Ala Arg Trp  
 20 25 30  
 Tyr Lys Val Ala Glu His Gln Leu Phe Asn Ala Thr Met Arg Val Lys  
 35 40 45  
 Asp Ser Leu Arg Glu His Asn Glu Ala Arg Val Ala Phe Glu Lys Glu  
 50 55 60  
 Arg Ser Lys Glu Asn Gln Arg Gln Val Gln Lys Lys Lys Glu Lys Arg  
 65 70 75 80  
 Leu Arg Asp Leu Lys Glu Leu His Asp Gln Glu Leu Pro Arg Ala Gln  
 85 90 95  
 Glu Arg Leu Arg Glu Leu Gln Ala Leu Tyr Pro Glu Ile Ala Val Ser  
 100 105 110  
 Val Val Glu Ala Arg Arg Glu Val Ala Ser Asp Leu Glu Lys Ala His  
 115 120 125  
 Glu Ser Ile Asp Lys His Tyr Gln Ser Cys Val Arg Glu Gln Glu Leu  
 130 135 140

Tyr

145

&lt;210&gt;62

&lt;211&gt;279

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;62

Glu Glu Glu Glu Lys Gln Glu Ala Glu Phe Arg Glu Asn Gly Thr Lys  
 1 5 10 15  
 Ile Arg Ser Met Glu Glu Val Ser Glu Tyr Leu Gln Gln Val Glu Asn  
 20 25 30  
 Gln Leu Glu Ser Cys Ser Lys Arg Leu Thr Lys Met Glu Thr Phe Ala  
 35 40 45  
 Leu Gly Val Arg Leu Glu Ala Lys Glu Glu Ile Glu Ser Ile Ile Leu  
 50 55 60  
 Ser Asp Val Val Asn Arg Phe Glu Val Leu Cys Arg Asp Ile Glu Asp  
 65 70 75 80  
 Met Leu Ser Arg Val Glu Glu Ile Glu Arg Met Leu Arg Met Ala Glu  
 85 90 95  
 Leu Pro Val Leu Pro Ile Lys Glu Ala Leu Thr Lys Ala Phe Val Gln  
 100 105 110  
 His Asn Ser Cys Lys Glu Lys Leu Thr Lys Val Glu Pro Tyr Phe Lys  
 115 120 125  
 Glu Ser Pro Ala Tyr Leu Thr Ser Glu Asn Arg Leu Gln Ser Leu Asn  
 130 135 140  
 Gln Thr Leu Gln Arg Ala Tyr Lys Glu Ser Gln Lys Val Ser Gly Leu  
 145 150 155 160  
 Glu Ser Glu Val Arg Ala Cys Arg Glu Gln Leu Lys Asp Gln Val Arg  
 165 170 175  
 Gln Phe Glu Thr Gln Gly Val Ser Leu Ile Lys Glu Glu Ile Leu Phe  
 180 185 190

Val Thr Ser Thr Phe Arg Thr Lys Phe Ser Tyr His Ser Phe Arg Leu  
 195 200 205  
 His Val Pro Cys Met Arg Leu Tyr Glu Glu Tyr Tyr Asp Asp Ile Asp  
 210 215 220  
 Leu Glu Arg Thr Arg Ala Arg Trp Met Ala Met Ser Glu Arg Tyr Arg  
 225 230 235 240  
 Asp Ala Phe Gln Ala Phe Gln Glu Met Leu Lys Glu Gly Leu Val Glu  
 245 250 255  
 Glu Ala Gln Ala Leu Arg Glu Thr Glu Tyr Trp Leu Tyr Arg Glu Glu  
 260 265 270  
 Arg Lys Ser Lys Lys Lys His  
 275  
 <210>63  
 <211>644  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>63  
 Cys Lys Tyr Leu Tyr His His Ser Tyr Pro Pro Pro Pro Pro Pro  
 1 5 10 15  
 Asp Gln Ser Val Gly Ala Ser Phe Cys Leu Ser Lys Phe Arg Val Leu  
 20 25 30  
 Ala Ile Thr Phe Leu Val Leu Gly Val Leu Leu Leu Ile Ser Gly Ala  
 35 40 45  
 Leu Phe Leu Thr Leu Gly Ile Ser Gly Val Ser Leu Gly Val Gly Leu  
 50 55 60  
 Gly Leu Ser Ala Leu Gly Ser Val Leu Val Ile Ser Gly Phe Leu Leu  
 65 70 75 80  
 Leu Leu Glu Arg Arg Glu Val Ser Gly Val Gly Leu Glu Gly Ile Pro  
 85 90 95  
 Thr Gly Ile Pro Val Gly Pro Ser Ala Glu Pro Ser Ser Glu Glu Ile  
 100 105 110  
 Gln Lys Lys Gln Lys Ala Lys Gln Ile Leu Asp Gln Leu Pro Gln Glu  
 115 120 125  
 Leu Asp Gln Leu Asp Thr Asp Ile Gln His Val Leu Ser Cys Leu Gly  
 130 135 140  
 Lys Leu Lys Asp Leu Lys Cys Lys Asp Arg Gly Leu Leu Lys Asp Ala  
 145 150 155 160  
 Lys Glu Lys Leu Gln Val Phe Asp Phe Val Trp Lys Asp Met Met Met  
 165 170 175  
 Glu Phe Val Glu Leu Gln Gln Val Met Asp Gln Glu Ser Arg Tyr Leu  
 180 185 190  
 Glu Gly Leu Ile His Glu Val Gln Ser Ile Ala His Lys Leu Phe Val  
 195 200 205  
 Asp Asp Val Asn Ile Arg Ser His Leu Gly Glu Ser Cys Gly Tyr Leu  
 210 215 220  
 Pro Ser Glu Asp Val Arg Gly Glu Leu Leu Lys Arg Phe Ala Lys Glu  
 225 230 235 240  
 Val Val Ala Arg Phe Met Lys Val Thr Arg Asp Ile Arg Lys Ile Ala  
 245 250 255  
 Met Ala Phe Asn Lys Asn Ala Tyr Gly Ala Ala Lys Asn Ala Phe Asp  
 260 265 270  
 Lys Ala Phe Gly Ser Leu Glu Thr Cys Leu Tyr Lys Ser Leu Thr Lys  
 275 280 285  
 Ser Tyr Arg Asp Thr Phe Cys Asp Tyr Lys Arg Ala Lys Ile Leu Pro  
 290 295 300  
 Asp Glu Asn Asn Ser Ala Arg Ala Glu Gln Arg Phe Arg Glu Val Lys  
 305 310 315 320  
 Asp His Trp Glu Asp Leu Asn Glu Thr Val Phe Trp Val Lys Glu Asp  
 325 330 335  
 Gly Arg Ile Asp Ile Glu Val Leu Thr Ala Val Gly Gly Trp Pro Asp  
 340 345 350  
 Arg Tyr Pro Glu His Leu Ile Leu Glu Lys Arg Lys Asp Lys Val Met  
 355 360 365  
 Ser His Gln Leu Trp Glu Ala Thr Met Arg Val Lys Glu Ala Glu Val

370 375 380  
 Thr Tyr Ser Val Ala Arg Val Ala Phe Glu Lys Asp Gly Ser Gln Gln  
 385 390 395 400  
 Asn Gln Lys Lys Phe Gln Glu Lys Thr Lys Glu Arg Leu Arg Cys Leu  
 405 410 415  
 Lys Asp Leu Arg Asp Gln Glu Cys His Arg Ala Gln Glu Arg Leu Glu  
 420 425 430  
 Lys Leu Thr Ala Leu Tyr Pro Glu Val Ser Val Ser Val Val Glu Thr  
 435 440 445  
 Glu Arg Glu Arg Lys Phe Asn Leu Glu Lys Ala Tyr Gly Asn Leu Glu  
 450 455 460  
 Glu Arg Tyr Gln Ser Val Val Gln Asp Gln Glu Asp Tyr Trp Thr Glu  
 465 470 475 480  
 Gln Lys Asn Arg Glu Ala Glu Phe Arg Ala Lys Gly Thr Lys Val Arg  
 485 490 495  
 Ser Met Glu Glu Val Ala Glu His Leu Gln Ile Leu Glu Asn Leu Leu  
 500 505 510  
 Glu Asp Cys Tyr Lys Arg Leu Ser Lys Ala Glu Thr Phe Ala Leu Gly  
 515 520 525  
 Val Glu Arg Glu Ala Thr Glu Glu Ile Glu Tyr Thr Ile Leu Ser Asp  
 530 535 540  
 Ala Ala Asn Arg Leu Lys Val Leu Cys Glu Asp Ile Glu Asp Thr Leu  
 545 550 555 560  
 Pro Arg Val Glu Glu Ile Glu Met Met Leu Arg Met Ala Glu Arg Pro  
 565 570 575  
 Leu His Pro Ile Lys Gln Ala Phe Thr Lys Ala Phe Val Gln Tyr Asn  
 580 585 590  
 Arg Cys Lys Glu Arg Leu Ala Lys Val Glu Pro Tyr Tyr Lys Glu Ser  
 595 600 605  
 Pro Ala Tyr Val Asn Ser Glu Glu Arg Leu Gln Ser Leu Asp Gln Ala  
 610 615 620  
 Ser Gln Cys Ile Gln Arg Val Pro Lys Gly Phe Lys Phe Arg Asn Gly  
 625 630 635 640  
 Ser Met Tyr Ile

&lt;210&gt;64

&lt;211&gt;114

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;64

Ser Lys Ile Cys Phe Ala Phe Cys Phe Phe Cys Ile Ser Ser Glu Glu  
 1 5 10 15  
 Gly Ser Ala Glu Gly Pro Thr Gly Ile Pro Val Gly Ile Pro Ser Lys  
 20 25 30  
 Pro Thr Pro Glu Thr Ser Arg Leu Ser Lys Ser Asn Arg Asn Pro Glu  
 35 40 45  
 Ile Thr Ser Thr Leu Pro Asn Ala Glu Ser Pro Lys Pro Thr Pro Arg  
 50 55 60  
 Glu Thr Pro Glu Ile Pro Asn Val Arg Lys Arg Ala Pro Glu Ile Ser  
 65 70 75 80  
 Lys Ser Thr Pro Arg Thr Lys Lys Val Ile Ala Lys Thr Arg Asn Leu  
 85 90 95  
 Asp Arg Gln Lys Glu Ala Pro Thr Asp Trp Ser Gly Gly Gly Gly Gly  
 100 105 110  
 Gly Gly

&lt;210&gt;65

&lt;211&gt;167

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;65

Ile Ala Lys Ser Asp Cys Arg Val Trp Ile Arg Leu His Ser Ala Tyr  
 1 5 10 15  
 Lys Glu Ser Gln Lys Val Ser Ser Leu Glu Thr Glu Ala Cys Thr Tyr

20 25 30  
 Arg Glu Tyr Leu Arg Glu Gln Val Gln Gln Phe Glu Thr Gln Gly Val  
 35 40 45  
 Ser Leu Ile Lys Glu Glu Leu Leu Phe Leu Ser Ser Thr Leu Lys Ser  
 50 55 60  
 Lys Leu Ser Tyr Asp Pro Leu Ile Ala Asn Ile Pro Cys Met Lys Phe  
 65 70 75 80  
 Tyr Tyr Gln Tyr Tyr Asp Asp Ile Asp Lys Ala Arg Ala Gln Ser Arg  
 85 90 95  
 Trp Leu Glu Lys Ser Glu Arg Tyr Arg Asn Ala Lys Arg Arg Phe Gln  
 100 105 110  
 Glu Ile Val Lys Lys Gly Leu Phe Lys Glu Ala Lys Pro Leu Lys Lys  
 115 120 125  
 Glu Glu Tyr Arg Leu Leu Gln Glu Glu Arg Ser Asn Lys Glu Lys Arg  
 130 135 140  
 Leu Ile Tyr Asn Lys Met Ala Val Ala Arg Gln Arg Val Gln Glu Phe  
 145 150 155 160  
 Glu Ser Met Glu Ile Pro Glu  
 165

&lt;210&gt;66

&lt;211&gt;235

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;66

Cys Lys Tyr Thr Tyr His Pro Pro Gln Leu Pro Pro Asp His Ser Val  
 1 5 10 15  
 Gly Ala Thr Ser Trp Gln Pro Lys Leu Arg Ile Leu Thr Ile Thr Phe  
 20 25 30  
 Leu Val Leu Gly Val Leu Leu Leu Ile Ser Gly Ala Leu Phe Leu Thr  
 35 40 45  
 Leu Gly Val Pro Gly Leu Ala Ala Gly Leu Ser Phe Gly Leu Gly Ile  
 50 55 60  
 Gly Leu Ser Ala Leu Gly Gly Val Leu Val Val Ser Gly Leu Leu Phe  
 65 70 75 80  
 Phe Leu Ile Arg Arg Gly Val Ser Lys Val Arg Pro Glu Glu Ile Pro  
 85 90 95  
 Val Thr Pro Ser His Glu Ala Gln Lys Ile Leu Cys Gln Leu Pro Gln  
 100 105 110  
 Glu Leu Asp Gln Leu Asp Thr Ser Ile Gln Glu Val Val Ser Cys Leu  
 115 120 125  
 Gly Lys Leu Lys Asp Leu Lys Tyr Glu Asp Gln Gly Leu Leu Thr Glu  
 130 135 140  
 Val Gln Glu Lys Leu Arg Val Phe Asp Phe Val Arg Lys Asp Met Val  
 145 150 155 160  
 Thr Glu Phe Leu Glu Leu Gln Gln Val Val Ala Gln Glu Gly Gln Phe  
 165 170 175  
 Leu Asp Tyr Leu Ile Asn Gln Val Gln Ser Ile Ser His Lys Leu Phe  
 180 185 190  
 Val Pro Asp Val Asn Ile Gly Ala His Leu Ala Glu Leu Cys Gly Tyr  
 195 200 205  
 Leu Pro Ser Gly Asp Val Arg Val Glu Arg Leu Lys Arg Ser Ala Arg  
 210 215 220  
 Gln Val Val Asp Arg Phe His Glu Gly Asp Leu  
 225 230 235

&lt;210&gt;67

&lt;211&gt;526

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;67

Arg Glu Cys Cys Gly Val Ala Lys Asn Ala Phe Asp Lys Ala Phe Gly  
 1 5 10 15  
 Ala Leu Glu Glu Cys Val Tyr Lys Ser Leu Thr Glu Ser Tyr Arg Glu  
 20 25 30  
 Ala Phe Tyr Glu Tyr Glu Lys Ala Lys Ile Leu Arg Asn Glu Asp Val



35 40 45  
 Glu Trp Leu Gln Asp Lys Asn Lys Ser Ala Arg Ala Glu Gln Arg Phe  
 50 55 60  
 Arg Glu Val Lys Asp Arg Trp Glu Asp Leu Lys Glu Thr Val Phe Trp  
 65 70 75 80  
 Val Lys Glu Asn Gly Cys Ile Asp Leu Glu Val Leu Thr Ala Val Gly  
 85 90 95  
 Gly Trp Pro Asp Arg Gly Pro Glu His Leu Ile Pro Glu Lys Arg Arg  
 100 105 110  
 Asn Lys Val Met Ser His Lys Leu Trp Glu Ala Thr Met Arg Met Lys  
 115 120 125  
 Gly Ala Glu Gly Thr Tyr Ser Val Ala Arg Val Ala Phe Glu Lys Asp  
 130 135 140  
 Gly Ser Arg Lys Asn Gln Lys Lys Phe Gln Glu Lys Thr Lys Glu Trp  
 145 150 155 160  
 Leu Arg Cys Leu Lys Asp Leu His Asp Gln Glu Cys His Arg Ala Arg  
 165 170 175  
 Glu Arg Leu Ala Glu Leu Glu Ala Leu Tyr Pro Glu Val Ser Val Ser  
 180 185 190  
 Val Val Glu Thr Glu Arg Glu Thr Lys Phe Lys Leu Glu Thr Ala Tyr  
 195 200 205  
 Gly Asn Leu Glu Glu Arg Tyr Gln Ser Val Val Arg Asp Gln Glu Asp  
 210 215 220  
 Tyr Trp Lys Glu Glu Glu Asn Lys Glu Ala Glu Phe Arg Glu Lys Gly  
 225 230 235 240  
 Thr Lys Val Arg Ser Pro Glu Glu Val Val Glu Tyr Leu Gln Ile Leu  
 245 250 255  
 Glu Asn Leu Leu Glu Asp Cys Ser Lys Gln Leu Thr Ile Ala Glu Val  
 260 265 270  
 Val Val Leu Gly Val Glu Leu Glu Ala Thr Ala Glu Phe Glu Tyr Thr  
 275 280 285  
 Ile Leu Ser Asp Ala Ala Asn Arg Leu Lys Val Leu Cys Glu Asp Ile  
 290 295 300  
 Glu Asp Ile Leu Pro Arg Val Glu Glu Ile Glu Ile Met Leu Arg Ile  
 305 310 315 320  
 Ala Glu Leu Pro Phe Leu Pro Ile Lys Gln Ala Phe Thr Lys Ala Phe  
 325 330 335  
 Leu Gln Tyr Asn Ser Cys Lys Asp Lys Leu Ala Lys Val Glu Pro Tyr  
 340 345 350  
 Cys Gln Glu Ser Val Asp Tyr Arg Arg Asn Lys Glu Arg Phe Gln Ser  
 355 360 365  
 Leu Asn Gln Asp Leu Gln Asn Val Tyr Gln Glu Cys Gln Lys Ala Thr  
 370 375 380  
 Gly Leu Glu Ser Glu Val Ser Ala Tyr Arg Asp His Leu Arg Glu Gln  
 385 390 395 400  
 Ile Thr Glu Phe Glu Thr Gln Gly Leu Asp Val Ile Lys Glu Glu Leu  
 405 410 415  
 Leu Phe Val Ser Ser Thr Leu Lys Ser Lys Leu Ser Tyr Asp Pro Leu  
 420 425 430  
 Ile Ala Asp Ile Pro Cys Met Lys Phe Tyr Glu Glu Tyr Tyr Asp Gly  
 435 440 445  
 Ile Asp Lys Ala Arg Val Gln Ser Arg Trp Leu Glu Lys Ser Glu Arg  
 450 455 460  
 Tyr Arg Lys Ala Lys Lys Gly Phe Gln Glu Met Leu Lys Glu Gly Leu  
 465 470 475 480  
 Phe Lys Glu Asp Gln Ala Leu Lys Lys Ala Glu Tyr Arg Leu Leu Arg  
 485 490 495  
 Glu Lys Arg Met Asn Lys Glu Lys Leu Leu Ile Cys Asn Lys Ile Glu  
 500 505 510  
 Ala Ala Gln Arg Val Gln Glu Phe Gly Pro Ser Asp Ser  
 515 520 525

&lt;210&gt;68

&lt;211&gt;705

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;68

```

Met Lys Glu Leu Arg His Glu Ser Tyr Asn Arg Ala Leu His Lys Leu
 1          5          10          15
Ser His Gln Trp Val Arg Tyr Phe Leu Tyr Thr Phe Val Ser Cys Ser
          20          25          30
Phe Ile Val Ala Ile Phe Thr Phe Ala Trp Leu Lys Val Leu Tyr Val
          35          40          45
Pro Glu Xaa Lys Ala Gly Glu Ile Ser Arg Ile Ser Leu Thr Ala Pro
          50          55          60
Met Asp Phe Xaa Leu Ser Trp Ser Ala His Lys Phe Tyr Lys Arg Thr
          65          70          75          80
Ala His Ile Ser Glu Ala Phe Gly Lys Val Tyr His Leu Thr Leu Ser
          85          90          95
Pro Gly Ser Leu Leu Ser Lys Glu Gly Asn Ala Asp Glu Asn Thr Asp
          100          105          110
Tyr Trp Phe Lys Lys Ala Ala Asp Phe Leu Leu Ser Thr Asn Phe Val
          115          120          125
Asp Ser Ser Thr Gln Lys Cys Leu Lys Asp Leu Cys Ile Tyr Pro Pro
          130          135          140
Leu Leu Gly Lys Glu Lys Lys Thr Leu Glu Ile Asn Ile Asn Ser Asn
          145          150          155          160
Lys Gly Asn Val Ile Ala Gln Cys Phe Cys His Leu Lys Ile Phe Leu
          165          170          175
Ile Gln Glu Asn Cys Pro Gln Pro Cys Phe Asp Ala Ile Met Asp Ile
          180          185          190
Leu Lys Ile Ala Asn Phe Glu Val Ala Val Asp Lys Glu Met Ser Gly
          195          200          205
Cys Val Lys Gly Glu Leu Leu Gly Lys Arg Cys Ile Glu Lys Ile Thr
          210          215          220
Lys Gly Thr Pro Ile Leu Glu Lys Tyr Gln Arg Ile Asp Asp Arg Asp
          225          230          235          240
Ala Lys Ile Leu Lys Gln Leu Arg Ala Gln Leu Leu Ser Val His Thr
          245          250          255
Leu Phe Ser Cys Arg Ser Leu Trp Gly Ala Ile Phe Val Val Leu Leu
          260          265          270
Ile Leu Leu Trp Gly Tyr Gly Ala Leu Lys Ala Leu Cys Pro Glu Met
          275          280          285
Leu Lys Ser Pro Gln Arg Phe Met Leu Tyr Ile Ala Ile Leu Thr Leu
          290          295          300
Ser Leu Leu Trp Cys Arg Gly Thr Glu Ile Phe Cys Ala Tyr Trp Val
          305          310          315          320
Ser Tyr Leu Ser Tyr Pro Pro Ile Leu Pro Phe Thr Ala Val Leu Leu
          325          330          335
Gly Tyr Phe Leu Gly Leu Pro Ile Ala Gly Phe Ser Cys Thr Phe Leu
          340          345          350
Ala Leu Leu Tyr Thr Leu Gly Ser Asp Leu Trp Asn Asn Ser Trp Phe
          355          360          365
Leu Ser Ile Asn Leu Leu Cys Ser Trp Arg Ile Leu Val Ser Leu His
          370          375          380
Arg Val Ser Arg Leu Ser Ser Val Phe Trp Ala Cys Met Lys Leu Gly
          385          390          395          400
Gly Val Ala Met Gly Ser Leu Leu Met Phe Arg Ile Phe Thr Asn Thr
          405          410          415
Ile Ser Arg Glu Ala Leu Tyr Ala Asp Gly Ile Glu Ser Phe Val Tyr
          420          425          430
Ser Leu Ile Thr Ala Ile Ser Val Val Ala Leu Ile Pro Val Phe Glu
          435          440          445
Ala Ser Phe Gly Ala Ser Thr Asn Phe Ser Leu Leu Thr Tyr Leu Ser
          450          455          460
Pro Glu Asn Ala Leu Leu Lys Arg Leu Phe Lys Glu Ala Pro Gly Thr
          465          470          475          480
Tyr Gln His Ser Val Leu Val Gly Ser Leu Ala Glu Ala Ala Ala Gln
          485          490          495

```

Ala Ile Gly Ala Asp Ser Leu Tyr Cys Leu Val Ala Ala His Tyr His  
 500 505 510  
 Asp Ile Gly Lys Leu Ile Asn Pro Gly Phe Phe Ser Glu Asn Gln Lys  
 515 520 525  
 Ile Leu Gln Gln Ser Gly His Ser Leu Ser Pro Leu Glu Cys Ala Lys  
 530 535 540  
 Met Ile Met Arg His Ile Pro Glu Gly Val Asn Leu Ala Arg Gln Xaa  
 545 550 555 560  
 Gly Leu Pro Glu Ser Asp Ile Gln Val Ile Glu Glu His His Gly Thr  
 565 570 575  
 Ser Val Ile Arg Ser Ala Tyr Tyr Ser His Met Val Glu Asn Pro Ser  
 580 585 590  
 Thr Gly Ser Phe Asp Glu Glu Leu Phe Arg Tyr Ser Gly Asn Lys Pro  
 595 600 605  
 Ser Ser Lys Glu Thr Thr Ile Ile Met Ile Ala Asp Ser Phe Glu Ala  
 610 615 620  
 Ala Ser Arg Ser Leu Lys Asn Ala Ser Leu Pro Asp Leu Gln Arg Leu  
 625 630 635 640  
 Ile Asp Gln Ile Ile Gln Gly Lys Leu Gln Asp Gly Gln Phe Ser Cys  
 645 650 655  
 Ser Pro Ile Thr Leu Asp Glu Leu Ala Leu Ile Ser Lys Ser Met Val  
 660 665 670  
 Gln Thr Leu Tyr Gly Ala Leu His Ser Arg Met Lys Tyr Pro Glu Ile  
 675 680 685  
 Ser Tyr Gln Ile Ser Met Asp Ser Cys Pro Lys Pro Ser Ile Gly Gly  
 690 695 700

Thr

705

&lt;210&gt;69

&lt;211&gt;224

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;69

Val Ile Ser Cys Gln Gly Lys Arg Pro Leu Arg Tyr Cys Phe Leu Glu  
 1 5 10 15  
 Ile Gln Ile Leu Ala Lys Ala Gln Val His Glu Cys Ile Ser Phe Xaa  
 20 25 30  
 Arg Ser Trp Tyr Pro Lys Leu Trp Phe Gln Leu Ser Thr Glu Thr  
 35 40 45  
 Thr Gly Asp Arg Glu Lys Lys Ile Pro Leu His Leu Val Glu Asn Ser  
 50 55 60  
 Tyr Phe Phe Thr Asp Gly Val Asp Ala Leu Val His Lys Gly Val Cys  
 65 70 75 80  
 Asp Leu Ala Ile His Ser Ala Lys Asp Leu Pro Glu Thr Pro Ser Leu  
 85 90 95  
 Pro Val Val Ala Ile Thr Arg Cys Leu His Pro Ala Asp Leu Leu Val  
 100 105 110  
 Tyr Ala Asp His Tyr Val His Glu Pro Leu Pro Leu Ser Pro Arg Leu  
 115 120 125  
 Gly Ser Ser Ser Leu Arg Arg Ser Ala Val Leu Lys Gln Leu Phe Pro  
 130 135 140  
 Gln Gly Gln Ile Leu Asp Ile Arg Gly Thr Ile Glu Glu Arg Leu Asp  
 145 150 155 160  
 Gln Leu His Arg Gly His Tyr Asp Ala Ile Val Leu Ala Lys Ala Ala  
 165 170 175  
 Ser Leu Arg Leu His Leu His His Ala Tyr Ser Ile Glu Leu Pro Pro  
 180 185 190  
 Pro Tyr His Ala Leu Gln Gly Ser Leu Ala Ile Thr Ala Lys Asp His  
 195 200 205  
 Ala Gly Lys Trp Lys Gln Leu Phe Thr Pro Ile His Cys His Ser Ser  
 210 215 220

&lt;210&gt;70

&lt;211&gt;334

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;70

Arg Ile Cys Asn Ala Asp Val Phe Glu Ser Glu Ala Leu Asn Ile Ser  
 1 5 10 15  
 Ser Pro Leu Ile Tyr Leu Phe Pro Glu Thr Asn Leu Asp Asn Ile Lys  
 20 25 30  
 Gln Gln Ile Ala Thr Leu Glu Pro Asp Ile Leu Ile Ile Asp Ser Ile  
 35 40 45  
 Gln Ile Ile Phe Asn Pro Thr Leu Asn Ser Ala Pro Gly Ser Val Ala  
 50 55 60  
 Gln Val Arg Glu Val Thr Tyr Glu Leu Met Gln Ile Ala Lys Ser Ala  
 65 70 75 80  
 Gln Ile Thr Thr Phe Ile Ile Gly His Val Thr Lys Ser Gly Glu Ile  
 85 90 95  
 Ala Gly Pro Arg Val Leu Glu His Leu Val Asp Thr Val Leu Tyr Phe  
 100 105 110  
 Glu Gly Asn Ser His Ala Asn Tyr Arg Met Ile Arg Ser Val Lys Asn  
 115 120 125  
 Arg Phe Gly Pro Thr Asn Glu Leu Leu Ile Leu Ser Met His Ala Asp  
 130 135 140  
 Gly Leu Lys Glu Val Ser Asn Pro Ser Gly Leu Phe Leu Gln Glu Lys  
 145 150 155 160  
 Thr Gly Pro Thr Thr Gly Ser Met Ile Ile Pro Ile Ile Glu Gly Ser  
 165 170 175  
 Gly Ala Leu Leu Ile Glu Leu Gln Ala Leu Val Ser Ser Ser Pro Phe  
 180 185 190  
 Ala Asn Pro Val Arg Lys Thr Ala Gly Phe Asp Pro Asn Arg Phe Ser  
 195 200 205  
 Leu Leu Leu Ala Val Leu Glu Lys Arg Ala Gln Val Lys Leu Phe Thr  
 210 215 220  
 Met Asp Val Phe Leu Ser Ile Thr Gly Gly Leu Lys Ile Ile Glu Pro  
 225 230 235 240  
 Ala Ala Asp Leu Gly Ala Leu Leu Ala Val Ala Ser Ser Leu Tyr Asn  
 245 250 255  
 Arg Leu Leu Pro Asn Asn Ser Ile Val Ile Gly Glu Val Gly Leu Gly  
 260 265 270  
 Gly Glu Ile Arg His Val Ala His Leu Glu Arg Arg Ile Lys Glu Gly  
 275 280 285  
 Lys Leu Met Gly Phe Glu Gly Ala Ile Leu Pro Glu Gly Gln Ile Ser  
 290 295 300  
 Ser Leu Pro Lys Glu Ile Arg Glu Asn Phe Arg Leu Gln Gly Val Lys  
 305 310 315 320  
 Thr Ile Lys Arg Cys Tyr Pro Ser Val Thr Leu Thr Pro Val  
 325 330

&lt;210&gt;71

&lt;211&gt;97

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;71

Glu Thr Tyr Val Pro Leu Leu Pro Pro Arg Glu Glu Ile Leu Pro Leu  
 1 5 10 15  
 Met Ser Gly Asn Pro Lys Asn Leu Leu Gln Gln Phe Thr Gln Lys Gln  
 20 25 30  
 Phe Arg Val Leu Pro Val Tyr Gln Ser Thr Ala Val Thr Asp Ala Gln  
 35 40 45  
 Gly Asn Val Ser Tyr Gln Ile Gln Val Leu Val Asn Gln Glu Val Trp  
 50 55 60  
 Gly Glu Gly Asn Ala Ser Ser Lys Lys Glu Ala Glu Lys Ile Ala Ala  
 65 70 75 80  
 Gln Gln Ala Leu Asp Thr Tyr Gly Asn Lys Asn Gln Asn Thr Met Asp  
 85 90 95  
 Val

&lt;210&gt;72

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;72

```

Ile Pro Asn Ser Lys Phe Lys Asp Gly Ala Leu Leu Ser Met His Pro
 1           5           10           15
Pro Ile Asp Ile Thr Ala Ile Glu Ala Lys Leu Asn Phe Thr Phe Thr
          20           25           30
Gln Pro Lys Leu Leu Glu Ile Ala Leu Thr His Pro Ser Tyr Lys Asn
          35           40           45
Glu Ser Ala Val Gln Ile Glu Asp Ser Glu Arg Leu Glu Phe Leu Gly
          50           55           60
Asp Ala Val Leu Gly Leu Ile Val Thr Glu His Leu Phe Leu Leu Phe
        65           70           75           80
Pro Ser Met Asp Glu Gly Thr Leu Ser Thr Ala Arg Ala Ser Leu Val
          85           90           95
Asn Ala Lys Ala Cys Cys Arg Tyr Thr Thr Met Leu Gly Ile Gly Asp
          100          105          110
Tyr Leu Leu Ile Gly Lys Gly Glu Lys Ile Gln Ser Glu Arg Gly Arg
          115          120          125
Leu Ser Ala Tyr Ala Asn Leu Phe Glu Ser Ile Leu Gly Ala Val Tyr
          130          135          140
Leu Asp Gly Gly Leu Ser Pro Ala Arg Lys Leu Thr Phe Pro Ser Phe
        145          150          155          160
Leu Leu Glu Lys Lys Phe Phe Leu
          165

```

&lt;210&gt;73

&lt;211&gt;165

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;73

```

Cys Phe Trp Ile Cys Tyr Leu Ile Arg Ile Arg Met Arg Ser Ala Leu
 1           5           10           15
His Leu Gln His Leu Arg His Phe His Asn His Gly Ser Ile Leu Phe
          20           25           30
Glu Asn Leu Leu Thr Ile Lys Asp Cys Phe Leu Leu Glu Thr Lys Leu
          35           40           45
Gln Asn Phe Ile Ala Lys Ala Ser Lys Thr Ile Asp Thr Val Arg Trp
          50           55           60
Arg Glu Asn Ile Phe Arg Ser Met Pro Glu Ile Tyr Thr Val Val Arg
        65           70           75           80
Lys Arg Arg Leu Asp Phe Phe Ala Ala Glu Leu Val His Arg Pro Lys
          85           90           95
Leu Ser Leu Val Arg Asp Leu Trp Val Phe Pro Gly Glu Glu Ile Leu
          100          105          110
Glu Gly Glu Glu Asp Cys Met Leu Phe Leu Leu Leu Ser Gly Asp Arg
          115          120          125
Ala Gly Ser Gly Ile Phe Phe Thr Gly Pro Tyr Pro Ser Asp Leu Tyr
          130          135          140
Glu Leu Glu Lys Gly Thr Thr Gly Leu Leu Leu Ala Phe Ser Ser Val
        145          150          155          160
Gly Ile Pro Val Ile
          165

```

&lt;210&gt;74

&lt;211&gt;595

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;74

```

Glu Phe Leu Lys Leu Ser Leu His Arg Ile Ser Leu Met Lys Glu Val
 1           5           10           15
Glu Gln Arg Ile Arg Ser Leu Tyr Asp Ala Val Thr Ala Glu Asn Ile
          20           25           30
Cys Arg Trp Leu Ser Asn Asp Cys Thr Gln Gln Asp Ala Lys Thr Ile
          35           40           45

```

```

Leu Gly Trp Leu Asp Thr Asp Pro Ala Gln Leu Glu Asp Leu Phe Gly
  50                      55                      60
Ala Thr Leu Thr Phe Gly Thr Gly Gly Leu Arg Ser Leu Met Gly Ile
  65                      70                      75                      80
Gly Thr Asn Arg Ile Asn Leu Phe Thr Ile Arg Arg Thr Thr Gln Gly
                      85                      90                      95
Leu Val Gln Val Leu Arg Ala His Leu Pro His Pro Gly Asp Pro Met
                      100                      105                      110
Arg Val Val Val Gly Cys Asp Thr Arg His Asn Ser Ile Glu Phe Ala
                      115                      120                      125
Gln Glu Thr Ala Lys Val Leu Ala Gly Asn Gly Cys Glu Val Phe Leu
                      130                      135                      140
Phe Gln Tyr Pro Glu Pro Leu Ala Leu Val Ser Phe Thr Val Arg Tyr
  145                      150                      155                      160
Glu Arg Ala Ile Gly Gly Val Met Ile Thr Ala Ser His Asn Pro Pro
                      165                      170                      175
Asn Tyr Asn Gly Tyr Lys Val Tyr Met Ala Ser Gly Gly Gln Val Leu
                      180                      185                      190
Pro Pro Leu Asp Gln Glu Ile Val Ala Ala Cys Ser Ala Val Asn Glu
                      195                      200                      205
Ile Leu Ser Val Pro Ser Ile Asp His Pro Asn Ile His Leu Ile Gly
                      210                      215                      220
Lys Glu Tyr Glu Ala Leu Tyr Arg Asp Thr Leu Lys Gln Leu Gln Leu
  225                      230                      235                      240
Tyr Pro Glu Ala Asn Arg Ile Ser Gly Arg Ser Leu Ser Ile Ser Tyr
                      245                      250                      255
Ser Pro Leu His Gly Thr Gly Ile Ser Leu Val Pro His Val Leu Lys
                      260                      265                      270
Asp Trp Gly Phe Leu Ser Val His Leu Val Glu Lys Gln Ala Ile Gly
                      275                      280                      285
Asp Gly Asp Phe Pro Thr Val Gln Leu Pro Asn Pro Glu Asp Pro Glu
  290                      295                      300
Ala Leu Thr Leu Gly Thr Glu Gln Met Leu Ala Asn Asp Asp Asp Leu
  305                      310                      315                      320
Phe Ile Ala Thr Asp Pro Asp Ala Asp Arg Val Gly Val Val Cys Leu
                      325                      330                      335
Glu Asp Gly Gln Pro Tyr Arg Phe Asn Gly Asn Gln Met Ala Ser Leu
                      340                      345                      350
Leu Ala Asp His Ile Leu Gly Ala Trp Ser Lys Thr Arg His Leu Gly
                      355                      360                      365
Glu His Asp Lys Leu Val Lys Ser Leu Val Thr Thr Glu Met Leu Ser
  370                      375                      380
Ala Ile Ala Lys His Tyr His Val Asp Leu Ile Asn Val Gly Thr Gly
  385                      390                      395                      400
Phe Lys Tyr Ile Gly Glu Lys Ile Glu Ser Trp Arg Asn Ser Thr Asn
                      405                      410                      415
Lys Phe Val Phe Gly Ala Glu Glu Ser Tyr Gly Cys Leu Tyr Gly Thr
                      420                      425                      430
His Val Glu Asp Lys Asp Ala Ile Ile Ala Ser Ala Leu Ile Ala Glu
                      435                      440                      445
Ala Ala Leu Gln Gln Lys Leu Gln Gly Lys Thr Leu Cys Asp Ala Leu
  450                      455                      460
Leu Ser Leu Tyr Glu Thr Tyr Gly Tyr Phe Ala Asn Lys Thr Glu Ser
  465                      470                      475                      480
Val Val Phe Ser Ala Lys Thr Asp Glu Gln Glu Ile Arg Lys Lys Leu
                      485                      490                      495
Ser His Leu Glu Glu Ile Ser Ser Ala Asn Phe Phe Ser Gly Lys Tyr
                      500                      505                      510
Gln Val Glu Lys Phe Glu Asn Tyr Lys Gln Gly Ile Gly Phe Asn Leu
                      515                      520                      525
Leu Ser Lys Asp Ser Tyr Ala Leu Thr Leu Pro Lys Thr Ser Met Leu
  530                      535                      540
Cys Tyr Tyr Phe Ser Gly Gly Gly Arg Val Ile Ile Arg Pro Ser Gly
  545                      550                      555                      560

```

```
<210>75
<211>214
<212>PRT
<213>Chlamydia pneumoniae
<400>75
```

```
<210>76
<211>255
<212>PRT
<213>Chlamydia pneumoniae
```

375

Ile Ile Val Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ser Val Phe  
 165 170 175  
 Ser Leu Met Gln Met Val Lys Thr Ser Ala Ala Leu Ala Lys Leu His  
 180 185 190  
 Glu Ala Gly Leu Pro Tyr Ile Ser Val Leu Thr Asn Pro Thr Ser Gly  
 195 200 205  
 Gly Val Thr Ala Ser Phe Ala Ala Leu Gly Asp Ile Ile Ile Ala Glu  
 210 215 220  
 Pro Lys Ala Leu Ile Cys Phe Ala Gly Pro Arg Val Val Ala Gln Val  
 225 230 235 240  
 Ile Gly Glu Asp Leu Pro Glu Gly Phe Lys Asn Leu Asn Ser Tyr  
 245 250 255

&lt;210&gt;77

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;77

Ile Cys Asn Ala Ile Leu Met Thr Val Phe Cys Glu Leu Asp Ser Gly  
 1 5 10 15  
 Gly Glu Leu Pro Glu Tyr Thr Thr Pro Gly Ala Ala Gly Ala Asp Leu  
 20 25 30  
 Arg Ala Asn Ile Glu Glu Pro Ile Ala Leu Leu Pro Gly Gln Arg Ala  
 35 40 45  
 Leu Ile Pro Thr Gly Ile Lys Ala Glu Ile Pro Glu Val Arg Ala Thr  
 50 55 60  
 Gly Pro Ser Ser Glu Arg Phe Gly Phe Lys Ala Arg His Tyr Cys Phe  
 65 70 75 80  
 Lys Phe Pro Arg Asp Tyr Arg Phe Arg Leu  
 85 90

&lt;210&gt;78

&lt;211&gt;101

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;78

Ser Leu Pro Glu Ser Lys Gln Lys Phe Pro Lys Tyr Glu Leu Gln Val  
 1 5 10 15  
 Arg Pro Arg Ser Gly Leu Ala Leu Lys His Gly Ile Thr Val Leu Asn  
 20 25 30  
 Ser Pro Gly Thr Ile Asp Ser Asp Tyr Arg Gly Glu Ile Arg Val Ile  
 35 40 45  
 Leu Ile Asn Phe Gly Asp Ser Thr Phe Ile Ile Glu Pro Lys Met Arg  
 50 55 60  
 Ile Ala Gln Val Val Leu Ser Pro Val Val Gln Ala Thr Phe Val Val  
 65 70 75 80  
 Lys Gln Xaa Ser Leu Ala Glu Thr Ala Arg Gly Ser Gly Gly Phe Gly  
 85 90 95  
 His Thr Gly Ala Ser  
 100

&lt;210&gt;79

&lt;211&gt;169

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;79

Val Glu Val Leu Val Ile Leu Glu Gln Ala Lys Met Pro Ser Tyr Cys  
 1 5 10 15  
 Gln Asn Gln Gln Asp Phe Ser Leu Phe Ser Leu Leu Ser Pro Arg Leu  
 20 25 30  
 Val Met Phe Leu Gly Lys His Ser Arg Asp Glu Ile Leu Gln Asp Leu  
 35 40 45  
 Thr Asp Leu Val Asp Ala Ala Gly Leu Leu Glu Asp Lys Gln Ala Phe  
 50 55 60  
 Phe Asp Ala Leu Val Arg Glu Asn Ile Met Ser Thr Gly Ile Gly  
 65 70 75 80  
 Met Gly Val Ala Ile Pro His Gly Lys Leu Glu Ser Cys Ser Asn Phe



85 90 95  
 Phe Ile Ala Ile Gly Ile His Thr Gln Gly Ile Leu Trp Asp Ala Ile  
 100 105 110  
 Asp Gly Ala Leu Val Arg Leu Val Phe Leu Ile Gly Gly Pro Glu Asn  
 115 120 125  
 Ala Gln Ala Glu Tyr Leu Lys Leu Leu Ser Thr Leu Thr Leu Ser Leu  
 130 135 140  
 Arg Glu Glu Ser Arg Arg Gln Gln Leu Leu Gln Val Asn Thr Ile Glu  
 145 150 155 160  
 Glu Val Met Asn Val Phe Val Gly Met  
 165

&lt;210&gt;80

&lt;211&gt;225

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;80

Met Asp Leu Lys Leu Asp Glu Val Ala Ser Leu Leu Asp Val Ser Glu  
 1 5 10 15  
 His Thr Val Leu Gln Trp Leu Lys Glu Gly Ala Ile Pro Ser Tyr Ser  
 20 25 30  
 Met Asn Asn Glu Tyr Arg Phe Ser Arg Glu Glu Ile Glu Asp Trp Leu  
 35 40 45  
 Leu His Asn Gln Ala Leu Met Ile Gln Glu Arg Gly Glu Asp Lys Glu  
 50 55 60  
 Ala Leu Lys Asp Leu Ser Leu Lys Tyr Ser Leu Tyr Lys Ala Ile His  
 65 70 75 80  
 Arg Gly Gly Val Leu Cys Asp Val Val Val His Ser Lys Glu Glu Ala  
 85 90 95  
 Leu Gln Tyr Ala Ser Lys Tyr Ile Ala Gln Lys Phe Gln Leu Asp Glu  
 100 105 110  
 Ser Val Leu Phe Glu Met Leu Ser His Arg Glu Asn Leu Met Ser Thr  
 115 120 125  
 Gly Ile Gly Glu Gly Ile Ala Leu Pro His Ala Lys Asp Phe Leu Ile  
 130 135 140  
 Asn Ala Tyr Tyr Asp Ile Val Val Pro Met Phe Leu Ala Glu Pro Ile  
 145 150 155 160  
 Glu Tyr Gly Ala Leu Asp Gly Lys Pro Val Gly Ile Leu Phe Phe Leu  
 165 170 175  
 Phe Ala Cys Gln Asp Lys Ser His Leu Asn Leu Val Asn Lys Ile Val  
 180 185 190  
 His Leu Gly Met Ser Leu Asn Ala Arg Ser Phe Phe Lys Asn Tyr Pro  
 195 200 205  
 Asn Lys Asp Gln Leu Leu Ala Tyr Val Lys Glu Trp Glu Ser Gln Thr  
 210 215 220

His

225

&lt;210&gt;81

&lt;211&gt;480

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;81

Lys Lys Ser Phe Cys Cys Tyr Gly Asp Pro His Arg Leu Pro Gly Asp  
 1 5 10 15  
 Cys Ser Arg Met Met Ser Ser Lys Arg Thr Ser Lys Ile Ala Val Leu  
 20 25 30  
 Ser Ile Leu Leu Thr Phe Thr His Ser Ile Gly Phe Ala Asn Ala Asn  
 35 40 45  
 Ser Ser Val Gly Leu Gly Thr Val Tyr Ile Thr Ser Glu Val Val Lys  
 50 55 60  
 Lys Pro Gln Lys Gly Ser Glu Arg Lys Gln Ala Lys Lys Glu Pro Arg  
 65 70 75 80  
 Ala Arg Lys Gly Tyr Leu Val Pro Ser Ser Arg Thr Leu Ser Ala Arg  
 85 90 95  
 Ala Gln Lys Met Lys Asn Ser Ser Arg Lys Glu Ser Ser Gly Gly Cys

100 105 110  
 Asn Glu Ile Ser Ala Asn Ser Thr Pro Arg Ser Val Lys Leu Arg Arg  
 115 120 125  
 Asn Lys Arg Ala Glu Gln Lys Ala Ala Lys Gln Gly Phe Ser Ala Phe  
 130 135 140  
 Ser Asn Leu Thr Leu Lys Ser Leu Leu Pro Lys Leu Pro Ser Lys Gln  
 145 150 155 160  
 Lys Thr Ser Ile His Glu Arg Glu Lys Ala Thr Ser Arg Phe Val Asn  
 165 170 175  
 Glu Ser Gln Leu Ser Ser Ala Arg Lys Arg Tyr Cys Thr Pro Ser Ser  
 180 185 190  
 Ala Ala Pro Ser Leu Phe Leu Glu Thr Glu Ile Val Arg Ala Pro Val  
 195 200 205  
 Glu Arg Thr Lys Glu Leu Gln Asp Asn Glu Ile His Ile Pro Val Val  
 210 215 220  
 Gln Val Gln Thr Asn Pro Lys Glu Gln Asn Thr Lys Thr Thr Lys Gln  
 225 230 235 240  
 Leu Ala Ser Gln Ala Ser Ile Gln Gln Ser Glu Gly Thr Glu Gln Ser  
 245 250 255  
 Leu Arg Glu Leu Ala Gln Gly Ala Ser Leu Pro Val Leu Val Arg Ser  
 260 265 270  
 Asn Pro Glu Val Ser Val Gln Arg Gln Lys Glu Glu Leu Lys Glu  
 275 280 285  
 Leu Val Ala Glu Arg Arg Gln Cys Lys Arg Lys Ser Val Arg Gln Ala  
 290 295 300  
 Leu Glu Ala Arg Ser Leu Thr Lys Lys Val Ala Arg Gly Gly Ser Val  
 305 310 315 320  
 Thr Ser Thr Leu Arg Tyr Asp Pro Glu Lys Ala Ala Glu Ile Lys Ser  
 325 330 335  
 Arg Arg Asn Cys Lys Val Ser Pro Glu Ala Arg Glu Gln Lys Tyr Ser  
 340 345 350  
 Ser Cys Lys Arg Asp Ala Arg Ala Asn Gly Lys Gln Asp Lys Thr Thr  
 355 360 365  
 Pro Ser Glu Asp Ala Ser Gln Glu Glu Gln Gln Thr Gly Ala Gly Leu  
 370 375 380  
 Val Arg Lys Thr Pro Lys Ser Gln Val Ala Ser Asn Ala Gln Asn Phe  
 385 390 395 400  
 Tyr Arg Asn Ser Lys Asn Thr Asn Ile Asp Ser Tyr Leu Thr Ala Asn  
 405 410 415  
 Gln Tyr Ser Cys Ser Ser Glu Glu Thr Asp Trp Pro Cys Ser Ser Cys  
 420 425 430  
 Val Ser Lys Arg Arg Thr His Asn Ser Ile Ser Val Cys Thr Met Val  
 435 440 445  
 Val Thr Val Ile Ala Met Ile Val Gly Ala Leu Ile Ile Ala Asn Ala  
 450 455 460  
 Thr Glu Ser Gln Thr Thr Ser Asp Pro Thr Pro Thr Pro Thr Pro  
 465 470 475 480  
 <210>82  
 <211>590  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>82  
 Tyr Asp Tyr Tyr Lys Tyr Asn Met Phe Phe Lys Lys Asn Tyr Met Thr  
 1 5 10 15  
 Asp Phe Pro Thr His Phe Lys Gly Pro Lys Leu Asn Pro Ile Lys Val  
 20 25 30  
 Asn Pro Asn Phe Phe Glu Arg Asn Pro Lys Val Ala Arg Val Leu Gln  
 35 40 45  
 Ile Thr Ala Val Val Leu Gly Ile Ile Ala Leu Leu Ser Gly Ile Val  
 50 55 60  
 Leu Ile Ile Gly Thr Pro Leu Gly Ala Pro Ile Ser Met Ile Leu Gly  
 65 70 75 80  
 Gly Cys Leu Leu Ala Ser Gly Gly Ala Leu Phe Val Gly Gly Thr Ile  
 85 90 95

Ala Thr Ile Leu Gln Ala Arg Asn Ser Tyr Lys Lys Ala Val Asn Gln  
 100 105 110  
 Lys Lys Leu Ser Glu Pro Leu Met Glu Arg Pro Glu Leu Lys Ala Leu  
 115 120 125  
 Asp Tyr Ser Leu Asp Leu Lys Glu Val Trp Asp Leu His His Ser Cys  
 130 135 140  
 Cys Gln His Leu Lys Lys Ile Asp Leu Asn Leu Ser Glu Thr Gln Arg  
 145 150 155 160  
 Glu Val Leu Asn Gln Ile Lys Ile Asp Asp Glu Gly Pro Ser Leu Gly  
 165 170 175  
 Glu Cys Ala Ala Met Ile Ser Glu Asn Tyr Asp Ala Cys Leu Lys Met  
 180 185 190  
 Leu Ala Tyr Arg Glu Glu Leu Leu Lys Glu Gln Thr Gln Tyr Gln Glu  
 195 200 205  
 Thr Arg Phe Asn Gln Asn Leu Thr His Arg Asn Lys Val Leu Leu Ser  
 210 215 220  
 Ile Leu Ser Arg Ile Thr Asp Asn Ile Ser Lys Ala Gly Gly Val Phe  
 225 230 235 240  
 Ser Leu Lys Phe Ser Thr Leu Ser Ser Arg Met Ser Arg Ile His Thr  
 245 250 255  
 Thr Thr Thr Val Ile Leu Ala Leu Ser Ala Val Val Ser Val Met Val  
 260 265 270  
 Val Ala Ala Leu Ile Pro Gly Gly Ile Leu Ala Leu Pro Ile Leu Leu  
 275 280 285  
 Ala Val Ala Ile Ser Ala Gly Val Ile Val Thr Gly Leu Ser Tyr Leu  
 290 295 300  
 Val Arg Gln Ile Leu Ser Asn Thr Lys Arg Asn Arg Gln Asp Phe Tyr  
 305 310 315 320  
 Lys Asp Phe Val Lys Asn Val Asp Ile Glu Leu Leu Asn Gln Thr Val  
 325 330 335  
 Thr Leu Gln Arg Phe Leu Phe Glu Met Leu Lys Gly Val Leu Lys Glu  
 340 345 350  
 Glu Glu Glu Val Ser Leu Glu Gly Gln Asp Trp Tyr Thr Gln Tyr Ile  
 355 360 365  
 Thr Asn Ala Pro Ile Glu Lys Arg Leu Ile Glu Glu Ile Arg Val Thr  
 370 375 380  
 Tyr Lys Glu Ile Asp Ala Gln Thr Lys Lys Met Lys Thr Asp Leu Glu  
 385 390 395 400  
 Phe Leu Glu Asn Glu Val Arg Ser Gly Arg Leu Ser Val Ala Ser Pro  
 405 410 415  
 Ser Glu Asp Pro Ser Glu Thr Pro Ile Phe Thr Gln Gly Lys Glu Phe  
 420 425 430  
 Ala Lys Leu Arg Arg Gln Thr Ser Gln Asn Ile Ser Thr Ile Tyr Gly  
 435 440 445  
 Pro Asp Asn Glu Asn Ile Asp Pro Glu Phe Ser Leu Pro Trp Met Pro  
 450 455 460  
 Lys Lys Glu Glu Glu Ile Asp His Ser Leu Glu Pro Val Thr Lys Leu  
 465 470 475 480  
 Glu Pro Gly Ser Arg Glu Glu Leu Leu Leu Val Glu Gly Val Asn Pro  
 485 490 495  
 Thr Leu Arg Glu Leu Asn Met Arg Ile Ala Leu Leu Gln Gln Gln Leu  
 500 505 510  
 Ser Ser Val Arg Lys Trp Arg His Pro Arg Gly Glu His Tyr Gly Asn  
 515 520 525  
 Val Ile Tyr Ser Asp Thr Glu Leu Asp Arg Ile Gln Met Leu Glu Gly  
 530 535 540  
 Ala Phe Tyr Asn His Leu Arg Glu Ala Gln Glu Glu Ile Thr Gln Ser  
 545 550 555 560  
 Leu Gly Asp Leu Val Asp Ile Gln Asn Arg Ile Leu Gly Ile Ile Val  
 565 570 575  
 Glu Gly Asp Ser Asp Ser Arg Thr Glu Glu Glu Pro Gln Glu  
 580 585 590

&lt;210&gt;83

&lt;211&gt;580

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;83

Gly Val Tyr Met Ala Asn Pro Thr Gln Ser Arg Pro Pro Ser Pro Glu  
 1 5 10 15  
 Ile Ser Ile Glu Leu Glu Leu Gln Glu Leu Ala Gly Ser Ser Asn  
 20 25 30  
 Thr Glu Thr Ile Ser Asn Thr Pro Pro Pro Ser Cys Ala Ala Thr Ala  
 35 40 45  
 Glu Glu Val Ser Leu Phe Ile Glu Gly Gly Arg Arg Asn Ser Glu Asp  
 50 55 60  
 Glu Glu Gly Pro Leu Gly Ser Cys Glu Val Tyr Asp Val Val Cys Ile  
 65 70 75 80  
 Thr Asn Gln Gly Asp Pro Glu Val Arg Asp His Glu Val Arg Val Met  
 85 90 95  
 Tyr Ile Asn Gly Ser Gly Arg Thr Gln His Glu Gly Ile Leu Asp Ala  
 100 105 110  
 Met Asn Ile Cys Asp Leu Arg Gly Glu Pro Val Arg Phe Ile His Asn  
 115 120 125  
 Ser Gly Tyr Gly Leu Gly Ser Cys Phe Leu Gly Ile Arg Asn Arg Ile  
 130 135 140  
 Pro Pro Arg Asp Asn Val Ile Ser Gln Ala Ile Gln Ala Arg Trp Asn  
 145 150 155 160  
 Glu Phe Phe Ile Phe Ala Glu Asn Ala Asn Arg Asp Tyr Ile Val Leu  
 165 170 175  
 Phe Ser Gly Asn Gly Gly Leu Tyr Leu Gln Val Ala Leu Asp Asn Ser  
 180 185 190  
 Ile Tyr Ser His His Ile Leu Cys Val Gly Ile Gly Ser Ser Tyr Tyr  
 195 200 205  
 Ile Gln Gly Asn Tyr Arg Val His Asn Tyr Arg Val Thr Gly Asp Trp  
 210 215 220  
 Thr Thr Leu Leu Asp Arg Arg Gly Ala Thr Ala Val Asn Thr Thr Thr  
 225 230 235 240  
 Leu Pro Tyr Ala Asp Ser Ala Glu Gly Leu Phe Leu Pro Ser Val Arg  
 245 250 255  
 Cys Pro Ser Tyr Gln Trp Ala Leu Arg Cys Gly Glu Gln Cys Leu Ile  
 260 265 270  
 Met Asp Asn Asn Gln Gln Val Gly Phe Arg Pro Gln Asp Ser Ser Ser  
 275 280 285  
 Glu Ile Ala Leu Val Val Asn Leu Asn Gln Asp His Ser Thr Trp Thr  
 290 295 300  
 Arg Leu Ile Glu Trp Ile Asp Arg Gly Asp Ser Gln Ala Val Leu Glu  
 305 310 315 320  
 Leu Asn Pro Gln Pro Ser His Cys Arg Asp Ile Ala Leu Thr Ala Leu  
 325 330 335  
 Tyr Ala Thr Thr Arg Ile Ser Ser Leu Leu Gln Glu Cys Leu Met Ile  
 340 345 350  
 Ser Val Thr Tyr Ala Pro Glu Val Phe Val Thr Tyr Ala Ile Val Thr  
 355 360 365  
 Gly Tyr Ser Ile Met Thr Leu Arg Tyr Phe Ile Leu Leu Leu Thr Asn  
 370 375 380  
 Arg Pro Gly Cys Arg Arg His Phe Arg Val Leu Arg Leu Ala Ala Leu  
 385 390 395 400  
 Gly Leu Gln Ser Leu Gly Phe Leu Thr Val Leu Leu Asp His Ile Asn  
 405 410 415  
 Val Thr Arg Arg Val Asn Arg Arg Pro Pro Leu Ile Ser Val Ile Phe  
 420 425 430  
 Cys Thr Ala Ser Phe Ala Thr Gly Ser Phe Ile Tyr Val Asp Leu Thr  
 435 440 445  
 Arg Met Phe Phe Thr Ser Leu Arg Ser Arg Leu Gln Leu Phe Val Gln  
 450 455 460  
 Arg Arg Leu Thr Gly Arg Gly Leu Pro Leu Arg Arg Val Phe Val Asn  
 465 470 475 480  
 His Leu Asp Ser Leu Arg Phe Ser Gln Asn Ala Leu Ile Thr Phe His

485 490 495  
 Gly Gly Leu Phe Met Pro Leu Ile Ile Gly Phe Phe Asn Gln Leu Val  
 500 505 510  
 Ile Gln Val Pro Arg Val Val Ile Arg Pro Asn Thr Thr Ala Val Tyr  
 515 520 525  
 Asp Leu Asn Gln Thr Ser Gln Glu Ala Trp Asp Ser Gly Asp Val Leu  
 530 535 540  
 Ala Ile Gly Gln Thr Ile Asn Phe Leu Leu Cys Met Ile Leu Leu Val  
 545 550 555 560  
 Ile Asn Thr Phe Phe Phe Val Arg Ser Val Arg Arg Asn Leu His Arg  
 565 570 575  
 Arg Pro His Arg  
 580

&lt;210&gt;84

&lt;211&gt;264

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;84

Lys Gly Ser Gly Tyr Ser Tyr Arg Gly Pro Pro Met Ala Val Glu Gly  
 1 5 10 15  
 Arg Val Asn Ser Ser Gln Ala Leu Asn Gln Asp Cys Gln Glu Val Leu  
 20 25 30  
 Ala Asn Lys Gln Ser Lys Gly Leu Arg Cys Arg Ile Leu Ser Ile  
 35 40 45  
 Val Val Ala Val Ile Thr Phe Ile Ala Gly Val Val Leu Ile Ala Leu  
 50 55 60  
 Thr Leu Ala Ser Ile Leu Thr Ser Val Pro Tyr Leu Ala Leu Gly Val  
 65 70 75 80  
 Phe Leu Leu Ile Val Thr Leu Gly Cys Ile Ile Phe Ala Leu Cys Ser  
 85 90 95  
 Glu Lys Ile Lys Lys Val Pro Pro Thr Pro Ile Ser His Lys Glu Glu  
 100 105 110  
 Ile Ile Ala Trp Phe Glu Glu Arg Lys Asn Ile Asp Met Glu Lys Glu  
 115 120 125  
 Lys Glu Asp Pro Glu His Phe Gly Arg Thr Ala Thr Asp Ile Pro Met  
 130 135 140  
 Arg Ser Ala Leu Asp Gln Phe Asn His Ser Cys His His Ile His Glu  
 145 150 155 160  
 Ser Pro Ala Leu Thr Glu Thr Tyr Arg Ser His Gln Asp Val Leu Leu  
 165 170 175  
 Phe Lys Asp Trp Cys Pro Val Thr Leu Pro Asp Val Thr Ser Glu Glu  
 180 185 190  
 Glu Val Leu Ile Arg Ser Val Val Gly Ser Tyr Leu Leu Met Glu Ala  
 195 200 205  
 Cys Val Pro Lys Val Ser Met Leu Ile Asp Glu Leu His Asn Lys Leu  
 210 215 220  
 Xaa Ser Pro Ser Glu Arg Glu Cys Leu Phe Ile Asp Lys Lys Thr Leu  
 225 230 235 240  
 Gln Arg Lys Ala Ser Phe Leu Phe Thr Gln Lys Asp Leu Ala Thr Phe  
 245 250 255  
 Phe Leu Asp Leu Tyr Ala Gly Glu  
 260

&lt;210&gt;85

&lt;211&gt;193

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;85

Ser Phe Met Ile Lys Lys Phe Phe Ile Tyr Ser Leu Ile Phe Ser Cys  
 1 5 10 15  
 Ser Phe Ser Ala Pro Leu Lys Gly Ile Cys Asn Glu Asp Val Ser Ser  
 20 25 30  
 Gln Ser Arg Ile Glu Glu Asp Pro Glu Val Leu Ile Thr Gln Leu Asn  
 35 40 45  
 Glu Leu Ile Glu Thr Pro Ile Glu Glu Gly Lys Glu Ile Arg Asn Glu

50 55 60  
 Leu Gln Ala Ile Ser Asp Gly Gln Lys Ser Ser Glu Glu Ile Glu Glu  
 65 70 75 80  
 Ser Cys Gly Thr Ser Asp Ser Glu Gly Leu Ser Glu Lys Thr Asp Lys  
 85 90 95  
 Glu Ser Ser Asn Glu Tyr Val Leu Asp Phe Phe Asp Ser Met Val Gln  
 100 105 110  
 Arg Leu Glu Gly Ile Ser Lys Met Cys Gln Ser Gly Gln Val Ala Gln  
 115 120 125  
 Ile Ile Asp Cys Phe Asn Arg Glu Phe Asp Ile Arg Asn Arg Glu Leu  
 130 135 140  
 Glu Leu Lys Asn Arg Glu Leu Glu Leu Arg Glu Lys Asp Leu Glu Phe  
 145 150 155 160  
 Lys Lys Ser Ile Leu Asp Trp Asn Lys Glu Lys Val Ser Arg Glu Leu  
 165 170 175  
 Ala Phe Gln Arg Glu Gln Asp Ile Lys Gln Thr Leu Met Leu Leu Lys  
 180 185 190

Lys

&lt;210&gt;86

&lt;211&gt;297

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;86

Asn Phe Lys Ile Trp Gly Ile Arg Ile Thr Ile Ala Val Glu Leu Pro  
 1 5 10 15  
 Pro Pro Glu Val Gly Gly Glu Leu Pro Pro Tyr Phe Ser Ala Ser Asn  
 20 25 30  
 Phe Val Val Ile Glu Arg Gly Ala Pro Ser Leu Pro Ser Pro Gln Gln  
 35 40 45  
 Leu Leu Ser Leu Pro Glu Tyr Ser Arg Gln Pro Pro Gly Tyr Phe  
 50 55 60  
 Asp Glu Thr Ala Ser Ile Thr Ser Arg Thr Ser Glu Glu Met Phe Gly  
 65 70 75 80  
 Thr Leu Val Ser Thr Leu Cys Cys Pro Ala Asn Ser Glu Arg Asp Trp  
 85 90 95  
 Glu Asp His Glu Val Asn Cys Ile Tyr Ile Ala Ser Thr Ser Asp Thr  
 100 105 110  
 Gln Leu Glu Ala Val Gln Gly Gly Met His Ile Thr Glu Leu Arg Gly  
 115 120 125  
 Glu Pro Val Arg Val Leu Tyr Glu Thr Gly His Leu Tyr Ala Phe Ala  
 130 135 140  
 Arg Glu Asn Thr Cys His Ser Arg Leu Glu Val Ser His Thr Val Arg  
 145 150 155 160  
 Ala Met Thr Tyr Phe Trp Asp Arg Phe Phe Ser Arg His Trp Asn Val  
 165 170 175  
 Gly Arg Arg Phe Leu Val Phe Tyr Gln Gly Asn Gly Gly Ala Tyr Val  
 180 185 190  
 Gln Ala Ala Leu Asp Ser Ser Met His Thr Gln Asp Ile Tyr Val Leu  
 195 200 205  
 Gly Leu Ser Pro Thr Val Tyr Ile Arg Gly Asn Tyr His Val Gln His  
 210 215 220  
 Tyr Arg Val Arg Gly Phe Trp Pro Ser Cys Leu Asp Ser Leu Ala Ala  
 225 230 235 240  
 Cys Ala Glu Asn Thr Ser Val Leu Pro Thr Gly Asn Arg Val Thr Glu  
 245 250 255  
 Ser Phe Thr Pro Leu Tyr Ser Ala Thr His Leu Ile Thr Arg Tyr Gly  
 260 265 270  
 Met Val Arg Asp Ala Cys Trp Phe Val Leu Arg Ala Trp Glu Cys Phe  
 275 280 285  
 Gln Lys Arg Asn Asn Lys His Leu Leu  
 290 295

&lt;210&gt;87

&lt;211&gt;380

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;87

Arg Glu Leu Ser Arg Thr Ala Leu Pro Cys Ser Arg Ile Leu Ala Leu  
 1 5 10 15  
 Leu Pro Gly Phe Ser Ser Gly Leu Cys Gly Lys Tyr Ile Ser Thr Ser  
 20 25 30  
 Tyr Gly Glu Ser Ser Asp Gly Ile Phe Tyr Pro Ser Leu Phe Ser His  
 35 40 45  
 Thr Phe Asp Asn Ala Ile Arg Tyr Gly Glu Arg Cys Leu Leu Val Cys  
 50 55 60  
 Ser Glu Gly Met Gly Met Leu Pro Glu Thr Gln Gln Thr Ser Pro  
 65 70 75 80  
 Leu Thr Ser Leu Glu Gly Gly His Glu Val Ala Leu Val Leu Asn Pro  
 85 90 95  
 Gln Gln Asn Pro Glu Ala Leu Ser Ile Ala Ser Arg Leu Met His Glu  
 100 105 110  
 Glu Arg Gly Gly Arg Leu Glu Ser Asn Tyr Met Pro Gly Arg Ser Ser  
 115 120 125  
 Asn Pro Phe Met Thr Ser Met Tyr Val Leu Val Arg Leu Asn Thr Leu  
 130 135 140  
 Ala Gln Ile Tyr Leu Met Ser Pro Tyr Tyr Ser Phe Gln Ser Asn Asp  
 145 150 155 160  
 Ile Val Cys Leu Ile Phe Ile Ser Ser Ala Ala Val Glu Thr Val Ser  
 165 170 175  
 Tyr Ile Phe Leu Thr Val Thr Asp Ser Thr Cys Gly Arg Arg Tyr Leu  
 180 185 190  
 Arg Val Pro Arg Leu Val Cys Thr Gly Leu Arg Asn Leu Ala Leu Pro  
 195 200 205  
 Thr Thr Leu Leu Glu Leu Leu Ile Leu Ser Tyr Pro Arg Ser Val Glu  
 210 215 220  
 Gly Val Pro Phe Asn Val Arg Phe Ile Leu Gly Tyr Met Cys Thr Thr  
 225 230 235 240  
 Arg Val Val Phe Phe Ala Trp Asn Leu Ile Leu His Trp Pro Phe Arg  
 245 250 255  
 Cys Leu Arg His Gly Ile Gln Leu Phe Val His Arg Ser Ile Ile Gly  
 260 265 270  
 His Thr Leu Gly Ala Arg Ile Thr Asp Leu Thr Leu Ala Ser Met Arg  
 275 280 285  
 Tyr Ala Ile Val Phe Pro Ser Ile Val Ser Ser Cys Leu Leu Thr Ala  
 290 295 300  
 Leu Ala His Ala Asn Thr Asn Ile Leu Ala Leu Asp Pro Tyr Arg Leu  
 305 310 315 320  
 Ile Glu Ser Gly Asp Leu Arg Arg Pro Ala Phe Asn Asp Asp Glu Met  
 325 330 335  
 Gln Gln Ala Asp Asn Pro Trp Asp Ala Tyr Ser Ile Gly Leu Val Ile  
 340 345 350  
 Asn Thr Cys Ile Tyr Met Leu Ile Leu Phe Ala Asn Leu Ile Phe Met  
 355 360 365  
 Val Tyr Ser Val Arg Arg Tyr His Arg Ser Arg Arg  
 370 375 380

&lt;210&gt;88

&lt;211&gt;156

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;88

Ile Lys Ser Leu Arg Ser Ile Leu Glu Phe Ile Cys Pro Leu Gln His  
 1 5 10 15  
 Ala Arg Cys Leu Lys Lys Gln His Lys Ile Ile Glu Glu Leu Phe Pro  
 20 25 30  
 Glu Pro Phe Gln Lys Asp His Leu Tyr Leu Lys Leu Met Glu Asn Ser  
 35 40 45  
 Ser Ser Arg Asp Ala Phe Asp Lys Lys Arg Met Leu Lys Glu Asn Leu  
 50 55 60

Val Val Gly Cys Gln Ser Asp Leu Tyr Leu Tyr Glu Val Tyr Gln Asp  
 65 70 75 80  
 Gly Ile Leu Phe Phe Phe Thr Tyr Thr Lys Ala Leu Val Ser Ser Gly  
 85 90 95  
 Ile Ala Ser Leu Phe Thr Glu Val Tyr Ser Gly Glu Thr Pro Ser Thr  
 100 105 110  
 Ile Leu Thr Cys Lys Pro Ile Phe Phe Gln Arg Leu Thr Pro Tyr Leu  
 115 120 125  
 Ser Phe Gly Arg Leu Asn Gly Gly Glu Ser Leu Tyr Met Arg Met Lys  
 130 135 140  
 Gln Ile Ala Val Gln Tyr Leu Lys Pro Pro Gln Thr  
 145 150 155  
 <210>89  
 <211>345  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>89  
 Cys Leu Leu Phe Tyr Phe Phe His Tyr Arg Met Ser Thr Pro Leu Ser  
 1 5 10 15  
 Ser Gly Gly Ile Ser Pro Ser Asp Gln Tyr Val Pro Gln Glu Leu Phe  
 20 25 30  
 Cys Asp Arg Leu Ser Ser Ser Arg Ser Asn Ser Pro Asp Ser Asn Ala  
 35 40 45  
 Ser Gly Asp Ser Pro Ile Val Ser Pro Pro Ile Ser Ala Leu Val Ala  
 50 55 60  
 Leu Thr Asp Leu Lys Leu Val Pro Tyr Asn Gln Asn Ser Phe Ser Trp  
 65 70 75 80  
 Thr Thr Arg Leu Lys Asn Ala Val Glu Lys Ile Gly Leu Phe Leu Gln  
 85 90 95  
 Arg Asn Trp Lys Tyr Ile Leu Leu Tyr Ile Leu Ala Trp Ala Leu Ile  
 100 105 110  
 Leu Val Cys His His Thr Val Ala Leu Thr Leu Thr Ile Trp Leu Gly  
 115 120 125  
 Val Gly Leu Gly Ile Gly Val Val Phe Gly Ile Phe Thr Ala Thr Cys  
 130 135 140  
 Leu Asp Lys Glu Asn Lys His Arg His Val Asn Ser Leu Trp Asn Leu  
 145 150 155 160  
 Ile Asn His Gly Ile Leu Gln Leu Asp Pro Asn Gly Thr Arg Gln Ile  
 165 170 175  
 Leu Leu Ala Thr Met Ile Ala Ser Ile Ser Ala Leu Ile Tyr Ala Val  
 180 185 190  
 Pro Gln Ala Val Gly Leu Val Ile Gly Phe Ser Ile Gly Asn Gln Leu  
 195 200 205  
 Ser Ile Asn Thr Val Tyr Gly Ala Arg Leu Gly Asp Glu Ala Thr Tyr  
 210 215 220  
 Ala Ile Asp Arg Lys Ala His Lys Lys Arg Ile Glu Asn Ile Glu Gln  
 225 230 235 240  
 Ala Ile Asn Gln His Gln Ile Ile Lys His Gln Met Ile Asn Gln Lys  
 245 250 255  
 Gln Leu Asn Ala Leu Ile Glu Ile Asn Arg Asn Asn Gln Thr Asp Pro  
 260 265 270  
 Ala Thr Ala Asn Leu Leu Ala Ser Leu Lys Leu Asn Leu Asn Gln Pro  
 275 280 285  
 Met Pro Tyr Cys Phe Ser Met Pro Glu Cys Gly Val Thr Ser Ser Tyr  
 290 295 300  
 Leu Asp Leu Asn Asn Asn Ser Pro Asp Asp Ile Ile Ala Arg Ala Asp  
 305 310 315 320  
 Gln Cys Ile Met Thr Leu Ser Gln Thr Leu Gln Gln Ile Lys Lys Glu  
 325 330 335  
 Pro Asp Arg Ile Ile Glu Ser Asn His  
 340 345  
 <210>90  
 <211>394  
 <212>PRT



&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;90

Met Ser Lys Glu Thr Phe Gln Arg Asn Lys Pro His Ile Asn Ile Gly  
 1 5 10 15  
 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile  
 20 25 30  
 Thr Arg Ala Leu Ser Gly Asp Gly Leu Ala Ser Phe Arg Asp Tyr Ser  
 35 40 45  
 Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn  
 50 55 60  
 Ala Ser His Val Glu Tyr Glu Thr Pro Asn Arg His Tyr Ala His Val  
 65 70 75 80  
 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala  
 85 90 95  
 Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala  
 100 105 110  
 Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val  
 115 120 125  
 Pro Tyr Ile Val Val Phe Leu Asn Lys Val Asp Met Ile Ser Gln Glu  
 130 135 140  
 Asp Ala Glu Leu Ile Asp Leu Val Glu Met Glu Leu Ser Glu Leu Leu  
 145 150 155 160  
 Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu  
 165 170 175  
 Lys Ala Leu Glu Gly Asp Ala Asn Tyr Ile Glu Lys Val Arg Glu Leu  
 180 185 190  
 Met Gln Ala Val Asp Asp Xaa Ile Pro Thr Pro Glu Arg Glu Ile Asp  
 195 200 205  
 Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg  
 210 215 220  
 Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser  
 225 230 235 240  
 Asp Lys Val Gln Leu Val Gly Leu Gly Glu Thr Lys Glu Thr Ile Val  
 245 250 255  
 Thr Gly Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly  
 260 265 270  
 Glu Asn Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu  
 275 280 285  
 Arg Gly Met Val Val Cys Gln Pro Asn Ser Val Lys Pro His Thr Lys  
 290 295 300  
 Phe Lys Ser Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His  
 305 310 315 320  
 Lys Pro Phe Phe Ser Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr  
 325 330 335  
 Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met Val Met  
 340 345 350  
 Pro Gly Asp Asn Val Glu Leu Asp Val Glu Leu Ile Gly Thr Val Ala  
 355 360 365  
 Leu Glu Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile  
 370 375 380  
 Gly Ala Gly Thr Ile Ser Lys Ile Asn Ala  
 385 390

&lt;210&gt;91

&lt;211&gt;88

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;91

Ser Arg Ser Trp Phe Met Lys Gln Gln His Asn Arg Lys Ala Leu Ser  
 1 5 10 15  
 Arg Lys Ile Gly Thr Val Lys Lys Gln Ala Lys Phe Ala Gly Ser Phe  
 20 25 30  
 Leu Asp Glu Ile Lys Lys Ile Glu Trp Val Ser Lys His Asp Leu Lys  
 35 40 45  
 Lys Tyr Ile Lys Val Val Leu Ile Ser Ile Phe Gly Phe Gly Phe Ala

<210>92

$\langle 211 \rangle 190$

<212>PRT

<213>Chlamydia pneumoniae

<400>92

<210>93

$\langle 211 \rangle 150$

<212>PRT

<213>Chlamydia pneumoniae

<400>93

<210>94

**<211>232**

<212>PRT

<213>Chlamydia pneumoniae

<400>94

Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Leu Lys Asn Tyr Asp  
 1 5 10 15  
 Phe Ser Lys Ser Tyr Ser Leu Arg Glu Ala Ile Asp Ile Leu Lys Gln  
 20 25 30  
 Cys Pro Pro Val Arg Phe Asp Gln Thr Val Asp Val Ser Ile Lys Leu  
 35 40 45  
 Gly Ile Asp Pro Lys Lys Ser Asp Gln Gln Ile Arg Gly Ala Val Phe  
 50 55 60  
 Leu Pro Asn Gly Thr Gly Lys Thr Leu Arg Ile Leu Val Phe Ala Ser  
 65 70 75 80  
 Gly Asn Lys Val Lys Glu Ala Val Glu Ala Gly Ala Asp Phe Met Gly  
 85 90 95  
 Ser Asp Asp Leu Val Glu Lys Ile Lys Ser Gly Trp Leu Glu Phe Asp  
 100 105 110  
 Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly  
 115 120 125  
 Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Thr Gly Thr  
 130 135 140  
 Val Thr Thr Asp Val Ala Lys Ala Ile Ser Glu Leu Arg Lys Gly Lys  
 145 150 155 160  
 Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Gly  
 165 170 175  
 Lys Leu Ser Phe Glu Ser Ser Gln Ile Lys Glu Asn Ile Glu Ala Leu  
 180 185 190  
 Ser Ser Ala Leu Ile Lys Ala Lys Pro Pro Ala Ala Lys Gly Gln Tyr  
 195 200 205  
 Leu Val Ser Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Ile Ser Ile  
 210 215 220  
 Asp Thr Arg Glu Leu Met Ala Ser  
 225 230

&lt;210&gt;95

&lt;211&gt;170

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;95

Met Lys Gln Glu Lys Thr Leu Leu Leu Gln Glu Val Glu Asp Lys Ile  
 1 5 10 15  
 Ser Ala Ala Gln Gly Phe Ile Leu Leu Arg Tyr Leu Arg Phe Thr Ala  
 20 25 30  
 Ala Tyr Ser Arg Glu Phe Arg Asn Ser Leu Ser Gly Val Ser Ala Glu  
 35 40 45  
 Phe Glu Val Leu Lys Lys Arg Ile Phe Phe Lys Ala Ile Glu Ala Ala  
 50 55 60  
 Gly Leu Glu Val Asp Cys Ser Asp Thr Asp Gly His Leu Gly Val Val  
 65 70 75 80  
 Phe Ser Cys Gly Asp Pro Val Ser Ala Ala Lys Gln Val Leu Asp Phe  
 85 90 95  
 Asn Lys Gln His Lys Asp Ser Leu Val Phe Leu Ala Gly Arg Met Asp  
 100 105 110  
 Asn Ala Ser Leu Ser Gly Ala Glu Val Glu Ala Val Ala Lys Leu Pro  
 115 120 125  
 Ser Leu Lys Glu Leu Arg Gln Gln Val Val Gly Leu Phe Ala Ala Pro  
 130 135 140  
 Met Ser Gln Val Val Gly Ile Met Asn Ser Val Leu Ser Gly Val Ile  
 145 150 155 160  
 Ser Cys Val Asp Gln Lys Ala Gly Lys Asn  
 165 170

&lt;210&gt;96

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;96

Val Thr Lys Val Thr Thr Glu Ser Leu Glu Thr Leu Val Glu Lys Leu  
 1 5 10 15

Ser Asn Leu Thr Val Leu Glu Leu Ser Gln Leu Lys Lys Leu Leu Glu  
 20 25 30  
 Glu Lys Trp Asp Val Thr Ala Ser Ala Pro Val Val Ala Val Ala Ala  
 35 40 45  
 Gly Gly Gly Gly Glu Ala Pro Val Ala Ala Glu Pro Thr Glu Phe Ala  
 50 55 60  
 Val Thr Leu Glu Asp Val Pro Ala Asp Lys Lys Ile Gly Val Leu Lys  
 65 70 75 80  
 Val Val Arg Glu Val Thr Gly Leu Ala Leu Lys Glu Ala Lys Glu Met  
 85 90 95  
 Thr Glu Gly Leu Pro Lys Thr Val Lys Glu Lys Thr Ser Lys Ser Asp  
 100 105 110  
 Ala Glu Asp Thr Val Lys Lys Leu Gln Asp Ala Gly Ala Lys Ala Ser  
 115 120 125  
 Phe Lys Gly Leu  
 130

&lt;210&gt;97

&lt;211&gt;1262

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;97

Leu Ser His Gln Asn Ser Arg Arg Thr Arg Thr Leu Lys Cys Pro Glu  
 1 5 10 15  
 Arg Val Ser Val Lys Lys Lys Glu Asp Ile Pro Asp Leu Pro Asn Leu  
 20 25 30  
 Ile Glu Ile Gln Ile Lys Ser Tyr Lys Gln Phe Leu Gln Ile Gly Lys  
 35 40 45  
 Leu Ala Glu Glu Arg Glu Asn Ile Gly Leu Glu Glu Val Phe Arg Glu  
 50 55 60  
 Ile Phe Pro Ile Lys Ser Tyr Asn Glu Ala Thr Val Leu Glu Tyr Leu  
 65 70 75 80  
 Ser Tyr Asn Leu Gly Val Pro Lys Tyr Ser Pro Glu Glu Cys Ile Arg  
 85 90 95  
 Arg Gly Ile Thr Tyr Ser Val Thr Leu Lys Val Arg Phe Arg Leu Thr  
 100 105 110  
 Asp Glu Thr Gly Ile Lys Glu Glu Glu Val Tyr Met Gly Thr Ile Pro  
 115 120 125  
 Leu Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Ala Glu Arg Val  
 130 135 140  
 Val Val Ser Gln Val His Arg Ser Pro Gly Ile Asn Phe Glu Gln Glu  
 145 150 155 160  
 Lys His Ser Lys Gly Asn Ile Leu Phe Ser Phe Arg Ile Ile Pro Tyr  
 165 170 175  
 Arg Gly Ser Trp Leu Glu Ala Ile Phe Asp Ile Asn Asp Leu Ile Tyr  
 180 185 190  
 Ile His Ile Asp Arg Lys Lys Arg Arg Arg Lys Ile Leu Ala Ile Thr  
 195 200 205  
 Phe Ile Arg Ala Leu Gly Tyr Ser Ser Asp Ala Asp Ile Ile Glu Glu  
 210 215 220  
 Phe Phe Thr Ile Gly Glu Ser Ser Leu Arg Ser Glu Lys Asp Phe Ala  
 225 230 235 240  
 Leu Leu Val Gly Arg Ile Leu Ala Asp Asn Ile Ile Asp Glu Ala Ser  
 245 250 255  
 Ser Leu Val Tyr Gly Lys Ala Gly Glu Lys Leu Ser Thr Ala Met Leu  
 260 265 270  
 Lys Arg Met Leu Asp Ala Gly Ile Ala Ser Val Lys Ile Ala Val Asp  
 275 280 285  
 Ala Asp Glu Asn His Pro Ile Ile Lys Met Leu Ala Lys Asp Pro Thr  
 290 295 300  
 Asp Ser Tyr Glu Ala Ala Leu Lys Asp Phe Tyr Arg Arg Leu Arg Pro  
 305 310 315 320  
 Gly Glu Pro Ala Thr Leu Ala Asn Ala Arg Ser Thr Ile Met Arg Leu  
 325 330 335  
 Phe Phe Asp Pro Lys Arg Tyr Asn Leu Gly Arg Val Gly Arg Tyr Lys

```

      340      345      350
Leu Asn Arg Lys Leu Gly Phe Ser Ile Asp Asp Glu Ala Leu Ser Gln
      355      360      365
Val Thr Leu Arg Lys Glu Asp Val Ile Gly Ala Leu Lys Tyr Leu Ile
      370      375      380
Arg Leu Lys Met Gly Asp Glu Lys Ala Cys Val Asp Asp Ile Asp His
385      390      395      400
Leu Ala Asn Arg Arg Val Arg Ser Val Gly Glu Leu Ile Gln Asn Gln
      405      410      415
Cys Arg Ser Gly Leu Ala Arg Met Glu Lys Ile Val Arg Glu Arg Met
      420      425      430
Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu Thr Pro Gly Lys Val Val
      435      440      445
Ser Ala Lys Gly Leu Ala Ser Val Leu Lys Asp Phe Phe Gly Arg Ser
      450      455      460
Gln Leu Ser Gln Phe Met Asp Gln Thr Asn Pro Val Ala Glu Leu Thr
465      470      475      480
His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Asn Arg Glu
      485      490      495
Arg Ala Gly Phe Glu Val Arg Asp Val His Ala Ser His Tyr Gly Arg
      500      505      510
Ile Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile Thr
      515      520      525
Ser Leu Ser Ser Phe Ala Lys Ile Asn Glu Phe Gly Phe Ile Glu Thr
      530      535      540
Pro Tyr Arg Ile Val Arg Asp Gly Ile Val Thr Asp Glu Ile Glu Tyr
545      550      555      560
Met Thr Ala Asp Val Glu Glu Glu Cys Val Ile Ala Gln Ala Ser Ala
      565      570      575
Ser Leu Asp Glu Tyr Asn Met Phe Thr Glu Pro Val Cys Trp Val Arg
      580      585      590
Tyr Ala Gly Glu Ala Phe Glu Ala Asp Thr Ser Thr Val Thr His Met
      595      600      605
Asp Val Ser Pro Lys Gln Leu Val Ser Ile Val Thr Gly Leu Ile Pro
      610      615      620
Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ser Asn Met
625      630      635      640
Gln Arg Gln Ala Val Pro Leu Leu Lys Thr Glu Ala Pro Val Val Gly
      645      650      655
Thr Gly Leu Glu Cys Arg Ala Ala Lys Asp Ser Gly Ala Ile Val Val
      660      665      670
Ala Glu Glu Asp Gly Val Val Asp Phe Val Asp Gly Tyr Lys Val Val
      675      680      685
Val Ala Ala Lys His Asn Pro Thr Ile Lys Arg Thr Tyr His Leu Lys
      690      695      700
Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys Ile Asn Gln Gln Pro Leu
705      710      715      720
Cys Ala Val Gly Asp Val Ile Thr Lys Gly Asp Val Ile Ala Asp Gly
      725      730      735
Pro Ala Thr Asp Arg Gly Glu Leu Ala Leu Gly Lys Asn Val Leu Val
      740      745      750
Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe Glu Asp Ala Ile Ile Ile
      755      760      765
Ser Glu Lys Leu Ile Arg Glu Asp Ala Tyr Thr Ser Ile Tyr Ile Glu
      770      775      780
Glu Phe Glu Leu Thr Ala Arg Asp Thr Lys Leu Gly Lys Glu Glu Ile
785      790      795      800
Thr Arg Asp Ile Pro Asn Val Ser Asp Glu Val Leu Ala Asn Leu Gly
      805      810      815
Glu Asp Gly Ile Ile Arg Ile Gly Ala Glu Val Lys Pro Gly Asp Ile
      820      825      830
Leu Val Gly Lys Ile Thr Pro Lys Ser Glu Thr Glu Leu Ala Pro Glu
      835      840      845
Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Ala Asp Val Lys

```

850 855 860  
 Asp Ala Ser Leu Thr Val Pro Pro Gly Thr Glu Gly Val Val Met Asp  
 865 870 875 880  
 Val Lys Val Phe Ser Arg Lys Asp Arg Leu Ser Lys Ser Asp Asp Glu  
 885 890 895  
 Leu Val Glu Glu Ala Val His Leu Lys Asp Leu Gln Lys Gly Tyr Lys  
 900 905 910  
 Asn Gln Val Ala Thr Leu Lys Thr Glu Tyr Arg Glu Lys Leu Gly Ala  
 915 920 925  
 Leu Leu Leu Asn Glu Lys Ala Pro Ala Ala Ile Ile His Arg Arg Thr  
 930 935 940  
 Ala Glu Ile Val Val His Glu Gly Leu Leu Phe Asp Gln Glu Thr Ile  
 945 950 955 960  
 Glu Arg Ile Glu Gln Glu Asp Leu Val Asp Leu Leu Met Pro Asn Cys  
 965 970 975  
 Glu Met Tyr Glu Val Leu Lys Gly Leu Leu Ser Asp Tyr Glu Thr Ala  
 980 985 990  
 Leu Gln Arg Leu Glu Ile Asn Tyr Lys Thr Glu Val Glu His Ile Arg  
 995 1000 1005  
 Glu Gly Asp Ala Asp Leu Asp His Gly Val Ile Arg Gln Val Lys Val  
 1010 1015 1020  
 Tyr Val Ala Ser Lys Arg Lys Leu Gln Val Gly Asp Lys Met Ala Gly  
 1025 1030 1035 1040  
 Arg His Gly Asn Lys Gly Val Val Ser Lys Ile Val Pro Glu Ala Asp  
 1045 1050 1055  
 Met Pro Tyr Leu Ser Asn Gly Glu Thr Val Gln Met Ile Leu Asn Pro  
 1060 1065 1070  
 Leu Gly Val Pro Ser Arg Met Asn Leu Gly Gln Val Leu Glu Thr His  
 1075 1080 1085  
 Leu Gly Tyr Ala Ala Lys Thr Ala Gly Ile Tyr Val Lys Thr Pro Val  
 1090 1095 1100  
 Phe Glu Gly Phe Pro Glu Gln Arg Ile Trp Asp Met Met Ile Glu Gln  
 1105 1110 1115 1120  
 Gly Leu Pro Glu Asp Gly Lys Ser Phe Leu Tyr Asp Gly Lys Thr Gly  
 1125 1130 1135  
 Glu Arg Phe Asp Asn Lys Val Val Ile Gly Tyr Ile Tyr Met Leu Lys  
 1140 1145 1150  
 Leu Ser His Leu Ile Ala Asp Lys Ile His Ala Arg Ser Ile Gly Pro  
 1155 1160 1165  
 Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Met Gly  
 1170 1175 1180  
 Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly  
 1185 1190 1195 1200  
 Val Ala His Met Leu Gln Glu Ile Leu Thr Val Lys Ser Asp Asp Val  
 1205 1210 1215  
 Ser Gly Arg Thr Arg Ile Tyr Glu Ser Ile Val Lys Gly Glu Asn Leu  
 1220 1225 1230  
 Leu Arg Ser Gly Thr Pro Glu Ser Phe Asn Val Leu Ile Lys Glu Met  
 1235 1240 1245  
 Gln Gly Leu Gly Leu Asp Val Arg Pro Met Val Val Asp Ala  
 1250 1255 1260  
 <210>98  
 <211>1218  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>98  
 Leu Glu Lys Ile Met Phe Gly Glu Asn Ser Arg Asp Ile Gly Val Leu  
 1 5 10 15  
 Ser Lys Glu Gly Leu Phe Asp Lys Leu Glu Ile Gly Ile Ala Ser Asp  
 20 25 30  
 Ile Thr Ile Arg Asp Lys Trp Ser Cys Gly Glu Ile Lys Lys Pro Glu  
 35 40 45  
 Thr Ile Asn Tyr Arg Thr Phe Lys Pro Glu Lys Gly Gly Leu Phe Cys  
 50 55 60

Glu Lys Ile Leu Gly Pro Thr Lys Asp Trp Glu Cys Cys Cys Gly Lys  
 65 70 75 80  
 Tyr Lys Lys Ile Lys His Lys Gly Ile Val Cys Asp Arg Cys Gly Val  
 85 90 95  
 Glu Val Thr Leu Ser Lys Val Arg Arg Glu Arg Met Ala His Ile Glu  
 100 105 110  
 Leu Ala Val Pro Ile Val His Ile Trp Phe Phe Lys Thr Thr Pro Ser  
 115 120 125  
 Arg Ile Gly Asn Val Leu Gly Met Thr Ala Ser Asp Leu Glu Arg Val  
 130 135 140  
 Ile Tyr Tyr Glu Glu Tyr Val Val Ile Asp Pro Gly Lys Thr Asp Leu  
 145 150 155 160  
 Thr Lys Lys Gln Leu Leu Asn Asp Ala Gln Tyr Arg Glu Val Val Glu  
 165 170 175  
 Lys Trp Gly Lys Asp Ala Phe Val Ala Lys Met Gly Gly Glu Ala Ile  
 180 185 190  
 Tyr Asp Leu Leu Lys Ser Glu Asp Leu Gln Ser Leu Leu Lys Asp Leu  
 195 200 205  
 Lys Glu Arg Leu Arg Lys Thr Lys Ser Gln Gln Ala Arg Met Lys Leu  
 210 215 220  
 Ala Lys Arg Leu Lys Ile Ile Glu Gly Phe Val Ser Ser Ser Asn His  
 225 230 235 240  
 Pro Glu Trp Met Val Leu Lys Asn Ile Pro Val Val Pro Pro Asp Leu  
 245 250 255  
 Arg Pro Leu Val Pro Leu Asp Gly Gly Arg Phe Ala Thr Ser Asp Leu  
 260 265 270  
 Asn Asp Leu Tyr Arg Arg Val Ile Asn Arg Asn Asn Arg Leu Lys Ala  
 275 280 285  
 Ile Leu Arg Leu Lys Thr Pro Glu Val Ile Val Arg Asn Glu Lys Arg  
 290 295 300  
 Met Leu Gln Glu Ala Val Asp Ala Leu Phe Asp Asn Gly Arg His Gly  
 305 310 315 320  
 His Pro Val Met Gly Ala Gly Asn Arg Pro Leu Lys Ser Leu Ser Glu  
 325 330 335  
 Met Leu Lys Gly Lys Asn Gly Arg Phe Arg Gln Asn Leu Leu Gly Lys  
 340 345 350  
 Arg Val Asp Tyr Ser Gly Arg Ser Val Ile Ile Val Gly Pro Glu Leu  
 355 360 365  
 Lys Phe Asn Gln Cys Gly Leu Pro Lys Glu Met Ala Leu Glu Leu Phe  
 370 375 380  
 Glu Pro Phe Ile Ile Xaa Arg Leu Lys Asp Gln Gly Ser Val Tyr Thr  
 385 390 395 400  
 Ile Arg Ser Ala Lys Lys Met Ile Gln Arg Gly Ala Pro Glu Val Trp  
 405 410 415  
 Asp Val Leu Glu Glu Ile Ile Lys Gly His Pro Val Leu Leu Asn Arg  
 420 425 430  
 Ala Pro Thr Leu His Arg Leu Gly Ile Gln Ala Phe Glu Pro Val Leu  
 435 440 445  
 Ile Glu Gly Lys Ala Ile Arg Ile His Pro Leu Val Cys Ala Ala Phe  
 450 455 460  
 Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu Ser  
 465 470 475 480  
 Val Glu Ala Gln Leu Glu Ala Lys Val Leu Met Met Ala Pro Asp Asn  
 485 490 495  
 Ile Phe Leu Pro Ser Ser Gly Lys Pro Val Ala Ile Pro Ser Lys Asp  
 500 505 510  
 Met Thr Leu Gly Leu Tyr Tyr Leu Met Ala Asp Pro Thr Tyr Phe Pro  
 515 520 525  
 Glu Glu His Gly Gly Lys Thr Lys Ile Phe Lys Asp Glu Ile Glu Val  
 530 535 540  
 Leu Arg Ala Leu Asn Asn Gly Gly Phe Ile Asp Asp Val Phe Gly Asp  
 545 550 555 560  
 Arg Arg Asp Glu Thr Gly Arg Gly Ile His Ile His Glu Lys Ile Lys  
 565 570 575

392



Ile Ala Ile Tyr Asp Asp Ala Asp Leu Ser Glu Leu Val Gly Thr Tyr  
 1090 1095 1100  
 Ala Ile Pro Ser Gly Ala Ile Ile Ser Val Glu Glu Gly Gln Arg Val  
 1105 1110 1115 1120  
 Asp Pro Gly Met Leu Leu Ala Arg Leu Pro Arg Gly Ala Ile Lys Thr  
 1125 1130 1135  
 Lys Asp Ile Thr Gly Gly Leu Pro Arg Val Ala Glu Leu Val Glu Ala  
 1140 1145 1150  
 Arg Lys Pro Glu Asp Ala Ala Asp Ile Ala Lys Ile Asp Gly Val Val  
 1155 1160 1165  
 Asp Phe Lys Gly Ile Gln Lys Asn Lys Arg Ile Leu Val Val Cys Asp  
 1170 1175 1180  
 Glu Met Thr Gly Met Glu Glu Glu His Leu Ile Pro Leu Thr Lys His  
 1185 1190 1195 1200  
 Leu Ile Val Gln Arg Gly Asp Ser Val Ile Lys Gly Ser Ser Leu Pro  
 1205 1210 1215  
 Met Val

&lt;210&gt;99

&lt;211&gt;186

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;99

Gly Gln Gln Leu Thr Asp Gly Leu Val Val Pro His Glu Ile Leu Glu  
 1 5 10 15  
 Ile Cys Gly Val Arg Glu Leu Gln Lys Tyr Leu Val Asn Glu Val Gln  
 20 25 30  
 Glu Val Tyr Arg Leu Gln Gly Val Asp Ile Asn Asp Lys His Ile Glu  
 35 40 45  
 Ile Ile Val Arg Gln Met Leu Gln Lys Val Arg Ile Thr Asp Pro Gly  
 50 55 60  
 Asp Thr Thr Leu Leu Phe Gly Glu Asp Val Asn Lys Lys Glu Phe Tyr  
 65 70 75 80  
 Glu Glu Asn Arg Arg Thr Glu Glu Asp Gly Gly Lys Pro Ala Gln Ala  
 85 90 95  
 Val Pro Val Leu Leu Gly Ile Thr Lys Ala Ser Leu Gly Thr Glu Ser  
 100 105 110  
 Phe Ile Ser Ala Ala Ser Phe Gln Asp Thr Thr Arg Val Leu Thr Asp  
 115 120 125  
 Ala Ala Cys Cys Ser Lys Thr Asp Tyr Leu Leu Gly Phe Lys Glu Asn  
 130 135 140  
 Val Ile Met Gly His Met Ile Pro Gly Gly Thr Gly Phe Glu Thr His  
 145 150 155 160  
 Lys Arg Ile Lys Gln Tyr Leu Glu Lys Glu Gln Glu Asp Leu Val Phe  
 165 170 175  
 Asp Phe Val Ser Glu Thr Glu Cys Val Xaa  
 180 185

&lt;210&gt;100

&lt;211&gt;337

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;100

Leu Glu Ile Asn Ser Asp Ala Lys Val Pro Met Ser Asn Gln Phe Asp  
 1 5 10 15  
 Gln Leu Lys Lys Leu Ser Thr Ile Val Cys Asp Ser Gly Asp Pro Glu  
 20 25 30  
 Leu Val Lys Ala Ser Gly Ser Gln Asp Ala Thr Thr Asn Pro Ser Leu  
 35 40 45  
 Ile Leu Lys Val Ala Gln Glu Pro Lys Phe Gln Glu Leu Leu Asn Glu  
 50 55 60  
 Ala Val Val Trp Gly Ile Arg Gln Asn Gly Asp Asp Leu Gln Thr Leu  
 65 70 75 80  
 Ser Phe Ile Leu Asp Lys Ile Gln Val Asn Phe Ala Leu Glu Ile Ile  
 85 90 95

Lys Asn Ile Pro Gly Arg Ile Ser Leu Glu Ile Asp Ala Arg Leu Ser  
                   100                  105                  110  
 Phe Asn Val Glu Ala Met Val Gln Arg Ala Val Phe Leu Ser Gln Leu  
                   115                  120                  125  
 Phe Glu Ala Met Gly Gly Asp Lys Lys Arg Leu Leu Val Lys Ile Pro  
                   130                  135                  140  
 Gly Thr Trp Glu Gly Ile Arg Ala Val Glu Phe Leu Glu Ala Lys Gly  
 145                  150                  155                  160  
 Ile Ala Cys Asn Val Thr Leu Ile Phe Asn Leu Val Gln Ala Ile Ala  
                   165                  170                  175  
 Ala Ala Lys Ala Lys Ala Thr Leu Ile Ser Pro Phe Val Gly Arg Ile  
                   180                  185                  190  
 Tyr Asp Trp Trp Ile Ala Ala Tyr Gly Asp Glu Gly Tyr Ser Ile Asp  
                   195                  200                  205  
 Ala Asp Pro Gly Val Ala Ser Val Ser Asn Ile Tyr Ala Tyr Tyr Lys  
                   210                  215                  220  
 Lys Phe Gly Ile Pro Thr Gln Ile Met Ala Ala Ser Phe Arg Thr Lys  
 225                  230                  235                  240  
 Glu Gln Val Leu Ala Leu Ala Gly Cys Asp Leu Leu Thr Ile Ser Pro  
                   245                  250                  255  
 Lys Leu Leu Asp Glu Leu Lys Lys Ser Gln His Pro Val Lys Lys Glu  
                   260                  265                  270  
 Leu Asp Pro Ala Glu Ala Lys Lys Leu Asp Val Gln Pro Ile Glu Leu  
                   275                  280                  285  
 Thr Glu Ser Phe Phe Arg Phe Leu Met Asn Glu Asp Ala Met Ala Thr  
                   290                  295                  300  
 Xaa Lys Leu Ala Glu Gly Ile Arg Ile Phe Ala Gly Asp Thr Gln Ile  
 305                  310                  315                  320  
 Leu Glu Thr Ala Ile Thr Glu Phe Ile Lys Gln Ile Ala Ala Glu Gly  
                   325                  330                  335  
 Ala

&lt;210&gt;101

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;101

Ser Glu Met Lys Asn Lys Met Asp Tyr Lys Ser Gln Leu Val Phe Ser  
   1                  5                  10                  15  
 Cys Pro Cys Cys Cys Lys Gly Asn Val Cys Phe Ser Val Phe Asn Leu  
                   20                  25                  30  
 Asp Val Ile Leu Thr Cys Asn Val Cys Ser Ser Thr Tyr Thr Phe Asp  
                   35                  40                  45  
 Ser Val Ile Arg Asn Glu Ile Arg Gln Phe Val Ala Leu Cys Lys Arg  
                   50                  55                  60  
 Ile His Asp Ala Asn Ser Ile Leu Gly Asn Ala Thr Val Ser Val Ser  
                   65                  70                  75                  80  
 Val Glu Asp Asn Gln Met Asp Ile Pro Phe Gln Leu Leu Phe Ser Arg  
                   85                  90                  95  
 Phe Pro Val Val Leu Asn Leu Ser Leu Asp Gly Lys Lys Ile Ala Ile  
                   100                  105                  110  
 Arg Phe Leu Phe Asp Ala Leu Asn Thr Ser Ile Leu His Gln Glu Ser  
                   115                  120                  125  
 Asp Leu Ile Ser  
                   130

&lt;210&gt;102

&lt;211&gt;192

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;102

Asn Lys Ser Thr Ala Arg Lys Lys Ile Gly Lys Phe Glu Lys Lys Pro  
   1                  5                  10                  15  
 Ser Leu Ser Pro Val Gln Trp Val Arg Tyr Ser Gly Lys Asn Tyr Ser  
                   20                  25                  30

Ile Gln Thr Pro Ser Leu Trp Gln Cys Ile Asp Asp Lys Thr Gln Leu  
                   35                  40                  45  
 Pro Glu Lys Leu Asp Val Leu Leu Ile Gly Lys Gly Lys Gly Asn Leu  
           50                  55                  60  
 Thr Pro Thr Ile Asn Ile Ala Gln Glu Ile Thr Ser Lys Ser Ser Lys  
   65                  70                  75                  80  
 Glu Tyr Ile Glu Glu Ile Leu Ala Tyr His Lys Ala Asn Glu Met Thr  
                   85                  90                  95  
 Leu Glu Ser Gly Ile Phe Thr Gln Ile Gln Ser Pro Ser Gly Glu Phe  
                   100                  105                  110  
 Thr Ile Ile Lys Thr Glu Lys Asn Ser Ser Trp Gly Arg Val Phe Cys  
           115                  120                  125  
 Leu Gln Ala Thr Thr Val Ile Asp His Thr Ala Tyr Ile Phe Thr Ser  
   130                  135                  140  
 Thr Ala Thr Leu Asp Asp Tyr Ala Glu Leu Ser Phe Thr Phe Leu Lys  
  145                  150                  155                  160  
 Val Val Ser Ser Phe Gln Ile Arg Gly Gly Lys Glu Ala Thr Ser Gly  
                   165                  170                  175  
 Asp Ala Ile Leu Glu Lys Ala Leu Glu Ala Leu Gln Asn Glu Asn Lys  
                   180                  185                  190

&lt;210&gt;103

&lt;211&gt;163

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;103

Asn Ile Met Ala Asn Leu Asn Ala Asp Gly Lys Leu Lys Gln Ile Cys  
   1                  5                  10                  15  
 Asp Ala Leu Arg Leu Asp Thr Leu Lys Pro Ala Glu Asp Glu Ala Ala  
           20                  25                  30  
 Ala Leu Leu His Asn Ala Lys Glu Gln Ala Lys Arg Ile Ile Gln Glu  
           35                  40                  45  
 Ala Gln Glu Glu Ala Arg Lys Ile Leu Glu Thr Ala Glu Glu Arg Ala  
   50                  55                  60  
 His Gln Lys Ile Lys Gln Gly Glu Val Ala Leu Ser Gln Ala Gly Lys  
   65                  70                  75                  80  
 Arg Ala Leu Glu Ala Leu Lys Gln Ala Val Glu Asn Lys Ile Phe Arg  
                   85                  90                  95  
 Glu Ser Leu Val Glu Trp Leu Glu His Val Thr Thr Asp Pro Glu Val  
                   100                  105                  110  
 Ser Thr Lys Leu Ile Gln Ala Leu Val Gln Ala Leu Glu Ala Gln Gly  
           115                  120                  125  
 Val Ser Gly Asn Leu Thr Ala Tyr Ile Gly Lys His Val Ser Pro Arg  
   130                  135                  140  
 Ala Val Asn Glu Leu Leu Arg Lys Gly Cys Asn Asn Lys Asn Tyr Glu  
  145                  150                  155                  160  
 Arg Lys Val

&lt;210&gt;104

&lt;211&gt;211

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;104

Ser His Glu Lys Ile Phe Ser Ile Phe Lys Val Val Val Met Thr Gln  
   1                  5                  10                  15  
 Tyr Tyr Phe Leu Ser Ser Phe Leu Pro Thr Gln Leu Pro Glu Ser Val  
           20                  25                  30  
 Pro Leu Phe Ser Ile Ser Asp Leu Asp Asp Leu Leu Tyr Leu Asn Leu  
           35                  40                  45  
 Ser Glu Asn Asp Leu Cys Asn Tyr Gly Leu Leu Lys Arg Phe Phe Asp  
   50                  55                  60  
 Phe Glu Asn Phe Ala Phe Phe Trp Ala Gly Lys Pro Ile Pro Phe Ser  
   65                  70                  75                  80  
 Phe Gly Glu Val Thr Gln Glu Asn Val Glu Arg Met Leu Ser Ser Gln  
                   85                  90                  95

Gln Trp Ser Asp Asp Asn Asp Phe Glu Asp Phe Phe Lys Asp Phe Leu  
 100 105 110  
 Met Asn His Lys Ser Ser Gln Asp Arg Leu Asn His Phe Ser Asp Leu  
 115 120 125  
 Phe Arg Glu Phe Leu Ser Tyr His Gln Thr Asn Ser Ser Lys Phe Leu  
 130 135 140  
 Gln Asp Tyr Phe Arg Phe Gln Gln Gln Leu Arg Val Val Leu Ala Gly  
 145 150 155 160  
 Phe Arg Ala Arg Val Leu Asn Met Asp Val Ser Tyr Val Leu Arg Asp  
 165 170 175  
 Glu Asp Ser Ser Asp Pro Val Val Leu Glu Val Leu Met Gln Lys Asp  
 180 185 190  
 Ser Pro Asn Tyr Glu Xaa Pro Glu Glu Phe Xaa Asp Leu Gln Gly Val  
 195 200 205  
 Leu Asp Asp  
 210  
 <210>105  
 <211>440  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>105  
 Lys Arg Gln Ser Asn Gly Asn Ser Phe Arg Thr Lys Leu Ala Gln Gly  
 1 5 10 15  
 His Val Ile Glu Ala Tyr Gly Asn Leu Leu Arg Val Arg Phe Asp Gly  
 20 25 30  
 Tyr Val Arg Gln Gly Glu Val Ala Tyr Val Asn Val Asp Asn Thr Trp  
 35 40 45  
 Leu Lys Ala Glu Val Ile Glu Val Ala Asp Gln Glu Val Lys Val Gln  
 50 55 60  
 Val Phe Glu Asp Thr Gln Gly Ala Cys Arg Gly Ala Leu Val Thr Phe  
 65 70 75 80  
 Ser Gly His Leu Leu Glu Ala Glu Leu Gly Pro Gly Leu Leu Gln Gly  
 85 90 95  
 Ile Phe Asp Gly Leu Gln Asn Arg Leu Glu Val Leu Ala Glu Asp Ser  
 100 105 110  
 Ser Phe Leu Gln Arg Gly Lys His Val Asn Ala Ile Ser Asp His Asn  
 115 120 125  
 Leu Trp Asn Tyr Thr Pro Val Ala Ser Val Gly Asp Thr Leu Arg Arg  
 130 135 140  
 Gly Asp Leu Leu Gly Thr Val Pro Glu Gly Arg Phe Thr His Lys Ile  
 145 150 155 160  
 Met Val Pro Phe Ser Cys Phe Gln Glu Val Thr Leu Thr Trp Val Ile  
 165 170 175  
 Ser Glu Gly Thr Tyr Asn Ala His Thr Val Val Ala Lys Ala Arg Asp  
 180 185 190  
 Ala Gln Gly Lys Glu Cys Ala Phe Thr Met Val Gln Arg Trp Pro Ile  
 195 200 205  
 Lys Gln Ala Phe Ile Glu Gly Glu Lys Ile Pro Ala His Lys Ile Met  
 210 215 220  
 Asp Val Gly Leu Arg Ile Leu Asp Thr Gln Ile Pro Val Leu Lys Gly  
 225 230 235 240  
 Gly Thr Phe Cys Thr Pro Gly Pro Phe Gly Ala Gly Lys Thr Val Leu  
 245 250 255  
 Gln His His Leu Ser Lys Tyr Ala Ala Val Asp Ile Val Ile Leu Cys  
 260 265 270  
 Ala Cys Gly Glu Arg Ala Gly Glu Val Val Glu Val Leu Gln Glu Phe  
 275 280 285  
 Pro His Leu Ile Asp Pro His Thr Gly Lys Ser Leu Met His Arg Thr  
 290 295 300  
 Cys Ile Ile Cys Asn Thr Ser Ser Met Pro Val Ala Ala Arg Glu Ser  
 305 310 315 320  
 Ser Ile Tyr Leu Gly Val Thr Ile Ala Glu Tyr Tyr Arg Gln Met Gly  
 325 330 335  
 Leu Asp Ile Leu Leu Leu Ala Asp Ser Thr Ser Arg Trp Ala Gln Ala

340 345 350  
 Leu Arg Glu Ile Ser Gly Arg Leu Glu Glu Ile Pro Gly Glu Glu Ala  
 355 360 365  
 Phe Pro Ala Tyr Leu Ser Ser Arg Ile Ala Ala Phe Tyr Glu Arg Gly  
 370 375 380  
 Gly Ala Ile Thr Thr Lys Asp Gly Ser Glu Gly Ser Leu Thr Ile Cys  
 385 390 395 400  
 Gly Ala Val Ser Pro Ala Gly Gly Asn Phe Glu Glu Pro Val Thr Gln  
 405 410 415  
 Ser Thr Leu Ala Val Val Gly Ala Phe Cys Gly Leu Ser Lys Ala Arg  
 420 425 430  
 Leu Thr His Val Gly Ile Leu Gln  
 435 440

&lt;210&gt;106

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;106

Arg Thr Ser His Ser Ile Tyr Ile Ser Cys Ser Arg Ser Val Leu Trp  
 1 5 10 15  
 Ser Phe Lys Ser Thr Thr Asp Ala Arg Arg Tyr Pro Ser Ile Asp Pro  
 20 25 30  
 Leu Ile Ser Trp Ser Lys Tyr Leu Asn Gln Val Gly Gln Ile Leu Glu  
 35 40 45  
 Glu Lys Val Ser Gly Trp Gly Gly Ala Val Lys Lys Ala Ala Gln Phe  
 50 55 60  
 Leu Glu Lys Gly Ser Glu Ile Gly Lys Arg Met Glu Val Val Gly Glu  
 65 70 75 80  
 Glu Gly Val Ser Met Glu Asp Met Glu Ile Tyr Leu Lys Ala Glu Leu  
 85 90 95  
 Tyr Asp Phe Cys Tyr Leu Gln Gln Asn Ala Phe Asp Pro Val Asp Cys  
 100 105 110  
 Tyr Cys Pro Phe Glu Arg Gln Ile Glu Leu Phe Ser Leu Ile Ser Arg  
 115 120 125  
 Ile Phe Asp Ala Lys Phe Val Phe Asp Ser Pro Asp Asp Ala Arg Ser  
 130 135 140  
 Phe Phe Leu Glu Leu Gln Ser Lys Ile Lys Thr Leu Asn Gly Leu Lys  
 145 150 155 160  
 Phe Leu Ser Glu Glu Tyr His Glu Ser Lys Glu Val Ile Val Arg Leu  
 165 170 175  
 Leu Glu Lys Thr Met Val Gln Met Ala  
 180 185

&lt;210&gt;107

&lt;211&gt;438

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;107

Met Gln Thr Ile Tyr Thr Lys Ile Thr Asp Ile Lys Gly Asn Leu Ile  
 1 5 10 15  
 Thr Val Glu Ala Glu Gly Ala Arg Leu Gly Glu Leu Ala Thr Ile Thr  
 20 25 30  
 Arg Ser Asp Gly Arg Ser Ser Tyr Ala Ser Val Leu Arg Phe Asp Leu  
 35 40 45  
 Lys Lys Val Thr Leu Gln Val Phe Gly Gly Thr Ser Gly Leu Ser Thr  
 50 55 60  
 Gly Asp His Val Thr Phe Leu Gly Arg Pro Met Glu Val Thr Phe Gly  
 65 70 75 80  
 Ser Ser Leu Leu Gly Arg Arg Leu Asn Gly Ile Gly Lys Pro Ile Asp  
 85 90 95  
 Asn Glu Gly Glu Cys Phe Gly Glu Pro Ile Glu Ile Ala Thr Pro Thr  
 100 105 110  
 Phe Asn Pro Val Cys Arg Ile Val Pro Arg Ser Met Val Arg Thr Asn  
 115 120 125  
 Ile Pro Met Ile Asp Val Phe Asn Cys Leu Val Lys Ser Gln Lys Ile

130 135 140  
 Pro Ile Phe Ser Ser Ser Gly Glu His His Asn Ala Leu Leu Met Arg  
 145 150 155 160  
 Ile Ala Ala Gln Thr Asp Ala Asp Ile Val Val Ile Gly Gly Met Gly  
 165 170 175  
 Leu Thr Phe Val Asp Tyr Ser Phe Phe Val Glu Glu Ser Lys Lys Leu  
 180 185 190  
 Gly Phe Ala Asp Lys Cys Val Met Phe Ile His Lys Ala Val Asp Ala  
 195 200 205  
 Pro Val Glu Cys Val Leu Val Pro Asp Met Ala Leu Ala Cys Ala Glu  
 210 215 220  
 Lys Phe Ala Val Glu Glu Lys Lys Asn Val Leu Val Leu Leu Thr Asp  
 225 230 235 240  
 Met Thr Ala Phe Ala Asp Ala Leu Lys Glu Ile Ser Ile Thr Met Asp  
 245 250 255  
 Gln Ile Pro Ala Asn Arg Gly Tyr Pro Gly Ser Leu Tyr Ser Asp Leu  
 260 265 270  
 Ala Leu Arg Tyr Glu Lys Ala Val Glu Ile Ala Asp Gly Gly Ser Ile  
 275 280 285  
 Thr Leu Ile Thr Val Thr Thr Met Pro Ser Asp Asp Ile Thr His Pro  
 290 295 300  
 Val Pro Asp Asn Thr Gly Tyr Ile Thr Glu Gly Gln Phe Tyr Leu Arg  
 305 310 315 320  
 Asn Asn Arg Ile Asp Pro Phe Gly Ser Leu Ser Arg Leu Lys Gln Leu  
 325 330 335  
 Val Ile Gly Lys Val Thr Arg Glu Asp His Gly Asp Leu Ala Asn Ala  
 340 345 350  
 Leu Ile Arg Leu Tyr Ala Asp Ser Arg Lys Ala Thr Glu Arg Met Ala  
 355 360 365  
 Met Gly Phe Lys Leu Ser Asn Trp Asp Lys Lys Leu Leu Ala Phe Ser  
 370 375 380  
 Glu Leu Phe Glu Thr Arg Leu Met Ser Leu Glu Val Asn Ile Pro Leu  
 385 390 395 400  
 Glu Glu Ala Leu Asp Ile Gly Trp Lys Ile Leu Ala Gln Ser Phe Thr  
 405 410 415  
 Ser Glu Glu Val Gly Ile Lys Ala Gln Leu Ile Asn Lys Tyr Trp Pro  
 420 425 430  
 Lys Ala Cys Leu Ser Lys  
 435  
 <210>108  
 <211>214  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>108  
 Val Leu Ala Lys Ser Met Ser Val Gln Val Lys Leu Thr Lys Asn Ser  
 1 5 10 15  
 Phe Arg Leu Glu Lys Gln Lys Leu Ala Arg Leu Gln Thr Tyr Leu Pro  
 20 25 30  
 Thr Leu Lys Leu Lys Lys Ala Leu Leu Gln Ala Glu Val Gln Asn Ala  
 35 40 45  
 Val Lys Asp Ala Ala Glu Cys Asp Lys Asp Tyr Val Gln Ala Tyr Glu  
 50 55 60  
 Arg Ile Tyr Ala Phe Ala Glu Leu Phe Ser Ile Pro Leu Cys Thr Asp  
 65 70 75 80  
 Cys Val Glu Lys Ser Phe Glu Ile Gln Ser Ile Asp Asn Asp Phe Glu  
 85 90 95  
 Asn Ile Ala Gly Val Glu Val Pro Ile Val Arg Glu Val Thr Leu Phe  
 100 105 110  
 Pro Ala Ser Tyr Ser Leu Leu Gly Thr Pro Ile Trp Leu Asp Thr Met  
 115 120 125  
 Leu Ser Ala Ser Lys Glu Leu Val Val Lys Lys Val Met Ala Glu Val  
 130 135 140  
 Ser Lys Glu Arg Leu Lys Ile Leu Glu Glu Glu Leu Arg Ala Val Ser  
 145 150 155 160

Ile Arg Val Asn Leu Phe Glu Lys Lys Leu Ile Pro Glu Thr Thr Lys  
 165 170 175  
 Ile Leu Lys Lys Ile Ala Val Phe Leu Ser Asp Arg Ser Ile Thr Asp  
 180 185 190  
 Val Gly Gln Val Lys Met Ala Lys Lys Lys Ile Glu Leu Arg Lys Ala  
 195 200 205  
 Arg Gly Asp Glu Cys Val  
 210  
 <210>109  
 <211>660  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>109  
 Val Arg Leu Asn Ile His Lys Tyr Leu Phe Ile Gly Arg Asn Lys Ala  
 1 5 10 15  
 Asp Phe Phe Ser Ala Ser Arg Glu Leu Gly Val Val Glu Phe Ile Ser  
 20 25 30  
 Lys Lys Cys Phe Ile Thr Thr Glu Gln Gly His Arg Phe Val Glu Cys  
 35 40 45  
 Leu Lys Val Phe Asp His Leu Glu Ala Glu Tyr Ser Leu Glu Ala Leu  
 50 55 60  
 Glu Phe Val Lys Asp Glu Ser Val Ser Val Glu Asp Ile Val Ser Glu  
 65 70 75 80  
 Val Leu Thr Leu Asn Lys Glu Ile Lys Gly Leu Leu Glu Thr Val Lys  
 85 90 95  
 Ala Leu Arg Lys Glu Ile Val Arg Val Lys Pro Leu Gly Ala Phe Ser  
 100 105 110  
 Ser Ser Glu Ile Ala Glu Leu Ser Arg Lys Thr Gly Ile Ser Leu Arg  
 115 120 125  
 Phe Phe Tyr Arg Thr His Lys Asp Asn Glu Asp Leu Glu Glu Asp Ser  
 130 135 140  
 Pro Asn Val Phe Tyr Leu Ser Thr Ala Tyr Asn Phe Asp Tyr Tyr Leu  
 145 150 155 160  
 Val Leu Gly Val Val Asp Leu Pro Arg Asp Arg Tyr Thr Glu Ile Glu  
 165 170 175  
 Ala Pro Arg Ser Val Asn Glu Leu Gln Val Asp Leu Ala Asn Leu Gln  
 180 185 190  
 Arg Glu Ile Arg Asn Arg Ser Asp Arg Leu Cys Asp Leu Tyr Ala Tyr  
 195 200 205  
 Arg Arg Glu Val Leu Arg Gly Leu Cys Asn Tyr Asp Asn Glu Gln Arg  
 210 215 220  
 Leu His Gln Ala Lys Glu Cys Cys Glu Asp Leu Phe Asp Gly Lys Val  
 225 230 235 240  
 Phe Ala Val Ala Gly Trp Val Ile Val Asp Arg Ile Lys Glu Leu Gln  
 245 250 255  
 Ser Leu Cys Asn Arg Tyr Gln Ile Tyr Met Glu Arg Val Pro Val Asp  
 260 265 270  
 Pro Asp Glu Thr Ile Pro Thr Tyr Leu Glu Asn Lys Gly Val Gly Val  
 275 280 285  
 Met Gly Glu Asp Leu Val Gln Ile Tyr Asp Thr Pro Ala Tyr Ser Asp  
 290 295 300  
 Lys Asp Pro Ser Thr Trp Val Phe Phe Ala Phe Val Leu Phe Phe Ser  
 305 310 315 320  
 Met Ile Val Asn Asp Ala Gly Tyr Gly Leu Leu Phe Leu Met Ser Ser  
 325 330 335  
 Leu Leu Phe Ser Trp Lys Phe Arg Arg Lys Met Lys Phe Ser Lys His  
 340 345 350  
 Leu Ser Arg Met Leu Lys Met Thr Ala Ile Leu Gly Leu Gly Cys Ile  
 355 360 365  
 Cys Trp Gly Thr Thr Thr Thr Ser Phe Phe Gly Met Ser Phe Ser Lys  
 370 375 380  
 Thr Ser Val Phe Arg Glu Tyr Ser Met Thr His Val Leu Ala Leu Lys  
 385 390 395 400  
 Lys Ala Glu Tyr Tyr Leu Gln Met Arg Pro Lys Ala Tyr Lys Glu Leu

405 410 415  
 Thr Asn Glu Tyr Pro Ser Leu Lys Ala Ile Arg Asp Pro Lys Ala Phe  
 420 425 430  
 Leu Leu Ala Thr Glu Ile Gly Ser Ala Gly Ile Glu Ser Arg Tyr Val  
 435 440 445  
 Val Tyr Asp Lys Phe Ile Asp Asn Ile Leu Met Glu Leu Ala Leu Phe  
 450 455 460  
 Ile Gly Val Val His Leu Ser Leu Gly Met Leu Arg Tyr Leu Arg Tyr  
 465 470 475 480  
 Arg Tyr Ser Gly Ile Gly Trp Ile Leu Phe Met Val Ser Ala Tyr Leu  
 485 490 495  
 Tyr Val Pro Ile Tyr Leu Gly Thr Val Ser Leu Ile His Tyr Leu Phe  
 500 505 510  
 His Val Pro Tyr Glu Leu Gly Gly Gln Ile Gly Tyr Tyr Gly Met Phe  
 515 520 525  
 Gly Gly Ile Gly Leu Ala Val Val Leu Ala Met Ile Gln Arg Ser Trp  
 530 535 540  
 Arg Gly Val Glu Glu Ile Ile Ser Val Ile Gln Val Phe Ser Asp Val  
 545 550 555 560  
 Leu Ser Tyr Leu Arg Ile Tyr Ala Leu Gly Leu Ala Gly Ala Met Met  
 565 570 575  
 Gly Ala Thr Phe Asn Gln Met Gly Ala Arg Leu Pro Met Leu Leu Gly  
 580 585 590  
 Ser Ile Val Ile Leu Leu Gly His Ser Val Asn Ile Ile Leu Ser Ile  
 595 600 605  
 Met Gly Gly Val Ile His Gly Leu Arg Leu Asn Phe Ile Glu Trp Tyr  
 610 615 620  
 His Tyr Ser Phe Asp Gly Gly Gly Arg Pro Leu Arg Pro Leu Arg Lys  
 625 630 635 640  
 Ile Val Cys Ser Glu Asp Ala Glu Ala Ser Gly Ile His Leu Asp Asn  
 645 650 655  
 Asn Ser Ile Val  
 660

&lt;210&gt;110

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;110

Leu Lys Gly Ala His Glu Val Ser Met Ile Asp Met Ser Val Val Gly  
 1 5 10 15  
 Pro Ala Leu Val Leu Gly Leu Ala Met Ile Gly Ser Ala Ile Gly Cys  
 20 25 30  
 Gly Met Ala Gly Val Ala Ser His Ala Val Met Ser Arg Ile Asp Glu  
 35 40 45  
 Gly His Gly Lys Leu Ile Gly Met Ser Ala Met Pro Ser Ser Gln Ser  
 50 55 60  
 Ile Tyr Gly Phe Ile Leu Met Leu Leu Met Gln Ala Ala Ile Lys Asn  
 65 70 75 80  
 Gly Thr Leu Ser Pro Val Gly Gly Ile Ala Ile Gly Leu Ser Val Gly  
 85 90 95  
 Ala Ala Leu Leu Val Ser Ser Val Met Gln Gly Lys Cys Cys Val Ser  
 100 105 110  
 Gly Ile Gln Ala Tyr Ala Arg Ser Ser Ile Tyr Gly Lys Cys Tyr  
 115 120 125  
 Ala Ala Ile Gly Ile Val Glu Ser Phe Ser Leu Phe Ala Val Val Phe  
 130 135 140  
 Ala Leu Leu Leu Leu  
 145

&lt;210&gt;111

&lt;211&gt;940

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;111

Met Thr Thr Glu Asp Phe Pro Lys Ala Tyr Asn Phe Gln Asp Thr Glu



```

      1              5              10              15
Pro Glu Leu Tyr Val Phe Trp Glu Lys Asn Gly Met Phe Lys Ala Glu
      20              25              30
Ala Ser Ser Asp Lys Pro Pro Tyr Ser Val Ile Met Pro Pro Pro Asn
      35              40              45
Val Thr Gly Val Leu His Met Gly His Ala Leu Val Asn Thr Leu Gln
      50              55              60
Asp Val Leu Val Arg Tyr Lys Arg Met Ser Gly Phe Glu Val Cys Trp
      65              70              75              80
Ile Pro Gly Thr Asp His Ala Gly Ile Ala Thr Gln Ala Val Val Glu
      85              90              95
Arg His Leu Gln Ala Ser Glu Gly Lys Arg Arg Thr Asp Tyr Ser Arg
      100              105              110
Glu Asp Phe Leu Lys His Ile Trp Ala Trp Lys Glu Lys Ser Glu Lys
      115              120              125
Val Val Leu Ser Gln Leu Arg Gln Leu Gly Cys Ser Cys Asp Trp Asp
      130              135              140
Arg Lys Arg Phe Thr Met Glu Pro Leu Ala Asn Arg Ala Val Lys Lys
      145              150              155              160
Ala Phe Lys Thr Leu Phe Glu Asn Gly Tyr Ile Tyr Arg Gly Tyr Tyr
      165              170              175
Leu Val Asn Trp Asp Pro Val Leu Gln Thr Ala Leu Ala Asp Asp Glu
      180              185              190
Val Glu Tyr Glu Glu Lys Asp Gly Trp Leu Tyr Tyr Ile Arg Tyr Arg
      195              200              205
Met Val Gly Ser Gln Glu Ser Ile Val Val Ala Thr Thr Arg Pro Glu
      210              215              220
Thr Ser Leu Gly Asp Thr Gly Ile Ala Val Ser Pro Asn Asp Glu Arg
      225              230              235              240
Tyr Ala Ser Trp Ile Gly Ala Ser Val Glu Val Pro Phe Val Asn Arg
      245              250              255
Gln Ile Pro Ile Ile Gly Asp Ala Ser Val Asp Pro Thr Phe Gly Thr
      260              265              270
Gly Ala Val Lys Val Thr Pro Ala His Asp Lys Asp Asp Tyr Leu Met
      275              280              285
Gly Thr Asn His His Leu Pro Met Ile Asn Ile Leu Thr Pro Ser Gly
      290              295              300
Gly Ile Asn Glu Asn Gly Gly Pro Phe Ala Gly Met Ala Lys Glu Lys
      305              310              315              320
Ala Arg Glu Glu Ile Leu Ile Ala Leu Glu Glu Gln Gly Leu Phe Val
      325              330              335
Arg Lys Glu Pro Tyr Lys Leu Arg Val Gly Val Ser Tyr Arg Ser Gly
      340              345              350
Ala Val Ile Glu Pro Tyr Leu Ser Lys Gln Trp Phe Val Ser Val Ser
      355              360              365
Glu Phe Arg Gly Ala Leu Arg Glu Phe Val Glu Ser Gln Asp Ile Lys
      370              375              380
Ile Phe Pro Lys Asp Phe Val Lys Asn Tyr Leu Ser Trp Val Asn His
      385              390              395              400
Leu Arg Asp Trp Cys Ile Ser Arg Gln Leu Trp Trp Gly His Arg Ile
      405              410              415
Pro Val Trp Tyr His Lys Asn His Asp Glu Arg Val Leu Cys Tyr Asp
      420              425              430
Gly Glu Gly Ile Pro Glu Glu Val Ala Gln Asp Pro Asp Ser Trp Tyr
      435              440              445
Gln Asp Pro Asp Val Leu Asp Thr Trp Phe Ser Ser Gly Leu Trp Pro
      450              455              460
Leu Thr Cys Leu Gly Trp Pro Asp Glu Asn Ser Pro Asp Leu Lys Lys
      465              470              475              480
Phe Tyr Pro Thr Ala Leu Leu Val Thr Gly His Asp Ile Leu Phe Phe
      485              490              495
Trp Val Thr Arg Met Val Leu Leu Cys Ser Ser Met Ser Gly Glu Lys
      500              505              510
Pro Phe Ser Glu Val Phe Leu His Gly Leu Ile Phe Gly Lys Ser Tyr

```

515 520 525  
 Lys Arg Tyr Asn Asp Phe Gly Glu Trp Ser Tyr Ile Ser Gly Lys Glu  
 530 535 540  
 Lys Leu Ala Tyr Asp Met Gly Glu Ala Leu Pro Asp Gly Val Val Ala  
 545 550 555 560  
 Lys Trp Glu Lys Leu Ser Lys Ser Lys Gly Asn Val Ile Asp Pro Leu  
 565 570 575  
 Glu Met Ile Ala Thr Tyr Gly Thr Asp Ala Val Arg Leu Thr Leu Cys  
 580 585 590  
 Ser Cys Ala Asn Arg Gly Glu Gln Ile Asp Leu Asp Tyr Arg Leu Phe  
 595 600 605  
 Glu Glu Tyr Lys His Phe Ala Asn Lys Val Trp Asn Gly Ala Arg Phe  
 610 615 620  
 Ile Phe Gly His Ile Ser Asp Leu Gln Gly Lys Asp Leu Leu Ala Gly  
 625 630 635 640  
 Ile Asp Glu Asp Ser Leu Gly Leu Glu Asp Phe Tyr Ile Leu Asp Gly  
 645 650 655  
 Phe Asn Gln Leu Ile His Gln Leu Glu Glu Ala Tyr Ala Thr Tyr Ala  
 660 665 670  
 Phe Asp Lys Val Ala Thr Leu Ala Tyr Glu Phe Phe Arg Asn Asp Leu  
 675 680 685  
 Cys Ser Thr Tyr Ile Glu Ile Ile Lys Pro Thr Leu Phe Gly Lys Gln  
 690 695 700  
 Gly Asn Glu Ala Ser Gln Ser Thr Lys Arg Thr Leu Leu Ala Val Leu  
 705 710 715 720  
 Leu Ile Asn Val Leu Gly Val Leu His Pro Val Ala Pro Phe Ile Thr  
 725 730 735  
 Glu Ser Leu Phe Leu Arg Ile Gln Asp Thr Leu Gly Ala Leu Pro Glu  
 740 745 750  
 Gly Asp Gly Asp Ala Phe Thr Gly His Ala Leu Arg Met Leu Arg Ser  
 755 760 765  
 Arg Ala Cys Met Glu Ala Pro Tyr Pro Lys Ala Phe Asp Val Lys Ile  
 770 775 780  
 Pro Gln Asp Leu Arg Glu Ser Phe Thr Leu Ala Gln Arg Leu Val Tyr  
 785 790 795 800  
 Thr Ile Arg Asn Ile Arg Gly Glu Met Gln Leu Asp Pro Arg Leu His  
 805 810 815  
 Leu Lys Ala Phe Val Val Cys Ser Asp Thr Thr Glu Ile Gln Ser Cys  
 820 825 830  
 Ile Pro Ile Leu Gln Ala Leu Gly Glu Leu Glu Ser Ile Gln Leu Leu  
 835 840 845  
 Asp Lys Glu Pro Glu Lys Gly Leu Tyr Ser Phe Gly Val Val Asp Thr  
 850 855 860  
 Ile Arg Leu Gly Ile Phe Val Pro Glu Glu His Leu Leu Lys Glu Lys  
 865 870 875 880  
 Gly Arg Leu Glu Lys Glu Arg Val Arg Leu Glu Arg Ala Val Glu Asn  
 885 890 895  
 Leu Glu Arg Leu Leu Gly Asp Glu Ser Phe Cys Gln Lys Ala Asn Pro  
 900 905 910  
 Asn Leu Val Val Ala Lys Gln Glu Ala Leu Lys Asn Asn Arg Ile Glu  
 915 920 925  
 Leu Gln Gly Ile Leu Asp Lys Leu Ala Ser Phe Ala  
 930 935 940  
 <210>112  
 <211>945  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>112  
 Ala Cys Ile Val Cys Leu Asp Arg Glu Asp Gln Arg Ser Leu Glu Arg  
 1 5 10 15  
 Tyr Asp Ile Val Arg Ile Ile Gly Lys Gly Gly Met Gly Glu Val Tyr  
 20 25 30  
 Leu Ala Tyr Asp Pro Val Cys Ser Arg Lys Val Ala Leu Lys Lys Ile  
 35 40 45

Arg Glu Asp Leu Ala Glu Asn Pro Leu Leu Lys Arg Arg Phe Leu Arg  
 50 55 60  
 Glu Ala Arg Ile Ala Ala Asp Leu Ile His Pro Gly Val Val Pro Val  
 65 70 75 80  
 Tyr Thr Ile Tyr Ser Glu Lys Asp Pro Val Tyr Tyr Thr Met Pro Tyr  
 85 90 95  
 Ile Glu Gly Tyr Thr Leu Lys Thr Leu Lys Ser Val Trp Gln Lys  
 100 105 110  
 Glu Ser Leu Ser Lys Glu Leu Ala Glu Lys Thr Ser Val Gly Ala Phe  
 115 120 125  
 Leu Ser Ile Phe His Lys Ile Cys Cys Thr Ile Glu Tyr Val His Ser  
 130 135 140  
 Arg Gly Ile Leu His Arg Asp Leu Lys Pro Asp Asn Ile Leu Leu Gly  
 145 150 155 160  
 Leu Phe Ser Glu Ala Val Ile Leu Asp Trp Gly Ala Ala Val Ala Cys  
 165 170 175  
 Gly Glu Glu Glu Asp Leu Leu Asp Ile Asp Val Ser Lys Glu Glu Val  
 180 185 190  
 Leu Ser Ser Arg Met Thr Ile Pro Gly Arg Ile Val Gly Thr Pro Asp  
 195 200 205  
 Tyr Met Ala Pro Glu Arg Leu Leu Gly His Pro Ala Ser Lys Ser Thr  
 210 215 220  
 Asp Ile Tyr Ala Leu Gly Val Val Leu Tyr Gln Met Leu Thr Leu Ser  
 225 230 235 240  
 Phe Pro Tyr Arg Arg Lys Lys Gly Lys Lys Ile Val Leu Asp Gly Gln  
 245 250 255  
 Arg Ile Pro Ser Pro Gln Glu Val Ala Pro Tyr Arg Glu Ile Pro Pro  
 260 265 270  
 Phe Leu Ser Ala Val Val Met Arg Met Leu Ala Val Asp Pro Gln Glu  
 275 280 285  
 Arg Tyr Ser Ser Val Thr Glu Leu Lys Glu Asp Ile Glu Ser His Leu  
 290 295 300  
 Lys Gly Ser Pro Lys Trp Thr Leu Thr Thr Ala Leu Pro Pro Lys Lys  
 305 310 315 320  
 Ser Ser Ser Trp Lys Leu Asn Glu Pro Ile Leu Leu Ser Lys Tyr Phe  
 325 330 335  
 Pro Met Leu Glu Val Ser Pro Ala Ser Trp Tyr Ser Leu Ala Ile Ser  
 340 345 350  
 Asn Ile Glu Ser Phe Ser Glu Met Arg Leu Glu Tyr Thr Leu Ser Lys  
 355 360 365  
 Lys Gly Leu Asn Glu Gly Phe Gly Ile Leu Leu Pro Thr Ser Glu Asn  
 370 375 380  
 Ala Leu Gly Gly Asp Phe Tyr Gln Gly Tyr Gly Phe Trp Leu His Ile  
 385 390 395 400  
 Lys Glu Arg Thr Leu Ser Val Ser Leu Val Lys Asn Ser Leu Glu Ile  
 405 410 415  
 Gln Arg Cys Ser Gln Asp Leu Glu Ser Asp Lys Glu Thr Phe Leu Ile  
 420 425 430  
 Ala Leu Glu Gln His Asn His Ser Leu Ser Leu Phe Val Asp Gly Thr  
 435 440 445  
 Thr Trp Leu Ile His Met Asn Tyr Leu Pro Ser Arg Ser Gly Arg Val  
 450 455 460  
 Ala Ile Ile Val Arg Asp Met Glu Asp Ile Leu Glu Asp Ile Gly Ile  
 465 470 475 480  
 Phe Glu Ser Ser Gly Ser Leu Arg Val Ser Cys Leu Ala Val Pro Asp  
 485 490 495  
 Ala Phe Leu Ala Glu Lys Leu Tyr Asp Arg Ala Leu Val Leu Tyr Arg  
 500 505 510  
 Arg Ile Ala Glu Ser Phe Pro Gly Arg Lys Glu Gly Tyr Glu Ala Arg  
 515 520 525  
 Phe Arg Ala Gly Ile Thr Val Leu Glu Lys Ala Ser Thr Asp Asn Asn  
 530 535 540  
 Glu Gln Glu Phe Ala Leu Ala Ile Glu Glu Phe Ser Lys Leu His Asp  
 545 550 555 560

Gly Val Ala Ala Pro Leu Glu Tyr Leu Gly Lys Ala Leu Val Tyr Gln  
 565 570 575  
 Arg Leu Gln Glu Tyr Asn Glu Glu Ile Lys Ser Leu Leu Leu Ala Leu  
 580 585 590  
 Lys Arg Tyr Ser Gln His Pro Glu Ile Phe Arg Leu Lys Asp His Val  
 595 600 605  
 Val Tyr Arg Leu His Glu Ser Phe Tyr Lys Arg Asp Arg Leu Ala Leu  
 610 615 620  
 Val Phe Met Ile Leu Val Leu Glu Ile Ala Pro Gln Ala Ile Thr Pro  
 625 630 635 640  
 Gly Gln Glu Glu Lys Ile Leu Val Trp Leu Lys Asp Lys Ser Arg Ala  
 645 650 655  
 Thr Leu Phe Cys Leu Leu Asp Pro Thr Val Leu Glu Leu Arg Ser Ser  
 660 665 670  
 Lys Met Glu Leu Phe Leu Ser Tyr Trp Ser Gly Phe Ile Pro His Leu  
 675 680 685  
 Asn Ser Leu Phe His Arg Ala Trp Asp Gln Ser Asp Val Arg Ala Leu  
 690 695 700  
 Ile Glu Ile Phe Tyr Val Ala Cys Asp Leu His Lys Trp Gln Phe Leu  
 705 710 715 720  
 Ser Ser Cys Ile Asp Ile Phe Lys Glu Ser Leu Glu Asp Gln Lys Ala  
 725 730 735  
 Thr Glu Glu Ile Val Glu Phe Ser Phe Glu Asp Leu Gly Ala Phe Leu  
 740 745 750  
 Phe Ala Ile Gln Ser Ile Phe Asn Lys Glu Asp Ala Glu Lys Ile Phe  
 755 760 765  
 Val Ser Asn Asp Gln Leu Ser Pro Ile Leu Leu Val Tyr Ile Phe Asp  
 770 775 780  
 Leu Phe Ala Asn Arg Ala Leu Leu Glu Ser Gln Gly Glu Ala Ile Phe  
 785 790 795 800  
 Gln Ala Leu Asp Leu Ile Arg Ser Lys Val Pro Glu Asn Phe Tyr His  
 805 810 815  
 Asp Tyr Leu Arg Asn His Glu Ile Arg Ala His Leu Trp Cys Arg Asn  
 820 825 830  
 Glu Lys Ala Leu Ser Thr Ile Phe Glu Asn Tyr Thr Glu Lys Gln Leu  
 835 840 845  
 Lys Asp Glu Gln His Glu Leu Phe Val Leu Tyr Gly Cys Tyr Leu Ala  
 850 855 860  
 Leu Ile Gln Gly Ala Glu Ala Ala Lys Gln His Phe Asp Val Cys Arg  
 865 870 875 880  
 Glu Asp Arg Ile Phe Pro Ala Ser Leu Leu Ala Arg Asn Tyr Asn Arg  
 885 890 895  
 Leu Gly Leu Pro Lys Asp Ala Leu Ser Tyr Gln Glu Arg Arg Leu Leu  
 900 905 910  
 Leu Arg Gln Lys Phe Leu Tyr Phe His Cys Leu Gly Asn His Asp Glu  
 915 920 925  
 Arg Asp Leu Cys Gln Thr Met Tyr His Leu Leu Thr Glu Glu Phe Gln  
 930 935 940  
 Leu  
 945  
 <210>113  
 <211>1826  
 <212>PRT  
 <213>Chlamydia pneumoniae.  
 <400>113  
 Met Lys Ser Leu Pro Val Tyr Val Ser Gly Ile Lys Val Arg Asn Leu  
 1 5 10 15  
 Lys Asn Val Ser Ile His Phe Asn Ser Glu Glu Ile Val Leu Leu Thr  
 20 25 30  
 Gly Val Ser Gly Ser Gly Lys Ser Ser Ile Ala Phe Asp Thr Leu Tyr  
 35 40 45  
 Ala Ala Gly Arg Lys Arg Tyr Ile Ser Thr Leu Pro Thr Phe Phe Ala  
 50 55 60  
 Thr Thr Ile Thr Thr Leu Pro Asn Pro Lys Val Glu Glu Ile His Gly

```

65              70              75              80
Leu Ser Pro Thr Ile Ala Ile Lys Gln Asn His Phe Ser His Tyr Ser
                        85              90              95
His Ala Thr Val Gly Ser Thr Thr Glu Leu Phe Ser His Leu Ala Leu
                        100              105              110
Leu Phe Thr Leu Glu Gly Gln Ala Arg Asp Pro Lys Thr Lys Glu Val
                        115              120              125
Leu Asp Leu Tyr Ser Lys Glu Lys Val Leu Ser Thr Ile Met Glu Leu
                        130              135              140
Ser Glu Gly Val Gln Ile Ser Ile Leu Ala Pro Leu Leu Arg Lys Asp
145              150              155              160
Ile Ala Ala Ile His Glu Tyr Ala Gln Gln Gly Phe Thr Lys Val Arg
                        165              170              175
Cys Asn Gly Thr Ile His Pro Ile Tyr Ser Phe Leu Thr Ser Gly Ile
                        180              185              190
Pro Glu Asp Cys Ser Val Asp Ile Val Ile Asp Thr Leu Ile Lys Ser
                        195              200              205
Glu Asn Asn Ile Ala Arg Leu Lys Val Ser Leu Phe Thr Ala Leu Glu
                        210              215              220
Phe Gly Glu Gly His Cys Ser Val Leu Ser Asp Glu Glu Leu Met Thr
225              230              235              240
Phe Ser Thr Lys Gln Gln Ile Asp Asp Val Thr Tyr Thr Pro Leu Thr
                        245              250              255
Gln Gln Leu Phe Ser Pro His Ala Leu Glu Ser Arg Cys Ser Leu Cys
                        260              265              270
Gln Gly Ser Gly Ile Phe Ile Ser Ile Asp Asn Pro Leu Leu Ile Asp
                        275              280              285
Glu Asn Leu Ser Ile Lys Glu Asn Cys Cys Ser Phe Ala Gly Asn Cys
                        290              295              300
Ser Ser Tyr Leu Tyr His Thr Ile Tyr Gln Ala Leu Ala Asp Ala Leu
305              310              315              320
Asn Phe Asn Leu Glu Thr Pro Trp Lys Asp Leu Ser Pro Glu Ile Gln
                        325              330              335
Asn Ile Phe Leu Arg Gly Lys Asn Asn Leu Val Leu Pro Val Arg Leu
                        340              345              350
Phe Asp Gln Thr Leu Gly Lys Lys Asn Leu Thr Tyr Lys Val Trp Arg
                        355              360              365
Gly Val Leu Asn Asp Ile Gly Asp Lys Val Arg Tyr Thr Thr Lys Pro
370              375              380
Ser Arg Tyr Leu Ser Lys Gly Met Ser Ala His Ser Cys Ser Leu Cys
385              390              395              400
Lys Gly Thr Gly Leu Gly Asp Tyr Ala Ser Val Ala Thr Trp Glu Gly
                        405              410              415
Lys Thr Phe Thr Glu Phe Gln Gln Met Ser Leu Asn Asn Trp His Val
                        420              425              430
Phe Phe Ser Lys Val Lys Ser Pro Ser Leu Ser Ile Gln Glu Ile Leu
                        435              440              445
Gln Gly Leu Lys Gln Arg Leu Ser Phe Leu Ile Asp Leu Gly Leu Gly
450              455              460
Tyr Leu Thr Pro Asn Arg Ala Leu Ala Thr Leu Ser Gly Gly Glu Gln
465              470              475              480
Glu Arg Thr Ala Ile Ala Lys His Leu Gly Gly Glu Leu Phe Gly Ile
                        485              490              495
Thr Tyr Ile Leu Asp Glu Pro Ser Ile Gly Leu His Pro Gln Asp Thr
                        500              505              510
Glu Lys Leu Ile Gly Val Ile Lys Lys Leu Arg Asp Gln Gly Asn Thr
515              520              525
Val Ile Leu Val Glu His Glu Glu Arg Met Ile Ser Leu Ala Asp Arg
530              535              540
Ile Ile Asp Ile Gly Pro Gly Ala Gly Ile Phe Gly Gly Glu Val Leu
545              550              555              560
Phe Asn Gly Lys Pro Glu Asp Phe Leu Met Asn Ser Ser Ser Leu Thr
                        565              570              575
Ala Lys Tyr Leu Arg Gln Glu Leu Thr Ile Pro Ile Pro Glu Ser Arg

```

406

1090 1095 1100  
 Lys Glu Gly Phe Ile Lys Leu Tyr Ser Glu Gly Asn Leu Tyr Asp Leu  
 1105 1110 1115 1120  
 Asp Glu Arg Leu Pro Leu Asn Leu Ile Glu Pro Ala Ile Val Ile Gln  
 1125 1130 1135  
 His Thr Lys Val Ser Pro Lys Asn Ser Ser Ser Leu Leu Ser Ala Ile  
 1140 1145 1150  
 Ser Val Ala Phe Ser Leu Ser Ser Glu Ile Trp Ile Tyr Ile Ser Gln  
 1155 1160 1165  
 Lys Lys Gln Arg Lys Leu Ser Tyr Ser Leu Gly Trp Lys Asp Lys Lys  
 1170 1175 1180  
 Gly Arg Leu Tyr Pro Glu Ile Thr His Gln Leu Leu Xaa Ser Asp His  
 1185 1190 1195 1200  
 Pro Glu Gly Arg Cys Leu Thr Cys Gly Gly Arg Gly Glu Ile Leu Lys  
 1205 1210 1215  
 Ile Ser Leu Glu Glu His Lys Glu Lys Ile Ala His Tyr Thr Pro Leu  
 1220 1225 1230  
 Glu Phe Phe Ser Leu Phe Phe Pro Lys Ser Tyr Met Lys Pro Val Gln  
 1235 1240 1245  
 Lys Leu Leu Lys Asp Glu Asn Ala Ser Gln Pro Leu Lys Leu Leu Thr  
 1250 1255 1260  
 Thr Lys Glu Phe Leu Asn Phe Cys Arg Gly Ser Ser Glu Phe Pro Gly  
 1265 1270 1275 1280  
 Met Asn Ala Leu Leu Met Glu Gln Leu Asp Thr Glu Ser Asp Ser Pro  
 1285 1290 1295  
 Leu Ile Lys Pro Leu Leu Ala Leu Thr Ser Cys Pro Ala Cys Lys Gly  
 1300 1305 1310  
 Ser Gly Leu Asn Asp Tyr Ala Asn Tyr Val Arg Ile Asn Asn Thr Ser  
 1315 1320 1325  
 Leu Leu Asp Ile Tyr Gln Glu Asp Ala Thr Phe Leu Glu Ser Phe Leu  
 1330 1335 1340  
 Asn Thr Ile Gly Thr Asp Asp Thr Arg Ser Ile Ile Gln Asp Leu Met  
 1345 1350 1355 1360  
 Asn Arg Leu Thr Phe Ile Ser Lys Val Gly Leu Ser Tyr Ile Thr Leu  
 1365 1370 1375  
 Gly Gln Arg Gln Asp Thr Leu Ser Asp Gly Glu Asn Tyr Arg Leu His  
 1380 1385 1390  
 Leu Ala Lys Lys Ile Ser Ile Asn Leu Thr Asn Ile Val Tyr Leu Phe  
 1395 1400 1405  
 Glu Glu Pro Leu Ser Gly Leu His Pro Gln Asp Leu Pro Thr Ile Val  
 1410 1415 1420  
 Gln Leu Leu Lys Glu Leu Val Ala Asn Asn Asn Thr Val Ile Ala Thr  
 1425 1430 1435 1440  
 Asp Arg Ser Cys Ser Leu Ile Pro His Ala Asp His Ala Ile Phe Leu  
 1445 1450 1455  
 Gly Pro Gly Ser Gly Pro Gln Gly Gly Phe Leu Met Asp Ser Asp Thr  
 1460 1465 1470  
 Glu Val Cys Pro Ser Val Asp Leu His Ala Asn Val Pro Gln Thr Glu  
 1475 1480 1485  
 Val Cys Pro Lys Ala Pro Leu Ser Ile Ser Lys Ala Asn His Thr Arg  
 1490 1495 1500  
 Gly Ser Asp Arg Thr Leu Lys Val Asn Leu Ser Ile His His Ile Gln  
 1505 1510 1515 1520  
 Asn Leu Lys Val Ser Ala Pro Leu His Ala Leu Val Ala Ile Gly Gly  
 1525 1530 1535  
 Val Ser Gly Ser Gly Lys Thr Ser Leu Leu Leu Glu Gly Phe Lys Lys  
 1540 1545 1550  
 Gln Ala Glu Leu Leu Ile Ala Lys Gly Thr Thr Thr Phe Ser Asp Leu  
 1555 1560 1565  
 Val Val Ile Asp Ser His Pro Ile Ala Ser Ser Gln Arg Ser Asp Ile  
 1570 1575 1580  
 Ser Thr Tyr Phe Asp Ile Ala Pro Ser Leu Arg Ala Phe Tyr Ala Ser  
 1585 1590 1595 1600  
 Leu Thr Gln Ala Lys Ala Leu Asn Ile Ser Ser Thr Met Phe Ser Thr

```

      1605      1610      1615
Asn Thr Lys Gln Gly Gln Cys Ser Asp Cys Gln Gly Leu Gly Tyr Gln
      1620      1625      1630
Trp Ile Asp Arg Ala Phe Tyr Ala Leu Glu Lys Arg Pro Cys Pro Thr
      1635      1640      1645
Cys Ser Gly Phe Arg Ile Gln Pro Leu Ala Gln Glu Val Leu Tyr Glu
      1650      1655      1660
Gly Lys His Phe Gly Glu Leu Leu His Thr Pro Ile Glu Thr Val Ala
      1665      1670      1675      1680
Leu Arg Phe Pro Phe Ile Lys Lys Ile Gln Lys Pro Leu Lys Ala Leu
      1685      1690      1695
Leu Asp Ile Gly Leu Gly Tyr Leu Pro Ile Gly Gln Lys Leu Ser Ser
      1700      1705      1710
Leu Ser Val Ser Glu Lys Thr Ala Leu Lys Thr Ala Tyr Phe Leu Tyr
      1715      1720      1725
Gln Thr Pro Glu Thr Pro Thr Leu Phe Leu Ile Asp Glu Leu Phe Ser
      1730      1735      1740
Ser Leu Asp Pro Ile Lys Lys Gln His Leu Pro Glu Lys Leu Arg Ser
      1745      1750      1755      1760
Leu Ile Asn Ser Gly His Ser Val Ile Tyr Ile Asp His Asp Val Lys
      1765      1770      1775
Leu Leu Lys Ser Ala Asp Tyr Leu Ile Glu Ile Gly Pro Gly Ser Gly
      1780      1785      1790
Lys Gln Gly Gly Lys Leu Leu Phe Ser Gly Ser Pro Lys Asp Ile Tyr
      1795      1800      1805
Ala Ser Lys Asp Ser Leu Leu Lys Lys Tyr Ile Cys Asn Glu Glu Leu
      1810      1815      1820
Asp Ser
1825
<210>114
<211>486
<212>PRT
<213>Chlamydia pneumoniae
<400>114
Asp Ser Met Ile Thr Arg Thr Lys Ile Ile Cys Thr Ile Gly Pro Ala
  1           5           10           15
Thr Asn Ser Pro Glu Met Leu Ala Lys Leu Leu Asp Ala Gly Met Asn
      20      25      30
Val Ala Arg Leu Asn Phe Ser His Gly Ser His Glu Thr His Gly Gln
      35      40      45
Ala Ile Gly Phe Leu Lys Glu Leu Arg Glu Gln Lys Arg Val Pro Leu
      50      55      60
Ala Ile Met Leu Asp Thr Lys Gly Pro Glu Ile Arg Leu Gly Asn Ile
      65      70      75      80
Pro Gln Pro Ile Ser Val Ser Gln Gly Gln Lys Leu Arg Leu Val Ser
      85      90      95
Ser Asp Ile Asp Gly Ser Ala Glu Gly Gly Val Ser Leu Tyr Pro Lys
      100      105      110
Gly Ile Phe Pro Phe Val Pro Glu Gly Ala Asp Val Leu Ile Asp Asp
      115      120      125
Gly Tyr Ile His Ala Val Val Val Ser Ser Glu Ala Asp Ser Leu Glu
      130      135      140
Leu Glu Phe Met Asn Ser Gly Leu Leu Lys Ser His Lys Ser Leu Ser
      145      150      155      160
Ile Arg Gly Val Asp Val Ala Leu Pro Phe Met Thr Glu Lys Asp Ile
      165      170      175
Ala Asp Leu Lys Phe Gly Val Glu Gln Asn Met Asp Val Val Ala Ala
      180      185      190
Ser Phe Val Arg Tyr Gly Glu Asp Ile Glu Thr Met Arg Lys Cys Leu
      195      200      205
Ala Asp Leu Gly Asn Pro Lys Met Pro Ile Ile Ala Lys Ile Glu Asn
      210      215      220
Arg Leu Gly Val Glu Asn Phe Ser Lys Ile Ala Lys Leu Ala Asp Gly
      225      230      235      240

```



Ile Met Ile Ala Arg Gly Asp Leu Gly Ile Glu Leu Ser Val Val Glu  
 245 250 255  
 Val Pro Asn Leu Gln Lys Met Met Ala Lys Val Ser Arg Glu Thr Gly  
 260 265 270  
 His Phe Cys Val Thr Ala Thr Gln Met Leu Glu Ser Met Ile Arg Asn  
 275 280 285  
 Val Leu Pro Thr Arg Ala Glu Val Ser Asp Ile Ala Asn Ala Ile Tyr  
 290 295 300  
 Asp Gly Ser Ser Ala Val Met Leu Ser Gly Glu Thr Ala Ser Gly Ala  
 305 310 315 320  
 His Pro Val Ala Ala Val Lys Ile Met Arg Ser Val Ile Leu Glu Thr  
 325 330 335  
 Glu Lys Asn Leu Ser His Asp Ser Phe Leu Lys Leu Asp Glu Ser Asn  
 340 345 350  
 Ser Ala Leu Gln Val Ser Pro Tyr Leu Ser Ala Ile Gly Leu Ala Gly  
 355 360 365  
 Ile Gln Ile Ala Glu Arg Ala Asp Ala Lys Ala Leu Ile Val Tyr Thr  
 370 375 380  
 Glu Ser Gly Ser Ser Pro Met Phe Leu Ser Lys Tyr Arg Pro Lys Phe  
 385 390 395 400  
 Pro Ile Ile Ala Val Thr Pro Ser Thr Ser Val Tyr Tyr Arg Leu Ala  
 405 410 415  
 Leu Glu Trp Gly Val Tyr Pro Met Leu Thr Gln Glu Ser Asp Arg Ala  
 420 425 430  
 Val Trp Arg His Gln Ala Cys Ile Tyr Gly Ile Glu Gln Gly Ile Leu  
 435 440 445  
 Ser Asn Tyr Asp Arg Ile Leu Val Leu Ser Arg Gly Ala Cys Met Glu  
 450 455 460  
 Glu Thr Asn Asn Leu Thr Leu Thr Ile Val Asn Asp Ile Leu Thr Gly  
 465 470 475 480  
 Ser Glu Phe Pro Glu Thr  
 485

&lt;210&gt;115

&lt;211&gt;463

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;115

Leu Val Gly Lys Lys Phe His Gln Ile Lys Arg Thr Ile Leu Glu Ala  
 1 5 10 15  
 Pro Leu Tyr Tyr Leu Val Ser Gly Ile Ile Ala Leu Cys Arg His Thr  
 20 25 30  
 Pro Arg Ser Phe Leu Thr Gly Leu Gly Lys Gly Phe Gly Phe Leu Ala  
 35 40 45  
 Phe Tyr Ile Ile Ser Asp Tyr Arg Lys Thr Ala Leu Thr Asn Leu Ala  
 50 55 60  
 Leu Ala Phe Pro Glu Lys Thr Phe Asp Glu Arg Tyr Lys Ile Ala Arg  
 65 70 75 80  
 Gln Ser Leu Gln His Leu Ile Ile Thr Leu Leu Glu Leu Leu Ala Ile  
 85 90 95  
 Glu Gln Leu Val Gly Asn Ile Asp Lys Leu Ile Thr Ile Val Thr Ser  
 100 105 110  
 Ser Arg Asn Pro Lys Gly Phe Ser Ser Glu Glu Val Ile Ser Asn Glu  
 115 120 125  
 Asp Leu Glu Glu Thr Phe Lys Asn Leu Gln Glu Lys Gln Gly Leu Ile  
 130 135 140  
 Leu Phe Cys Gly His Gln Ala Asn Trp Glu Leu Pro Phe Leu Tyr Ile  
 145 150 155 160  
 Thr Lys Asn Tyr Pro Gly Ile Ala Phe Ala Lys Ala Ile Lys Asn Gln  
 165 170 175  
 Arg Leu Ser Lys Lys Ile Phe Ala Leu Arg Glu Val Phe Lys Gly Lys  
 180 185 190  
 Ile Val Pro Pro Lys Asn Gly Ile Gln Gln Gly Ile Glu Ala Leu Asn  
 195 200 205  
 Gln Gly Lys Leu Val Gly Ile Val Gly Asp Gln Ala Leu Leu Met Ser

210 215 220  
 Ser Tyr Thr Tyr Pro Leu Phe Gly Ser Pro Ala Phe Thr Thr Thr Ser  
 225 230 235 240  
 Pro Ala Leu Leu Ala Tyr Lys Thr Gly Phe Pro Val Ile Ala Val Asn  
 245 250 255  
 Val Ser Arg Gln Ala Lys Gly Phe Glu Val Ile Pro Ser Ala Lys Leu  
 260 265 270  
 Tyr Ala Asn Lys Ser Leu Pro Met Lys Glu Ser Val Ala Ile Leu Met  
 275 280 285  
 Asp Gln Met Met Gly Phe Leu Glu Lys Gly Ile Ala Ser Gln Pro Glu  
 290 295 300  
 Gln Trp Met Trp Ile His Lys Arg Trp Lys Arg Lys Ile Ser Asn Val  
 305 310 315 320  
 Ile Lys Lys Lys Tyr Arg Tyr Ser His Ile Leu Val Phe Val Asp Gln  
 325 330 335  
 Val Ser Ser His Phe Ser Phe Leu Lys Ala Leu Ala Glu Cys Phe Ser  
 340 345 350  
 Gly Thr Thr Leu His Leu Thr Leu Gly Asn Ala Asp His Leu Glu Glu  
 355 360 365  
 Leu Gln Glu Gln Phe Pro Glu Tyr Ser Leu Ile Gln Leu Arg Asn Asp  
 370 375 380  
 Gln Asp Ile Leu Ala Leu Pro Asn Cys Tyr Pro Ala Ile Phe Asp Leu  
 385 390 395 400  
 Thr Asn Asn Leu Gln His Leu Tyr Lys His Phe Arg Lys Thr Gly Ser  
 405 410 415  
 Cys Ala Val Tyr Ser Lys Arg Phe Leu Glu Lys Ser Leu Asp His Pro  
 420 425 430  
 Gln Ala Pro Leu Lys Asn Ser Leu Arg Ile Phe Tyr Ser Lys Asn Leu  
 435 440 445  
 Lys Asp Lys Glu Arg Lys Asn Phe Lys Val Lys Ser Lys Gly Pro  
 450 455 460

&lt;210&gt;116

&lt;211&gt;114

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;116

Ile Ile Leu Leu Cys Phe Leu Leu Ser Gln Asp Phe Ser Phe Cys Ser  
 1 5 10 15  
 Glu Asp Ala Pro Glu Arg Asn Met Leu Asn Ser Ile Val Thr Lys Arg  
 20 25 30  
 Thr Arg Thr Ala Ala Thr Leu Leu Ile Pro Lys Val Ile Pro Glu Ala  
 35 40 45  
 Pro Ser Thr Pro Val Gln Ile Lys Met Ile Ser Ile Lys Glu Thr Ile  
 50 55 60  
 Ala Val Arg Ala Lys Ser Pro Ala Asp Thr Val Ala Thr Phe Ala Leu  
 65 70 75 80  
 Asp Ser Glu Leu Ser Glu Gln Gln Gln Thr Val Leu Ile Ala Ala Ser  
 85 90 95  
 Lys Pro Trp Pro Lys Gln Ser Ile Lys His Ile Lys Phe Pro Leu Thr  
 100 105 110  
 Lys Phe

&lt;210&gt;117

&lt;211&gt;104

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;117

Asn Leu Val Arg Gly Asn Phe Met Cys Leu Ile Asp Cys Leu Gly Gln  
 1 5 10 15  
 Gly Phe Glu Ala Ala Ile Asn Thr Val Cys Cys Cys Ser Asp Ser Ser  
 20 25 30  
 Glu Ser Lys Ala Asn Val Ala Thr Val Ser Ala Gly Leu Leu Ala Leu  
 35 40 45  
 Thr Ala Ile Val Ser Phe Ile Leu Ile Ile Leu Ile Cys Thr Gly Val

50 55 60  
 Leu Gly Ala Ser Gly Met Thr Phe Gly Met Ser Asn Val Ala Ala Val  
 65 70 75 80  
 Leu Val Leu Leu Val Thr Ile Leu Leu Ser Met Phe Leu Ser Gly Ala  
 85 90 95  
 Ser Ser Leu Gln Asn Glu Lys Ser  
 100  
 <210>118  
 <211>434  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>118  
 Arg Thr Gln Lys Lys Thr Phe Ile Leu Leu Asp Leu Glu Thr Met Ile  
 1 5 10 15  
 Lys Phe Leu Ser Gln Leu Phe Ile Arg His Trp Pro Arg Lys Val Val  
 20 25 30  
 Ser Leu Gly Phe Ala Ile Ile Ile Trp Ile Leu Val Gly Gln Ser Val  
 35 40 45  
 Thr Ile Thr Arg Thr Leu Thr Asn Val Pro Val Arg Ile Val Asp Leu  
 50 55 60  
 His Pro Asp Gln Thr Val Leu Gly Leu Gln Lys Ser Gly Phe Leu Asn  
 65 70 75 80  
 Lys Lys Val Ser Leu Thr Ile Thr Gly Asn Lys Asn Thr Val Gln Asp  
 85 90 95  
 Leu Arg Pro Ser Asn Leu Glu Val Val Ile Ser Ala Ala Asn His Thr  
 100 105 110  
 Glu Ser Trp Ile Ala Thr Ile Asp Lys His Asn Leu Val Ser Val Asp  
 115 120 125  
 His Glu Ile Asn Ile Arg Lys Asp Ile His Ser Val Asp Ala Asn Asp  
 130 135 140  
 Ile Phe Val Arg Leu Thr Gln Tyr Val Thr Glu Asp Ile Leu Leu Thr  
 145 150 155 160  
 Ile Thr Lys Pro Ile Gly Ser Pro Pro Lys Gly Tyr Glu Tyr Leu Asp  
 165 170 175  
 Val Trp Pro Lys Tyr Leu Asn Gln Lys Val Ser Gly Pro Lys Glu Tyr  
 180 185 190  
 Ile Asn Ala Leu Lys Glu Gln Gly Leu Glu Leu Thr Phe Asn Leu Asn  
 195 200 205  
 Lys Ile Ser Phe Glu Glu Leu Glu Arg Asn Arg Ile Ala Gln Gly Ser  
 210 215 220  
 His Asp Glu Ile Ile Phe Pro Ile Pro Lys Glu Trp Lys Lys Ile Leu  
 225 230 235 240  
 Ile Pro Phe Glu Asn Thr Phe Met Asp Leu Asn Asp Pro Gln Ala Asp  
 245 250 255  
 Phe Leu Arg Leu Leu Phe Leu Lys Arg Glu Cys Ile Pro Leu Asn Leu  
 260 265 270  
 Asn Leu Pro Val Phe Leu Phe Phe Pro Val Thr Phe Ile Gln Thr Met  
 275 280 285  
 Asn Pro Leu Glu Tyr Ser Leu Asp Pro Val Pro Pro Ile Ile Leu Asn  
 290 295 300  
 His Gly Ile His Gln Ile Asn Ile Pro Leu Tyr Val Lys Asp Val Ser  
 305 310 315 320  
 Arg Gln Phe Leu Asp Val Val Lys Asn Asn Met Val Leu Thr Ile Val  
 325 330 335  
 Met Pro Ser Pro Gln Asp Pro Ser Ser Ile Asn Trp Ala Ile Glu Phe  
 340 345 350  
 Leu Asp Glu Lys Thr Leu Glu Asn Thr Phe Leu Gln Thr Ile Ile Ala  
 355 360 365  
 Gln Glu His Gly Ile Leu His Asp Ile Ala Leu Ile Asp Glu Ala Gly  
 370 375 380  
 Ile Arg His Arg Phe Arg Glu Tyr Leu Arg Lys Leu Ala Leu Phe Thr  
 385 390 395 400  
 Ala Asp Gly Glu Pro Leu Asn Leu Ile Ala Glu Ile Lys Asn Asn Lys  
 405 410 415

Val Val Ile Gln Thr Lys Thr Lys Glu Thr Thr Lys Leu Tyr Lys Lys  
 420 425 430

Glu Trp

<210>119

<211>279

<212>PRT

<213>Chlamydia pneumoniae

<400>119

Leu Cys Asn Phe Ser Gln Tyr Thr Thr Gln Gly Pro Ser Lys Thr Met  
 1 5 10 15  
 Pro Phe Asp Ile Thr Tyr Tyr Thr Thr Pro Leu Leu Glu Ile Ile Leu  
 20 25 30  
 Ile Trp Val Met Leu Asn Tyr Leu Leu Lys Phe Phe Trp Gly Thr Arg  
 35 40 45  
 Ala Met Asp Val Val Phe Gly Leu Leu Ala Phe Leu Phe Leu Phe Val  
 50 55 60  
 Leu Ala Asp Lys Leu His Leu Pro Ile Ile Arg Arg Leu Met Leu His  
 65 70 75 80  
 Val Val Asn Ile Ala Ala Ile Val Val Phe Ile Ile Phe Gln Pro Glu  
 85 90 95  
 Ile Arg Leu Ala Leu Ser Arg Ile Arg Phe His Gly Lys Lys Phe Phe  
 100 105 110  
 Ile Asp Thr Gln Glu Gln Phe Val Glu Gln Leu Ala Ala Ser Ile Tyr  
 115 120 125  
 Gln Leu Ser Glu Arg Gln Ile Gly Ala Leu Val Val Leu Glu Asn Lys  
 130 135 140  
 Asp Ser Phe Asp Glu Tyr Leu Ser Phe Ser Ser Val Lys Ile Asn Ala  
 145 150 155 160  
 Thr Phe Ser Glu Glu Leu Leu Glu Thr Ile Phe Glu Pro Ser Ser Pro  
 165 170 175  
 Leu His Asp Gly Ala Val Ile Leu Arg Gly Asp Ile Leu Ala Tyr Ala  
 180 185 190  
 Arg Val Val Leu Pro Leu Ala His Asp Thr Thr Gln Leu Ser Arg Ser  
 195 200 205  
 Met Gly Thr Arg His Arg Ala Ala Leu Gly Ala Ser Gln Arg Ser Asp  
 210 215 220  
 Ala Leu Ile Ile Thr Val Ser Glu Glu Asn Gly Ser Val Ser Leu Ser  
 225 230 235 240  
 Arg Asp Gly Leu Leu Thr Arg Gly Val Lys Ile Asp Arg Phe Lys Ala  
 245 250 255  
 Val Leu Arg Ser Ile Leu Ser Pro Lys Glu His Lys Arg Lys Pro Leu  
 260 265 270  
 Phe Ser Trp Ile Trp Lys Arg  
 275

<210>120

<211>448

<212>PRT

<213>Chlamydia pneumoniae

<400>120

Met Asp Ala Leu Ile Leu Ser Arg Ile Gln Phe Gly Leu Phe Ile Thr  
 1 5 10 15  
 Phe His Tyr Leu Phe Val Pro Leu Ser Met Gly Leu Ser Met Met Leu  
 20 25 30  
 Val Ile Met Glu Gly Leu Tyr Leu Val Thr Lys Lys Gln Ile Tyr Lys  
 35 40 45  
 Gln Met Thr Trp Phe Trp Val Gly Ile Phe Ala Leu Thr Phe Val Leu  
 50 55 60  
 Gly Val Val Thr Gly Ile Met Gln Ile Phe Ser Phe Gly Ser Asn Trp  
 65 70 75 80  
 Ala Asn Phe Ser Glu Tyr Thr Gly Asn Ile Phe Gly Thr Leu Leu Gly  
 85 90 95  
 Ser Glu Gly Val Phe Ala Phe Phe Leu Glu Ser Gly Phe Leu Gly Ile  
 100 105 110

Leu Leu Phe Gly Arg His Lys Val Ser Lys Lys Met His Phe Phe Ser  
 115 120 125  
 Thr Cys Met Val Ala Leu Gly Ala His Met Ser Ala Phe Trp Ile Ile  
 130 135 140  
 Cys Ala Asn Ser Trp Met Gln Thr Pro Ser Gly Tyr Glu Met Val Met  
 145 150 155 160  
 His Lys Gly Lys Leu Ile Pro Ala Leu Thr Ser Phe Trp Gly Val Val  
 165 170 175  
 Phe Ser Pro Thr Thr Ile Asp Arg Phe Ile His Ala Val Leu Gly Thr  
 180 185 190  
 Trp Leu Ser Gly Val Phe Leu Val Ile Ser Val Ser Ala Tyr Tyr Leu  
 195 200 205  
 Trp Lys Lys Arg His His Glu Phe Ala Lys Gln Gly Met Lys Ile Gly  
 210 215 220  
 Thr Ile Cys Ala Val Ile Val Leu Val Leu Gln Leu Trp Ser Ala Asp  
 225 230 235 240  
 Val Thr Ala Arg Gly Val Ala Lys Asn Gln Pro Ala Lys Leu Ala Ala  
 245 250 255  
 Phe Glu Gly Ile Phe Lys Thr Glu Glu Tyr Thr Pro Ile Trp Ala Phe  
 260 265 270  
 Gly Tyr Val Asp Met Glu Lys Glu Arg Val Ile Gly Leu Pro Ile Pro  
 275 280 285  
 Gly Ala Leu Ser Phe Leu Val His Arg Asn Ile Lys Thr Pro Val Thr  
 290 295 300  
 Gly Leu Asp Gln Ile Pro Arg Asp Glu Trp Pro Asn Val Gln Ala Val  
 305 310 315 320  
 Phe Gln Leu Tyr His Leu Met Ile Met Leu Trp Gly Val Met Val Ala  
 325 330 335  
 Leu Thr Leu Ile Ser Trp Ser Ala Tyr Lys Gly Trp Arg Trp Ala Leu  
 340 345 350  
 Lys Pro Phe Phe Leu Val Ile Leu Thr Phe Ser Val Leu Leu Pro Glu  
 355 360 365  
 Ile Cys Asn Glu Cys Gly Trp Cys Ala Ala Glu Met Gly Arg Gln Pro  
 370 375 380  
 Trp Val Val Gln Gly Leu Leu Lys Thr Lys Asp Ala Val Ser Pro Ile  
 385 390 395 400  
 Val Gln Ala Asn Lys Ile Val Gln Ser Leu Val Ile Phe Ser Leu Val  
 405 410 415  
 Phe Ile Ala Leu Leu Thr Leu Phe Ile Thr Val Leu Cys Lys Lys Ile  
 420 425 430  
 Lys His Gly Pro Glu Glu Glu Asn Asp Leu Thr Glu Phe Glu Val Lys  
 435 440 445  
 <210>121  
 <211>268  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>121  
 Met Glu Leu Ser Leu Thr Ser Leu Leu Pro Leu Ala Trp Tyr Val Ile  
 1 5 10 15  
 Leu Gly Val Ala Val Phe Ala Tyr Ser Phe Gly Asp Gly Phe Asp Leu  
 20 25 30  
 Gly Leu Gly Ala Val Tyr Leu Lys Ala Lys Glu Asp Lys Glu Arg Arg  
 35 40 45  
 Ile Leu Leu Asn Ser Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp  
 50 55 60  
 Leu Val Ile Ile Val Gly Gly Leu Phe Ala Gly Phe Pro Ala Cys Tyr  
 65 70 75 80  
 Ala Thr Leu Leu Ser Ile Phe Tyr Met Pro Ile Trp Thr Leu Val Leu  
 85 90 95  
 Leu Tyr Ile Phe Arg Gly Cys Ser Leu Glu Phe Arg Ser Lys Ser Glu  
 100 105 110  
 Ser Val Ser Trp Lys Ile Phe Trp Asp Ile Ile Phe Ile Cys Ser Gly  
 115 120 125  
 Thr Ala Ile Ser Phe Phe Leu Gly Thr Ile Val Gly Asn Leu Ile Leu

130 135 140  
 Gly Leu Pro Leu Ser Pro Asp Thr Ser Tyr Ala Ser Leu Ser Trp Ile  
 145 150 155 160  
 Leu Phe Phe Arg Pro Tyr Ala Ala Leu Cys Gly Ala Val Val Ala Ser  
 165 170 175  
 Ala Phe Ala Thr His Gly Ser Phe Phe Ala Leu Met Lys Thr Ser Asp  
 180 185 190  
 Ser Leu Asn Ala Arg Ile Ala Gln Gln Phe Pro Tyr Ile Leu Ser Ser  
 195 200 205  
 Phe Leu Val Phe Tyr Val Leu Phe Leu Gly Ala Ser Leu Ile Ser Ile  
 210 215 220  
 Pro Lys Arg Phe Asp Ala Phe Pro Thr Tyr Pro Leu Leu Ile Leu Leu  
 225 230 235 240  
 Ile Ala Leu Thr Ser Cys Cys Cys Val Ala Ala Lys Thr Ser Val Ser  
 245 250 255  
 Lys Lys His Tyr Gly Thr His Leu Phe Ile Leu His  
 260 265  
 <210>122  
 <211>403  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>122  
 Glu Lys Ser Met Arg Met Leu Gln Ile Ser Met Leu Leu Leu Ala Leu  
 1 5 10 15  
 Gly Thr Ala Ile Asn Ser Pro Ala Ile Tyr Ala Ala Asp Ser Gln Ser  
 20 25 30  
 Val Ser Phe Pro Glu Gln Leu Pro Ser Ser Phe Thr Gly Glu Ile Lys  
 35 40 45  
 Gly Asn His Val Arg Met Arg Leu Ala Pro His Thr Asp Gly Thr Ile  
 50 55 60  
 Ile Arg Glu Phe Ser Lys Gly Asp Leu Val Ala Val Ile Gly Glu Ser  
 65 70 75 80  
 Lys Asp Tyr Tyr Val Ile Ser Ala Pro Pro Gly Ile Thr Gly Tyr Val  
 85 90 95  
 Phe Arg Ser Phe Val Leu Asp Asn Val Val Glu Gly Glu Gln Val Asn  
 100 105 110  
 Val Arg Leu Glu Pro Ser Thr Ser Ala Pro Val Leu Val Arg Leu Ser  
 115 120 125  
 Arg Gly Thr Gln Ile Gln Pro Ala Ser Gln Glu Pro His Gly Lys Trp  
 130 135 140  
 Leu Glu Val Val Leu Pro Ser Gln Cys Val Phe Tyr Val Ala Lys Asn  
 145 150 155 160  
 Phe Val Ala Asn Lys Gly Pro Ile Glu Leu Tyr Thr Gln Arg Glu Gly  
 165 170 175  
 Gln Lys Lys Ile Ala Met Asp Leu Ile Asn Ser Ala Leu Asn Phe Ala  
 180 185 190  
 His Ile Glu Leu Glu Lys Ser Leu Asn Glu Ile Asp Leu Glu Ala Ile  
 195 200 205  
 Tyr Lys Lys Ile Asn Leu Val Gln Ser Glu Glu Phe Lys Asp Val Pro  
 210 215 220  
 Gly Ile Gln Gly Leu Ile Gln Lys Ala Leu Glu Glu Ile Gln Asp Ala  
 225 230 235 240  
 Tyr Leu Ser Lys Ser Leu Glu Ser Gln Asn Thr Ser Ile Ala Ser Ser  
 245 250 255  
 Gln Cys Ser Thr Pro Lys Val Ser Ser Glu Val Thr Thr Ser Leu  
 260 265 270  
 Leu Ser Arg His Ile Arg Lys Gln Thr Ala Leu Lys Thr Ala Pro Leu  
 275 280 285  
 Thr Gln Gly Arg Glu Asn Leu Glu Tyr Ser Leu Phe Arg Ile Trp Ala  
 290 295 300  
 Ser Met Gln Gln Gly Asn Asp His Ser Glu Ala Leu Thr Gln Glu Ala  
 305 310 315 320  
 Phe Tyr Arg Ala Glu Gln Lys Lys Lys Gln Val Leu Ala Gly Val Leu  
 325 330 335

Glu Val Tyr Pro His Val Val Lys Asn Asn Pro Gly Asp Tyr Leu Leu  
                           340                          345                          350  
 Lys Ala Gln Glu Asn Thr Ile Ala Phe Leu Tyr Gly Thr Ser Ile Asn  
                           355                          360                          365  
 Leu Glu Gln Trp Leu Gly Lys Arg Val Thr Val Glu Cys Leu Pro Arg  
                           370                          375                          380  
 Pro Asn Asn His Phe Ala Phe Pro Ala Tyr Tyr Val Val Gly Ile Lys  
                           385                          390                          395                          400  
 Glu Ala Ser

&lt;210&gt;123

&lt;211&gt;255

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;123

Tyr Val Pro Phe Arg Lys Phe Ser Asn Gln Asn Pro Met Leu Leu Ile  
   1                          5                          10                          15  
 Tyr Cys Lys Lys Lys Glu Ile His Leu Gln Trp Pro Gln Thr Ala Lys  
                           20                          25                          30  
 Ile Arg Phe Thr Pro Lys Ile Ala Met Lys Val Lys Ile Asn Asp Gln  
                           35                          40                          45  
 Leu Ile Cys Ile Pro Pro Phe Ile Ser Ala Arg Trp Ser Gln Ile Ala  
   50                          55                          60  
 Phe Ile Glu Ser Gln Glu Gly Glu Asn Lys Asp Gln Gly Thr Leu Arg  
   65                          70                          75                          80  
 Leu His Leu Ile Asp Gly Lys Ile Ile Ser Ile Pro Asn Leu Asp Gln  
                           85                          90                          95  
 Ser Ile Ile Asp Ile Ala Phe Gln Glu His Leu Leu Tyr Leu Glu Thr  
                           100                          105                          110  
 Ser Gln Ser Gly Lys Glu Asp Ser Arg Asp Asp Asp Lys Leu Gly Val  
                           115                          120                          125  
 Gly Val Leu Met Asn Val Leu Gln Gln Ile Thr Lys Gly Asn Asp Ile  
   130                          135                          140  
 Gln Val Leu Pro Lys Asn Leu Ile Ser Pro Leu Phe Ser Gly Thr Asn  
   145                          150                          155                          160  
 Pro Ile Glu Ala Ile Leu Gln His Thr Pro Glu His Lys Asp His Pro  
                           165                          170                          175  
 Asp Ala Pro Thr Asp Val Leu Glu Lys Met Ala Asp Val Ile Arg Val  
                           180                          185                          190  
 Leu Ser Gly Asn Asn Ala Thr Leu Leu Pro Arg Pro Glu Pro His Cys  
                           195                          200                          205  
 Asn Cys Met His Cys Gln Ile Gly Arg Val Met Asn Glu Glu Asp Thr  
                           210                          215                          220  
 Leu Ala Val Ser Asp Lys Asp Leu Thr Phe Arg Thr Trp Asp Ile Met  
   225                          230                          235                          240  
 Gln Ser Gly Asp Lys Val Val Tyr Cys Asn Glu Ser Leu Lys Ser  
                           245                          250                          255

&lt;210&gt;124

&lt;211&gt;432

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;124

Val Arg Thr Gln Met Lys Lys Thr Met Val Ile Asp Thr Ser Val Phe  
   1                          5                          10                          15  
 Ile Tyr Asp Pro Glu Ala Leu Phe Ser Phe Glu Asn Thr Arg Ile Ile  
                           20                          25                          30  
 Ile Pro Phe Pro Val Ile Glu Glu Leu Glu Ala Phe Gly Lys Phe Arg  
                           35                          40                          45  
 Asp Glu Ser Ala Lys Asn Ala Ser Arg Ala Leu Ser Asn Ile Arg Leu  
   50                          55                          60  
 Leu Leu Glu Asn Ala Lys Thr Lys Val Thr Asp Gly Val Leu Leu Pro  
   65                          70                          75                          80  
 Ser Gly Ser Glu Leu Arg Ile Glu Val Ala Pro Leu Ser Asn Asp Asp  
                           85                          90                          95

Arg Arg Gly Lys Leu Leu Thr Leu Glu Leu Leu Lys Ile Ile Ala Lys  
 100 105 110  
 Arg Glu Pro Met Val Phe Val Thr Lys Ser Leu Gly Arg Arg Val Arg  
 115 120 125  
 Ala Glu Ala Leu Gln Ile Glu Ser Arg Asp Tyr Glu Ser Lys Arg Phe  
 130 135 140  
 Ser Phe Arg Ser Leu Tyr Arg Gly Phe Arg Glu Leu Gln Val Ser Gln  
 145 150 155 160  
 Glu Asp Ile Glu Asn Phe Tyr Lys Asn Gly Tyr Leu Asp Leu Pro Leu  
 165 170 175  
 Asp Val Val Ser Ser Pro Asn Glu Tyr Phe Phe Met Ser Ala Gly Glu  
 180 185 190  
 Asn His Phe Ala Leu Gly Arg Tyr Tyr Val Ser Glu Gly Lys Ile Ile  
 195 200 205  
 Ala Leu Lys Ala Met Asp Lys Ser Val Trp Gly Ile Lys Pro Leu Asn  
 210 215 220  
 Thr Glu Gln Arg Cys Ala Leu Asp Leu Leu Leu Arg Asp Asp Val Lys  
 225 230 235 240  
 Leu Val Thr Leu Ile Gly Gln Ala Gly Ser Gly Lys Thr Ile Leu Ala  
 245 250 255  
 Leu Ala Ala Ala Met His Lys Val Phe Asp Lys Glu Thr Tyr Asn Lys  
 260 265 270  
 Val Leu Val Ser Arg Pro Ile Val Pro Met Gly Arg Asp Ile Gly Phe  
 275 280 285  
 Leu Pro Gly Leu Lys Glu Asp Lys Leu Met His Trp Met Gln Pro Ile  
 290 295 300  
 Tyr Asp Asn Met Glu Val Leu Phe Ser Ile Asn Gln Met Gly Asn Ser  
 305 310 315 320  
 Ser Glu Ala Leu Gln Ala Leu Met Asp Ala Lys Lys Leu Glu Met Glu  
 325 330 335  
 Ala Leu Thr Tyr Ile Arg Gly Arg Ser Leu Pro Lys Ala Phe Ile Ile  
 340 345 350  
 Ile Asp Glu Ala Gln Asn Leu Thr Pro His Glu Ile Lys Thr Ile Ile  
 355 360 365  
 Ser Arg Ala Gly Lys Gly Thr Lys Ile Val Leu Thr Gly Asp Pro Thr  
 370 375 380  
 Gln Ile Asp Ser Leu Tyr Phe Asp Glu Asn Ser Asn Gly Leu Thr Tyr  
 385 390 395 400  
 Leu Val Gly Lys Phe His His Leu Ala Leu Tyr Gly His Met Phe Met  
 405 410 415  
 Thr Arg Thr Glu Arg Ser Glu Leu Ala Ala Ala Ala Thr Ile Leu  
 420 425 430

&lt;210&gt;125

&lt;211&gt;184

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;125

Asn Asn Glu Ser Arg Trp Gly Gly Tyr Lys Ser Ser Ser Ile Gly Ser  
 1 5 10 15  
 Ser Gln Cys Arg Phe Leu Gly Leu Ser Gln Arg Pro Leu Asn Pro Glu  
 20 25 30  
 Arg Gln Gly Thr Pro Leu Asn Glu Gly Glu Cys Arg Ala Gly Met Trp  
 35 40 45  
 Arg Asn Ala Asp Gly Ser Asn His Thr Gly Lys Gln Gly Lys Pro His  
 50 55 60  
 Tyr Leu Ala Gln Leu Leu Gly Pro Lys Ala Val Asp His His Asn Lys  
 65 70 75 80  
 Ser Gln Ala Ala Phe Asp Arg Cys Lys Asn Ala Tyr Leu Asn Cys Phe  
 85 90 95  
 Ser Leu Ala Gln Thr Leu Gly Val Thr Phe Leu Gln Ile Pro Leu Ile  
 100 105 110  
 Ser Ser Gly Ile Tyr Ala Pro Pro Glu Asn Arg Lys Lys Pro Asn Ser  
 115 120 125  
 Glu Glu Asn Lys Val Arg Met Arg Trp Ile His Ala Val Lys Cys Ala



130 135 140  
 Leu Val Ala Ala Met Gln Glu Phe Gly Asn Glu Pro Gly Asn Thr Asp  
 145 150 155 160  
 Arg Arg Met Leu Ile Val Leu Thr Asp Leu Lys Thr Pro Ala Ile Thr  
 165 170 175  
 Asp Pro Lys Lys Lys Ser His Leu  
 180

&lt;210&gt;126

&lt;211&gt;195

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;126

Lys Asn Leu Phe His Tyr Lys Ala Ile Leu Met Ser Ile Phe Asn Glu  
 1 5 10 15  
 Glu Val Phe Ile Ile Ser His Arg His Thr Pro Leu Gly Gln Thr Ser  
 20 25 30  
 Thr Ala Leu Arg Asn Thr Pro Leu Val Asn Pro Leu His Arg Thr Asn  
 35 40 45  
 Leu Gln Arg Ile Ala Ser Tyr Ile Pro Ile Phe Ser Thr Phe Ile Gly  
 50 55 60  
 Ile Lys Thr Leu Lys Gly Ile Ser Ser Leu Gln Tyr Ser Met Val Leu  
 65 70 75 80  
 Met Thr Gly Asn Phe Ser Ser Val Cys Lys Thr Leu Pro Cys Pro Glu  
 85 90 95  
 Ile Tyr Glu Glu Leu Pro Lys Val Arg Lys Glu Ala Trp Leu Glu Ile  
 100 105 110  
 Phe Gly Ile Lys Ala Leu Tyr Tyr Leu Val Leu Gly Val Ile Lys Ile  
 115 120 125  
 Ile Lys Leu Ile Val Arg Tyr Leu Cys Pro Cys Cys Arg Pro Pro Glu  
 130 135 140  
 Pro Arg Glu Pro Gln Asn Pro Leu Thr Pro Thr Pro Leu Asp Met Gly  
 145 150 155 160  
 Gln Gln Ile Asp Ala Ile Phe Ser Thr Pro Thr Ser Pro Thr Gly Phe  
 165 170 175  
 Lys Asp Pro Phe Leu Asp Asp Leu Leu Gln Glu Asp Lys Lys Lys Ala  
 180 185 190  
 Pro His Leu  
 195

&lt;210&gt;127

&lt;211&gt;1043

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;127

Met Thr Ala Asp Glu Val Gly Lys Asn Ser Phe Ala Lys Lys Glu Glu  
 1 5 10 15  
 Gln Val Leu Lys Phe Trp Lys Asp Asn Gln Ile Phe Glu Lys Ser Leu  
 20 25 30  
 Gln Asn Arg Gln Gly Lys Thr Leu Tyr Ser Phe Tyr Asp Gly Pro Pro  
 35 40 45  
 Phe Ala Thr Gly Leu Pro His Tyr Gly His Leu Leu Ala Ser Thr Ile  
 50 55 60  
 Lys Asp Val Val Gly Arg Tyr Ala Thr Met Asp Gly Tyr Tyr Val Pro  
 65 70 75 80  
 Arg Arg Phe Gly Trp Asp Cys His Gly Val Pro Val Glu Tyr Glu Val  
 85 90 95  
 Glu Lys Ser Leu Ser Leu Thr Ala Pro Gly Pro Ile Glu Asp Phe Gly  
 100 105 110  
 Ile Ala Ser Phe Asn Glu Glu Cys Arg Lys Ile Val Phe Arg Tyr Val  
 115 120 125  
 His Glu Trp Glu Tyr Tyr Ile Asn Arg Ile Gly Arg Trp Val Asp Phe  
 130 135 140  
 Ser Ser Thr Trp Lys Thr Met Asp Ala Ser Phe Met Glu Ser Val Trp  
 145 150 155 160  
 Trp Val Phe Gln Ser Leu Tyr Asn Gln Gly Leu Val Tyr Glu Gly Thr

```

      165      170      175
Lys Val Val Pro Phe Ser Thr Ala Leu Gly Thr Pro Leu Ser Asn Phe
      180      185      190
Glu Ala Ser Gln Asn Tyr Lys Glu Val Asp Asp Pro Ser Leu Val Val
      195      200      205
Arg Met Pro Leu Gln Asn Asp Ser Ala Ser Leu Leu Val Trp Thr Thr
      210      215      220
Thr Pro Trp Thr Leu Pro Ser Asn Met Ala Ile Ala Val Gly Glu Thr
      225      230      235      240
Leu Val Tyr Val Arg Ile Gln Asp Lys Lys Ser Gly Glu Gln Trp Ile
      245      250      255
Leu Ser Gln Gly Cys Val Ser Arg Trp Phe Ser Asn Pro Glu Glu Phe
      260      265      270
Val Ile Leu Glu Ser Phe Ser Gly Lys Asp Leu Val Gly Arg Thr Tyr
      275      280      285
Glu Pro Pro Phe Thr Phe Phe Gln Ser Lys Arg Glu Glu Gly Ala Phe
      290      295      300
Arg Val Ile Ala Ala Ser Phe Val Glu Glu Ser Glu Gly Thr Gly Val
      305      310      315      320
Val His Met Ala Pro Ala Phe Gly Glu Gly Asp Phe Leu Val Cys Lys
      325      330      335
Glu Asn His Val Pro Leu Val Cys Pro Val Asp Ala His Gly Ser Phe
      340      345      350
Thr Glu Glu Ile Pro Gln Tyr Gln Gly Gln Tyr Ile Lys His Ala Asp
      355      360      365
Lys Glu Ile Ile Lys Phe Leu Lys Lys Glu Gly Arg Ile Phe Tyr His
      370      375      380
Gly Thr Val Lys His Arg Tyr Pro Phe Cys Trp Arg Thr Asp Thr Pro
      385      390      395      400
Leu Ile Tyr Lys Ala Val Asn Ser Trp Phe Val Ala Val Glu Lys Ile
      405      410      415
Lys Asp Lys Met Leu Arg Ala Asn Ser Ser Ile His Trp Val Pro Glu
      420      425      430
His Ile Gln Glu Gly Arg Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp
      435      440      445
Trp Ala Ile Ser Arg Asn Arg Tyr Trp Gly Thr Pro Ile Pro Ile Trp
      450      455      460
Lys Ser Ala Asp Gly Glu Ile Leu Val Val Gly Ser Ile Arg Glu Leu
      465      470      475      480
Glu Glu Leu Thr Gly Thr Gln Ile Thr Asp Ile His Arg His Phe Ile
      485      490      495
Asp Asp Leu Asn Ile Val Lys Asp Gly Lys Pro Phe His Arg Ile Pro
      500      505      510
Tyr Val Phe Asp Cys Trp Phe Asp Ser Gly Ala Met Pro Tyr Ala Gln
      515      520      525
Asn His Tyr Pro Phe Glu Asn Gln Lys Glu Thr Glu Glu Ala Phe Pro
      530      535      540
Ala Asp Phe Ile Ala Glu Gly Leu Asp Gln Thr Arg Gly Trp Phe Tyr
      545      550      555      560
Thr Leu Thr Val Ile Ser Ala Ile Leu Phe Asp Arg Pro Ala Phe Arg
      565      570      575
Asn Ala Ile Val Asn Gly Ile Ile Leu Ala Glu Asp Gly Asn Lys Met
      580      585      590
Ser Lys Arg Leu Asn Asn Tyr Pro Ser Pro Lys Tyr Val Leu Asp Thr
      595      600      605
Tyr Gly Ala Asp Ala Leu Arg Leu Tyr Leu Leu His Ser Val Val Val
      610      615      620
Lys Ala Glu Asp Leu Arg Phe Ser Asp Lys Gly Ile Glu Gly Val Leu
      625      630      635      640
Lys Gln Ile Leu Leu Pro Leu Thr Asn Val Leu Ser Phe Phe Asn Thr
      645      650      655
Tyr Ala Glu Leu Tyr Gly Phe Asp Pro Lys Ser Gln Asp Ile Glu Pro
      660      665      670
Ala Tyr Thr Glu Ile Asp Gln Trp Ile Leu Ser Asn Leu Tyr Ser Val

```

675 680 685  
 Val Gly Lys Val Arg Glu Ser Met Ser Gln Tyr His Leu Asn Phe Ala  
 690 695 700  
 Val Glu Pro Phe Val Thr Phe Ile Asp Asp Leu Thr Asn Trp Tyr Ile  
 705 710 715  
 Arg Arg Cys Arg Arg Phe Trp Glu Ala Glu Asp Thr Pro Asp Arg  
 725 730 735  
 Arg Ala Ala Phe Ser Thr Leu Tyr Glu Val Leu Thr Val Phe Cys Lys  
 740 745 750  
 Val Ile Ala Pro Phe Val Pro Phe Leu Ala Glu Asp Ile Tyr Gln Lys  
 755 760 765  
 Leu Lys Leu Glu Lys Glu Pro Glu Ser Val His Leu Cys Asp Phe Pro  
 770 775 780  
 Gln Val Glu Met Asp Lys Ile Leu Pro Asp Leu Glu Lys Arg Met His  
 785 790 795  
 Asp Ile Arg Glu Ile Val Gly Leu Gly His Ser Leu Arg Lys Glu His  
 805 810 815  
 Lys Leu Lys Val Arg Gln Pro Leu Ala Asn Phe Tyr Val Val Gly Ser  
 820 825 830  
 Lys Asp Arg Leu Ser Leu Leu Lys Thr Phe Glu Gly Leu Ile Ala Glu  
 835 840 845  
 Glu Leu Asn Val Lys Asn Val Ile Phe Tyr Glu Glu Ala Pro Ser Phe  
 850 855 860  
 Ile Tyr Thr Thr Val Lys Pro Asn Phe Arg Met Leu Gly Lys Lys Val  
 865 870 875  
 Gly Ser Lys Met Lys Glu Val Gln Lys Ala Leu Ser Glu Leu Pro Asn  
 885 890 895  
 Asn Ala Ile Asp Lys Leu Ile Gln Glu Glu Thr Trp Val Leu Thr Ile  
 900 905 910  
 Asp Asp Arg Glu Ile Ala Leu Asp Gly Asp Asp Val Val Ile Cys Arg  
 915 920 925  
 His Thr Asp Pro Gly Tyr Ile Ala Arg Ser Ser Ala Leu Phe Ser Val  
 930 935 940  
 Ile Leu Asp Cys Gln Leu Arg Glu Pro Leu Ile Val Glu Gly Ile Ala  
 945 950 955  
 Arg Glu Leu Val Asn Lys Ile Asn Thr Met Arg Arg Asn Gln Gln Leu  
 965 970 975  
 His Val Ser Asp Arg Ile Ala Leu Arg Ile Lys Thr Thr Glu Ala Val  
 980 985 990  
 His Arg Ala Phe Leu Asp Tyr Glu Asn Tyr Ile Cys Glu Glu Thr Leu  
 995 1000 1005  
 Ile Ile Ala Tyr Asp Phe Thr Gln Asp Ser Asp Phe Gln Gly Glu Asn  
 1010 1015 1020  
 Trp Asp Ile Asn Gly His Ala Thr Gln Ile Glu Ile Thr Val Ser Ser  
 1025 1030 1035 1040  
 Ile Asp Ser

&lt;210&gt;128

&lt;211&gt;636

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;128

Met Lys Gln His Tyr Ser Leu Asn Lys Ser Arg His Ile Leu Arg Ser  
 1 5 10 15  
 Thr Tyr Lys Leu Leu Lys Ser Lys Lys Leu Ala His Ser Pro Ala Asp  
 20 25 30  
 Lys Lys Gln Leu Gln Glu Leu Leu Glu Gln Leu Glu Glu Ala Ile Phe  
 35 40 45  
 Glu His Asp Gln Glu Thr Ala Ser Asp Leu Ala Gln Ala Leu Ala  
 50 55 60  
 Phe Ser Asn Arg Tyr Pro Asn Ser Phe Gly Arg Lys Thr Tyr Glu Leu  
 65 70 75 80  
 Ile Lys Ala Leu Leu Phe Ala Gly Val Val Ala Phe Leu Val Arg Gln  
 85 90 95

Phe	Trp	Phe	Glu	Leu	Tyr	Glu	Val	Pro	Thr	Gly	Ser	Met	Arg	Pro	Thr
			100					105					110		
Ile	Leu	Glu	Gln	Asp	Arg	Ile	Leu	Val	Ser	Lys	Thr	Thr	Phe	Gly	Leu
		115					120					125			
His	Cys	Pro	Phe	Ala	Lys	Lys	Pro	Leu	Ala	Phe	Asn	Pro	Glu	Ser	Val
	130					135					140				
Thr	Arg	Gly	Gly	Leu	Val	Val	Phe	Thr	Val	Gly	Asp	Leu	Pro	Ile	Pro
145					150					155					160
Asp	Ala	Asp	Thr	Lys	Tyr	Phe	Gly	Leu	Ile	Pro	Gly	Lys	Lys	Arg	Tyr
				165				170						175	
Ile	Lys	Arg	Cys	Met	Gly	Arg	Pro	Gly	Asp	Phe	Leu	Tyr	Phe	Tyr	Gly
			180					185					190		
Gly	Lys	Ile	Tyr	Gly	Leu	Asp	Asp	Ala	Gly	Lys	Arg	Ile	Glu	Phe	Pro
	195					200						205			
Ser	Val	His	Gly	Leu	Glu	Asn	Leu	Tyr	His	Val	Pro	Tyr	Ile	Ser	Phe
	210					215				220					
Asp	Gly	Thr	Thr	Ser	Ser	His	Thr	Glu	Gly	Gln	Lys	Thr	Ile	Ile	Asp
225					230					235					240
Phe	Lys	Gln	Phe	Asn	Gln	Ser	Tyr	Gly	Arg	Leu	Ile	Phe	Pro	Gln	Thr
				245				250						255	
Ser	Met	Tyr	Gly	Gln	Phe	Phe	Asp	His	Lys	Glu	Trp	His	Gln	Asp	Glu
			260				265						270		
Pro	Asn	Lys	Leu	Lys	Asp	Pro	His	Leu	Ser	Pro	Val	Ser	Tyr	Ala	Asp
	275					280						285			
Leu	Phe	Gly	Met	Gly	Asn	Tyr	Ala	Met	Val	Arg	Ile	Leu	Thr	Glu	His
	290				295					300					
Gln	Ala	Arg	Thr	Ser	His	Leu	Leu	Pro	Asn	Pro	Gly	Ser	Pro	Thr	Lys
305					310					315					320
Val	Tyr	Leu	Glu	Ile	Cys	His	Thr	Ala	Asn	Leu	Ser	Tyr	Pro	Lys	Pro
				325				330						335	
Leu	Leu	Arg	His	Tyr	Glu	His	Gln	Leu	Ser	Pro	Ala	Ile	Gln	Pro	Met
		340					345						350		
Lys	Thr	Leu	Leu	Pro	Leu	Arg	Lys	Glu	His	Leu	His	Leu	Ile	Arg	Asn
		355					360					365			
Asn	Leu	Thr	Thr	Ser	Arg	Phe	Ile	Val	Ala	Gln	Gly	Cys	Ala	Tyr	Lys
	370					375					380				
Tyr	His	Gln	Phe	Lys	Ile	Asn	Thr	Ser	Gly	Ile	Ala	Lys	Ala	Tyr	Ala
385					390					395					400
Ile	Leu	Leu	Pro	Lys	Val	Pro	Asp	Gly	Cys	Tyr	Glu	Tyr	Ser	Lys	Gly
				405					410					415	
Glu	Ala	Tyr	Gln	Ile	Gly	Phe	Gly	Glu	Ile	Arg	Tyr	Lys	Leu	Lys	Ser
			420				425						430		
Ser	His	Pro	Leu	Thr	Gln	Leu	Asn	Asp	Lys	Gln	Val	Ile	Glu	Leu	Phe
		435					440					445			
Asn	Cys	Gly	Ile	Asn	Phe	Ser	Ser	Ile	Tyr	Asn	Pro	Val	Asn	Pro	Leu
	450					455					460				
Gln	Ala	Pro	Leu	Pro	Asn	Arg	Tyr	Ala	Phe	Phe	Asn	Gln	Gly	Asn	Leu
465					470					475					480
Tyr	Ile	Met	Asp	Ser	Pro	Val	Phe	Ile	Lys	Asn	Asp	Pro	Thr	Leu	Gln
				485					490					495	
Lys	Phe	Val	Thr	Ser	Glu	Thr	Glu	Lys	Gln	Glu	Gly	Ser	Ser	Glu	Thr
		500						505					510		
Gln	Pro	Tyr	Ile	Ala	Phe	Val	Asp	Lys	Gly	Leu	Pro	Pro	Glu	Asp	Phe
	515						520					525			
Lys	Glu	Phe	Val	Glu	Phe	Ile	His	Asn	Phe	Gly	Ile	Gln	Val	Pro	Lys
	530					535					540				
Gly	His	Val	Leu	Val	Leu	Gly	Asp	Asn	Tyr	Pro	Met	Ser	Ala	Asp	Ser
545					550					555					560
Arg	Glu	Phe	Gly	Phe	Val	Pro	Met	Glu	Asn	Leu	Leu	Gly	Ser	Pro	Leu
				565				570						575	
Cys	Thr	Phe	Trp	Pro	Ile	Gly	Arg	Met	Gly	Arg	Leu	Thr	Gly	Val	Ser
		580					585						590		
Ala	Pro	Thr	Leu	Ser	Gly	Tyr	Leu	Val	Ser	Gly	Ile	Ala	Leu	Ala	
		595					600					605			

Thr Gly Leu Ser Leu Ile Gly Tyr Val Tyr Tyr Gln Lys Arg Arg Arg  
 610 615 620  
 Leu Phe Pro Lys Lys Glu Glu Lys Asn His Lys Lys  
 625 630 635  
 <210>129  
 <211>276  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>129  
 Gln Leu Gln Asn Arg Tyr Pro Ile Met Pro Asn Asp Ser Ser Thr Tyr  
 1 5 10 15  
 Phe Glu Arg Ile Leu Gln Lys Tyr Leu Met Lys Lys Gln Gly Lys Thr  
 20 25 30  
 Leu Phe Leu Phe Leu Phe Leu Ser Phe Leu Phe Ser Thr Ala Phe Ser  
 35 40 45  
 Gly Leu Phe Ala Ser Gln Thr Ser Ser Leu Arg Thr Ile Gln Glu Asn  
 50 55 60  
 Ile Phe Leu Ala Lys Thr Gly Asp Tyr Thr Val Leu Ser Arg Gly Ser  
 65 70 75 80  
 Gln Arg Thr Phe Val Leu Val Lys Ser Thr Thr Pro Lys Thr Val Trp  
 85 90 95  
 Ile Glu Ile Ile His Phe Pro Cys Ile Ala His Lys Glu Arg Pro Ser  
 100 105 110  
 Leu Glu Gln Ala Ser Trp Lys Thr Val Ile His Gln Leu Glu Ser Pro  
 115 120 125  
 Ser Gln Val Phe Val Val Ser Leu Ser Ser Glu Gly Ser Gln Phe Phe  
 130 135 140  
 Ser Leu Asn Thr Arg Thr Lys Ser Leu Glu Pro Val Gly Lys Ser Thr  
 145 150 155 160  
 Thr Val Pro Ala Phe Leu Gln Ile Phe Asp Leu Pro Leu Ser Pro Ala  
 165 170 175  
 Pro Ala Asn Val Ile Lys Thr Lys Gly Lys Glu Asn Lys Pro Trp Ser  
 180 185 190  
 Pro Lys Val Ser Phe Glu Gly Ala Pro Leu Thr Ser Ile Ser Val Asn  
 195 200 205  
 Ala Trp Gln Gly Leu Trp Pro Lys Asp Arg Gly Pro Leu Ser Glu Thr  
 210 215 220  
 Gly Ile Leu Met Tyr Phe Thr Gln Pro Asp Ile Ser Val Phe Pro Leu  
 225 230 235 240  
 Trp Val Ser Ile Glu Thr Pro Lys Gly Thr Ser Ile Val Arg Ala Val  
 245 250 255  
 Asp Ile Gly His Gly Ala Thr Ser Pro Tyr Val Tyr Ser Leu Pro Asp  
 260 265 270  
 Ser Lys Thr Gln  
 275  
 <210>130  
 <211>109  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>130  
 Met Lys Lys Asn Thr His Pro Glu Tyr Arg Gln Val Leu Phe Val Asp  
 1 5 10 15  
 Xaa Ser Thr Gly Tyr Lys Phe Val Cys Gly Xaa Thr Tyr Gln Ser Glu  
 20 25 30  
 Lys Thr Glu Val Phe Glu Gly Lys Glu Tyr Pro Val Cys Tyr Val Ser  
 35 40 45  
 Val Ser Ser Ser Ser His Pro Phe Phe Thr Gly Ser Lys Lys Phe Val  
 50 55 60  
 Asp Ala Glu Gly Arg Val Asp Lys Phe Leu Lys Arg Tyr Ser Asn Val  
 65 70 75 80  
 Arg Gln Pro Ala Gln Gln Pro Gln Pro Glu Glu Asp Ala Leu Pro Ala  
 85 90 95  
 Ala Lys Gly Lys Lys Lys Val Val Thr Lys Lys Lys Lys  
 100 105

&lt;210&gt;131

&lt;211&gt;359

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;131

Gly Phe Met Lys Lys Lys Val Ala Glu Tyr Leu Asn Arg Leu Ala Glu  
 1 5 10 15  
 Val Glu Ile Lys Ile Ser Asn Pro Glu Ile Phe Ser Asn Ser Lys Glu  
 20 25 30  
 Tyr Ser Ala Leu Ser Lys Glu His Ser Tyr Leu Leu Glu Leu Lys Asn  
 35 40 45  
 Ala Tyr Asp Lys Ile Leu Asn Leu Glu Lys Val Leu Ala Asp Asp Lys  
 50 55 60  
 Gln Ala Leu Ala Ile Glu Lys Asp Pro Glu Met Val Val Met Leu Glu  
 65 70 75 80  
 Glu Gly Ile Asn Glu Asn Lys Val Glu Leu Glu Lys Leu Asn Lys Ile  
 85 90 95  
 Leu Glu Ser Leu Leu Val Pro Pro Asp Pro Asp Asp Asp Leu Asn Val  
 100 105 110  
 Ile Met Glu Leu Arg Ala Gly Thr Gly Gly Glu Glu Ala Ala Leu Phe  
 115 120 125  
 Val Gly Asp Cys Val Arg Met Tyr His Leu Tyr Ala Ser Ser Lys Gly  
 130 135 140  
 Trp Lys Tyr Glu Val Leu Ser Ala Ser Glu Ser Asp Leu Lys Gly Tyr  
 145 150 155 160  
 Lys Glu Tyr Val Met Gly Ile Ser Gly Thr Gly Val Lys Arg Leu Leu  
 165 170 175  
 Gln Tyr Glu Ala Gly Thr His Arg Val Gln Arg Val Pro Glu Thr Glu  
 180 185 190  
 Thr Gln Gly Arg Val His Thr Ser Ala Ile Thr Ile Ala Val Leu Pro  
 195 200 205  
 Glu Pro Ser Glu Glu Asp Thr Glu Leu Leu Ile Asn Glu Lys Asp Leu  
 210 215 220  
 Lys Ile Asp Thr Phe Arg Ala Ser Gly Ala Gly Gly Gln His Val Asn  
 225 230 235 240  
 Val Thr Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Val Val  
 245 250 255  
 Val Thr Cys Gln Asp Glu Arg Ser Gln His Lys Asn Lys Asp Lys Ala  
 260 265 270  
 Met Arg Ile Leu Lys Ala Arg Ile Arg Asp Ala Glu Met Gln Lys Arg  
 275 280 285  
 His Asn Glu Ala Ser Ala Met Arg Ser Ala Gln Val Gly Ser Gly Asp  
 290 295 300  
 Arg Ser Glu Arg Ile Arg Thr Tyr Asn Phe Ser Gln Asn Arg Val Thr  
 305 310 315 320  
 Asp His Arg Ile Gly Leu Thr Leu Tyr Asn Leu Asp Lys Val Met Glu  
 325 330 335  
 Gly Asp Leu Asp Pro Ile Thr Thr Ala Met Val Ser His Ala Tyr His  
 340 345 350  
 Gln Leu Leu Glu His Gly Asn  
 355

&lt;210&gt;132

&lt;211&gt;296

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;132

Met Pro Thr Thr Ser Tyr Ser Asn Met Glu Ile Lys Lys Ala Ile Gln  
 1 5 10 15  
 Glu Gly Thr Ala Tyr Leu Asp Tyr Tyr Gly Val Pro Leu Ser Asp Cys  
 20 25 30  
 Glu Ala Leu Tyr Ile Leu Met Asp Leu Leu Glu Val Ser Arg Ala  
 35 40 45  
 Lys Leu Phe Asp Leu Val Gly Ile Ser Glu Thr Met Leu Met Glu Tyr  
 50 55 60

Arg Lys Arg Leu Ala Leu Arg Gly Gln Arg Cys Pro Thr Ala Tyr Leu  
 65 70 75 80  
 Asn Gly Ala Val Ser Phe Leu Gly Leu Arg Leu Arg Val Asp Ser Arg  
 85 90 95  
 Val Leu Ile Pro Arg Thr Glu Thr Glu Leu Leu Ala Glu Tyr Ile Ile  
 100 105 110  
 Asn Tyr Leu Leu Ser His Ser Glu Ile Gln Thr Phe Tyr Asp Ile Cys  
 115 120 125  
 Cys Gly Ser Gly Cys Leu Gly Leu Ala Ile Lys Lys Ser Cys Pro His  
 130 135 140  
 Val Glu Val Val Leu Ser Asp Val Cys Pro Gln Ala Val Ala Val Ala  
 145 150 155 160  
 Asn Glu Asn Ala Lys Ser Asn Gly Leu Asp Val Lys Ile Leu Leu Gly  
 165 170 175  
 Asp Leu Ser Ala Pro Tyr Thr Arg Pro Ala Asp Ala Phe Val Cys Asn  
 180 185 190  
 Pro Pro Tyr Leu Ser Phe Asn Glu Ile Ile His Ile Asp Pro Glu Val  
 195 200 205  
 Arg Cys Tyr Glu Pro Trp Lys Ala Leu Val Gly Gly Ser Thr Gly Leu  
 210 215 220  
 Glu Phe Tyr Gln Arg Ile Ala Gln Glu Leu Pro Lys Ile Val Thr Ser  
 225 230 235 240  
 Thr Gly Val Gly Trp Leu Glu Ile Gly Ser Ser Gln Gly Glu Ser Ile  
 245 250 255  
 Lys Asn Ile Phe Ser Lys His Gly Ile Tyr Gly Arg Leu His Gln Asp  
 260 265 270  
 Leu Ser Gly Arg Asp Arg Ile Phe Phe Leu Glu Met Asp Gly Arg Asp  
 275 280 285  
 Pro Val Ser Ser Gly Ala Tyr Ser  
 290 295

&lt;210&gt;133

&lt;211&gt;448

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;133

Met Ile Asn Ser Leu Ser Gln Lys Leu Ser Ser Ile Phe Ser Phe Leu  
 1 5 10 15  
 Val Ser Ser Arg Arg Ile Asn Glu Glu Asn Ile Ser Glu Ser Ile Arg  
 20 25 30  
 Glu Val Arg Leu Ala Leu Leu Asp Ala Asp Val Asn Tyr His Val Val  
 35 40 45  
 Lys Asp Phe Ile Ser Lys Val Lys Xaa Lys Ile Leu Gly Glu Glu Ile  
 50 55 60  
 Trp Lys His Val Ser Pro Gly Lys Gln Phe Ile Arg Cys Leu His Glu  
 65 70 75 80  
 Glu Leu Val Ala Phe Leu Ser Asp Gly Arg Glu Glu Phe Thr Ile Gln  
 85 90 95  
 Lys Thr Pro Ser Ile Ile Leu Leu Cys Gly Leu Gln Gly Ala Gly Lys  
 100 105 110  
 Thr Thr Thr Ala Ala Lys Leu Ala Asp Tyr Val Ile Lys Asn Lys Lys  
 115 120 125  
 Ala Lys Lys Val Leu Val Val Pro Cys Asp Leu Lys Arg Phe Ala Ala  
 130 135 140  
 Val Asp Gln Leu Lys Ile Leu Val Ala Gln Thr Lys Ala Glu Phe Tyr  
 145 150 155 160  
 Gln Ser Gln Glu Asn Lys Pro Ile Asp Val Val Val Lys Ala Leu Ala  
 165 170 175  
 Tyr Ala Lys Glu Asn Gly His Asp Phe Val Ile Leu Asp Thr Ala Gly  
 180 185 190  
 Arg Leu Asn Ile Asp Asn Glu Leu Met Glu Glu Leu Thr Ala Ile Gln  
 195 200 205  
 Lys Val Ser Gln Ala Asn Glu Arg Leu Phe Val Met Asn Val Ala Met  
 210 215 220  
 Gly Gln Asp Val Leu Ala Thr Val Gln Ala Phe Asp Gln Ser Leu Asp

225 230 235 240  
 Leu Thr Gly Val Ile Leu Ser Met Thr Asp Gly Asp Ala Arg Ala Gly  
 245 250 255  
 Ala Val Phe Ser Ile Lys His Val Leu Gly Lys Pro Ile Lys Phe Glu  
 260 265 270  
 Gly Cys Gly Glu Arg Ile Gln Asp Leu Arg Ser Phe Asp Pro Gln Ser  
 275 280 285  
 Met Ala Glu Arg Ile Leu Gly Met Gly Asp Thr Ile Asn Phe Val Lys  
 290 295 300  
 Glu Met Arg Glu Tyr Ile Ser Glu Glu Glu Asp Ala Glu Leu Gly Lys  
 305 310 315 320  
 Lys Leu Val Thr Ala Ala Phe Thr Tyr Glu Asp Tyr Tyr Lys Gln Met  
 325 330 335  
 Lys Ala Phe Arg Arg Met Gly Pro Leu Arg Lys Leu Leu Gly Met Met  
 340 345 350  
 Pro Gly Phe Asn Asn Ala Lys Pro Ser Gln Lys Glu Ile Glu Asp Ser  
 355 360 365  
 Glu Gln Gln Met Lys Arg Thr Glu Ala Ile Ile Leu Ser Met Thr Pro  
 370 375 380  
 Glu Glu Arg Lys Glu Leu Val Glu Leu Asp Met Ser Arg Met Lys Arg  
 385 390 395 400  
 Ile Ala Ser Gly Cys Gly Leu Thr Leu Gly Asp Val Asn Gln Phe Arg  
 405 410 415  
 Lys Gln Met Ser Gln Ser Lys Lys Phe Lys Gly Met Ser Lys Gly  
 420 425 430  
 Lys Met Glu Gln Val Arg Lys Lys Met Ser Gly Gly Asn Gln Trp Arg  
 435 440 445

&lt;210&gt;134

&lt;211&gt;208

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;134

Met Lys Ile Asp Ile Leu Ser Leu Ser Pro Gly Tyr Phe Asp Gly Pro  
 1 5 10 15  
 Leu Gln Thr Ser Ile Leu Gly Arg Ala Ile Lys Gln Arg Leu Leu Asp  
 20 25 30  
 Val Gln Leu Thr Asn Leu Arg Asp Phe Gly Leu Gly Lys Trp Lys Gln  
 35 40 45  
 Val Asp Asp Thr Pro Phe Ser Gly Gly Gly Met Leu Leu Met Ala Glu  
 50 55 60  
 Pro Val Thr Ser Ala Ile Arg Ser Val Arg Lys Glu Asn Ser Lys Val  
 65 70 75 80  
 Ile Tyr Leu Ser Pro Gln Gly Ala Leu Leu Thr Ala Glu Lys Ser Arg  
 85 90 95  
 Glu Leu Ala Ala Ala Ser His Leu Ile Leu Leu Cys Gly His Tyr Glu  
 100 105 110  
 Gly Ile Asp Glu Arg Ala Ile Glu Ser Glu Val Asp Glu Ile Ser  
 115 120 125  
 Ile Gly Asp Tyr Val Leu Thr Asn Gly Gly Ile Ala Ala Leu Val Leu  
 130 135 140  
 Ile Asp Ala Val Ser Arg Phe Ile Pro Gly Val Leu Gly Asn Gln Glu  
 145 150 155 160  
 Ser Ala Glu Arg Asp Ser Leu Glu Asn Gly Leu Leu Glu Gly Pro Gln  
 165 170 175  
 Tyr Thr Arg Pro Arg Glu Phe Glu Gly Lys Glu Val Pro Glu Val Leu  
 180 185 190  
 Leu Gln Gly Asp His Lys Ala Ile Ser Ser Val Glu Ile Gly Ala Lys  
 195 200 205

&lt;210&gt;135

&lt;211&gt;189

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;135

Lys Asp Leu Ser Ile His Ala Leu Glu Ser Leu Lys Gly Lys Lys Phe



1 5 10 15  
 Gln Lys Tyr Cys Cys Lys Gly Ile Thr Lys Pro Phe His Gln Trp Arg  
 20 25 30  
 Leu Glu Gln Ser Glu Arg Arg Thr Tyr Glu Arg Arg Pro Asp Leu Tyr  
 35 40 45  
 Leu Asn Tyr Leu Tyr Lys Arg Ser Ile Asp His Lys Phe Asp Glu Glu  
 50 55 60  
 Thr Thr Thr Asn Arg Asp His Phe Lys Cys Asp Lys Ile Ser Val Val  
 65 70 75 80  
 Leu Glu Val Asn Lys Leu Lys Arg Ala Lys Asn Phe Tyr Cys Lys Val  
 85 90 95  
 Phe Gly Leu Asp Ala Met Ser Cys Glu Asn Lys Phe Cys Leu Pro His  
 100 105 110  
 Glu Gly Lys Thr Ile Phe Trp Leu Arg Glu Val Gln Ala Glu Lys Lys  
 115 120 125  
 Asn Ile Val Thr Leu Ser Leu Ser Leu Asp Cys Ala Cys Glu Glu Asp  
 130 135 140  
 Phe Cys Tyr Leu Leu Arg Arg Trp Glu Leu Phe Gly Gly Lys Leu Leu  
 145 150 155 160  
 Glu Lys Gln Ala Asp Glu His Ala Val Trp Ala Leu Ala Gln Asp Leu  
 165 170 175  
 Asp Gly His Ala Trp Ile Phe Ser Trp His Arg Met Lys  
 180 185

&lt;210&gt;136

&lt;211&gt;121

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;136

Met Val Asn Leu Leu Lys Glu Leu Glu Gln Glu Gln Cys Arg Asn Asp  
 1 5 10 15  
 Leu Pro Glu Phe His Val Gly Asp Thr Ile Arg Leu Ala Thr Lys Ile  
 20 25 30  
 Ser Glu Gly Gly Lys Glu Arg Val Gln Val Phe Gln Gly Thr Val Met  
 35 40 45  
 Ala Arg Arg Gly Gly Gly Ser Gly Glu Thr Val Ser Leu His Arg Val  
 50 55 60  
 Ala Tyr Gly Glu Gly Met Glu Lys Ser Phe Leu Asn Ser Pro Arg  
 65 70 75 80  
 Ile Val Ser Ile Glu Ile Val Lys Arg Gly Lys Val Ala Arg Ala Arg  
 85 90 95  
 Leu Tyr Tyr Leu Arg Gly Lys Thr Gly Lys Ala Ala Lys Val Lys Glu  
 100 105 110  
 Phe Val Gly Pro Arg Ser Ser Lys Lys  
 115 120

&lt;210&gt;137

&lt;211&gt;214

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;137

Met Asn Thr Ser Ile Ser Glu Ile Gln Arg Phe Leu Ser Met Ile Ala  
 1 5 10 15  
 Phe Glu Lys Glu Leu Val Ser Glu Asp Phe Ser Val Val Ala Gly Ile  
 20 25 30  
 Asp Glu Ala Gly Arg Gly Pro Leu Ala Gly Pro Val Val Ala Ser Ala  
 35 40 45  
 Cys Ile Leu Pro Lys Gly Lys Val Phe Pro Gly Val Asn Asp Ser Lys  
 50 55 60  
 Lys Leu Ser Pro Lys Gln Arg Ala Gln Val Arg Asp Ala Leu Met Gln  
 65 70 75 80  
 Asp Pro Glu Val Cys Phe Gly Ile Gly Val Ile Ser Val Glu Arg Ile  
 85 90 95  
 Asp Gln Val Asn Ile Leu Glu Ala Thr Lys Glu Ala Met Leu Gln Ala  
 100 105 110  
 Ile Ser Ser Leu Pro Ile Ser Pro Asp Ile Leu Leu Val Asp Gly Leu

115 120 125  
 Tyr Leu Pro His Asp Ile Pro Cys Lys Lys Ile Ile Gln Gly Asp Ala  
 130 135 140  
 Lys Ser Ala Ser Ile Ala Ala Ser Ile Leu Ala Lys Glu His Arg  
 145 150 155 160  
 Asp Asp Leu Met Leu Gln Leu His Arg Leu Tyr Pro Glu Tyr Gly Phe  
 165 170 175  
 Asp Arg His Lys Gly Tyr Gly Thr Ser Leu His Val Glu Ala Ile Arg  
 180 185 190  
 Arg Tyr Gly Pro Ser Pro Cys His Arg Lys Ser Phe Ser Pro Ile Lys  
 195 200 205  
 Gln Met Cys Ala Ile Val  
 210

&lt;210&gt;138

&lt;211&gt;209

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;138

Val Cys Tyr Cys Met Asn Lys Ile Leu Val Asp Ser Pro Phe Ser Pro  
 1 5 10 15  
 Asp His Gln Lys Cys Cys Pro Lys Leu Phe Thr Ile Ser Ala Pro Ala  
 20 25 30  
 Gly Val Gly Lys Thr Thr Leu Val Arg Met Leu Glu Gln Glu Phe Ser  
 35 40 45  
 Ser Ala Phe Ala Glu Thr Ile Ser Val Thr Thr Arg Lys Pro Arg Glu  
 50 55 60  
 Gly Glu Val Pro Gly Lys Asp Tyr His Phe Val Ser His Glu Glu Phe  
 65 70 75 80  
 Gln Arg Leu Leu Asp Arg Gln Ala Leu Leu Glu Trp Val Phe Leu Phe  
 85 90 95  
 Gly Glu Cys Tyr Gly Thr Ser Met Leu Glu Ile Glu Arg Ile Trp Ser  
 100 105 110  
 Leu Gly Lys His Ala Val Ala Val Ile Asp Ile Gln Gly Ala Leu Phe  
 115 120 125  
 Ile Arg Ser Arg Met Pro Ser Val Ser Ile Phe Ile Ala Pro Pro Ser  
 130 135 140  
 Gln Glu Glu Leu Glu Arg Arg Leu Ala Ser Arg Gly Ser Glu Glu Gly  
 145 150 155 160  
 Ser Gln Arg Lys Glu Arg Leu Glu His Ser Leu Ile Glu Leu Ala Ala  
 165 170 175  
 Ala Asn Gln Phe Asp Tyr Val Ile Ile Asn Asp Asp Leu Asn Gln Ala  
 180 185 190  
 Tyr Arg Val Leu Lys Ser Ile Phe Ile Ala Glu Glu His Arg Asn Ile  
 195 200 205  
 Leu

&lt;210&gt;139

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;139

Glu His Ile Met Ile Lys Lys Asp Arg Phe Thr Asn Glu Lys Leu Asn  
 1 5 10 15  
 Lys Leu Phe Asp Ser Pro Phe Ser Leu Val Asn Tyr Ala Ile Lys Gln  
 20 25 30  
 Ala Lys Ile Lys Ile Ala Lys Gly Asp Val Arg Ser Ser Asn Val Ala  
 35 40 45  
 Ile Glu Thr Leu Val Leu Leu Asp Arg Glu Gly Ile Gln Pro Glu Phe  
 50 55 60  
 Thr Glu Glu Ile Val Val Thr Ala Ser Pro Thr Val Glu Arg Lys Arg  
 65 70 75 80  
 Ser Glu His Thr Asn Ser Arg Lys Lys Asp Pro Ser Ala Tyr Thr Trp  
 85 90 95  
 Ser Asp Val Lys

100

&lt;210&gt;140

&lt;211&gt;554

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;140

Cys Lys Val Met Pro Gln Lys Val Leu Ile Thr Ser Ala Leu Pro Tyr  
 1 5 10 15  
 Ala Asn Gly Pro Leu His Phe Gly His Ile Ala Gly Val Tyr Leu Pro  
 20 25 30  
 Ala Asp Val Tyr Ala Arg Phe Arg Arg Leu Leu Gly Asp Asp Val Leu  
 35 40 45  
 Tyr Ile Cys Gly Ser Asp Glu Phe Gly Ile Ala Ile Thr Leu Asn Ala  
 50 55 60  
 Asp Arg Glu Gly Leu Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys  
 65 70 75 80  
 Leu His Lys Asp Thr Phe Glu Lys Leu Gly Phe Ala Leu Asp Phe Phe  
 85 90 95  
 Ser Arg Thr Thr Asn Pro Phe His Ala Glu Leu Val Gln Asp Phe Tyr  
 100 105 110  
 Ser Gln Leu Lys Ala Ser Gly Leu Ile Glu Asn Arg Ile Ser Glu Gln  
 115 120 125  
 Leu Tyr Ser Glu Gln Glu Gln Arg Phe Leu Ala Asp Arg Tyr Val Glu  
 130 135 140  
 Gly Thr Cys Pro Arg Cys Gly Phe Asp His Ala Arg Gly Asp Glu Cys  
 145 150 155 160  
 Gln Ser Cys Gly Ala Asp Tyr Glu Ala Ile Asp Leu Ile Asp Pro Lys  
 165 170 175  
 Ser Lys Ile Ser Gly Val Glu Leu Val Lys Lys Glu Thr Glu His Ser  
 180 185 190  
 Tyr Phe Leu Leu Asp Arg Met Lys Asp Ala Leu Leu Ser Phe Ile Gln  
 195 200 205  
 Gly Cys Tyr Leu Pro Asp His Val Arg Lys Phe Val Val Asp Tyr Ile  
 210 215 220  
 Glu His Val Arg Ser Arg Ala Ile Thr Arg Asp Leu Ser Trp Gly Ile  
 225 230 235 240  
 Pro Val Pro Asp Phe Pro Gly Lys Val Phe Tyr Val Trp Phe Asp Ala  
 245 250 255  
 Pro Ile Gly Tyr Ile Ser Gly Thr Met Glu Trp Ala Ala Ser Gln Gly  
 260 265 270  
 Asn Pro Asp Glu Trp Lys Arg Phe Trp Leu Glu Asp Gly Val Glu Tyr  
 275 280 285  
 Val Gln Phe Ile Gly Lys Asp Asn Leu Pro Phe His Ser Val Val Phe  
 290 295 300  
 Pro Ala Met Glu Leu Gly Gln Lys Leu Asp Tyr Lys Lys Val Asp Ala  
 305 310 315 320  
 Leu Val Val Ser Glu Phe Tyr Leu Leu Glu Gly Arg Gln Phe Ser Lys  
 325 330 335  
 Ser Glu Gly Asn Tyr Val Asp Met Asp Lys Phe Leu Ser Ser Tyr Ser  
 340 345 350  
 Leu Asp Lys Leu Arg Tyr Val Leu Ala Ala Thr Ala Pro Glu Thr Ser  
 355 360 365  
 Asp Ser Glu Phe Thr Phe Leu Asp Phe Lys Thr Arg Cys Asn Ser Glu  
 370 375 380  
 Leu Val Gly Lys Phe Gly Asn Phe Ile Asn Arg Val Leu Ala Phe Ala  
 385 390 395 400  
 Glu Lys Asn His Tyr Asp Lys Leu Ser Tyr His Ser Val Val Leu Glu  
 405 410 415  
 Asp Ser Asp Arg Ala Phe Leu Glu Glu Val Arg Gln Leu Val Arg Asp  
 420 425 430  
 Ala Glu Lys Cys Tyr Arg Glu Tyr Ser Leu Arg Lys Ala Thr Ser Val  
 435 440 445  
 Ile Met Ser Leu Ala Ala Leu Gly Asn Val Tyr Phe Asn Gln Gln Ala  
 450 455 460

Pro Trp Lys Leu Leu Lys Glu Gly Thr Arg Glu Arg Val Glu Ala Ile  
 465 470 475 480  
 Leu Phe Cys Ala Cys Tyr Cys Gln Lys Leu Leu Ala Leu Ile Ser Tyr  
 485 490 495  
 Pro Ile Ile Pro Glu Ser Ala Val Ala Ile Trp Glu Met Ile Ser Pro  
 500 505 510  
 Lys Ser Leu Glu Asn Cys Asn Leu Asp Thr Met Tyr Ala Arg Asp Leu  
 515 520 525  
 Trp Lys Glu Glu Ile Leu Asp Val Ile Asn Glu Glu Phe His Leu Lys  
 530 535 540  
 Ser Pro Arg Leu Leu Phe Thr Thr Val Glu  
 545 550  
 <210>141  
 <211>408  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>141  
 Ser Gln Ala His Phe Ile Phe Phe Glu Glu Asn Pro Phe Tyr Arg Arg  
 1 5 10 15  
 Arg Lys Ser Asn Cys Leu Gly Arg Gly Lys Leu Ser Ile Asp Leu Ala  
 20 25 30  
 Glu Gln Gln Arg Glu Ala Ile Lys Ala Cys Phe Ser Glu Lys Leu Leu  
 35 40 45  
 Ile Ile Thr Gly Gly Pro Gly Thr Gly Lys Ser Thr Ile Thr Gln Ala  
 50 55 60  
 Ile Leu Lys Ile Phe Glu Gln Val Thr His Lys Ile Ile Leu Ala Ala  
 65 70 75 80  
 Pro Thr Gly Lys Ala Ala Lys Arg Met Thr Glu Ile Thr Gln Lys His  
 85 90 95  
 Ser Val Thr Ile His Ala Leu Leu Gln Tyr Asp Phe Lys Thr Lys Ser  
 100 105 110  
 Phe Arg Lys Asn His Asp Asn Pro Ile Asp Cys Asp Leu Ile Ile Val  
 115 120 125  
 Asp Glu Ser Gly Met Met Asp Thr His Leu Leu His His Phe Leu Lys  
 130 135 140  
 Ala Leu Pro Asp Tyr Thr Thr Leu Val Phe Ile Gly Asp Ile His Gln  
 145 150 155 160  
 Leu Pro Ser Val Gly Pro Gly Asn Ile Leu Lys Asp Leu Ile Thr Ser  
 165 170 175  
 Asn Lys Met Thr Val Ile Arg Leu Asn Lys Ile Phe Arg Gln Val His  
 180 185 190  
 Asp Ser Gly Ile Val Thr Asn Ala His Arg Val Asn Glu Gly Glu Leu  
 195 200 205  
 Pro Ile Leu Tyr Ser Glu Thr Gly Arg Arg Asp Phe Leu Phe Phe Gln  
 210 215 220  
 Lys Asp Asp Gln Glu Glu Ala Leu Asn His Ile Ile His Leu Val Thr  
 225 230 235 240  
 Lys Phe Val Pro Gln Lys Tyr His Ile Tyr Pro Gln Asp Ile Gln Val  
 245 250 255  
 Leu Ala Pro Met Lys Lys Gly Thr Leu Gly Ile Tyr Asn Leu Asn Lys  
 260 265 270  
 Ala Leu Lys His Ala Leu Asn Pro Lys Lys Ala Asn Leu His Gly Arg  
 275 280 285  
 Phe Gln Ser Tyr Ala Val Gly Asp Lys Val Met Gln Ile Arg Asn Asn  
 290 295 300  
 Tyr Asn Lys Glu Val Phe Asn Gly Asp Ile Gly Tyr Val Ser Thr Ile  
 305 310 315 320  
 Asn Phe Glu Asp Lys Ala Val Val Val Arg Met Glu Gly Lys His Val  
 325 330 335  
 Gly Tyr Ser Phe Ser Glu Leu Asp Asp Leu Val Leu Ala Tyr Ala Thr  
 340 345 350  
 Ser Val His Lys Tyr Gln Gly Ser Glu Ser Pro Cys Ile Ile Ile Pro  
 355 360 365  
 Ile His Thr Ser His Phe Met Met Leu Tyr Arg Asn Leu Leu Tyr Thr

370 375 380  
 Ala Ile Thr Arg Gly Lys Lys Leu Val Ile Leu Val Gly Thr Lys Lys  
 385 390 395 400  
 Ala Ile Cys Tyr Cys Asn Lys Lys  
 405  
 <210>142  
 <211>313  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>142  
 Asn Ser Met Glu Lys Ile Cys Gly Tyr Leu Glu Gln Ile Leu Val Glu  
 1 5 10 15  
 Asn Lys Asp Ser Gly Asp Ile Thr Ala Tyr Ile Lys Ile Pro Asn Lys  
 20 25 30  
 Thr Thr Pro Ile Leu Ile Lys Gly Lys Leu Pro Gln Pro Leu Glu Leu  
 35 40 45  
 Gly Ser Pro Ile Gln Ile Tyr Gly Val Trp Ser His Ser Pro Ser Asn  
 50 55 60  
 Thr Lys Tyr Phe Gln Ile His Ser Tyr Asp Ser Pro Leu Leu Tyr Glu  
 65 70 75 80  
 Tyr Arg Gly Val Phe His Tyr Leu Thr Ser Lys Leu Ile Lys Gly Ile  
 85 90 95  
 Gly Pro Lys Ile Ala Glu Lys Ile Ile Glu Lys Phe Gln Glu Lys Thr  
 100 105 110  
 Cys Tyr Val Leu Asp Ile Thr Pro Glu Arg Leu Ser Glu Val Ser Gly  
 115 120 125  
 Ile Ser Glu Thr Arg Cys Val Ser Ile Cys Lys Gln Leu Cys Glu Gln  
 130 135 140  
 Lys Met Leu Arg Lys Thr Leu Leu Phe Leu Gln Glu Tyr Asn Ile Pro  
 145 150 155 160  
 Ile His Tyr Gly Val Arg Ile Phe Lys Lys Tyr Gln Glu Lys Ser Ile  
 165 170 175  
 Glu Lys Ile Cys Glu Asp Pro Phe Leu Leu Ala Arg Glu Met Glu Gly  
 180 185 190  
 Ile Gly Phe Lys Thr Ala Asp Phe Ile Ala Met Lys Leu Gly Val Pro  
 195 200 205  
 Arg Asn Ser Glu Ser Arg Leu Cys Ala Gly Ile Gln His Ser Leu Glu  
 210 215 220  
 Glu Leu Gln Glu Glu Gly His Thr Cys Tyr Pro Ile Glu Leu Leu Ile  
 225 230 235 240  
 Asp Val Val Ala Lys Leu Leu Asn Gln Asp Val Phe Asp Thr Pro Ile  
 245 250 255  
 Thr Leu Glu Glu Ile Asp Thr Gln Ile Leu Asn Met Gln Lys Arg Asn  
 260 265 270  
 Phe Tyr Ile Phe Lys Thr Phe Leu Gly His Ser Met Ser Gly His Val  
 275 280 285  
 Ile Ser Ile Ser Gln Arg Lys Leu Leu Phe Leu Ile Ser Ser Ala Phe  
 290 295 300  
 Tyr Phe Leu Arg Gly Glu Ser Val Leu  
 305 310  
 <210>143  
 <211>498  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>143  
 Ile Arg Ser Lys Gln Arg Thr Val Ala Ile Thr Leu Leu Val Leu Gly  
 1 5 10 15  
 Ile Leu Leu Ile Ala Ser Gly Ile Ile Phe Leu Ala Val Ala Ile Pro  
 20 25 30  
 Gly Leu Ser Ser Ala Val Ala Leu Gly Leu Gly Cys Gly Met Thr Ala  
 35 40 45  
 Leu Gly Thr Val Leu Leu Ile Thr Gly Leu Val Leu Leu Ile Arg Ser  
 50 55 60  
 Glu Lys Leu Ala Leu Glu Gln Val Glu Ile Lys Gln Ala Arg Thr Arg

65	70	75	80
Val Asn Asn Glu Leu Asp Gln Leu Ser Gln Tyr Val Phe Tyr Thr Glu			
	85	90	95
Asn Val Leu Asp Asn Leu Lys Arg Trp Ser Tyr Arg Asp Leu Gly Phe			
	100	105	110
Val Arg Gln Ala Gln Glu Glu Val Thr Asn Leu Glu Gln Asp Ile Glu			
	115	120	125
Glu Ile Phe Leu Thr Leu Arg Asp Ile Arg Asn Ala Leu Asp Asn Glu			
	130	135	140
Glu Phe Phe Met Thr His Ala Lys Gln Cys Leu Ala Gln Val Gly Glu			
	145	150	155
Ser Leu Phe Gln Asp Ala Ser Ile Asp Glu Phe Ile Asn Leu Ala His			
	165	170	175
Leu Ser Glu Ile Arg Gln His Leu Asp Ile Asn Asp Pro Arg Trp Ser			
	180	185	190
Met Ile Thr Lys Lys Val Lys Gly Thr Val Val Arg Phe Ile Tyr Val			
	195	200	205
Ser Thr Met Tyr Lys Gln Ile Lys Ser Asn Phe Glu Lys Ser Asp Phe			
	210	215	220
Gly Gln Leu Arg Lys Met Leu Leu Asn Asn Tyr Lys Thr Ile Glu Glu			
	225	230	235
Val Leu Tyr Gln Ser Phe Gln Arg Gly Tyr Asn Arg Ala Ala Leu Leu			
	245	250	255
Ser Glu Lys Thr Arg Ile Ile His Thr Ser Ser Leu Leu His Trp Glu			
	260	265	270
Lys Asp Glu Asp Lys His Leu Asn Ile Lys Asn Glu Cys Ala Ser Arg			
	275	280	285
Leu Glu Asn Phe Lys Lys Phe Arg Thr Leu Phe Leu Gly Leu Ser Glu			
	290	295	300
Glu Asp Val Ile Asp Phe Thr Gly Ala Ser Gly Trp Asp Cys Ser Lys			
	305	310	315
Leu Pro Arg Lys Glu Val Pro Leu Asp Gly Gly Lys Lys Lys Leu Arg			
	325	330	335
Phe Lys Arg Thr Phe Ala Asp Glu Gln Val Gly Asp Trp Asp Arg Thr			
	340	345	350
Thr Ser Leu Glu His Met Thr Pro Gln Glu Glu Asp Pro Leu Asp Arg			
	355	360	365
Leu Met Asp Gln Val Glu Gln Glu Ala Thr Ser Val Leu Lys Asp Gln			
	370	375	380
Asp Arg Tyr Trp Lys Glu Ile Glu Thr Ser Glu Ala Lys Phe Arg Ser			
	385	390	395
Leu Pro Arg Glu Asp Asp Phe Glu Lys Gln Ser Gln Ile Asp Ser Tyr			
	405	410	415
Ile Arg Asp Leu Asp Asp His Leu Ser Val Trp Ala Asn Gln Leu Ser			
	420	425	430
Ala Ala Glu Asp Ala Leu Ile Glu Val Thr Asp Val Gln Glu His Gly			
	435	440	445
Asn Arg Glu Met Leu Lys Asn Ile Gln Gln Gly Leu Glu Leu Ile Glu			
	450	455	460
Asp Ala Val Lys Ala Thr Leu Pro Arg Val Asp Phe Ile Gln Glu Leu			
	465	470	475
Leu Glu Lys Glu Glu Leu Pro Leu Val Ala Ala Arg Met Ser Leu Glu			
	485	490	495

Asn Ser

&lt;210&gt;144

&lt;211&gt;538

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;144

Pro Phe Phe Ser Lys Pro Pro Glu Glu Ile Ser Gln Leu Glu Ser Tyr			
1	5	10	15
Ile Arg Ser Ala Ala Asn Asp Leu Asn Thr Ile Lys Thr Trp Pro His			
20	25	30	

Lys Asp Gln Arg Leu Val Glu Thr Val Ser Arg Lys Leu Glu Arg Leu  
 35 40 45  
 Ala Ala Ala Gln Asn Tyr Met Ile Ser Glu Leu Cys Glu Ile Ser Glu  
 50 55 60  
 Ile Leu Glu Glu Glu Glu His His Leu Ile Leu Ala Gln Glu Ser Leu  
 65 70 75 80  
 Glu Trp Ile Gly Lys Ser Leu Phe Ser Thr Phe Leu Asp Met Glu Ser  
 85 90 95  
 Phe Leu Asn Leu Ser His Leu Ser Glu Val Arg Pro Tyr Leu Ala Val  
 100 105 110  
 Asn Asp Pro Arg Leu Leu Glu Ile Thr Glu Glu Ser Trp Glu Val Val  
 115 120 125  
 Ser His Phe Ile Asn Val Thr Ser Ala Phe Lys Lys Ala Gln Ile Leu  
 130 135 140  
 Phe Lys Asn Asn Glu His Ser Arg Met Lys Lys Lys Leu Glu Ser Val  
 145 150 155 160  
 Gln Glu Leu Leu Glu Thr Phe Ile Tyr Lys Ser Leu Lys Arg Ser Tyr  
 165 170 175  
 Arg Glu Leu Gly Cys Leu Ser Glu Lys Met Arg Ile Ile His Asp Asn  
 180 185 190  
 Pro Leu Phe Pro Trp Val Gln Asp Gln Gln Lys Tyr Ala His Ala Lys  
 195 200 205  
 Asn Glu Phe Gly Glu Ile Ala Arg Cys Leu Glu Glu Phe Glu Lys Thr  
 210 215 220  
 Phe Phe Trp Leu Asp Glu Glu Cys Ala Ile Ser Tyr Met Asp Cys Trp  
 225 230 235 240  
 Asp Phe Leu Asn Glu Ser Ile Gln Asn Lys Lys Ser Arg Val Asp Arg  
 245 250 255  
 Asp Tyr Ile Ser Thr Lys Lys Ile Ala Leu Lys Asp Arg Ala Arg Thr  
 260 265 270  
 Tyr Ala Lys Val Leu Leu Glu Glu Asn Pro Thr Thr Glu Gly Lys Ile  
 275 280 285  
 Asp Leu Gln Asp Ala Gln Arg Ala Phe Glu Arg Gln Ser Gln Glu Phe  
 290 295 300  
 Tyr Thr Leu Glu His Thr Glu Thr Lys Val Arg Leu Glu Ala Leu Gln  
 305 310 315 320  
 Gln Cys Phe Ser Asp Leu Arg Glu Ala Thr Asn Val Arg Gln Val Arg  
 325 330 335  
 Phe Thr Asn Ser Glu Asn Ala Asn Asp Leu Lys Glu Ser Phe Glu Lys  
 340 345 350  
 Ile Asp Lys Glu Arg Val Arg Tyr Gln Lys Glu Gln Arg Leu Tyr Trp  
 355 360 365  
 Glu Thr Ile Asp Arg Asn Glu Gln Glu Leu Arg Glu Glu Ile Gly Glu  
 370 375 380  
 Ser Leu Arg Leu Gln Asn Arg Arg Lys Gly Tyr Arg Ala Gly Tyr Asp  
 385 390 395 400  
 Ala Gly Arg Leu Lys Gly Leu Leu Arg Gln Trp Lys Lys Asn Leu Arg  
 405 410 415  
 Asp Val Glu Ala His Leu Glu Asp Ala Thr Met Asp Phe Glu His Glu  
 420 425 430  
 Val Ser Lys Ser Glu Leu Cys Ser Val Arg Ala Arg Leu Glu Val Leu  
 435 440 445  
 Glu Glu Glu Leu Met Asp Met Ser Pro Lys Val Ala Asp Ile Glu Glu  
 450 455 460  
 Leu Leu Ser Tyr Glu Glu Arg Cys Ile Leu Pro Ile Arg Glu Asn Leu  
 465 470 475 480  
 Glu Arg Ala Tyr Leu Gln Tyr Asn Lys Cys Ser Glu Ile Leu Ser Lys  
 485 490 495  
 Ala Lys Phe Leu Leu Ser Gly Arg Arg Ala Ile Ala Ser Phe Gly Ser  
 500 505 510  
 Glu Ser Lys Arg Gly Gly Cys Pro Val Lys Thr Ser Thr Gly Lys Met  
 515 520 525  
 Ser Arg Glu Gly Pro Lys Val Arg Asn Ile  
 530 535

&lt;210&gt;145

&lt;211&gt;201

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;145

```

Lys Gly His Thr Ser Asn Ile Ile Ser Val Leu Lys Phe Tyr Pro Arg
 1           5           10           15
Gln Ser Phe Phe Phe Pro Glu Asp Glu Gln Leu Leu Val Ser Glu Ala
          20           25           30
Asn Leu Arg Glu Val Gly Ala Gln Leu Lys Gln Val Gln Gly Lys Cys
          35           40           45
Gln Glu Arg Ala Gln Lys Phe Ala Ile Phe Glu Lys His Ile Gln Glu
          50           55           60
Gln Lys Ser Leu Ile Lys Glu Gln Val Arg Ser Phe Asp Leu Ala Gly
          65           70           75           80
Val Gly Phe Leu Lys Ser Glu Leu Leu Ser Ile Ala Cys Asn Leu Tyr
          85           90           95
Ile Lys Ala Val Val Lys Glu Ser Ile Pro Val Asp Val Pro Cys Met
          100          105          110
Gln Leu Tyr Tyr Ser Tyr Tyr Glu Asp Asn Glu Ala Val Val Arg Asn
          115          120          125
Arg Leu Leu Asn Met Thr Glu Arg Tyr Gln Asn Phe Lys Arg Ser Leu
          130          135          140
Asn Ser Ile Gln Phe Asn Gly Asp Val Leu Leu Arg Asp Pro Val Tyr
          145          150          155          160
Gln Pro Glu Gly His Glu Thr Arg Leu Lys Glu Arg Glu Leu Gln Glu
          165          170          175
Thr Thr Leu Ser Cys Lys Lys Leu Lys Val Ala Gln Asp Arg Leu Ser
          180          185          190
Glu Leu Glu Ser Arg Leu Ser Arg Arg
          195          200

```

&lt;210&gt;146

&lt;211&gt;259

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;146

```

Met Leu Arg Asn Gln Val Leu Val Tyr Cys Ser Glu Gly Val Ser Pro
 1           5           10           15
Tyr Tyr Leu Arg His Thr Ile Arg Phe Leu Lys Tyr Tyr Ser Thr Gln
          20           25           30
Glu Gly Ala Phe Asp Ile Leu Arg Val Xaa Gly Asn Phe Leu Ile Lys
          35           40           45
Asn Pro Phe Trp Glu Glu Thr Thr Arg Leu Leu Val Phe Pro Gly Gly
          50           55           60
Ala Asp Arg Pro Tyr His Arg Val Leu His Gly Leu Gly Thr Ala Arg
          65           70           75           80
Ile Phe Gln Tyr Val Ser Glu Gly Gly Asn Phe Leu Gly Ile Cys Ala
          85           90           95
Gly Ala Tyr Phe Gly Ser Lys Met Ile Tyr Phe Tyr Glu Pro Glu Gly
          100          105          110
Ala Pro Leu Gln Gly Ala Arg Asp Leu Gly Phe Phe Pro Gly Thr Ala
          115          120          125
Lys Gly Pro Ala Tyr Arg Gly Asn Phe Ser Tyr Val Ser Pro Ser Gly
          130          135          140
Val Arg Val Ser Pro Gln Leu Phe Ser Asp Phe Gly Leu Gly Tyr Ala
          145          150          155          160
Met Phe Asn Gly Gly Cys Phe Phe Glu Gly Ser Glu Gly Tyr Pro Gly
          165          170          175
Val Asn Ile Glu Ser Arg Tyr Asp Asp Leu Pro Gly Lys Pro Ala Ser
          180          185          190
Ile Val Ser Arg Ile Val Ser Lys Gly Leu Ala Val Leu Ser Gly Pro
          195          200          205
His Ile Glu Tyr Leu Pro His Tyr Cys Arg Met Val Lys Glu Asn Val
          210          215          220

```



Gln Lys Thr Arg Glu Phe Leu Gln Arg Glu Arg Thr Thr Leu Asp Arg  
 225 230 235 240  
 Tyr Cys Gln Asn Leu Val Gln Arg Leu Arg Gln Pro Ala Phe Ser Lys  
 245 250 255  
 Ala Asp Cys

&lt;210&gt;147

&lt;211&gt;396

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;147

Ser Ser Met Val Lys Cys Ser Ser Ile Ile His Glu Asn Lys Lys Pro  
 1 5 10 15  
 Ala Gln Leu Leu Pro Glu Ser Lys Phe Ala Ala Ile Thr Lys Leu Ser  
 20 25 30  
 Leu Ala Ile Leu Ser Leu Phe Leu Gly Ile Ala Ala Cys Ile Leu Ile  
 35 40 45  
 Ala Leu Ser Gly Leu Leu Pro Asn Thr Leu Leu Ile Ile Ala Leu Ser  
 50 55 60  
 Leu Ile Ser Ile Ile Val Leu Ser Thr Gly Ile Ser Leu Leu Ile Gly  
 65 70 75 80  
 Thr Gln Cys Ser Lys Ser Val Gln Lys Asp Glu Gln Lys Pro Lys Ser  
 85 90 95  
 Ile Phe Pro Lys Glu Thr Pro Ser Leu Asp Pro Trp Leu Leu Asn Pro  
 100 105 110  
 Leu Lys Asn Lys Ile Gln Ser Ser Glu Thr Leu Leu Leu Asp Pro Thr  
 115 120 125  
 Ser Ile Asn Leu Lys Asn Glu Leu Phe Phe Pro Ser Phe Glu Glu Trp  
 130 135 140  
 Lys Lys Ile Phe Leu Lys Asp Pro Asp Phe Leu Ile Lys Ser Ala Leu  
 145 150 155 160  
 Ala Asn Trp Lys Ile Leu Glu Gln Asp Glu Gln Tyr Ile Leu Ser His  
 165 170 175  
 Ile His Met Asp Pro Arg Ile Phe Val Thr Ser Glu Pro Leu Gln Lys  
 180 185 190  
 Thr Tyr Gln Lys Leu Gln Glu Lys His Val Asn Asn Leu Gly Ile Ala  
 195 200 205  
 Ser Gln Val Ser Leu Thr Asp Leu Gln Asn Lys Thr Gln Tyr Glu Asn  
 210 215 220  
 Asn Leu Ile Glu Thr Thr Thr Asn Glu Ile Thr Tyr Tyr Phe Pro Val  
 225 230 235 240  
 Val His Asn Pro Asp Ile Leu Arg Ser Glu Trp Asp Pro Ile Ser Asn  
 245 250 255  
 Gln Leu Tyr Leu Ile Phe Lys Lys Phe Phe Ile His Tyr His Asn Leu  
 260 265 270  
 Phe Ser Thr Ala Leu Glu Arg Asn Gln Ile Leu Leu Ile Asp Ser Leu  
 275 280 285  
 Asn Thr Gly Ser Ser Asn Pro Ile Ala Arg Gln Met Glu Leu Leu Ala  
 290 295 300  
 Phe Leu Cys Val Phe Glu Gln Leu Asp Tyr Asn Glu Asp Glu Tyr Thr  
 305 310 315 320  
 Ile Glu Pro Arg Asp Tyr Phe Asn Arg Phe Val Tyr Xaa Xaa Ser Xaa  
 325 330 335  
 Thr Ala Pro Gln Ile Gln Ser Phe Gly Leu Leu His Gly Tyr Glu Glu  
 340 345 350  
 Met Ser Tyr Ala Ser Asn Asn Ile Arg Asn Val Leu Thr His Ser Ile  
 355 360 365  
 Val Leu Cys Ser Pro Ile Leu Tyr Gln Leu Ile Thr Glu Phe Asp Thr  
 370 375 380  
 Thr Lys Ile His Ala Asp Phe Asp Cys Leu Ile  
 385 390 395

&lt;210&gt;148

&lt;211&gt;266

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;148

Phe Ser Ser Leu Lys Lys Glu Arg Phe Ser Leu Ser Leu Ala Ile Phe  
 1 5 10 15  
 Leu Ile Phe Phe Phe Thr Ser Ala Tyr Val Phe Pro Ser Ile Cys Phe  
 20 25 30  
 Leu Glu Leu Phe Met Glu Asn Ala Met Ser Ser Ser Phe Val Tyr Asn  
 35 40 45  
 Gly Pro Ser Trp Ile Leu Lys Thr Ser Val Ala Gln Glu Val Phe Lys  
 50 55 60  
 Lys His Gly Lys Gly Ile Gln Val Leu Leu Ser Thr Ser Val Met Leu  
 65 70 75 80  
 Phe Ile Gly Leu Gly Val Cys Ala Phe Ile Xaa Pro Gln Xaa Leu Ile  
 85 90 95  
 Val Phe Val Leu Thr Ile Asp Leu Leu Met Leu Ala Ile Ser Leu Val  
 100 105 110  
 Leu Phe Leu Leu Lys Val Leu Tyr Ala Pro Ser Met Val Asp Arg Leu  
 115 120 125  
 Trp Cys Ser Glu Lys Gly Tyr Ala Leu His Gln His Glu Asn Gly Pro  
 130 135 140  
 Phe Leu Asp Val Lys Arg Val Gln Gln Ile Leu Arg Ser Pro Tyr  
 145 150 155 160  
 Ile Lys Val Arg Ala Leu Trp Pro Ser Gly Asp Ile Pro Glu Asp Pro  
 165 170 175  
 Ser Gln Ala Ala Val Leu Leu Leu Ser Pro Trp Thr Phe Phe Ser Ser  
 180 185 190  
 Val Asp Val Glu Ala Leu Leu Pro Ser Pro Gln Glu Lys Glu Gly Lys  
 195 200 205  
 Tyr Ile Asp Pro Val Leu Pro Lys Leu Ser Arg Ile Glu Arg Val Ser  
 210 215 220  
 Leu Leu Val Phe Leu Ser Ala Phe Thr Leu Asp Asp Leu Asn Glu Gln  
 225 230 235 240  
 Gly Val Asn Pro Leu Met Asn Asn Glu Glu Phe Leu Phe Phe Ile Asn  
 245 250 255  
 Lys Lys Ala Arg Asp Met Gly Phe Arg Ile  
 260 265

&lt;210&gt;149

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;149

His Gly Ile Gln Asp Leu Lys His Glu Ile Met Ser Ser Leu Glu Lys  
 1 5 10 15  
 Thr Gly Val Pro Leu Asp Pro Ser Met Ser Phe Gln Val Ser Gln Ala  
 20 25 30  
 Met Phe Ser Val Tyr Arg Tyr Leu Arg Gln Arg Asp Leu Thr Thr Ser  
 35 40 45  
 Glu Leu Arg Cys Phe His Leu Leu Ser Cys Phe Lys Gly Asp Val Val  
 50 55 60  
 His Cys Leu Ala Ser Phe Glu Asn Pro Lys Asp Leu Ala Asp Ser Asp  
 65 70 75 80  
 Phe Leu Glu Ala Cys Lys Asn Val Glu Trp Gly Glu Phe Ile Ser Ala  
 85 90 95  
 Cys Glu Lys Ala Leu Leu Lys Asn Pro Gln Gly Ile Ser Ile Lys Asp  
 100 105 110  
 Leu Lys Gln Phe Leu Val Arg  
 115

&lt;210&gt;150

&lt;211&gt;326

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;150

Ser Met Ile Glu Phe Ala Phe Val Pro His Thr Ser Val Thr Ala Asp  
 1 5 10 15

Arg Ile Glu Asp Arg Met Ala Cys Arg Met Asn Lys Leu Ser Thr Leu  
                     20                    25                    30  
 Ala Ile Thr Ser Leu Cys Val Leu Ile Ser Ser Val Cys Ile Met Ile  
                     35                    40                    45  
 Gly Ile Leu Cys Ile Ser Gly Thr Val Gly Thr Tyr Ala Phe Val Val  
                     50                    55                    60  
 Gly Ile Ile Phe Ser Val Leu Ala Leu Val Ala Cys Val Phe Phe Leu  
                     65                    70                    75                    80  
 Tyr Phe Phe Tyr Phe Ser Ser Glu Glu Phe Lys Cys Ala Ser Ser Gln  
                     85                    90                    95  
 Glu Phe Arg Phe Leu Pro Ile Pro Ala Val Val Ser Ala Leu Arg Ser  
                     100                    105                    110  
 Tyr Glu Tyr Ile Ser Gln Asp Ala Ile Asn Asp Val Ile Lys Asp Thr  
                     115                    120                    125  
 Met Gln Leu Ser Thr Leu Ser Ser Leu Leu Asp Pro Glu Ala Phe Phe  
                     130                    135                    140  
 Leu Glu Phe Pro Tyr Phe Asn Ser Leu Ile Val Asn His Ser Met Lys  
                     145                    150                    155                    160  
 Glu Ala Asp Arg Leu Ser Arg Glu Ala Phe Leu Ile Leu Leu Gly Glu  
                     165                    170                    175  
 Ile Thr Trp Lys Asp Cys Glu Thr Lys Ile Leu Pro Trp Leu Lys Asp  
                     180                    185                    190  
 Pro Asn Ile Thr Pro Asp Asp Phe Trp Lys Leu Leu Lys Asp His Phe  
                     195                    200                    205  
 Asp Leu Lys Asp Phe Lys Lys Arg Ile Ala Thr Trp Ile Arg Lys Ala  
                     210                    215                    220  
 Tyr Pro Glu Ile Arg Leu Pro Lys Lys His Cys Leu Asp Lys Ser Ile  
                     225                    230                    235                    240  
 Tyr Lys Gly Cys Cys Lys Phe Leu Leu Leu Ala Glu Asn Asp Val Gln  
                     245                    250                    255  
 Tyr Gln Arg Leu Leu His Lys Val Cys Tyr Phe Ser Gly Glu Phe Pro  
                     260                    265                    270  
 Ala Met Val Leu Gly Leu Gly Ser Glu Val Pro Met Val Leu Gly Leu  
                     275                    280                    285  
 Pro Lys Val Pro Lys Asp Leu Thr Trp Glu Met Phe Met Glu Asn Met  
                     290                    295                    300  
 Pro Val Leu Leu Gln Ser Lys Arg Glu Gly His Trp Lys Ile Ser Leu  
                     305                    310                    315                    320  
 Glu Asp Val Ala Ser Leu  
                     325

&lt;210&gt;151

&lt;211&gt;257

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;151

Met Phe Lys Leu Leu Lys Asn Leu Phe Leu Ile Gly Cys Cys Ile Val  
                     1                    5                    10                    15  
 Gly Tyr Phe Trp Met Arg Lys Glu Ser Ile Val Glu Gln Trp Leu Ser  
                     20                    25                    30  
 Asn Arg Leu His Thr Gln Val Thr Val Gly Arg Val Ser Ile Arg Thr  
                     35                    40                    45  
 Ser Gly Ile Lys Ile Arg His Ile Cys Ile His Asn Pro Leu Ala Ser  
                     50                    55                    60  
 Glu Arg Phe Pro Tyr Ala Ala Glu Ile Glu Tyr Ala Asp Val Arg Phe  
                     65                    70                    75                    80  
 Ser Ser Ile Ser Met Leu Leu Thr Lys Gln Leu Glu Ile Ser Glu Leu  
                     85                    90                    95  
 Ile Ile His Gly Ala Asn Phe Thr Ile Phe Pro Tyr Asp Ser His Gly  
                     100                    105                    110  
 Thr Lys Thr Asn Trp Ser Leu Val Trp Lys Asn Phe His Pro Gln Lys  
                     115                    120                    125  
 Glu Thr Pro Ser Asn Leu Trp Ile Asp Arg Ala Pro Val Leu Ile Arg  
                     130                    135                    140  
 Arg Cys Leu Phe Leu Asn Thr Arg Leu Tyr Gly Leu Arg Ala Asn His

145                      150                      155                      160  
 Lys Asp Ile Pro His Leu Ser Val Pro Ser Leu Glu Phe His Ser His  
                                  165                      170                      175  
 Thr Ser Ser Ala Lys Glu Leu Pro Lys Leu Ser Glu Ala Leu Pro Ser  
                                  180                      185                      190  
 Leu Leu Tyr Leu Ala Leu Glu Glu Ser Leu Tyr His Leu Asn Leu Pro  
                                  195                      200                      205  
 Gly Asp Ile Ile Lys Pro Leu Ser Gln Gln Ala His Lys His Phe Tyr  
                                  210                      215                      220  
 Ser Ser Tyr Pro Gln Phe Gln Asp Arg Leu Asn Asp Ile Asn Thr Pro  
 225                      230                      235                      240  
 Gly Thr Pro Thr Glu Glu Ile Ile Gly Phe Ile Arg Gly Leu Phe Phe  
                                  245                      250                      255  
 His

&lt;210&gt;152

&lt;211&gt;83

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;152

Ser Lys Glu Gly Arg Ala Ser Glu Ser Phe Gly Asn Ser Leu Ala Glu  
 1                      5                      10                      15  
 Leu Val Trp Leu Trp Asn Ser Lys Asp Gly Thr Glu Arg Trp Gly Met  
                                  20                      25                      30  
 Ser Leu Trp Leu Ala Leu Ser Pro Tyr Asn Arg Val Phe Arg Asn Arg  
                                  35                      40                      45  
 His Leu Arg Met Ser Thr Gly Ala Arg Ser Ile His Lys Phe Glu Gly  
                                  50                      55                      60  
 Val Ser Phe Cys Gly Trp Lys Phe Phe His Thr Lys Asp Gln Phe Val  
 65                      70                      75                      80  
 Phe Val Pro

&lt;210&gt;153

&lt;211&gt;544

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;153

Met Ala Ala Lys Asn Ile Lys Tyr Asn Glu Glu Ala Arg Xaa Lys Ile  
 1                      5                      10                      15  
 His Lys Gly Val Lys Thr Leu Ala Glu Ala Val Lys Val Thr Leu Gly  
                                  20                      25                      30  
 Pro Lys Gly Arg His Val Val Ile Asp Lys Ser Phe Gly Ser Pro Gln  
                                  35                      40                      45  
 Val Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp  
                                  50                      55                      60  
 Lys His Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys  
 65                      70                      75                      80  
 Thr Ala Asp Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala  
                                  85                      90                      95  
 Glu Ala Ile Tyr Ser Glu Gly Leu Arg Asn Val Thr Ala Gly Ala Asn  
                                  100                      105                      110  
 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Lys Val Val Val  
                                  115                      120                      125  
 Asp Glu Leu Lys Lys Ile Ser Lys Pro Val Gln His His Lys Glu Ile  
 130                      135                      140  
 Ala Gln Val Ala Thr Ile Ser Ala Asn Asn Asp Ser Glu Ile Gly Asn  
 145                      150                      155                      160  
 Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Asn Gly Ser Ile Thr  
                                  165                      170                      175  
 Val Glu Glu Ala Lys Gly Phe Glu Thr Val Leu Asp Val Val Glu Gly  
                                  180                      185                      190  
 Met Asn Phe Asn Arg Gly Tyr Leu Ser Ser Tyr Phe Ser Thr Asn Pro  
                                  195                      200                      205  
 Glu Thr Gln Glu Cys Val Leu Glu Asp Ala Leu Ile Leu Ile Tyr Asp

210 215 220  
 Lys Lys Ile Ser Gly Ile Lys Asp Phe Leu Pro Val Leu Gln Gln Val  
 225 230 235 240  
 Ala Glu Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Glu Ile Glu Gly  
 245 250 255  
 Glu Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Ala Gly Phe Arg  
 260 265 270  
 Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met  
 275 280 285  
 Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Gln Leu Val Ser Glu Glu  
 290 295 300  
 Leu Gly Met Lys Leu Glu Asn Thr Thr Leu Ala Met Leu Gly Lys Ala  
 305 310 315 320  
 Lys Lys Val Ile Val Thr Lys Glu Asp Thr Thr Ile Val Glu Gly Leu  
 325 330 335  
 Gly Asn Lys Pro Asp Ile Gln Ala Arg Cys Asp Asn Ile Lys Lys Gln  
 340 345 350  
 Ile Glu Asp Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg  
 355 360 365  
 Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Arg Val Gly Ala Ala  
 370 375 380  
 Thr Glu Ile Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Gln  
 385 390 395 400  
 His Ala Thr Ile Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly Gly  
 405 410 415  
 Thr Ala Leu Val Arg Cys Ile Pro Thr Leu Glu Ala Phe Leu Pro Met  
 420 425 430  
 Leu Ala Asn Glu Asp Glu Ala Ile Gly Thr Arg Ile Ile Leu Lys Ala  
 435 440 445  
 Leu Thr Ala Pro Leu Lys Gln Ile Ala Ser Asn Ala Gly Lys Glu Gly  
 450 455 460  
 Ala Ile Ile Cys Gln Gln Val Leu Ala Arg Ser Ala Asn Glu Gly Tyr  
 465 470 475 480  
 Asp Ala Leu Arg Asp Ala Tyr Thr Asp Met Ile Asp Ala Gly Ile Leu  
 485 490 495  
 Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Glu Ser Ala Ala Ser Ile  
 500 505 510  
 Ala Gly Leu Leu Thr Thr Glu Ala Leu Ile Ala Asp Ile Pro Glu  
 515 520 525  
 Glu Lys Ser Ser Ser Ala Pro Ala Met Pro Ser Ala Gly Met Asp Tyr  
 530 535 540

&lt;210&gt;154

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;154

Met Ser Asp Gln Ala Thr Thr Leu Arg Ile Lys Pro Leu Gly Asp Arg  
 1 5 10 15  
 Ile Leu Val Lys Arg Glu Glu Glu Glu Ala Thr Ala Arg Gly Gly Ile  
 20 25 30  
 Ile Leu Pro Asp Thr Ala Lys Arg Lys Gln Asp Arg Ala Glu Val Leu  
 35 40 45  
 Val Leu Gly Thr Gly Lys Arg Thr Asp Asp Gly Thr Leu Leu Pro Phe  
 50 55 60  
 Glu Val Gln Val Gly Asp Ile Ile Leu Met Asp Lys Tyr Ala Gly Gln  
 65 70 75 80  
 Glu Ile Thr Ile Asp Asp Glu Glu Tyr Val Ile Leu Gln Ser Ser Glu  
 85 90 95  
 Ile Met Ala Val Leu Lys  
 100

&lt;210&gt;155

&lt;211&gt;617

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;155

Lys Gly Val Pro Ser Leu Met Thr Thr Glu Leu Lys Thr Glu Ala Leu  
 1 5 10 15  
 Pro Thr Arg Thr Gln Val Asp Pro Lys His Cys Trp Asp Thr Thr Leu  
 20 25 30  
 Met Tyr Ala Asn Arg Glu Glu Trp Lys Lys Asp Phe Asp Leu Cys Ser  
 35 40 45  
 Ser Gly Lys Asp Arg Ser Pro Ile Trp Pro Glu Phe Ser Pro Ser His  
 50 55 60  
 Tyr Gln Ile Asp Asn Pro Glu Ser Leu Leu Glu Leu Leu Ser Lys Lys  
 65 70 75 80  
 Phe Ser Val Glu Arg Lys Leu Asp Gln Leu Tyr Ile Tyr Ala His Leu  
 85 90 95  
 Ile His Asp Gln Asp Ile Thr Asn Pro Glu Gly Glu Ser Asp Tyr Gln  
 100 105 110  
 Ser Ile Val Tyr Leu Tyr Thr Leu Phe Ser Gln Glu Ile Ser Trp Ile  
 115 120 125  
 Gln Pro Ala Xaa Ile Ala Leu Ser Glu Glu Lys Val Ala Ala Leu Leu  
 130 135 140  
 Ser Ser Ser Val Leu Ala Pro Tyr Arg Phe Tyr Leu Glu Lys Ile Phe  
 145 150 155 160  
 Arg Leu Ser Pro His Thr Gly Thr Ala Asn Glu Glu Lys Ile Leu Ala  
 165 170 175  
 Ser Ser Phe Ala Ala Leu Asn Val Ser Asn Lys Ala Phe Ser Ser Leu  
 180 185 190  
 Ser Asp Ala Glu Ile Pro Phe Gly Ile Ala Lys Asp Ser Asn Gly Glu  
 195 200 205  
 Glu His Pro Leu Ser His Ala Leu Ala Ser Leu Tyr Met Gln Ser Pro  
 210 215 220  
 Asp Gln Glu Leu Arg Arg Thr Ala Tyr Leu Ala Gln Phe Gln Arg Tyr  
 225 230 235 240  
 Tyr Asp Tyr Arg Asn Thr Phe Ala Asn Leu Leu Asn Gly Lys Val Gln  
 245 250 255  
 Ala His Leu Phe Glu Ala Lys Ala Arg Asn Tyr Pro Ser Cys Leu Glu  
 260 265 270  
 Ala Ser Leu Phe Gln His Asn Ile Pro Thr Thr Val Tyr Ile Asn Leu  
 275 280 285  
 Ile Asn Glu Thr Lys Lys His Thr Ser Leu Ile Asn Arg Tyr Phe Asn  
 290 295 300  
 Leu Lys Lys Glu Ala Leu Asn Leu Lys Glu Phe His Phe Tyr Asp Val  
 305 310 315 320  
 Tyr Ala Pro Ile Ser Gln Thr Thr Ser Lys Asn Tyr Ser Tyr Glu Glu  
 325 330 335  
 Gly Val Asp Leu Val Cys Lys Ser Leu Leu Pro Leu Gly Thr His Tyr  
 340 345 350  
 Val Glu Ile Leu Arg Asn Gly Leu Leu Ser Asn Arg Trp Val Asp Arg  
 355 360 365  
 Tyr Glu Asn Lys His Lys Arg Ser Gly Ala Tyr Ser Ser Gly Cys Tyr  
 370 375 380  
 Asp Ser Ala Pro Tyr Ile Leu Leu Asn Tyr Thr Asn Thr Leu Tyr Asp  
 385 390 395 400  
 Val Ser Val Ile Ala His Glu Ala Gly His Ser Met His Ser Tyr Phe  
 405 410 415  
 Ser Arg Glu Ala Gln Pro Tyr His Asp Ala Gln Tyr Pro Leu Phe Leu  
 420 425 430  
 Ala Glu Ile Ala Ser Thr Phe Asn Glu Met Leu Leu Met Glu Ala Leu  
 435 440 445  
 Ser Lys Ser Asp Gln Ser Lys Glu Asp Lys Ile Val Ile Ile Thr Lys  
 450 455 460  
 Thr Leu Asp Thr Ile Phe Ala Thr Leu Phe Arg Gln Thr Phe Phe Ala  
 465 470 475 480  
 Ala Phe Glu Tyr Glu Ile His Ser Ala Ala Glu Gln Gly Thr Pro Leu  
 485 490 495  
 Thr Glu Glu Phe Leu Ser Ala Thr Tyr Gly Asn Leu Gln Lys Glu Phe

500 505 510  
 Tyr Gly Gly Val Val Thr Ser Asp Ser Leu Ser Ala Leu Glu Trp Ala  
 515 520 525  
 Arg Ile Pro His Phe Tyr Tyr Asn Phe Tyr Val Tyr Gln Tyr Ala Thr  
 530 535 540  
 Gly Ile Ile Ala Ala Leu Ser Phe Ala Glu Lys Xaa Leu Thr Gln Glu  
 545 550 555 560  
 Pro Gly Ala Leu Glu Leu Tyr Leu Lys Phe Leu Lys Ser Gly Arg Ser  
 565 570 575  
 Asp Phe Pro Leu Asn Ile Leu Lys Lys Ser Gly Leu Asp Met Thr Thr  
 580 585 590  
 Ser Ala Pro Leu Asp Lys Ala Phe Ala Phe Ile Thr Lys Lys Ile Asp  
 595 600 605  
 Leu Leu Ser Ser Leu Leu Ser Glu Asp  
 610 615  
 <210>156  
 <211>251  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>156  
 Met Asn Val Ala Asp Leu Leu Ser His Leu Glu Thr Leu Leu Ser Ser  
 1 5 10 15  
 Lys Ile Phe Gln Asp Tyr Gly Pro Asn Gly Leu Gln Val Gly Asp Pro  
 20 25 30  
 Gln Thr Pro Val Lys Lys Ile Ala Val Ala Val Thr Ala Asp Leu Glu  
 35 40 45  
 Thr Ile Lys Gln Ala Val Ala Ala Glu Ala Asn Val Leu Ile Val His  
 50 55 60  
 His Gly Ile Phe Trp Lys Gly Met Pro Tyr Pro Ile Thr Gly Met Ile  
 65 70 75 80  
 His Lys Arg Ile Gln Leu Leu Ile Glu His Asn Ile Gln Leu Ile Ala  
 85 90 95  
 Tyr His Leu Pro Leu Asp Ala His Pro Thr Leu Gly Asn Asn Trp Arg  
 100 105 110  
 Val Ala Leu Asp Leu Asn Trp His Asp Leu Lys Pro Phe Gly Ser Ser  
 115 120 125  
 Leu Pro Tyr Leu Gly Val Gln Gly Ser Phe Ser Pro Ile Asp Ile Asp  
 130 135 140  
 Ser Phe Ile Asp Leu Leu Ser Arg Tyr Tyr Gln Ala Pro Leu Lys Gly  
 145 150 155 160  
 Ser Ala Leu Gly Gly Pro Ser Arg Val Ser Ser Ala Ala Leu Ile Ser  
 165 170 175  
 Gly Gly Ala Tyr Arg Glu Leu Ser Ser Ala Ala Thr Ser Gln Val Asp  
 180 185 190  
 Cys Phe Ile Thr Gly Asn Phe Asp Glu Pro Ala Trp Ser Thr Ala Leu  
 195 200 205  
 Glu Ser Asn Ile Asn Phe Leu Ala Phe Gly His Thr Ala Thr Glu Lys  
 210 215 220  
 Val Gly Pro Lys Ser Leu Ala Glu His Leu Lys Ser Glu Phe Pro Ile  
 225 230 235 240  
 Ser Thr Thr Phe Ile Asp Ala Ala Asn Pro Phe  
 245 250  
 <210>157  
 <211>449  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>157  
 Met Trp Lys Leu Thr Lys Arg Asn Ser Met Leu Asn Cys Ser Asn Gln  
 1 5 10 15  
 Lys His Thr Val Thr Phe Glu Glu Ala Cys Gln Val Phe Pro Gly Gly  
 20 25 30  
 Val Asn Ser Pro Val Arg Ala Cys Arg Ser Val Gly Val Thr Pro Pro  
 35 40 45  
 Ile Val Ser Ser Ala Gln Gly Asp Ile Phe Leu Asp Thr His Gly Arg

```

      50              55              60
Glu Phe Ile Asp Phe Cys Gly Gly Trp Gly Ala Leu Ile His Gly His
 65              70              75              80
Ser His Pro Lys Ile Val Lys Ala Ile Gln Lys Thr Ala Leu Lys Gly
      85              90              95
Thr Ser Tyr Gly Leu Thr Ser Glu Glu Ile Leu Phe Ala Thr Met
 100              105              110
Leu Leu Ser Ser Leu Lys Leu Lys Glu His Lys Ile Arg Phe Val Ser
 115              120              125
Ser Gly Thr Glu Ala Thr Met Thr Ala Val Arg Leu Ala Arg Gly Ile
 130              135              140
Thr Asn Arg Ser Ile Ile Ile Lys Phe Ile Gly Gly Tyr His Gly His
 145              150              155              160
Ala Asp Thr Leu Leu Gly Gly Ile Ser Thr Thr Glu Glu Thr Ile Asp
      165              170              175
Asn Leu Thr Ser Leu Ile His Thr Pro Ser Pro His Ser Leu Leu Ile
      180              185              190
Ser Leu Pro Tyr Asn Asn Ser Gln Ile Leu His His Val Met Glu Ala
      195              200              205
Leu Gly Pro Gln Val Ala Gly Ile Ile Phe Glu Pro Ile Cys Ala Asn
      210              215              220
Met Gly Ile Val Leu Pro Lys Ala Glu Phe Leu Asp Asp Ile Ile Glu
 225              230              235              240
Leu Cys Lys Arg Phe Gly Ser Leu Ser Ile Met Asp Glu Val Val Thr
      245              250              255
Gly Phe Arg Val Ala Phe Gln Gly Ala Gln Asp Ile Phe Asn Leu Ser
      260              265              270
Pro Asp Ile Thr Ile Tyr Gly Lys Ile Leu Gly Gly Gly Leu Pro Ala
      275              280              285
Ala Ala Leu Val Gly His Arg Ser Ile Leu Asp His Leu Met Pro Glu
      290              295              300
Gly Thr Ile Phe Gln Ala Gly Thr Met Ser Gly Asn Phe Leu Ala Met
 305              310              315              320
Ala Thr Gly His Ala Ala Ile Gln Leu Cys Gln Ser Glu Gly Phe Tyr
      325              330              335
Asp His Leu Ser Gln Leu Glu Ala Leu Phe Tyr Ser Pro Ile Glu Glu
      340              345              350
Glu Ile Arg Ser Gln Gly Phe Pro Val Ser Leu Val His Gln Gly Thr
      355              360              365
Met Phe Ser Leu Phe Phe Thr Glu Ser Ala Pro Thr Asn Phe Asp Glu
      370              375              380
Ala Lys Asn Ser Asp Val Glu Lys Phe Gln Thr Phe Tyr Ser Glu Val
 385              390              395              400
Phe Asp Asn Gly Val Tyr Leu Ser Pro Ser Pro Leu Glu Ala Asn Phe
      405              410              415
Ile Ser Ser Ala His Thr Glu Glu Asn Leu Thr Tyr Ala Gln Asn Ile
      420              425              430
Ile Ile Asp Ser Leu Ile Lys Ile Phe Asp Ser Ser Ala Gln Arg Phe
      435              440              445

```

Xaa

&lt;210&gt;158

&lt;211&gt;174

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;158

```

Ser Leu Leu Leu Asn Ile Asn Gln Gly Val Phe Ala Arg Ser Val Ile
 1              5              10              15
Leu Leu Cys Glu His Ser Leu Asn Gly Ser Phe Gly Leu Ile Leu Asn
      20              25              30
Lys Thr Leu Gly Phe Glu Ile Ser Asp Asp Ile Phe Thr Phe Glu Lys
      35              40              45
Val Ser Asn His Asn Ile Arg Phe Cys Xaa Gly Gly Pro Leu Gln Ala
      50              55              60

```



Asn Gln Met Met Leu Leu His Ser Cys Ser Glu Ile Pro Glu Gln Thr  
 65 70 75 80  
 Leu Glu Ile Cys Pro Ser Val Tyr Leu Gly Gly Asp Leu Pro Phe Leu  
 85 90 95  
 Gln Glu Ile Ala Ser Ser Glu Ser Gly Pro Glu Ile Asn Leu Cys Phe  
 100 105 110  
 Gly Tyr Ser Gly Trp Gln Ala Gly Gln Leu Glu Lys Glu Phe Leu Ser  
 115 120 125  
 Asn Asp Trp Phe Leu Ala Pro Gly Asn Lys Asp Tyr Val Phe Tyr Ser  
 130 135 140  
 Glu Pro Glu Asp Leu Trp Ala Leu Val Leu Lys Asp Leu Gly Gly Lys  
 145 150 155 160  
 Tyr Ala Ser Leu Ser Thr Val Pro Asp Asn Leu Leu Leu Asn  
 165 170

&lt;210&gt;159

&lt;211&gt;124

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;159

Met Ser Leu Glu Lys Glu Leu Leu Glu Glu Thr Pro Leu Val Leu Leu  
 1 5 10 15  
 Asn Phe Tyr Lys Leu Val Ser Phe Cys Asn Tyr Ala Gly Met Ile Leu  
 20 25 30  
 Gly Thr Glu Glu Lys Lys Phe Ala Ile Tyr Gly His Val Ser Met Gly  
 35 40 45  
 Gln Ala Phe Gln Gly Ala Asp Thr Glu Gly His Ser Pro Gln Arg Pro  
 50 55 60  
 Phe Ala His Asp Leu Leu Asn Phe Val Phe Ser Gly Phe Asp Ile Gln  
 65 70 75 80  
 Val Leu Arg Val Val Ile Asn Asp Tyr Lys Asp Asn Val Phe Tyr Thr  
 85 90 95  
 Arg Leu Phe Leu Glu Gln Lys Asp Arg Glu Phe Leu Tyr Val Val Asp  
 100 105 110  
 Val Asp Ala Arg Pro Ser Asp Arg Ser Leu Ser Pro  
 115 120

&lt;210&gt;160

&lt;211&gt;140

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;160

Ser Arg Pro Ser Ile Ala Asp Asp Gln Arg Trp Trp Arg Thr Phe Phe  
 1 5 10 15  
 Arg Glu Lys Ile Leu Leu Arg Ala Ala Lys Arg Ser Ile Ile Leu Val  
 20 25 30  
 Asp Glu Ser Lys Leu Val Pro Val Leu Gly Lys Phe Arg Val Pro Leu  
 35 40 45  
 Glu Ile Ser Arg Phe Gly Arg Ser Ala Ile Ile Glu Glu Ile Arg His  
 50 55 60  
 Leu Gly Tyr Glu Gly Glu Trp Arg Leu Gln Asp Thr Gly Asp Leu Phe  
 65 70 75 80  
 Ile Thr Asp Ser Ser Asn Tyr Ile Tyr Asp Ile Phe Ser Pro Asn Ser  
 85 90 95  
 Tyr Pro Asn Pro Glu Lys Asp Leu Leu Lys Leu Ile Gln Ile His Gly  
 100 105 110  
 Val Ile Glu Val Gly Phe Val Ile Glu Lys Val Glu Val Trp Ser Ser  
 115 120 125  
 Asn Ser Gln Gly Leu Ile Ser Lys Lys Tyr Ser Val  
 130 135 140

&lt;210&gt;161

&lt;211&gt;112

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;161

Val Glu Lys Asp Leu His Leu His Glu Lys Lys Cys Leu Ala His Glu

1 5 10 15  
 Ala Ala Thr Gln Val Thr Ser Gly Met Ile Leu Gly Leu Gly Ser Gly  
 20 25 30  
 Ser Thr Ala Lys Glu Phe Ile Phe Ala Leu Ala His Arg Ile Gln Thr  
 35 40 45  
 Glu Ser Leu Ala Val His Ala Ile Ala Ser Ser Gln Asn Ser Tyr Ala  
 50 55 60  
 Leu Ala Lys Gln Leu Ala Ile Pro Leu Leu Asn Pro Glu Lys Phe Ser  
 65 70 75 80  
 Ser Leu Asp Leu Thr Val Asp Gly Ala Asp Glu Val Asp Pro Gln Leu  
 85 90 95  
 Arg Met Ile Lys Gly Gly Gly Gly Pro Phe Ser Glu Lys Arg Phe Phe  
 100 105 110  
 <210>162  
 <211>378  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>162  
 Arg Arg Thr Ile Met Asn Thr Ser Leu Lys Arg Pro Leu Lys Ser His  
 1 5 10 15  
 Phe Asp Val Val Gly Ser Phe Leu Arg Pro Glu His Leu Lys Lys Thr  
 20 25 30  
 Arg Glu Ser Leu Lys Glu Gly Ser Ile Ser Leu Asp Gln Leu Met Gln  
 35 40 45  
 Ile Glu Asp Ile Ala Ile Gln Asp Leu Ile Lys Lys Gln Lys Ala Ala  
 50 55 60  
 Gly Leu Ser Phe Ile Thr Asp Gly Glu Phe Arg Arg Ala Thr Trp His  
 65 70 75 80  
 Tyr Asp Phe Met Trp Gly Phe His Gly Val Gly His His Arg Ala Thr  
 85 90 95  
 Glu Gly Val Phe Phe Asp Gly Glu Arg Ala Met Ile Asp Asp Thr Tyr  
 100 105 110  
 Leu Thr Asp Lys Ile Ser Val Ser His His Pro Phe Val Asp His Phe  
 115 120 125  
 Lys Phe Val Lys Ala Leu Glu Asp Glu Phe Thr Thr Ala Lys Gln Thr  
 130 135 140  
 Leu Pro Ala Pro Ala Gln Phe Leu Lys Gln Met Ile Phe Pro Asn Asn  
 145 150 155 160  
 Ile Glu Val Thr Arg Lys Phe Tyr Pro Thr Asn Gln Glu Leu Ile Glu  
 165 170 175  
 Asp Ile Val Ala Gly Tyr Arg Lys Val Ile Arg Asp Leu Tyr Asp Ala  
 180 185 190  
 Gly Cys Arg Tyr Leu Gln Leu Asp Asp Cys Thr Arg Gly Gly Leu Val  
 195 200 205  
 Asp Pro Arg Val Cys Ser Trp Tyr Gly Ile Asp Glu Lys Gly Leu Gln  
 210 215 220  
 Asp Leu Ile Gln Gln Tyr Leu Leu Ile Asn Asn Leu Val Ile Ala Asp  
 225 230 235 240  
 Arg Pro Asp Asp Leu Val Val Asn Leu His Val Cys Arg Gly Asn Tyr  
 245 250 255  
 His Ser Lys Phe Phe Ala Ser Gly Ser Tyr Asp Phe Ile Ala Lys Pro  
 260 265 270  
 Leu Phe Glu Gln Thr Asn Val Asp Gly Tyr Tyr Leu Glu Phe Asp His  
 275 280 285  
 Glu Arg Ser Gly Asp Phe Ser Pro Leu Thr Phe Ile Ser Gly Glu Lys  
 290 295 300  
 Thr Val Cys Leu Gly Leu Val Thr Ser Lys Thr Pro Thr Leu Glu Asn  
 305 310 315 320  
 Lys Asp Glu Val Ile Ala Arg Ile His Gln Ala Ala Asp Tyr Leu Pro  
 325 330 335  
 Leu Glu Arg Leu Ser Leu Ser Pro Gln Cys Gly Phe Ala Ser Cys Glu  
 340 345 350  
 Ile Gly Asn Lys Leu Thr Glu Glu Glu Gln Trp Ala Lys Val Ala Leu  
 355 360 365

Val Lys Glu Ile Ser Glu Glu Val Trp Lys  
 370 375  
 <210>163  
 <211>872  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>163  
 Val Leu Gly Val Asn Phe Met Glu Lys Phe Ser Asp Ala Val Ser Glu  
 1 5 10 15  
 Ala Leu Glu Lys Ala Phe Glu Leu Ala Lys Ser Ser Lys His Thr Tyr  
 20 25 30  
 Val Thr Glu Asn His Leu Leu Leu Ala Leu Leu Glu Asn Thr Glu Ser  
 35 40 45  
 Leu Phe Tyr Leu Val Ile Lys Asp Ile His Gly Asn Pro Gly Leu Leu  
 50 55 60  
 Asn Thr Ala Val Lys Asp Ala Leu Ser Arg Glu Pro Thr Val Val Glu  
 65 70 75 80  
 Gly Glu Val Asp Pro Lys Pro Ser Pro Gly Leu Gln Thr Leu Leu Arg  
 85 90 95  
 Asp Ala Lys Gln Glu Ala Lys Thr Leu Gly Asp Glu Tyr Ile Ser Gly  
 100 105 110  
 Asp His Leu Leu Ala Phe Trp Ser Ser Asn Lys Glu Pro Phe Asn  
 115 120 125  
 Ser Trp Lys Gln Thr Thr Lys Val Ser Phe Lys Asp Leu Lys Asn Leu  
 130 135 140  
 Ile Thr Lys Ile Arg Arg Gly Asn Arg Met Asp Ser Pro Ser Ala Glu  
 145 150 155 160  
 Ser Asn Phe Gln Gly Leu Glu Lys Tyr Cys Lys Asn Leu Thr Ala Leu  
 165 170 175  
 Ala Arg Glu Gly Lys Leu Asp Pro Val Ile Gly Arg Asp Glu Glu Ile  
 180 185 190  
 Arg Arg Thr Ile Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Met  
 195 200 205  
 Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu  
 210 215 220  
 Ala Leu Arg Leu Ile Gln Gly Asp Val Pro Glu Ser Leu Lys Gly Lys  
 225 230 235 240  
 Gln Leu Tyr Val Leu Asp Met Gly Ala Leu Ile Ala Gly Ala Lys Tyr  
 245 250 255  
 Arg Gly Glu Phe Glu Glu Arg Leu Lys Ser Val Leu Lys Asp Val Glu  
 260 265 270  
 Ser Gly Asp Gly Glu His Ile Ile Phe Ile Asp Glu Val His Thr Leu  
 275 280 285  
 Val Gly Ala Gly Ala Thr Asp Gly Ala Met Asp Ala Ala Asn Leu Leu  
 290 295 300  
 Lys Pro Ala Leu Ala Arg Gly Thr Leu His Cys Ile Gly Ala Thr Thr  
 305 310 315 320  
 Leu Asn Glu Tyr Gln Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg  
 325 330 335  
 Arg Phe Gln Pro Ile Phe Val Thr Glu Pro Ser Leu Glu Asp Ala Val  
 340 345 350  
 Phe Ile Leu Arg Gly Leu Arg Glu Lys Tyr Glu Ile Phe His Gly Val  
 355 360 365  
 Arg Ile Thr Glu Gly Ala Leu Asn Ala Ala Val Leu Leu Ser Tyr Arg  
 370 375 380  
 Tyr Ile Pro Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp  
 385 390 395 400  
 Glu Ala Ala Ser Leu Ile Arg Met Gln Ile Gly Ser Leu Pro Leu Pro  
 405 410 415  
 Ile Asp Glu Lys Glu Arg Glu Leu Ala Ala Leu Ile Val Lys Gln Glu  
 420 425 430  
 Ala Ile Lys Arg Glu Gln Ser Pro Ser Tyr Gln Glu Glu Ala Asp Ala  
 435 440 445  
 Met Gln Lys Ser Ile Asp Ala Leu Arg Glu Glu Leu Ala Ser Leu Arg

450 455 460  
 Leu Gly Trp Asp Glu Glu Lys Lys Leu Ile Ser Gly Leu Lys Glu Lys  
 465 470 475 480  
 Lys Asn Ser Leu Glu Ser Met Lys Phe Ser Glu Glu Glu Ala Glu Arg  
 485 490 495  
 Val Ala Asp Tyr Asn Arg Val Ala Glu Leu Arg Tyr Ser Leu Ile Pro  
 500 505 510  
 Gln Leu Glu Glu Glu Ile Lys Gln Asp Glu Ala Ser Leu Asn Gln Arg  
 515 520 525  
 Asp Asn Arg Leu Leu Gln Glu Glu Val Asp Glu Arg Leu Ile Ala Gln  
 530 535 540  
 Val Val Ala Asn Trp Thr Gly Ile Pro Val Gln Lys Met Leu Glu Gly  
 545 550 555 560  
 Glu Ala Glu Lys Leu Leu Ile Leu Glu Glu Ser Leu Glu Glu Arg Val  
 565 570 575  
 Val Gly Gln Pro Phe Ala Val Ser Ala Val Ser Asp Ser Ile Arg Ala  
 580 585 590  
 Ala Arg Val Gly Leu Asn Asp Pro Gln Arg Pro Leu Gly Val Phe Leu  
 595 600 605  
 Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Ala Lys Ala Leu  
 610 615 620  
 Ala Asp Leu Leu Phe Asn Lys Glu Glu Ala Met Val Arg Phe Asp Met  
 625 630 635 640  
 Ser Glu Tyr Met Glu Lys His Ser Ile Ser Lys Leu Ile Gly Ser Ser  
 645 650 655  
 Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Ser Leu Ser Glu Ala Leu  
 660 665 670  
 Arg Arg Arg Pro Tyr Ser Val Val Leu Phe Asp Glu Ile Glu Lys Ala  
 675 680 685  
 Asp Lys Glu Val Leu Asn Ile Leu Leu Gln Val Phe Asp Asp Gly Ile  
 690 695 700  
 Leu Thr Asp Gly Lys Lys Arg Lys Val Asn Cys Lys Asn Ala Leu Phe  
 705 710 715 720  
 Ile Met Thr Ser Asn Ile Gly Ser Pro Glu Leu Ala Asp Tyr Cys Ser  
 725 730 735  
 Lys Lys Gly Ser Glu Leu Thr Lys Glu Ala Ile Leu Ser Val Val Ser  
 740 745 750  
 Pro Val Leu Lys Arg Tyr Leu Ser Pro Glu Phe Met Asn Arg Ile Asp  
 755 760 765  
 Glu Ile Leu Pro Phe Val Pro Leu Thr Lys Glu Asp Ile Val Lys Ile  
 770 775 780  
 Val Gly Ile Gln Met Arg Arg Ile Ala Gln Arg Leu Lys Ala Arg Arg  
 785 790 795 800  
 Ile Asn Leu Ser Trp Asp Asp Ser Val Ile Leu Phe Leu Ser Glu Gln  
 805 810 815  
 Gly Tyr Asp Ser Ala Phe Gly Ala Arg Pro Leu Lys Arg Leu Ile Gln  
 820 825 830  
 Gln Lys Val Val Ile Leu Leu Ser Lys Ala Leu Leu Lys Gly Asp Ile  
 835 840 845  
 Lys Pro Asp Thr Ser Ile Glu Leu Thr Met Ala Lys Glu Val Leu Val  
 850 855 860  
 Phe Lys Lys Val Glu Thr Pro Ser  
 865 870  
 <210>164  
 <211>182  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>164  
 Asn Cys Ala Ala Ser Phe Ile Trp Leu Asn Lys Ser Ser His Arg Asn  
 1 5 10 15  
 Leu Arg Ser Pro Met Phe Lys Ser Phe Ile Val Arg Tyr Met Phe Val  
 20 25 30  
 Gly Gly Leu Val Ser Phe Leu Leu Pro Ile Pro Asp Leu Glu Cys Ala  
 35 40 45

Asn Asn Val Thr Lys Thr Tyr Asp Lys Lys Ala Ser Val Ile Ser Arg  
 50 55 60  
 Asp Leu Lys Leu Gln Glu Asp Cys Gln Lys Phe Trp Asn Leu Asp Pro  
 65 70 75 80  
 Tyr Lys Leu Glu Ser Leu Cys Ala Tyr Gln Val Leu Tyr His Asp Asp  
 85 90 95  
 Tyr Ser Ser Lys Arg Ile Arg Glu Leu Phe Pro Gln Ile Gln Lys Asp  
 100 105 110  
 Glu Val Pro Ile Phe Ala Thr Met Ile Leu Thr Leu Gly Lys Val Asp  
 115 120 125  
 Arg Gly Phe Ser Pro Glu Glu Ile Ser Leu Ile Gln Lys Leu Ser Tyr  
 130 135 140  
 Pro Gly Leu Ser Leu Ala Ser Leu Arg Gly Ser Thr Glu Ile Arg Pro  
 145 150 155 160  
 Glu Tyr Arg Phe Gly Ser Cys Phe Ser Ser Val Gly Val Phe Trp Arg  
 165 170 175  
 Phe Arg Glu Glu Pro Ser  
 180

&lt;210&gt;165

&lt;211&gt;399

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;165

Glu Gly Leu Gln Lys Leu Asp Pro Asn Thr Asp Leu Ala Arg Ala Leu  
 1 5 10 15  
 Val Val Ser Glu Phe Ser Gly Asp Leu Gly Lys Asn Arg Ala Asp Tyr  
 20 25 30  
 Tyr Ser Asn Cys Leu Asp Ile Leu Ala Leu Arg Ile His Ala Glu Arg  
 35 40 45  
 Gln Arg Tyr Leu Asp Gln Ser Pro Cys Val Pro Gly Thr Ser Glu Phe  
 50 55 60  
 His Lys Ala Thr Ile Glu Ala Ile Asn Thr Ile Leu Phe Tyr Glu Glu  
 65 70 75 80  
 Ala Val Arg Tyr Pro Ser Lys Lys Glu Met Phe Ser Asp Glu Phe Ser  
 85 90 95  
 Phe Leu Ser Ser Val Thr Asp Arg Lys Phe Gly Val Cys Leu Gly Val  
 100 105 110  
 Ser Ser Leu Tyr Phe Ser Leu Ser Gln Arg Leu Asp Leu Pro Leu Glu  
 115 120 125  
 Ala Val Thr Pro Pro Gly His Ile Tyr Leu Arg Tyr Gln Gly Gly Glu  
 130 135 140  
 Val Asn Ile Glu Thr Thr Ala Gly Gly Arg His Leu Pro Thr Ala Ser  
 145 150 155 160  
 Tyr Cys Asp Cys Leu Asp Leu Glu Asp Leu Gln Val Arg Thr Pro Glu  
 165 170 175  
 Glu Met Ile Gly Leu Thr Phe Met Asn Gln Gly Ser Phe Ala Leu Gln  
 180 185 190  
 Lys Lys Lys Tyr Lys Glu Ala Glu Glu Ala Tyr Lys Lys Ala Gln Glu  
 195 200 205  
 Tyr Leu Gly Asp Glu Glu Leu Gln Glu Leu Leu Gly Phe Val Gln Ile  
 210 215 220  
 Leu Gly Gly Lys Lys Lys Glu Gly Lys Ser Leu Ile Gly Lys Ser Pro  
 225 230 235 240  
 Arg Ala Ser Gln Lys Gly Ser Val Ala Tyr Asp Tyr Leu Lys Gly Arg  
 245 250 255  
 Ile Asn Ile Pro Thr Leu Ala Leu Leu Phe Ser Tyr Pro Gly Ser Asn  
 260 265 270  
 Tyr Glu Glu Ile Ala Ser Tyr Glu Glu Glu Leu Lys Lys Ala Met Lys  
 275 280 285  
 Ser Ser Met Pro Cys Cys Glu Gly Gln Arg Arg Leu Ala Ser Val Ala  
 290 295 300  
 Phe His Leu Gly Lys Thr Ala Glu Ala Val Ala Leu Leu Glu Lys Cys  
 305 310 315 320  
 Val Glu Asp Ile Pro Asn Asp Leu Ser Leu His Leu Arg Leu Cys Lys

325 330 335  
 Ile Leu Cys Asp Arg His Glu Tyr Thr Lys Ala Leu Lys Tyr Phe Ile  
 340 345 350  
 Ile Ala Glu Arg Leu Met Glu Asp Gln Gly Phe Leu Lys Lys Asp Asn  
 355 360 365  
 Arg Ser Phe Ala Leu Phe Tyr Glu Val Lys Lys Ile Ile Ser Lys Val  
 370 375 380  
 Ala Pro Gln Lys Ala Asn Thr Leu Leu Leu Met Glu Ser Glu Arg  
 385 390 395  
 <210>166  
 <211>167  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>166  
 Ile Ile Val Gly Ile Ser Met Ser Ser Ser Glu Val Val Phe Gln Thr  
 1 5 10 15  
 Val His Gly Leu Gly Phe Gly Gly Leu Ser Ser Lys Ser Val Val Pro  
 20 25 30  
 Phe Lys Lys Ser Leu Ser Asp Ala Pro Arg Val Val Cys Ser Ile Leu  
 35 40 45  
 Val Leu Thr Leu Gly Leu Gly Ala Leu Val Cys Gly Ile Ala Ile Thr  
 50 55 60  
 Cys Trp Cys Val Pro Gly Val Ile Leu Met Gly Gly Ile Cys Ala Ile  
 65 70 75 80  
 Val Leu Gly Ala Ile Ser Leu Ala Leu Ser Leu Phe Trp Leu Trp Gly  
 85 90 95  
 Leu Phe Ser Asn Cys Cys Gly Ser Lys Arg Val Leu Pro Gly Glu Gly  
 100 105 110  
 Leu Leu Arg Asp Lys Leu Leu Asp Gly Gly Phe Ser Arg Ala Ala Pro  
 115 120 125  
 Ser Gly Met Gly Leu Pro Gly Asp Gly Ser Pro Arg Ala Ser Thr Pro  
 130 135 140  
 Ser Cys Leu Glu Glu Leu Gln Ala Glu Ile Gln Ala Val Thr Gln Ala  
 145 150 155 160  
 Ile Asp Gln Met Ser Asp Asp  
 165  
 <210>167  
 <211>145  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>167  
 Leu Pro Ala Pro Glu Leu Arg Ser Ser Trp Val Lys Gly Asp Pro Pro  
 1 5 10 15  
 Pro Arg Pro Ala Ser Pro Ala Thr Pro Pro Ser Arg Gly Gly Val Ala  
 20 25 30  
 Glu Phe Leu Ser Leu Gly Ser Pro Leu Phe Pro Gly Leu Gly Ile Ser  
 35 40 45  
 Ala Leu Gly Ile Leu Ser Ser Leu Lys Val Ile Ser Ile Ala Gln Ala  
 50 55 60  
 Asn Asn Ala Thr Pro Ser Ser Ile Val Ile Ala Pro Ala Ala Ile Pro  
 65 70 75 80  
 Lys Gly Gln Gln Pro Ala Arg Thr Thr Arg Pro Ser Pro Ser Lys Glu  
 85 90 95  
 Ile Ala Thr Thr Ala Met Ile Ala Ala Ile Thr Asp Leu Ala Ile Leu  
 100 105 110  
 Val Ala Leu Ser Ser Val Leu Asn Ala Gly Ile Ala Ser Leu Glu Gln  
 115 120 125  
 Phe Thr His Pro Thr Asp Val Ala Ala Asp Val Thr Ala Ser Phe Ile  
 130 135 140  
 Asp  
 145  
 <210>168  
 <211>538  
 <212>PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;168

Gly Lys Trp Trp Arg Val Ser Ser Met Glu Ser Glu Lys Asp Ile Gly  
 1 5 10 15  
 Ala Lys Phe Leu Gly Asp Tyr Arg Ile Leu Tyr Arg Lys Gly Gln Ser  
 20 25 30  
 Leu Trp Ser Glu Asp Leu Leu Ala Glu His Arg Phe Ile Lys Lys Arg  
 35 40 45  
 Tyr Leu Ile Arg Leu Leu Leu Pro Asp Leu Gly Ser Ser Gln Pro Phe  
 50 55 60  
 Met Glu Ala Phe His Asp Val Val Val Lys Leu Ala Lys Leu Asn His  
 65 70 75 80  
 Pro Gly Ile Leu Ser Ile Glu Asn Val Ser Glu Ser Glu Gly Arg Cys  
 85 90 95  
 Phe Leu Val Thr Gln Glu Gln Asp Ile Pro Ile Leu Ser Leu Thr Gln  
 100 105 110  
 Tyr Leu Lys Ser Ile Pro Arg Lys Leu Thr Glu Leu Glu Ile Val Asp  
 115 120 125  
 Ile Val Ser Gln Leu Ala Ser Leu Leu Asp Tyr Val His Ser Glu Gly  
 130 135 140  
 Leu Ala Gln Glu Glu Trp Asn Leu Asp Ser Val Tyr Ile His Ile Leu  
 145 150 155 160  
 Asn Gly Val Pro Lys Val Ile Leu Pro Asp Leu Gly Phe Ala Ser Leu  
 165 170 175  
 Ile Lys Glu Arg Ile Leu Asp Gly Phe Ile Ser Asp Glu Glu Asn Arg  
 180 185 190  
 Glu Ser Lys Ile Lys Glu Arg Val Leu Leu His Thr Ser Glu Gly Lys  
 195 200 205  
 Gln Gly Arg Glu Asp Thr Tyr Ala Phe Gly Ala Ile Thr Tyr Tyr Leu  
 210 215 220  
 Leu Phe Gly Phe Leu Pro Gln Gly Ile Phe Pro Met Pro Ser Lys Val  
 225 230 235 240  
 Phe Ser Asp Phe Ile Tyr Asp Trp Asp Phe Leu Ile Ser Ser Cys Leu  
 245 250 255  
 Ser Cys Phe Met Glu Glu Arg Ala Lys Glu Leu Phe Pro Leu Ile Arg  
 260 265 270  
 Lys Lys Thr Leu Gly Glu Glu Leu Gln Asn Val Val Thr Asn Cys Ile  
 275 280 285  
 Glu Ser Ser Leu Arg Glu Val Pro Asp Pro Leu Glu Ser Ser Gln Asn  
 290 295 300  
 Leu Pro Gln Ala Val Leu Lys Val Gly Glu Thr Lys Val Ser His Gln  
 305 310 315 320  
 Gln Lys Glu Ser Ala Glu His Leu Glu Phe Val Leu Val Glu Ala Cys  
 325 330 335  
 Ser Ile Asp Glu Ala Met Asp Thr Ala Ile Glu Ser Glu Ser Ser Ser  
 340 345 350  
 Gly Val Glu Glu Glu Gly Tyr Ser Leu Ala Leu Gln Ser Leu Leu Val  
 355 360 365  
 Arg Glu Pro Val Val Ser Arg Tyr Val Glu Ala Glu Lys Glu Glu Pro  
 370 375 380  
 Lys Pro Gln Pro Ile Leu Thr Glu Met Val Leu Ile Glu Gly Gly Glu  
 385 390 395 400  
 Phe Ser Arg Gly Ser Val Glu Gly Gln Arg Asp Glu Leu Pro Val His  
 405 410 415  
 Lys Val Ile Leu His Ser Phe Phe Leu Asp Val His Pro Val Thr Asn  
 420 425 430  
 Glu Gln Phe Asn Arg Tyr Leu Glu Cys Cys Gly Ser Glu Gln Asp Lys  
 435 440 445  
 Tyr Tyr Asn Glu Leu Ile Arg Leu Arg Asp Ser Arg Ile Gln Arg Arg  
 450 455 460  
 Ser Gly Arg Leu Val Ile Glu Pro Gly Tyr Ala Lys His Pro Val Val  
 465 470 475 480  
 Gly Val Thr Trp Tyr Gly Ala Ser Gly Tyr Ala Glu Trp Ile Gly Lys  
 485 490 495

Arg Leu Pro Thr Glu Ala Glu Trp Glu Ile Ala Ala Ser Gly Gly Val  
                   500                  505                  510  
 Ala Cys Tyr Ala Ile Pro Val Gly Arg Lys Ser Lys Lys Ala Gly Gln  
                   515                  520                  525  
 Ile Phe Ser Leu Arg Ile Arg Gln Gln Ser  
                   530                  535  
 <210>169  
 <211>662  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>169  
 Met Lys Glu Glu Asn Ser Gln Ala His Tyr Leu Ala Leu Cys Arg Glu  
   1                  5                  10                  15  
 Leu Glu Asp His Asp Tyr Ser Tyr Tyr Val Leu His Arg Pro Arg Ile  
                   20                  25                  30  
 Ser Asp Tyr Glu Tyr Asp Met Lys Leu Arg Lys Leu Leu Glu Ile Glu  
                   35                  40                  45  
 Arg Ser His Pro Glu Trp Lys Val Leu Trp Ser Pro Ser Thr Arg Leu  
                   50                  55                  60  
 Gly Asp Arg Pro Ser Gly Thr Phe Ser Val Val Ser His Lys Glu Pro  
   65                  70                  75                  80  
 Met Leu Ser Ile Ala Asn Ser Tyr Ser Lys Glu Glu Leu Ser Glu Phe  
                   85                  90                  95  
 Phe Ser Arg Val Glu Lys Ser Leu Gly Thr Ser Pro Arg Tyr Thr Val  
                   100                  105                  110  
 Glu Leu Lys Ile Asp Gly Ile Ala Val Ala Ile Arg Tyr Glu Asp Arg  
                   115                  120                  125  
 Val Leu Val Gln Ala Leu Ser Arg Gly Asn Gly Lys Gln Gly Glu Asp  
   130                  135                  140  
 Ile Thr Ser Asn Ile Arg Thr Ile Arg Ser Leu Pro Leu Arg Leu Pro  
  145                  150                  155                  160  
 Glu Asp Ala Pro Glu Phe Ile Glu Val Arg Gly Glu Val Phe Phe Ser  
                   165                  170                  175  
 Tyr Ser Thr Phe Gln Ile Ile Asn Glu Lys Gln Gln Gln Leu Glu Lys  
                   180                  185                  190  
 Thr Ile Phe Ala Asn Pro Arg Asn Ala Ala Gly Gly Thr Leu Lys Leu  
                   195                  200                  205  
 Leu Ser Pro Gln Glu Ser Arg Lys Arg Lys Leu Glu Ile Ser Ile Tyr  
  210                  215                  220  
 Asn Leu Ile Ala Pro Gly Asp Asn Asp Ser His Tyr Glu Asn Leu Gln  
  225                  230                  235                  240  
 Arg Cys Leu Glu Trp Gly Phe Pro Val Ser Gly Lys Pro Arg Leu Cys  
                   245                  250                  255  
 Ser Thr Pro Glu Glu Val Ile Ser Val Leu Lys Thr Ile Glu Thr Glu  
                   260                  265                  270  
 Arg Ala Ser Leu Pro Met Glu Ile Asp Gly Ala Val Ile Lys Val Asp  
                   275                  280                  285  
 Ser Leu Ala Ser Gln Arg Val Leu Gly Ala Thr Gly Lys His Tyr Arg  
  290                  295                  300  
 Trp Ala Leu Ala Tyr Lys Tyr Ala Pro Glu Glu Ala Glu Thr Leu Leu  
  305                  310                  315                  320  
 Glu Asp Ile Leu Val Gln Val Gly Arg Thr Gly Val Leu Thr Pro Val  
                   325                  330                  335  
 Ala Lys Leu Thr Pro Val Leu Leu Ser Gly Ser Leu Val Ser Arg Ala  
                   340                  345                  350  
 Ser Leu Tyr Asn Glu Asp Glu Ile His Arg Lys Asp Ile Arg Ile Gly  
                   355                  360                  365  
 Asp Thr Val Cys Val Ala Lys Gly Gly Glu Val Ile Pro Lys Val Val  
                   370                  375                  380  
 Arg Val Cys Arg Glu Lys Arg Pro Glu Gly Ser Glu Val Trp Asn Met  
  385                  390                  395                  400  
 Pro Glu Phe Cys Pro Val Cys His Ser His Val Val Arg Glu Glu Asp  
                   405                  410                  415  
 Arg Val Ser Val Arg Cys Val Asn Pro Glu Cys Val Ala Gly Ala Ile



420 425 430  
 Glu Lys Ile Arg Phe Phe Val Gly Arg Gly Ala Leu Asn Ile Asp His  
 435 440 445  
 Leu Gly Val Lys Val Ile Thr Lys Leu Phe Glu Leu Gly Leu Val His  
 450 455 460  
 Thr Cys Ala Asp Leu Phe Gln Leu Thr Thr Glu Asp Leu Met Gln Ile  
 465 470 475 480  
 Pro Gly Ile Arg Glu Arg Ser Ala Arg Asn Ile Leu Glu Ser Ile Glu  
 485 490 495  
 Gln Ala Lys His Val Asp Leu Asp Arg Phe Leu Val Ala Leu Gly Ile  
 500 505 510  
 Pro Leu Ile Gly Ile Gly Val Ala Thr Val Leu Ala Gly His Phe Glu  
 515 520 525  
 Thr Leu Asp Arg Val Ile Ser Ala Thr Phe Glu Glu Leu Leu Ser Leu  
 530 535 540  
 Glu Gly Ile Gly Glu Lys Val Ala His Ala Ile Ala Glu Tyr Phe Ser  
 545 550 555 560  
 Asp Ser Thr His Leu Asn Glu Ile Lys Lys Met Gln Asp Leu Gly Val  
 565 570 575  
 Cys Ile Ser Pro Tyr His Lys Ser Gly Ser Thr Cys Phe Gly Lys Ala  
 580 585 590  
 Phe Val Ile Thr Gly Thr Leu Glu Gly Met Ser Arg Leu Asp Ala Glu  
 595 600 605  
 Thr Ala Ile Arg Asn Cys Gly Gly Lys Val Gly Ser Ser Val Ser Lys  
 610 615 620  
 Gln Thr Asp Tyr Val Val Met Gly Asn Asn Pro Gly Ser Lys Leu Glu  
 625 630 635 640  
 Lys Ala Arg Lys Leu Gly Val Ser Ile Leu Asp Gln Glu Ala Phe Thr  
 645 650 655  
 Asn Leu Ile His Leu Glu  
 660  
 <210>170  
 <211>441  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>170  
 Ile Ile Tyr Tyr Lys Phe Phe Tyr Ser Tyr Asn Cys Pro Tyr Phe Ile  
 1 5 10 15  
 Ser Phe Phe Val Leu Leu Gly Val Asn Met Ala Ser Ser Ser Asn Asn  
 20 25 30  
 Ser Thr Lys Gln Asp Gly Ile Pro Ser Trp Val Asn Pro Asn Val Gln  
 35 40 45  
 Trp Asn Arg Ala Ser Gln Val Gly Asp Gln Glu Ala Asn Ser Leu Thr  
 50 55 60  
 Pro Glu Ala Gln Thr Ser Arg Ser Trp Phe Ser Asp Arg Lys His Phe  
 65 70 75 80  
 Leu Glu Val Leu Asp Val Ser Leu Glu Glu Met Glu Asn Asn Asp Leu  
 85 90 95  
 Lys Lys Tyr Ser Arg Tyr Lys Thr Ile Ile Leu Ile Ala Thr Leu Val  
 100 105 110  
 Thr Val Ala Ile Thr Cys Ile Val Pro Ile Ser Met Val Phe Gly Ile  
 115 120 125  
 Pro Met Trp Val Pro Cys Leu Ile Leu Phe Gly Ala Gly Leu Ser Ser  
 130 135 140  
 Ala Phe Leu Ser His Arg Leu Gln Ser Lys Cys Lys Glu Ile His Leu  
 145 150 155 160  
 Arg Tyr Arg Ala Tyr Gln Ile Tyr Arg Gln Gln Leu Leu Ser Gln Tyr  
 165 170 175  
 Pro Asp Leu Arg Lys Ser Thr Leu Tyr Lys Tyr Ser Ile Thr His Val  
 180 185 190  
 Lys Pro Lys Lys Gly Phe Val Gly Lys Leu Val Glu Asn Leu Arg Pro  
 195 200 205  
 Asp Leu His Lys Asn Lys Asp Asp Gly Gly Ala Ala Ala Asp Ser Arg  
 210 215 220

Leu Asp Phe Ala Gly Tyr Gly Val Lys His Tyr Gln Thr Asp Ala Leu  
 225 230 235 240  
 Leu Gly Val Ser Gly Val Asn Ser Val Glu Trp Gln Arg Leu Ala Ser  
 245 250 255  
 Leu Ile Met Ser Val Lys Asn Asp Ile Leu Asn Asp Val Gly Ser Arg  
 260 265 270  
 Glu Pro Ile Asp Lys Ala Gln Arg Ser Ala Leu Val Val Ser Gly Lys  
 275 280 285  
 Asp Ile Gly Gly Glu Ile Gln Pro Gly Gly Ile Leu Asp Ile Ser Arg  
 290 295 300  
 Asp Ile Leu Ala Ile Cys Gly Tyr Gly Met Asn Val Gly Val Glu Ala  
 305 310 315 320  
 Lys Lys Ala Ile Asp Gln Tyr Lys Lys Trp Tyr Leu Asn Ser Ser Thr  
 325 330 335  
 Phe Ile Ala Trp Asn Pro Gln Leu Pro Ala Ile Ala Gln Ser Tyr Leu  
 340 345 350  
 Leu Glu Gln Gln Arg His Leu Asp Tyr Ala Ala Lys Ile Phe Gln Asp  
 355 360 365  
 Leu Ser Ala Leu Thr Thr Ala His Gly Thr Gly Gln Ala Leu Glu Asp  
 370 375 380  
 Leu Asp Ser Leu Leu Cys Tyr Tyr Asp Gln Leu Ile Glu Ser Lys Gly  
 385 390 395 400  
 Val Gly Glu Lys Ile Ala Ser Ile His Gln Lys Ala Ser Arg Leu  
 405 410 415  
 Ser Asn Ala Arg Phe Leu Arg Ser Gly Thr Phe Lys Glu Met Val Glu  
 420 425 430  
 Ser Ile Pro Arg Val Phe Asn Tyr Tyr  
 435 440

&lt;210&gt;171

&lt;211&gt;1156

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;171

His Arg Phe Thr Arg Lys His Leu Asp Leu Ala Met Gln Asp Ser Cys  
 1 5 10 15  
 Asp Gln Glu His Leu Lys Lys Trp Ser Asn Leu Tyr His Val Phe Ser  
 20 25 30  
 Ile Thr Ile Lys Glu Phe Thr Glu Gly Lys Leu Glu Gln Asn Glu Val  
 35 40 45  
 Val Ser Arg Ile Gln Arg Leu Arg Gly Lys Leu Glu Lys Ser Lys Cys  
 50 55 60  
 Ser Ile Leu Gly Asn Cys Arg Thr Asn Ala Glu Tyr Ala Thr Lys Ser  
 65 70 75 80  
 Glu Lys Lys Leu Ala Asp Tyr Leu Leu Gln Ile Gly Asp Arg Glu Pro  
 85 90 95  
 Phe Leu Thr Gly Met His Lys Ala Ile Ala Thr Gly Lys Ala Ile Gln  
 100 105 110  
 Gly Lys Val Glu Gly Val Ile Ser Gln His Pro Glu Lys Gln Ile Met  
 115 120 125  
 Met Leu Arg Cys Ser Ile Glu Arg Leu Glu Gly Met Leu Arg Arg Glu  
 130 135 140  
 Asp Trp Gly Ala Ile Leu Gln Lys Asn Glu Asp Glu Val Leu Ala Leu  
 145 150 155 160  
 Lys Ser Thr Met Glu Ala Gln Leu Gln Gly Phe Lys Asp Leu Val Gly  
 165 170 175  
 Thr Trp Glu Gly Lys Tyr Gln Glu Phe Lys Lys Asn Lys Leu Ser Lys  
 180 185 190  
 Val Leu Val Tyr Asp Phe Thr Lys Ser Tyr Ser Asn Leu Leu Asn Arg  
 195 200 205  
 Leu Glu Val Leu His Ala Glu Ser Ser Thr Asp Asp Leu Val Leu His  
 210 215 220  
 Val Asp Arg Met Ser Glu Asp Leu Lys Lys Thr Ile Glu Glu Ile Asp  
 225 230 235 240  
 Gly Asn Leu Phe Gln Val Thr Pro Glu Glu Leu Ser Leu Leu Ala Arg

245 250 255  
 Glu Tyr Gln Gly Leu Met Asn Glu Leu Pro Leu Ile Val Gln Glu Gly  
 260 265 270  
 Asn Arg Leu Gln Glu Ala Ile Ser Ser Glu Gly Val Ser Gln Gly Leu  
 275 280 285  
 Met Leu Leu Asn Ser Leu Leu Asn Arg Asp Glu Lys Ile Asn Lys Asn  
 290 295 300  
 Ile Glu Ser Ser Arg Lys Asn Leu Val Ala Ile Ala Lys Gln Ala Arg  
 305 310 315 320  
 Ser Asp Ala Arg Asn Ile Asp Ser Gln Gly Leu Ala Pro Leu Ile Gln  
 325 330 335  
 Arg Asn Arg Ala Ser Leu Asp Asn Ile Leu Gln Asn Met Tyr Leu Phe  
 340 345 350  
 Asn Gly Ser Ile Arg Asn Ile His Ala Leu Asp Thr Glu Thr Leu Val  
 355 360 365  
 Ala Thr Ser Ser Asn Met Phe Ser Ala Met His Thr Phe Asp Trp Asn  
 370 375 380  
 Ile Tyr Thr Asn Leu Leu Asp Val Leu Glu Ile Gln Ser Lys Pro Ala  
 385 390 395 400  
 Pro Ala Pro Met Glu Asn Pro Asp Leu Pro Gly Ala Leu Pro Glu Glu  
 405 410 415  
 Val Gln Asp Ala Val Ala Glu Asp Val Ser Gly Thr His Arg Leu His  
 420 425 430  
 His Gln Val Leu Lys Arg Arg Cys Ala Asp Leu Lys Asn Met Ile Ser  
 435 440 445  
 Gln Leu Gln Lys Ser Ile Asn Lys Trp Gly Met Ala Lys Ala Ile Val  
 450 455 460  
 Leu Gly Ile Val Ala Val Leu Phe Cys Val Leu Ser Ala Ile Phe Ile  
 465 470 475 480  
 Gly Gln Asn Ile Leu Ser Leu Leu Ile Leu Ser Cys Val Gly Leu Leu  
 485 490 495  
 Leu Thr Gln Val Cys Pro Leu Ile Phe Asp Arg Ile Ser Lys Ser Lys  
 500 505 510  
 Glu Phe Glu Lys Gln Val Leu Glu Thr Ala Gln Ser Leu Ile Pro Ala  
 515 520 525  
 Thr Lys Ile Leu Pro Ser Glu Phe Asn Asn Lys Asp Leu Asn Arg Leu  
 530 535 540  
 Ala Lys Leu Gln Asp Asn Leu Asn Leu Glu Gly Phe Gly Pro Thr Trp  
 545 550 555 560  
 Ala Arg Asn Ile Val Ser Asp Leu Glu Gly Ile Pro Thr Lys Glu Lys  
 565 570 575  
 Ser Leu Lys Asp Leu Thr Lys Glu Phe Arg Lys Asp Ser Lys Asn Leu  
 580 585 590  
 Asn Lys Arg Ile Lys Arg Arg Phe Lys Glu Gly Leu Gly Gln Glu Ala  
 595 600 605  
 Pro Val Val Arg Pro Thr Ile Pro Gln Asp Ile Arg Gly Ala Glu Val  
 610 615 620  
 Phe Ala Glu Leu His Arg Glu Leu Glu His Leu Gln Lys Gln Lys Glu  
 625 630 635 640  
 Glu Ile Ser Ile Arg Gly Asp Ala Leu Val Gln Glu Arg Met Gly Leu  
 645 650 655  
 Cys Leu Glu Lys Ser Lys Tyr Asp Asn Glu Lys Ala His Ala Ala Ala  
 660 665 670  
 Met Thr Lys Lys Val Gly Lys Leu Gln Asn Ile Asp Arg Leu Gln Lys  
 675 680 685  
 Asn Asn Glu Thr Tyr Val Arg Ile Gln Asn Phe Phe Arg Thr Leu Ile  
 690 695 700  
 Gln Glu Lys Leu Gly Arg Asp Thr Val Gln Glu Ile Asp Val Val Lys  
 705 710 715 720  
 Glu Ala Lys Glu Leu His Glu Leu Ala Ala Ile Ile Tyr Gly Asn Thr  
 725 730 735  
 Ser Gly Lys Ser Gln Lys Gln Arg Ala Lys Lys Gln Phe Lys Glu Asn  
 740 745 750  
 Val Leu His Ile Ala Gly Lys Gly Gln Leu Glu Leu Leu Glu Ala Tyr

```

      755                      760                      765
Leu Asn Val Thr Ala Ser Gln Gly Leu Cys Arg His Gln Met Gln Ala
      770                      775                      780
Ser Phe Arg Glu Arg Ile Leu Leu Asn Pro Asp Gly Ala Lys His Gly
785                      790                      795                      800
Glu Ala Glu Arg Thr Leu Ala Ser Arg Glu Glu Met Leu Lys Thr Leu
      805                      810                      815
Gly Leu Ser Tyr Leu Thr Pro Phe Val Arg Phe Ser Ser Pro Glu Ser
      820                      825                      830
Thr Gln Ser Gly Tyr Asn Gln Ile Leu Lys Val Arg Glu Gln Leu Phe
      835                      840                      845
Asp Ile Glu Gln Arg Leu Gln Asn Gln Glu Thr Val Ser Pro Glu Asp
      850                      855                      860
Tyr Ala Ala Val Gln Ala Leu Ala Ala Tyr Val Arg Lys His Glu
865                      870                      875                      880
Ser Leu Ile Val Ser Thr Tyr Gly Leu Gly Ala Gln Glu Gly Gln Thr
      885                      890                      895
Ser Ser Lys Val Thr Thr Leu Met Arg Asp Leu His Ala Val Glu Glu
      900                      905                      910
Leu Val Glu Met Gly Val Glu Thr Tyr Arg Leu Asn Arg Ser Asp Gln
      915                      920                      925
Ile Leu His Arg Val His Ser Val Leu His Ser His Leu Arg Asp Ser
      930                      935                      940
Asp Ser Ser Gly Asn Gly Ile Ile Asp Val Val Lys Lys Leu Phe Glu
945                      950                      955                      960
Leu Leu Asn Asn Asn Gly Asn Asn Pro Asn Asp Pro Glu Cys Gln Lys
      965                      970                      975
Tyr Met Gln Ile Leu Leu Asp Ala Pro Val Ser Leu Leu Tyr Gly Ala
      980                      985                      990
Phe Lys Ser Phe Lys Asn Glu Phe Leu Leu Asn Phe Thr Glu Leu Asn
      995                      1000                      1005
Ile Ala Asn Ser Thr Lys Ala Ala Glu Glu Glu Ala Lys Arg Tyr Val
      1010                      1015                      1020
Glu Glu Lys Gly Arg Gly Phe Glu Thr Tyr Trp Glu Glu Ala Lys Gln
1025                      1030                      1035                      1040
Arg Leu Glu Ala Ile Ala Ala Glu Leu Asp Asp Leu Arg Asn Gln Glu
      1045                      1050                      1055
Thr Leu Leu Glu Gln Glu Ile Arg Leu Ala Asn Leu Lys Ile Ser Ile
      1060                      1065                      1070
Phe Ser Asp Leu Asn Leu Arg Glu Lys Val Ser Val Glu Lys Ala Ala
      1075                      1080                      1085
Leu Glu Glu Glu Ile Gln Gly Ile Gln Glu Gln Tyr Ala Glu Met Gln
      1090                      1095                      1100
Gly Ile Glu Asp Leu Glu Leu Lys Gln Lys Phe Glu Asp Leu Gln Lys
1105                      1110                      1115                      1120
Lys Leu Glu Ala Leu Glu Glu Arg Leu Leu Gln Ile Gly Arg Arg Ile
      1125                      1130                      1135
Asp Ser Ser Val Asp Lys Gln Lys Glu Leu Leu Gly Leu Leu Gly Arg
      1140                      1145                      1150
Glu Glu Ala Ala
      1155
<210>172
<211>518
<212>PRT
<213>Chlamydia pneumoniae
<400>172
Cys Tyr Glu Asn Leu Phe His Tyr Pro Arg Ala Ser Met Ala Asp Ile
  1                      5                      10                      15
Leu Val Ile Gly Ala Asn Pro Thr Gly Leu Ile Leu Ala Asn Met Leu
      20                      25                      30
Ile Gln His Gly Ile Ser Val Lys Val Ile Asp His Arg Ala Ser Pro
      35                      40                      45
Glu Asp Pro Ser Phe Leu Asp Cys Arg Lys Leu Pro Val Ile Leu Ser
      50                      55                      60

```

Cys Ser Ser Leu Glu Leu Leu His Asn Ser Glu Met Leu Gly Asp Phe  
 65 70 75 80  
 Ile Gln Ala Asn His Lys Ile Phe Gly Ala Arg Tyr His Trp Lys Lys  
 85 90 95  
 Arg Thr Leu Leu Phe Lys Phe Ser Gln Ala Thr Asp Ser Pro Val Pro  
 100 105 110  
 Phe Ser Leu Ser Thr Thr Tyr Gln Ser Leu Glu Gln His Leu Ile Asp  
 115 120 125  
 Glu Phe Leu Lys Arg Gly Gly Val Ile Asp Trp Ser Thr Arg Pro Val  
 130 135 140  
 Thr Leu Val Asp Asn Ser Ile Phe Ile Glu Ser Thr Lys Val Ser Gln  
 145 150 155 160  
 Asn Phe Glu Asn Arg Glu Ile Tyr Asn Pro Lys Trp Ile Ile Ala Cys  
 165 170 175  
 Glu Ala Asp Asn Asn Leu Asp Ile Arg Asp Leu Val Lys Ser Gln Leu  
 180 185 190  
 Arg Ala Arg Arg Ile Asn Arg Glu Val Ile Phe Ile Asn Cys Asp Glu  
 195 200 205  
 Gly Glu Pro Phe Glu Glu Asp His Ile His Leu Leu Pro Ile Thr Lys  
 210 215 220  
 Asn Phe Leu Asn Phe Val Phe Tyr Asn Pro Gln Glu Lys Thr Lys Gln  
 225 230 235 240  
 Leu Cys Leu Pro Gln Gly Thr His Ser Ile Ser Pro Lys Leu Lys Gln  
 245 250 255  
 Lys Leu Leu Tyr Thr Tyr Asn Leu Val Ile Ser Asp Glu Asn Phe His  
 260 265 270  
 Ile Lys Thr Ser His His Ala Phe Pro Pro Glu His Gly Asn Val Leu  
 275 280 285  
 Phe Leu Gly Ser Leu Ser Asn Thr Leu Leu Leu Ser Tyr Leu Asn Gly  
 290 295 300  
 Ile Asn Thr Asn Ile His Ala Ala Phe Asn Leu Ala Trp Lys Leu Leu  
 305 310 315 320  
 Pro Val Leu Lys Lys Ala Ala Leu Lys His Leu Val Ile Thr Lys Glu  
 325 330 335  
 Gln Glu Asp Gly Asn Ile Leu Pro Tyr Ile Ser Pro Thr Thr Glu Lys  
 340 345 350  
 Arg Ala Lys Lys Leu Pro Phe Ser Arg Phe Tyr Thr Pro Ala Leu Met  
 355 360 365  
 Tyr Tyr Phe Leu Lys Gly Cys Arg Lys Phe Asn Thr Thr Gly Glu Glu  
 370 375 380  
 Tyr Tyr Tyr Pro Pro His Gln Ala Leu Lys Tyr Arg Ser Ser Asp Ile  
 385 390 395 400  
 Ile Lys Met Ser Pro Gln Asp Lys Glu Ile His Gly Pro Gly Pro Gly  
 405 410 415  
 Met Arg Ala Ile Asp Ala Arg Leu Glu Asn Gly Ser Phe Leu Leu Asp  
 420 425 430  
 Pro Leu Lys Ser Ser Lys His Leu Leu Ile Phe Phe Lys Asp Ile Pro  
 435 440 445  
 Asp Leu Lys Glu Ala Leu Gln Glu Glu Tyr Gly Glu Trp Ile Glu Ile  
 450 455 460  
 Cys Asn Val Lys Glu Pro Arg Ile Leu Asn Leu Tyr His Ala Asn Pro  
 465 470 475 480  
 Asn Ser Leu Phe Ile Ile Arg Pro Asp Arg Tyr Ile Gly Tyr Arg Thr  
 485 490 495  
 His Thr Phe Lys Leu His Glu Leu Ile Ser Tyr Leu Leu Arg Ile Phe  
 500 505 510  
 Ala Ser Glu Lys Thr Ser  
 515  
 <210>173  
 <211>319  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>173  
 Leu Ile Lys Met Arg Lys Val Ala Phe Leu Val Ser Cys Leu Phe Ser

1 5 10 15  
 Val Ala Ile Gly Ala Ser Ala Ala Pro Val Arg Val Pro Gly Phe Pro  
 20 25 30  
 Gln Ile Pro Glu Asp Xaa Val Gln Ile Lys Thr Glu Val Cys Pro Lys  
 35 40 45  
 Gln Glu Val Cys Leu Ala Val Thr Ile Lys Cys Asp Asp His Asn Leu  
 50 55 60  
 Ile Gly Val Leu His Leu Pro Asn Thr Pro Thr Pro Glu Gly Gly Phe  
 65 70 75 80  
 Pro Thr Val Val Leu Phe His Gly Phe Arg Gly Thr Lys Phe Gly Gly  
 85 90 95  
 Leu Thr Gly Ala Tyr Arg Lys Leu Gly Arg Lys Phe Ala Ala Gly  
 100 105 110  
 Ile Ala Thr Leu Arg Val Asp Met Ala Gly Cys Gly Asp Ser Glu Gly  
 115 120 125  
 Val Ala Glu Glu Val Pro Ile Glu Thr Tyr Leu Arg Asp Ala Gln Thr  
 130 135 140  
 Ile Leu Glu Thr Val Gln Glu His Pro Asp Leu Asn Ala Tyr Arg Leu  
 145 150 155 160  
 Gly Ile Ser Gly Phe Ser Leu Gly Cys His Ile Ala Phe Glu Leu Ala  
 165 170 175  
 Lys Ile Tyr Asn Pro Arg Asp Leu Asn Ile Lys Ala Leu Ser Val Trp  
 180 185 190  
 Ala Pro Ile Ala Asp Gly Gly Ile Leu Leu Lys Glu Leu Tyr Glu Asn  
 195 200 205  
 Phe Ser Lys His Gly Glu Gly Asp Ile Ile Ser Val Gly Lys Asp Phe  
 210 215 220  
 Gly Phe Gly Pro Pro Pro Ile Ile Val Cys Ser Gly Asp Val Asp Leu  
 225 230 235 240  
 Leu Ile Arg Ile Gln Asp His Val Thr Ala Asn Ser Leu Pro Thr Lys  
 245 250 255  
 Pro Tyr Ile Leu His Gln Gln Gly Ile Asp Asp Thr Leu Val Ser Arg  
 260 265 270  
 Thr Gln Gln Thr Leu Phe Lys Asn Thr Ala Pro Gly Arg Met Thr Phe  
 275 280 285  
 Ile Ser Tyr Pro Asn Thr Gly His Asn Leu Ala Thr Ala Pro Asp Leu  
 290 295 300  
 Asp Met Ile Leu Asp Gln Ile Val Ser His Phe Gln Arg Thr Leu  
 305 310 315  
 <210>174  
 <211>507  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>174  
 Met Arg Tyr Asp Pro Asn Leu Ile Glu Lys Lys Trp Gln Gln Phe Trp  
 1 5 10 15  
 Lys Glu His Arg Ser Phe Gln Ala Asn Glu Asp Glu Asp Lys Val Lys  
 20 25 30  
 Tyr Tyr Val Leu Asp Met Phe Pro Tyr Pro Ser Gly Ala Gly Leu His  
 35 40 45  
 Val Gly His Leu Ile Gly Tyr Thr Ala Thr Asp Ile Val Ala Arg Tyr  
 50 55 60  
 Lys Arg Ala Arg Gly Phe Ser Val Leu His Pro Met Gly Trp Asp Ser  
 65 70 75 80  
 Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Arg Thr Gly Thr His Pro  
 85 90 95  
 Lys Val Thr Thr Gln Lys Asn Ile Ala Asn Phe Lys Lys Gln Leu Ser  
 100 105 110  
 Ala Met Gly Phe Ser Tyr Asp Glu Gly Arg Glu Phe Ala Thr Ser Asp  
 115 120 125  
 Pro Asp Tyr Tyr His Trp Thr Gln Lys Leu Phe Leu Phe Leu Tyr Asp  
 130 135 140  
 Gln Gly Leu Ala Tyr Met Ala Asp Met Ala Val Asn Tyr Cys Pro Glu  
 145 150 155 160

Leu Gly Thr Val Leu Ser Asn Glu Glu Val Glu Asn Gly Phe Ser Ile  
 165 170 175  
 Glu Gly Gly Tyr Pro Val Glu Arg Lys Met Leu Arg Gln Trp Ile Leu  
 180 185 190  
 Lys Ile Thr Ala Tyr Ala Asp Lys Leu Leu Glu Gly Leu Asp Ala Leu  
 195 200 205  
 Asp Trp Pro Glu Asn Val Lys Gln Leu Gln Lys Asn Trp Ile Gly Lys  
 210 215 220  
 Ser Glu Gly Ala Leu Val Thr Xaa His Leu Thr Gln Glu Gly Ser Leu  
 225 230 235 240  
 Glu Ala Phe Thr Thr Arg Leu Asp Thr Leu Leu Gly Val Ser Phe Leu  
 245 250 255  
 Val Ile Ala Pro Glu His Pro Asp Leu Asp Ser Ile Val Ser Glu Glu  
 260 265 270  
 Gln Arg Asp Glu Val Thr Ala Tyr Val Gln Glu Ser Leu Arg Lys Ser  
 275 280 285  
 Glu Arg Asp Arg Ile Ser Ser Val Lys Thr Lys Thr Gly Val Phe Thr  
 290 295 300  
 Gly Asn Tyr Ala Lys His Pro Ile Thr Gly Asn Leu Leu Pro Val Trp  
 305 310 315 320  
 Ile Ser Asp Tyr Val Val Leu Gly Tyr Gly Thr Gly Val Val Met Gly  
 325 330 335  
 Val Pro Ala His Asp Glu Arg Asp Arg Glu Phe Ala Glu Met Phe Ser  
 340 345 350  
 Leu Pro Ile His Glu Val Ile Asp Asp Asn Gly Val Cys Ile His Ser  
 355 360 365  
 Asn Tyr Asn Asp Phe Cys Leu Asn Gly Leu Ser Gly Gln Glu Ala Lys  
 370 375 380  
 Asp Tyr Val Ile Asn Tyr Leu Glu Met Arg Ser Leu Gly Arg Ala Lys  
 385 390 395 400  
 Thr Met Tyr Arg Leu Arg Asp Trp Leu Phe Ser Arg Gln Arg Tyr Trp  
 405 410 415  
 Gly Glu Pro Ile Pro Ile Ile His Phe Glu Asp Gly Thr His Arg Pro  
 420 425 430  
 Leu Glu Asp Asp Glu Leu Pro Leu Leu Pro Pro Asn Ile Asp Asp Tyr  
 435 440 445  
 Arg Pro Glu Gly Phe Gly Gln Gly Pro Leu Ala Lys Ala Gln Asp Trp  
 450 455 460  
 Val His Ile Tyr Asp Glu Lys Thr Gly Arg Pro Gly Cys Arg Glu Thr  
 465 470 475 480  
 Tyr Thr Met Pro Gln Trp Ala Gly Ser Cys Trp Tyr Tyr Leu Arg Phe  
 485 490 495  
 Cys Asp Ala His Asn Tyr Ser Val Ala Leu Glu  
 500 505

&lt;210&gt;175

&lt;211&gt;198

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;175

Arg Arg Leu Lys Ile Gly Cys Ile Ser Thr Thr Arg Arg Gln Val Asp  
 1 5 10 15  
 Gln Asp Val Glu Arg Leu Ile Leu Cys His Ser Gly Gln Ala Leu Ala  
 20 25 30  
 Gly Ile Ile Phe Val Ser Val Met His Thr Thr Thr Gln Leu Pro Trp  
 35 40 45  
 Ser Lys Glu Lys Glu Ser Tyr Trp Met Pro Val Asp Leu Tyr Ile Gly  
 50 55 60  
 Gly Ala Glu His Ala Val Leu His Leu Leu Tyr Ser Arg Phe Trp His  
 65 70 75 80  
 Arg Val Phe Tyr Asp Ala Gly Leu Val Ser Thr Pro Glu Pro Phe Lys  
 85 90 95  
 Lys Leu Ile Asn Gln Gly Leu Val Leu Ala Ser Ser Tyr Arg Ile Pro  
 100 105 110  
 Gly Lys Gly Tyr Val Ser Ile Glu Asp Val Arg Glu Glu Asn Gly Thr

115 120 125  
 Trp Ile Ser Thr Cys Gly Glu Ile Val Glu Val Arg Gln Glu Lys Met  
 130 135 140  
 Ser Lys Ser Lys Leu Asn Gly Val Asp Pro Gln Val Leu Ile Glu Glu  
 145 150 155 160  
 Tyr Gly Ala Asp Ala Leu Arg Met Tyr Ala Met Phe Ser Gly Pro Leu  
 165 170 175  
 Asp Lys Asn Lys Thr Trp Ser Asn Glu Gly Val Trp Gly Val Pro Ser  
 180 185 190  
 Phe Pro Lys Ser Phe Leu  
 195

&lt;210&gt;176

&lt;211&gt;163

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;176

Phe Gly Xaa Ser Ser Glu Val Gln Asp Ile Glu Asp Arg Asp Gly Leu  
 1 5 10 15  
 Val Leu Ala His Lys Leu Val Phe Arg Ile Thr Glu His Ile Glu Lys  
 20 25 30  
 Met Ser Leu Asn Thr Ile Pro Ser Ser Phe Met Glu Phe Leu Asn Asp  
 35 40 45  
 Phe Ser Lys Leu Pro Val Tyr Ser Lys Arg Ala Leu Ser Met Ala Val  
 50 55 60  
 Arg Val Leu Glu Pro Ile Xaa Pro His Ile Ser Glu Glu Leu Trp Val  
 65 70 75 80  
 Ile Leu Gly Asn Pro Pro Gly Ile Asp Gln Ala Ala Trp Pro Gln Ile  
 85 90 95  
 Asp Glu Ser Tyr Leu Val Ala Gln Thr Val Thr Phe Val Val Gln Val  
 100 105 110  
 Asn Gly Lys Leu Arg Gly Arg Leu Glu Val Ala Lys Glu Ala Pro Lys  
 115 120 125  
 Glu Glu Val Leu Ser Leu Ser Arg Ser Val Val Ala Lys Tyr Leu Glu  
 130 135 140  
 Asn Ala Gln Ile Arg Lys Glu Ile Tyr Val Pro Asn Lys Leu Val Asn  
 145 150 155 160  
 Phe Val Leu

&lt;210&gt;177

&lt;211&gt;437

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;177

Met Met Leu Arg Gly Val His Arg Ile Phe Lys Cys Phe Tyr Asp Val  
 1 5 10 15  
 Val Leu Val Cys Ala Phe Val Ile Ala Leu Pro Lys Leu Leu Tyr Lys  
 20 25 30  
 Met Leu Val Tyr Gly Lys Tyr Lys Lys Ser Leu Ala Val Arg Phe Gly  
 35 40 45  
 Leu Lys Lys Pro His Val Pro Gly Glu Gly Pro Leu Val Trp Phe His  
 50 55 60  
 Gly Ala Ser Val Gly Glu Val Arg Leu Leu Leu Pro Val Leu Glu Lys  
 65 70 75 80  
 Phe Cys Glu Glu Phe Pro Gly Trp Arg Cys Leu Val Thr Ser Cys Thr  
 85 90 95  
 Glu Leu Gly Val Gln Val Ala Ser Gln Val Phe Ile Pro Met Gly Ala  
 100 105 110  
 Thr Val Ser Ile Leu Pro Leu Asp Phe Ser Ile Ile Ile Lys Ser Val  
 115 120 125  
 Val Ala Lys Leu Arg Pro Ser Leu Ala Val Phe Ser Glu Gly Asp Cys  
 130 135 140  
 Trp Leu Asn Phe Ile Glu Glu Ala Lys Arg Ile Gly Ala Thr Thr Leu  
 145 150 155 160  
 Val Ile Asn Gly Arg Ile Ser Ile Asp Ser Ser Lys Arg Phe Lys Phe



165 170 175  
 Leu Lys Arg Leu Gly Lys Asn Tyr Phe Ser Pro Val Asp Gly Phe Leu  
 180 185 190  
 Leu Gln Asp Glu Val Gln Lys Gln Arg Phe Leu Ser Leu Gly Ile Pro  
 195 200 205  
 Glu His Lys Leu Gln Val Thr Gly Asn Ile Lys Thr Tyr Val Ala Ala  
 210 215 220  
 Gln Thr Ala Leu His Leu Glu Arg Glu Thr Trp Arg Asp Arg Leu Arg  
 225 230 235 240  
 Leu Pro Thr Asp Ser Lys Leu Val Ile Leu Gly Ser Met His Arg Ser  
 245 250 255  
 Asp Ala Gly Lys Trp Leu Pro Val Val Gln Lys Leu Ile Lys Glu Gly  
 260 265 270  
 Val Ser Val Leu Trp Val Pro Arg His Val Glu Lys Thr Lys Asp Val  
 275 280 285  
 Glu Glu Ser Leu His Arg Leu His Ile Pro Tyr Gly Leu Trp Ser Arg  
 290 295 300  
 Gly Ala Asn Phe Ser Tyr Val Pro Val Val Val Asp Glu Ile Gly  
 305 310 315 320  
 Leu Leu Lys Gln Leu Tyr Val Ala Gly Asp Leu Ala Phe Val Gly Gly  
 325 330 335  
 Thr Phe Asp Pro Lys Ile Gly Gly His Asn Leu Leu Glu Pro Leu Gln  
 340 345 350  
 Cys Glu Val Pro Leu Ile Phe Gly Pro His Ile Thr Ser Gln Ser Glu  
 355 360 365  
 Leu Ala Gln Arg Leu Leu Leu Ser Gly Ala Gly Leu Cys Leu Asp Glu  
 370 375 380  
 Ile Glu Pro Ile Ile Asp Thr Val Ser Phe Leu Leu Asn Asn Gln Glu  
 385 390 395 400  
 Val Arg Glu Ala Tyr Val Gln Lys Gly Lys Val Phe Val Lys Ala Glu  
 405 410 415  
 Thr Ala Ser Phe Asp Arg Thr Trp Arg Ala Leu Lys Ser Tyr Ile Pro  
 420 425 430  
 Leu Tyr Lys Asn Ser  
 435

&lt;210&gt;178

&lt;211&gt;179

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;178

Leu Leu Leu Glu Asp Leu Asp Thr Asp Ser Ile Pro Trp Pro Lys Leu  
 1 5 10 15  
 Tyr Leu Ser Glu Asp Phe Asp Phe Ala Tyr Tyr Pro Glu Ser Lys Ala  
 20 25 30  
 Ile Ile Asp Thr Val Ala Lys Leu Glu Lys Asn Asn Pro Gly Glu Glu  
 35 40 45  
 Phe Cys Leu Glu Ser Lys Lys Ile Leu Ala Arg Tyr Leu Leu Glu Gln  
 50 55 60  
 Leu Phe Lys Leu Glu Thr Gly Leu Asn Phe Pro Thr Ser Thr Ile Asp  
 65 70 75 80  
 Gly Gly Arg Glu Ser Phe Leu Ile Glu Phe Ser His Glu Thr Lys Lys  
 85 90 95  
 Pro Thr Val Trp Ala Phe Ile Tyr Phe Tyr Tyr Tyr His Ser Asn Gly  
 100 105 110  
 Pro Lys Leu Glu Lys Asp Phe Lys Gln Ala Gly Cys Glu Val His Asn  
 115 120 125  
 Arg Leu Leu Asn Leu Gly Leu Lys Tyr Arg Pro Gln Ala Gly Ala Gln  
 130 135 140  
 Asn Asp Gly Arg Asn Gly Gly Pro Tyr Gly Pro Ile Gly Phe Leu Ile  
 145 150 155 160  
 Val Trp Glu Glu Asn Tyr Gly Ser Val Leu Lys Asp His Gly Phe Ile  
 165 170 175  
 Lys Asp Asn

&lt;210&gt;179

&lt;211&gt;115

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;179

Cys Cys Phe Gly Gly Glu Thr Ala Thr Arg Ile Phe Ser Met Thr Pro  
 1 5 10 15  
 Ser Gly Phe Ser Leu Ala Thr Glu Glu Lys Val Gln Val Ser Thr Ala  
 20 25 30  
 Glu Lys Val Ile Lys Ile Leu Ala Leu Ile Phe Phe Pro Ile Ile Leu  
 35 40 45  
 Ile Ala Leu Ala Ile Arg Tyr Phe Leu His Arg Lys Phe Asp Arg Lys  
 50 55 60  
 Cys Phe Val Ile Pro Gln Asp Thr Pro Lys Glu Leu Glu Leu Ile Leu  
 65 70 75 80  
 Ala Ala Asn Pro Gln Leu Val Glu Lys Ala Ala Arg Glu Val His Pro  
 85 90 95  
 Gly Phe Phe Ala Leu Pro Thr Lys Tyr Gln Ser Met Tyr Ile Gln Thr  
 100 105 110  
 Ser Lys Gly  
 115

&lt;210&gt;180

&lt;211&gt;544

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;180

Thr Val Glu Leu Leu Ser Leu Asn Lys Ser Tyr Phe Glu Ile Gln Arg  
 1 5 10 15  
 Leu Arg Tyr Arg Pro Glu Ile Leu Thr Leu Leu Glu Thr Ile Arg Ser  
 20 25 30  
 Lys His Ile Gln Glu Thr Ser Ser Pro Ser Pro Pro Pro Glu Leu  
 35 40 45  
 Gln Lys His Ile Pro Asn Leu Cys Arg Ile Pro Glu Val Ser Ile Tyr  
 50 55 60  
 Thr Glu Gln Glu Thr Ser Ser Lys Pro Leu Lys Ile Gly Val Leu Leu  
 65 70 75 80  
 Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Val Ile Gly Leu Phe  
 85 90 95  
 Asp Ala Leu Arg Val Phe Asn Pro Lys Thr Arg Leu Phe Gly Phe Ile  
 100 105 110  
 Lys Gly Pro Leu Gly Leu Thr Arg Gly Leu Tyr Lys Asp Leu Asp Ile  
 115 120 125  
 Ser Val Ile Tyr Asp Tyr Tyr Asn Met Gly Gly Phe Asp Met Leu Ser  
 130 135 140  
 Ser Ser Arg Glu Lys Ile Lys Thr Glu Glu Gln Lys Lys Asn Ile Leu  
 145 150 155 160  
 Asn Thr Val Lys Gln Leu Lys Leu Asp Gly Leu Leu Ile Ile Gly Gly  
 165 170 175  
 Asn Asn Ser Asn Thr Asp Thr Ala Met Leu Ala Glu Tyr Phe Leu Ala  
 180 185 190  
 His Asn Cys Lys Thr Ser Val Ile Gly Val Pro Lys Thr Ile Asp Gly  
 195 200 205  
 Asp Leu Lys Asn Cys Trp Ile Glu Thr Ser Leu Gly Phe His Thr Ser  
 210 215 220  
 Cys Arg Thr Tyr Ser Glu Met Ile Gly Asn Leu Ala Lys Asp Ala Leu  
 225 230 235 240  
 Ser Ala Lys Lys Tyr His His Phe Ile Arg Leu Met Gly Gln Gln Ala  
 245 250 255  
 Ser Tyr Thr Thr Leu Glu Cys Gly Leu Gln Thr Leu Pro Asn Ile Ala  
 260 265 270  
 Leu Ile Ser Glu Leu Ile Ala Thr Arg Lys Ile Ser Leu Lys Gln Leu  
 275 280 285  
 Ser Glu Gln Leu Ala Leu Gly Leu Val Arg Arg Tyr Lys Ser Gly Lys  
 290 295 300

Asn Tyr Ser Thr Val Leu Ile Pro Glu Gly Leu Ile Glu His Ile Phe  
 305 310 315 320  
 Asp Thr Arg Lys Leu Ile Asp Glu Leu Asn Val Leu Leu Ala Asn Gly  
 325 330 335  
 Asp Ser Ser Met Lys Asn Ser Phe Gln Ala Leu Ser Arg Asp Ile Lys  
 340 345 350  
 Thr Phe His Leu Phe Pro Lys Asp Ile Ala Asn Gln Leu Leu Leu Ala  
 355 360 365  
 Arg Asp Ser His Gly Asn Val Arg Val Ser Lys Ile Ala Thr Glu Glu  
 370 375 380  
 Leu Leu Ala Val Met Val Lys Lys Glu Ile Glu Lys Ile Lys Pro His  
 385 390 395 400  
 Met Glu Phe His Ser Val Ser His Phe Phe Gly Tyr Glu Ala Arg Ala  
 405 410 415  
 Gly Phe Pro Ser Asn Phe Asp Cys Asn Tyr Gly Ile Ala Leu Gly Ile  
 420 425 430  
 Ile Ser Ala Leu Phe Leu Val Arg Gln Lys Thr Gly Tyr Met Ile Thr  
 435 440 445  
 Ile Asn Asn Leu Ala Gln Ser Tyr Thr Glu Trp Gln Gly Gly Ala Thr  
 450 455 460  
 Pro Leu Tyr Lys Met Met His Leu Glu Asn Arg Cys Gly Thr Glu Thr  
 465 470 475 480  
 Pro Val Ile Lys Thr Asp Ser Val Asp Pro Lys Ser Pro Ala Val Gln  
 485 490 495  
 His Leu Leu Gln Gln Ser Asp Ser Cys Leu Val Glu Asp Leu Tyr Arg  
 500 505 510  
 Phe Pro Gly Pro Leu Gln Tyr Phe Gly Lys Glu Glu Leu Ile Asp Gln  
 515 520 525  
 Arg Pro Leu Thr Leu Leu Trp Glu Asn Gln Thr His Ser Pro Leu Leu  
 530 535 540  
 <210>181  
 <211>275  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>181  
 Leu Ile Thr Gly Val Val Leu Glu Lys His Glu Gln Arg Thr Met Phe  
 1 5 10 15  
 Ser Leu Thr Leu Leu Asn Asn Phe Thr Thr Phe Gly Leu Leu His Thr  
 20 25 30  
 Pro Leu His Tyr Asn Pro Pro Tyr Pro Ile Val Ile Leu Leu His Gly  
 35 40 45  
 Leu Ala Ser Asp Lys Thr Gly Ser Lys Arg Ser His Val Arg Leu Ala  
 50 55 60  
 Gln Glu Leu Thr Arg Leu Gly Ile Ala Ala Leu Arg Val Asp Leu Leu  
 65 70 75 80  
 Gly His Gly Asp Cys Glu Gly Glu Leu Met Asp Phe Ser Leu Glu Asn  
 85 90 95  
 Tyr Lys Gln Asn Ile Arg Glu Ile Ile Glu Tyr Thr His Ser Leu Leu  
 100 105 110  
 His Ile Asp Gln Glu Arg Leu Ala Ile Phe Gly Ser Ser Leu Gly Gly  
 115 120 125  
 Thr Leu Ala Leu Gln Thr Leu Pro Phe Phe Asn Lys Ile Lys Ala Leu  
 130 135 140  
 Ala Val Trp Ala Pro Thr Ile Ser Gly Glu Leu Met Ala Ala Glu Ala  
 145 150 155 160  
 Gln Lys Asn Ala Pro Glu Val Ile Thr Met Ser Gln Lys Gly Ala Ile  
 165 170 175  
 Thr Tyr Ala Gly Met Thr Leu Asn Pro Asp Phe Tyr Thr Gln Phe Leu  
 180 185 190  
 Lys Ile Asp Ile Val Lys Glu Leu Met Pro Ser Ala Arg Asn Leu Pro  
 195 200 205  
 Pro Ile Leu Tyr Met Gln Gly Glu Gln Asp Leu Leu Val Ser Ile Asn  
 210 215 220  
 His Arg Thr Leu Phe Thr Glu Ala Phe Ala Asn Gln Asp Lys Pro Ile

460

115 120 125  
 Phe Ser Thr Tyr Ile Leu Ser Leu Arg Ser Tyr Gln Ala Asn Ser Pro  
 130 135 140  
 Ser Asp Asp Thr Trp Gly Ile Trp Phe Gly Ser Ile Asp Asp Pro Val  
 145 150 155 160  
 Gln Ala Val Ile Ser Phe Leu Lys Asp His Gly Phe Ala Leu Pro Ser  
 165 170 175  
 Thr Leu Ala Gln Asp Pro Leu Leu Cys Thr Asn Lys  
 180 185

&lt;210&gt;184

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;184

Leu Cys Phe Lys Cys Ile Tyr Ile Lys Ile Ile Phe Ser Phe Leu Lys  
 1 5 10 15  
 Gln Leu Met Thr Arg Ser Thr Ile Glu Ser Ser Asp Ser Leu Cys Ser  
 20 25 30  
 Arg Ser Phe Ser Gln Lys Leu Ser Val Gln Thr Leu Lys Asn Leu Cys  
 35 40 45  
 Glu Ser Arg Leu Met Lys Ile Thr Ser Leu Val Ile Ala Phe Leu Thr  
 50 55 60  
 Leu Ile Val Gly Gly Ala Leu Ile Ala Leu Ala Gly Gly Gly Val Leu  
 65 70 75 80  
 Ser Phe Pro Leu Gly Leu Ile Leu Gly Ser Val Leu Val Leu Phe Ser  
 85 90 95  
 Ser Ile Tyr Leu Val Ser Cys Cys Lys Phe Phe Thr Leu Lys Glu Met  
 100 105 110  
 Thr Met Thr Cys Ser Val Lys Ser Lys Ile Asn Ile Trp Phe Glu Lys  
 115 120 125  
 Gln Arg Asn Lys Asp Ile Glu Lys Ala Leu Glu Asn Pro Asp Leu Xaa  
 130 135 140  
 Gly Glu Asn Lys Arg Asn Val Gly Asn Arg Ser Ala Arg Asn Gln Leu  
 145 150 155 160  
 Glu Met Ile Leu His Glu Thr Asp Gly Ile Ile Leu Lys Arg Tyr Met  
 165 170 175  
 Lys Gly Ala Lys Met Tyr Phe Tyr Leu  
 180 185

&lt;210&gt;185

&lt;211&gt;200

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;185

Asn Val Leu Leu Phe Met Asn Trp Val Pro Lys Thr Ile Asp His Val  
 1 5 10 15  
 Asp Pro Glu Ser Glu Ile Asp Ile Arg Lys Val Val Ser Cys Tyr Lys  
 20 25 30  
 Leu Ile Lys Glu Cys Gln Pro Glu Phe Arg Ser Leu Ile Ser Glu Leu  
 35 40 45  
 Leu Gly Val Ile Arg Cys Gly Leu Arg Leu Leu Lys Arg Ser Lys Tyr  
 50 55 60  
 Gln Glu Gln Ala Arg Thr Val Ser Asp Glu Asp Ala Pro Leu Phe Cys  
 65 70 75 80  
 Leu Thr Arg Ser Tyr Tyr Gln Asp Gly Tyr Leu Thr Pro Leu Arg Ala  
 85 90 95  
 Gly Pro Arg Asp Leu Ile Asn His Tyr Ile His Leu Arg Arg Arg Glu  
 100 105 110  
 Asn Pro Lys His Phe Phe Ser Pro Lys His Pro Cys Tyr Ala Arg  
 115 120 125  
 Leu Ala Phe Asn Glu Ser Val Cys Val Tyr Arg Glu Leu Phe Asp Ile  
 130 135 140  
 Glu Arg Leu Thr Lys Met Tyr Val Glu Gly Asp Tyr Ser Lys Glu Gln  
 145 150 155 160  
 Glu Lys Asn Leu Gln Ala Ile Leu Ser Phe Val Lys Thr Leu Asp Glu

165 170 175  
 Gly Lys Asp Phe Leu Ile Glu His Lys Asp Thr Asp Leu Ile Gly Arg  
 180 185 190  
 Gly Phe Thr Asp Val Phe Cys Thr  
 195 200  
 <210>186  
 <211>111  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>186  
 Asn Leu Trp Ser His Phe Pro Arg Gly Phe Phe Met Leu Pro Phe Cys  
 1 5 10 15  
 Pro Thr Ile Leu Leu Ala Lys Pro Phe Leu Asn Ser Glu Asn Tyr Gly  
 20 25 30  
 Leu Glu Arg Leu Ala Ala Thr Val Asp Ser Tyr Phe Asp Leu Gly Gln  
 35 40 45  
 Ser Gln Ile Val Phe Leu Ser Lys Gln Asp Gln Gly Ile Thr Val Glu  
 50 55 60  
 Glu Leu Ser Ala Lys Asp Arg Lys Phe Lys Pro Gly Ser Met Asn Cys  
 65 70 75 80  
 Thr Leu Tyr Thr Glu Asp Pro Ile Leu Pro Ala His Asn Ser Phe Ser  
 85 90 95  
 Asn Cys Ser Asp Ile Gln Met Arg Thr Pro Ile Ser Pro Ile His  
 100 105 110  
 <210>187  
 <211>276  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>187  
 Ser Phe His Ile Glu Phe Thr Ile Gly Glu Asn Asn Met Lys Asn Val  
 1 5 10 15  
 Gly Ser Glu Cys Ser Gln Pro Leu Val Met Glu Leu Asn Thr Gln Pro  
 20 25 30  
 Leu Arg Asn Leu Cys Glu Ser Arg Leu Val Lys Ile Thr Ser Phe Val  
 35 40 45  
 Ile Ala Leu Leu Ala Leu Val Gly Gly Ile Thr Leu Thr Ala Leu Ala  
 50 55 60  
 Gly Ala Gly Ile Leu Ser Phe Leu Pro Trp Leu Val Leu Gly Ile Val  
 65 70 75 80  
 Leu Val Val Leu Cys Ala Leu Phe Leu Leu Phe Ser Tyr Lys Phe Cys  
 85 90 95  
 Pro Ile Lys Glu Leu Gly Val Val Tyr Asn Thr Asp Ser Gln Ile His  
 100 105 110  
 Gln Trp Phe Gln Lys Gln Arg Asn Lys Asp Leu Glu Lys Ala Thr Glu  
 115 120 125  
 Asn Pro Glu Leu Phe Gly Glu Asn Arg Ala Glu Asp Asn Asn Arg Ser  
 130 135 140  
 Ala Arg Ser Gln Val Lys Glu Thr Leu Arg Asp Cys Asp Gly Asn Val  
 145 150 155 160  
 Leu Lys Lys Ile Tyr Glu Arg Asn Leu Asp Val Leu Leu Phe Met Asn  
 165 170 175  
 Trp Val Pro Lys Thr Met Asp Asp Val Asp Pro Val Ser Glu Asp Ser  
 180 185 190  
 Ile Arg Thr Val Ile Ser Cys Tyr Lys Leu Ile Lys Ala Cys Lys Pro  
 195 200 205  
 Glu Phe Arg Ser Leu Ile Ser Glu Leu Leu Arg Ala Met Gln Ser Gly  
 210 215 220  
 Leu Gly Leu Leu Ser Arg Cys Ser Arg Tyr Gln Glu Arg Ala Lys Thr  
 225 230 235 240  
 Val Ser His Lys Asp Ala Pro Leu Phe Cys Pro Thr His Ser Tyr Tyr  
 245 250 255  
 Arg Asp Gly Tyr Leu Thr Pro Leu Arg Ala Gly Pro Arg Tyr Ile Ile  
 260 265 270  
 Asn Arg Ala Ile

275  
 <210>188  
 <211>358  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>188  
 Asn Val Arg Lys Asn His Ile Ile Arg Gly Glu Lys Tyr Asn Thr Cys  
 1 5 10 15  
 Thr Val Ile Ala Phe Val Leu Ser Met Ser Tyr Asp Thr Leu Phe Lys  
 20 25 30  
 Asn Leu Glu Lys Glu Asp Ser Val His Lys Ile Cys Asn Glu Ile Phe  
 35 40 45  
 Ala Leu Val Pro Arg Leu Asn Thr Ile Ala Cys Thr Glu Ala Ile Ile  
 50 55 60  
 Lys Asn Leu Pro Lys Ala Asp Ile His Val His Leu Pro Gly Thr Ile  
 65 70 75 80  
 Thr Pro Gln Leu Ala Trp Ile Leu Gly Val Lys Asn Gly Phe Leu Lys  
 85 90 95  
 Trp Ser Tyr Asn Ser Trp Thr Asn His Arg Leu Leu Ser Pro Lys Asn  
 100 105 110  
 Pro His Lys Gln Tyr Ser Asn Ile Phe Arg Asn Phe Gln Asp Ile Cys  
 115 120 125  
 His Glu Lys Asp Pro Asp Leu Ser Val Leu Gln Tyr Asn Ile Leu Asn  
 130 135 140  
 Tyr Asp Phe Asn Ser Phe Asp Arg Val Met Ala Thr Val Gln Gly His  
 145 150 155 160  
 Arg Phe Pro Pro Gly Gly Ile Gln Asn Glu Glu Asp Leu Leu Leu Ile  
 165 170 175  
 Phe Asn Asn Tyr Leu Gln Gln Cys Leu Asp Asp Thr Ile Val Tyr Thr  
 180 185 190  
 Glu Val Gln Gln Asn Ile Arg Leu Ala His Val Leu Tyr Pro Ser Leu  
 195 200 205  
 Pro Glu Lys His Ala Arg Met Lys Phe Tyr Gln Ile Leu Tyr Arg Ala  
 210 215 220  
 Ser Gln Thr Phe Ser Lys His Gly Ile Thr Leu Arg Phe Leu Asn Cys  
 225 230 235 240  
 Phe Asn Lys Thr Phe Ala Pro Gln Ile Asn Thr Gln Glu Pro Ala Gln  
 245 250 255  
 Glu Ala Val Gln Trp Leu Gln Glu Val Asp Ser Thr Phe Pro Gly Leu  
 260 265 270  
 Phe Val Gly Ile Gln Ser Ala Gly Ser Glu Ser Ala Pro Gly Ala Cys  
 275 280 285  
 Pro Lys Arg Leu Ala Ser Gly Tyr Arg Asn Ala Tyr Asp Ser Gly Phe  
 290 295 300  
 Gly Cys Ala Ala His Ala Gly Glu Gly Ile Glu Thr Arg Thr Ile Phe  
 305 310 315 320  
 Ser Ser Ala Lys Val Asn Pro Glu Gly Leu Ile Glu Ile Thr Arg Val  
 325 330 335  
 Thr Phe Ser Ser Leu Lys Arg Lys Gln Pro Ser Ser Leu Pro Ile Arg  
 340 345 350  
 Val Thr Cys Gln Leu Gly  
 355  
 <210>189  
 <211>429  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>189  
 Leu Gln Ser Ala Arg Arg His Leu Asn Thr Ile Phe Ile Leu Asp Phe  
 1 5 10 15  
 Gly Ser Gln Tyr Thr Tyr Val Leu Ala Lys Gln Val Arg Lys Leu Phe  
 20 25 30  
 Val Tyr Cys Glu Val Leu Pro Trp Asn Ile Ser Val Gln Cys Leu Lys  
 35 40 45  
 Glu Arg Ala Pro Leu Gly Ile Ile Leu Ser Gly Gly Pro His Ser Val

```

      50              55              60
Tyr Glu Asn Lys Ala Pro His Leu Asp Pro Glu Ile Tyr Lys Leu Gly
 65              70              75              80
Ile Pro Ile Leu Ala Ile Cys Tyr Gly Met Gln Leu Met Ala Arg Asp
      85              90
Phe Gly Gly Thr Val Ser Pro Gly Val Gly Glu Phe Gly Tyr Thr Pro
 100              105              110
Ile His Leu Tyr Pro Cys Glu Leu Phe Lys His Ile Val Asp Cys Glu
 115              120              125
Ser Leu Asp Thr Glu Ile Arg Met Ser His Arg Asp His Val Thr Thr
 130              135              140
Ile Pro Glu Gly Phe Asn Val Ile Ala Ser Thr Ser Gln Cys Ser Ile
 145              150              155              160
Ser Gly Ile Glu Asn Thr Lys Gln Arg Leu Tyr Gly Leu Gln Phe His
      165              170              175
Pro Glu Val Ser Asp Ser Thr Pro Thr Gly Asn Lys Ile Leu Glu Thr
 180              185              190
Phe Val Gln Glu Ile Cys Ser Ala Pro Thr Leu Trp Asn Pro Leu Tyr
 195              200              205
Ile Gln Gln Asp Leu Val Ser Lys Ile Gln Asp Thr Val Ile Glu Val
 210              215              220
Phe Asp Glu Val Ala Gln Ser Leu Asp Val Gln Trp Leu Ala Gln Gly
 225              230              235              240
Thr Ile Tyr Ser Asp Val Ile Glu Ser Ser Arg Ser Gly His Ala Ser
      245              250              255
Glu Val Ile Lys Ser His His Asn Val Gly Gly Leu Pro Lys Asn Leu
 260              265              270
Lys Leu Lys Leu Val Glu Pro Leu Arg Tyr Leu Phe Lys Asp Glu Val
 275              280              285
Arg Ile Leu Gly Glu Ala Leu Gly Leu Ser Ser Tyr Leu Leu Asp Arg
 290              295              300
His Pro Phe Pro Gly Pro Gly Leu Thr Ile Arg Val Ile Gly Glu Ile
 305              310              315              320
Leu Pro Glu Tyr Leu Ala Ile Leu Arg Arg Ala Asp Leu Ile Phe Ile
      325              330              335
Glu Glu Leu Arg Lys Ala Lys Leu Tyr Asp Lys Ile Ser Gln Ala Phe
 340              345              350
Ala Leu Phe Leu Pro Ile Lys Ser Val Ser Val Lys Gly Asp Cys Arg
 355              360              365
Ser Tyr Gly Tyr Thr Ile Ala Leu Arg Ala Val Glu Ser Thr Asp Phe
 370              375              380
Met Thr Gly Arg Trp Ala Tyr Leu Pro Cys Asp Val Leu Ser Ser Cys
 385              390              395              400
Ser Ser Arg Ile Ile Asn Glu Ile Pro Glu Val Ser Arg Val Val Tyr
      405              410              415
Asp Ile Ser Asp Lys Pro Pro Ala Thr Ile Glu Trp Glu
 420              425

```

&lt;210&gt;190

&lt;211&gt;266

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;190

```

Ala Pro Ile Gly Ala Ala Ile Gly Ile Gly Pro Leu Gly Ile Ser Arg
 1              5              10              15
Ala His His Leu Val Glu Ala Gly Ala Asn Val Leu Val Ile Asp Thr
      20              25              30
Ala His Ala His Ser Lys Gly Val Phe Gln Thr Val Leu Glu Ile Lys
      35              40              45
Ser Gln Phe Pro Gln Ile Ser Leu Val Val Gly Asn Leu Val Thr Ala
 50              55              60
Glu Ala Ala Val Ser Leu Ala Glu Ile Gly Val Asp Ala Val Lys Val
 65              70              75              80
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Ser Gly Val
      85              90              95

```



Gly Tyr Pro Gln Ile Thr Ala Ile Thr Asn Val Ala Lys Ala Leu Lys  
                   100                  105                  110  
 Asn Ser Ala Val Thr Val Ile Ala Asp Gly Arg Ile Arg Tyr Ser Gly  
                   115                  120                  125  
 Asp Val Val Lys Ala Leu Ala Gly Ala Asp Cys Val Met Leu Gly  
                   130                  135                  140  
 Ser Leu Leu Ala Gly Thr Asp Glu Ala Pro Gly Asp Ile Val Ser Ile  
 145                  150                  155                  160  
 Asp Glu Lys Leu Phe Lys Arg Tyr Arg Gly Met Gly Ser Leu Gly Ala  
                   165                  170                  175  
 Met Lys Gln Gly Ser Ala Asp Arg Tyr Phe Gln Thr Gln Gly Gln Lys  
                   180                  185                  190  
 Lys Leu Val Pro Gly Gly Val Glu Gly Leu Val Ala Tyr Lys Gly Ser  
                   195                  200                  205  
 Val His Asp Val Leu Tyr Gln Ile Leu Gly Gly Ile Arg Ser Gly Met  
                   210                  215                  220  
 Gly Tyr Val Gly Ala Glu Thr Leu Lys Asp Leu Lys Thr Lys Ala Ser  
 225                  230                  235                  240  
 Phe Val Arg Ile Thr Glu Ser Gly Arg Ala Glu Ser His Ile His Asn  
                   245                  250                  255  
 Ile Tyr Lys Val Gln Pro Thr Leu Asn Tyr  
                   260                  265

&lt;210&gt;191

&lt;211&gt;170

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;191

Lys Ile Phe Ile Trp Phe Val Glu Lys Ile Val Ile Leu Ser Met Ile  
   1                  5                  10                  15  
 Met Thr Thr Ile Ser Asn Ser Pro Ser Pro Ala Leu Asn Pro Glu Leu  
                   20                  25                  30  
 Ser Leu Ile Pro Pro Pro Thr Leu Val Ser Ser Gly Thr Gln Thr Ser  
                   35                  40                  45  
 Leu Ala Tyr Thr Ile Pro Ala Gln Gly Arg Arg Ser Thr Leu Arg Ile  
                   50                  55                  60  
 Ile Leu Asp Ile Phe Ile Ile Ile Leu Gly Leu Ala Thr Ile Ile Ser  
 65                  70                  75                  80  
 Thr Phe Ile Val Ile Phe Phe Leu Asn Gly Leu Asn Leu Leu Ser Thr  
                   85                  90                  95  
 Pro Ser Ile Ile Ser Ser Ser Cys Leu Ile Ile Val Gly Leu Leu Phe  
                   100                  105                  110  
 Leu Ile Met Gly Leu Tyr Phe Met Ile Ser Ser Leu Asp Gln Gly Leu  
                   115                  120                  125  
 Val Gly Leu Leu Gln Lys Glu Leu Ser Gln Ala Glu Glu Arg Glu Glu  
                   130                  135                  140  
 Glu Tyr Ile Gln Glu Ile Glu Ala Leu Arg Gly Ala Pro Arg Ala Glu  
 145                  150                  155                  160  
 Ser Pro Thr Glu Ser Pro Ser Thr Trp Leu  
                   165                  170

&lt;210&gt;192

&lt;211&gt;140

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;192

Leu Leu Leu Ala Cys Phe Gln Phe Leu Leu Arg Arg Arg Asp Met Glu  
   1                  5                  10                  15  
 Gln Pro Asn Cys Val Ile Gln Asp Thr Thr Thr Val Leu Tyr Ala Leu  
                   20                  25                  30  
 Asn Ser Phe Asp Pro Arg Leu Ser Asp Asp Thr His Arg Leu Gly Lys  
                   35                  40                  45  
 Gln Ser Pro Leu Glu Ala Glu Asn Ala Leu Gly Glu Phe Ile Glu Gly  
                   50                  55                  60  
 Leu Asp Thr Asn Ser Phe Pro Leu Glu Glu Val Ala Ile Pro Ile Leu  
                   65                  70                  75                  80

Pro Gly Tyr His Pro Lys Phe Tyr Leu Ser Phe Ile Asp Arg Asp Asp  
                             85                            90                            95  
 Gln Gly Val His Tyr Glu Val Leu Asp Gly Val Phe Leu Lys Thr Val  
                             100                            105                            110  
 Ala Ala Cys Ile Ile Glu Asn Ser Phe Leu Thr Asp Ser Met Ser Pro  
                             115                            120                            125  
 Glu Leu Leu Ser Glu Val Lys Glu Ala Leu Lys Arg  
                             130                            135                            140  
 <210>193  
 <211>416  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>193  
 Asn Asp Asp Asp Pro Met Asp Glu Ser Asp Gly Glu Glu Ala Ser Lys  
   1                            5                            10                            15  
 Asp Ser Ala Phe Ser Ala Ser Phe Ser Tyr Glu Phe Val Lys Ser Ser  
                             20                            25                            30  
 Thr Arg Glu Ser Lys Asn Thr Val Thr His Ser Thr Ala Ser Arg Thr  
                             35                            40                            45  
 Leu Tyr Ile Leu Arg Gln Asp Cys Ser Tyr Asp Pro Arg Ala Leu Lys  
                             50                            55                            60  
 Val Asp Asp Glu Phe Arg Tyr Trp Val Glu Lys Arg Leu Asp Ala Lys  
                             65                            70                            75                            80  
 Asn Pro Asp Ser Leu Asn Ala Phe Val Lys Glu Val Gly Thr His Tyr  
                             85                            90                            95  
 Val Ala Ser Val Thr Tyr Gly Gly Ile Gly Phe Gln Val Leu Lys Met  
                             100                            105                            110  
 Ser Tyr Leu Gln Val Glu Glu Leu Glu Lys Glu Lys Ile Ser Ile Ser  
                             115                            120                            125  
 Val Ala Ala Ala Ser Ser Leu Leu Lys Ser Lys Thr Ser Asn Ala Thr  
                             130                            135                            140  
 Glu Lys Gly Tyr Ser Ser Tyr Gln Ser Glu Ser Ser Ala Gln Thr Val  
   145                            150                            155                            160  
 Phe Leu Gly Gly Thr Val Leu Pro Asp Leu Gln Gln Asp Lys Leu Asp  
                             165                            170                            175  
 Phe Lys Asp Trp Ser Glu Ser Ile Pro Asn Glu Pro Ile Pro Leu Ala  
                             180                            185                            190  
 Ile Ser Val Ser Ser Ile Thr Asp Leu Ile Ile Pro Glu Leu Phe Pro  
                             195                            200                            205  
 Ser Glu Asp Ala Gln Val Leu Ser Gln Lys Lys Ser Ala Leu Gly Gln  
                             210                            215                            220  
 Val Ile Leu Asn Tyr Leu Glu Ser His Lys Pro Lys Glu Glu Gly Pro  
   225                            230                            235                            240  
 Lys Pro Val Gln Ile Thr Ser Gly Phe Asn Ser Ser Ser Ser Val Phe  
                             245                            250                            255  
 Thr Leu Gln Ala Ala Lys Ala Pro Lys Thr Val Ser Phe Pro Tyr Ile  
                             260                            265                            270  
 Asp Tyr Trp Ser Thr Ile Pro Tyr Leu Phe Pro Thr Leu Lys Glu Thr  
                             275                            280                            285  
 Ser Gly Ala Gln Pro Leu Ser Phe Tyr Leu Arg Phe Asp Asp Ile Phe  
                             290                            295                            300  
 Glu Gln Gln Asn Leu Val His Asn Thr Ser Tyr Ile Leu Ala Ser Thr  
   305                            310                            315                            320  
 Ser Val Arg Leu Gly Tyr Phe Gly Asp Ser Tyr Arg Asp Tyr Asp Ala  
                             325                            330                            335  
 Leu Ser Phe Tyr Gly Ser Trp Pro Gln Ala Tyr Phe Asp Trp Ala Gly  
                             340                            345                            350  
 Tyr Lys Asp Arg Cys Thr Trp Thr Leu Glu Lys Leu Asn Thr Thr Gly  
                             355                            360                            365  
 Asp Leu Phe Ile Arg Ser Gly Asp Glu Ile Arg Leu Lys His Asn Thr  
                             370                            375                            380  
 Ser Gly Lys Tyr Leu Ala Thr Thr Ser Met Ser Asp Gly Tyr Gln Thr  
   385                            390                            395                            400  
 Leu Thr Cys Thr Thr Gln Thr Ser Asp Ser Val Phe Ile Ile Thr Val

405 410 415  
 <210>194  
 <211>303  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>194  
 Val Gly Gln Lys Arg Ala Asn Xaa Ser Lys Phe Ile Phe Leu Ile Ser  
 1 5 10 15  
 Glu Glu Ser Met Lys Gln Pro Met Ser Leu Ile Phe Ser Ser Val Cys  
 20 25 30  
 Leu Gly Leu Gly Leu Gly Ser Leu Ser Ser Cys Asn Gln Lys Pro Ser  
 35 40 45  
 Trp Asn Tyr His Asn Thr Ser Thr Ser Glu Glu Phe Phe Val His Gly  
 50 55 60  
 Asn Lys Ser Val Ser Gln Leu Pro His Tyr Pro Ser Ala Phe Arg Thr  
 65 70 75 80  
 Thr Gln Ile Phe Ser Glu Glu His Asn Asp Pro Tyr Val Val Ala Lys  
 85 90 95  
 Thr Asp Glu Glu Ser Arg Lys Ile Trp Arg Glu Ile His Lys Asn Leu  
 100 105 110  
 Lys Ile Lys Gly Ser Tyr Ile Pro Ile Ser Thr Tyr Gly Ser Leu Met  
 115 120 125  
 His Pro Lys Ser Ala Ala Leu Thr Leu Lys Thr Tyr Arg Pro His Pro  
 130 135 140  
 Ile Trp Ile Asn Gly Tyr Glu Arg Ser Phe Asn Ile Asp Thr Gly Lys  
 145 150 155 160  
 Tyr Leu Lys Asn Gly Ser Arg Arg Arg Thr Ser His Asp Gly Pro Lys  
 165 170 175  
 Asn Arg Ala Val Leu Asn Leu Ile Lys Ser Ser Gly Arg Arg Cys Asn  
 180 185 190  
 Ala Ile Gly Leu Glu Met Thr Glu Glu Asp Phe Val Ile Ala Arg Arg  
 195 200 205  
 Arg Glu Gly Val Tyr Ser Leu Tyr Pro Val Glu Val Cys Ser Tyr Pro  
 210 215 220  
 Gln Gly Asn Pro Phe Val Ile Ala Tyr Ala Trp Ile Ala Asp Glu Ser  
 225 230 235 240  
 Ala Cys Ser Lys Glu Val Leu Pro Val Lys Gly Tyr Tyr Ser Leu Val  
 245 250 255  
 Trp Glu Ser Val Ser Ser Ser Asp Ser Leu Asn Ala Phe Gly Asp Ser  
 260 265 270  
 Phe Ala Glu Asp Tyr Leu Arg Ser Thr Phe Leu Ala Asn Gly Thr Ser  
 275 280 285  
 Ile Leu Cys Val His Glu Ser Tyr Lys Lys Val Pro Pro Gln Pro  
 290 295 300  
 <210>195  
 <211>88  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>195  
 Val Lys Glu Tyr Leu Asp Phe Leu Val Gln Arg Asn Val Glu Arg Asp  
 1 5 10 15  
 Pro Gln Thr Lys Arg His Cys Thr Val Ser Gln Lys Phe Gly Gly Glu  
 20 25 30  
 Ser Ile Asp Ala Lys Thr Thr Thr Gly Gln Leu Phe His Ile Ala Gly  
 35 40 45  
 Lys Thr Glu Pro Gly His Gly Lys Leu Cys Leu Gly Glu Ser Ile Leu  
 50 55 60  
 Lys Gln Leu Leu Ala Leu Gly Ile Ile Thr Gly Tyr Glu Asn Arg Glu  
 65 70 75 80  
 Arg Glu Val Trp Val Tyr Leu Asp  
 85  
 <210>196  
 <211>203  
 <212>PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;196

Thr Ser Leu His Lys Ile Leu Asp Cys Lys Tyr Lys Pro Val Phe Ile  
 1 5 10 15  
 Gln Asn Thr Val Ala Ser Glu Thr Tyr Pro Ser Gln Ile Leu His Ala  
 20 25 30  
 Gln Arg Glu Val Arg Asp Ala Tyr Phe Asn Gln Ala Asp Cys His Pro  
 35 40 45  
 Ala Arg Ala Asn Gln Ile Leu Glu Ala Lys Lys Ile Cys Leu Leu Asp  
 50 55 60  
 Val Tyr His Thr Asn His Tyr Ser Val Phe Thr Phe Cys Val Asp Asn  
 65 70 75 80  
 Tyr Pro Asn Leu Arg Phe Thr Phe Val Ser Ser Lys Asn Asn Glu Met  
 85 90 95  
 Asn Gly Leu Ser Asn Pro Leu Asp Asn Val Leu Val Glu Ala Met Val  
 100 105 110  
 Arg Arg Thr His Ala Arg Asn Leu Leu Ala Ala Cys Lys Ile Arg Asn  
 115 120 125  
 Ile Glu Val Pro Arg Val Val Gly Leu Asp Leu Arg Ser Gly Ile Leu  
 130 135 140  
 Ile Ser Lys Leu Glu Leu Lys Gln Pro Gln Phe Gln Ser Leu Thr Glu  
 145 150 155 160  
 Asp Phe Val Asn His Ser Thr Asn Gln Glu Glu Ala Arg Val His Gln  
 165 170 175  
 Lys His Val Leu Leu Ile Ser Leu Ile Leu Leu Cys Lys Gln Ala Ala  
 180 185 190  
 Leu Glu Ser Phe Gln Glu Lys Lys Arg Ser Ser  
 195 200

&lt;210&gt;197

&lt;211&gt;454

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;197

Met Lys Lys Val Leu Ile Ala Asn Arg Gly Glu Ile Ala Val Arg Ile  
 1 5 10 15  
 Ile Arg Ala Cys His Asp Leu Gly Leu Ser Thr Val Ala Val Tyr Ser  
 20 25 30  
 Leu Ala Asp Gln Glu Ala Leu His Val Leu Leu Ala Asp Glu Ala Ile  
 35 40 45  
 Cys Ile Gly Glu Pro Gln Ala Ala Lys Ser Tyr Leu Lys Ile Ser Asn  
 50 55 60  
 Ile Leu Ala Ala Cys Glu Ile Thr Gly Ala Asp Ala Val His Pro Gly  
 65 70 75 80  
 Tyr Gly Phe Leu Ser Glu Asn Ala Asn Phe Ala Ser Ile Cys Glu Ser  
 85 90 95  
 Cys Gly Leu Thr Phe Ile Gly Pro Ser Ser Glu Ser Ile Ala Met Met  
 100 105 110  
 Gly Asp Lys Ile Ala Ala Lys Ser Leu Ala Lys Lys Ile Lys Cys Pro  
 115 120 125  
 Val Ile Pro Gly Ser Glu Gly Ile Ile Glu Asp Glu Ser Glu Gly Leu  
 130 135 140  
 Lys Ile Ala Glu Lys Ile Gly Phe Pro Ile Val Ile Lys Ala Val Ala  
 145 150 155 160  
 Gly Gly Gly Gly Arg Gly Ile Arg Ile Val Lys Glu Lys Asp Glu Phe  
 165 170 175  
 Tyr Arg Ala Phe Ser Ala Ala Arg Ala Glu Ala Glu Ala Gly Phe Asn  
 180 185 190  
 Asn Pro Asn Val Tyr Ile Glu Lys Phe Ile Glu Asn Pro Arg His Leu  
 195 200 205  
 Glu Ile Gln Val Ile Gly Asp Thr His Gly Asn Tyr Val His Leu Gly  
 210 215 220  
 Glu Arg Asp Cys Thr Ile Gln Arg Arg Arg Gln Lys Leu Ile Glu Glu  
 225 230 235 240  
 Thr Pro Ser Pro Ile Leu Asn Ala Glu Ile Arg Val Lys Val Gly Lys

245 250 255  
 Val Ala Val Asp Leu Ala Arg Ser Ala Gly Tyr Phe Ser Val Gly Thr  
 260 265 270  
 Val Glu Phe Leu Leu Asp Lys Asp Lys Lys Phe Tyr Phe Met Glu Met  
 275 280 285  
 Asn Thr Arg Ile Gln Val Glu His Thr Ile Thr Glu Glu Val Thr Gly  
 290 295 300  
 Ile Asp Leu Val Lys Glu Gln Ile His Val Ala Met Gly Asn Lys Leu  
 305 310 315 320  
 Pro Trp Lys Gln Lys Asn Ile Glu Phe Ser Gly His Ile Ile Gln Cys  
 325 330 335  
 Arg Ile Asn Ala Glu Asp Pro Thr Asn Asn Phe Ser Pro Ser Pro Gly  
 340 345 350  
 Arg Leu Asp Tyr Tyr Leu Pro Pro Ala Gly Pro Ser Ile Arg Val Asp  
 355 360 365  
 Gly Ala Cys Tyr Ser Gly Tyr Ala Ile Pro Pro Tyr Tyr Asp Ser Met  
 370 375 380  
 Ile Ala Lys Val Ile Ala Lys Gly Lys Asn Arg Glu Glu Ala Ile Ala  
 385 390 395 400  
 Ile Met Lys Arg Ala Leu Lys Glu Phe His Ile Gly Gly Val Gln Ser  
 405 410 415  
 Thr Ile Pro Phe His Gln Phe Met Leu Asp Asn Pro Lys Phe Leu Glu  
 420 425 430  
 Ser Asn Tyr Asp Ile Asn Tyr Ile Asp Asn Leu Leu Ala Gln Gly Asn  
 435 440 445  
 Ser Phe Phe Lys Glu Phe  
 450  
 <210>198  
 <211>167  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>198  
 Met Asp Leu Lys Gln Ile Glu Lys Leu Met Ile Ala Met Gly Arg Asn  
 1 5 10 15  
 Gly Met Lys Arg Phe Ala Ile Lys Arg Glu Gly Leu Glu Leu Glu Leu  
 20 25 30  
 Glu Arg Asp Thr Arg Glu Gly Asn Arg Gln Glu Pro Val Phe Tyr Asp  
 35 40 45  
 Ser Arg Leu Phe Ser Gly Phe Ser Gln Glu Arg Pro Ile Pro Thr Asp  
 50 55 60  
 Pro Lys Lys Asp Thr Ile Lys Glu Thr Thr Thr Glu Asn Ser Glu Thr  
 65 70 75 80  
 Ser Thr Thr Thr Ser Ser Gly Asp Phe Ile Ser Ser Pro Leu Val Gly  
 85 90 95  
 Thr Phe Tyr Gly Ser Pro Ala Pro Asp Ser Pro Ser Phe Val Lys Pro  
 100 105 110  
 Gly Asp Ile Val Ser Glu Asp Thr Ile Val Cys Ile Val Glu Ala Met  
 115 120 125  
 Lys Val Met Asn Glu Val Lys Ala Gly Met Ser Gly Arg Val Leu Glu  
 130 135 140  
 Val Leu Ile Thr Asn Gly Asp Pro Val Gln Phe Gly Ser Lys Leu Phe  
 145 150 155 160  
 Arg Ile Ala Lys Asp Ala Ser  
 165  
 <210>199  
 <211>185  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>199  
 Met Val Leu Ser Ser Gln Leu Ser Val Gly Met Phe Ile Ser Thr Lys  
 1 5 10 15  
 Asp Gly Leu Tyr Lys Val Thr Ser Val Ser Lys Val Ala Gly Pro Lys  
 20 25 30  
 Gly Glu Ser Phe Ile Lys Val Ala Leu Gln Ala Ala Asp Ser Asp Val

```

      35      40      45
Val Ile Glu Arg Asn Phe Lys Ala Thr Gln Glu Val Lys Glu Ala Gln
      50      55      60
Phe Glu Thr Arg Thr Leu Glu Tyr Leu Tyr Leu Glu Asp Glu Ser Tyr
      65      70      75      80
Leu Phe Leu Asp Leu Gly Asn Tyr Glu Lys Leu Phe Ile Pro Gln Glu
      85      90      95
Ile Met Lys Asp Asn Phe Leu Phe Leu Lys Ala Gly Val Thr Val Ser
      100      105      110
Ala Met Val Tyr Asp Asn Val Val Phe Ser Val Glu Leu Pro His Phe
      115      120      125
Leu Glu Leu Met Val Ser Lys Thr Asp Phe Pro Gly Asp Ser Leu Ser
      130      135      140
Leu Ser Gly Gly Val Lys Lys Ala Leu Leu Glu Thr Gly Ile Glu Val
      145      150      155      160
Met Val Pro Pro Phe Val Glu Ile Gly Asp Val Ile Lys Ile Asp Thr
      165      170      175
Arg Thr Cys Glu Tyr Ile Gln Arg Val
      180      185

```

&lt;210&gt;200

&lt;211&gt;229

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;200

```

Val Lys Lys Gln Glu Ser Val Leu Val Gly Pro Ser Ile Met Gly Ala
  1      5      10      15
Asp Leu Thr Cys Leu Gly Val Glu Ala Lys Lys Leu Glu Gln Ala Gly
      20      25      30
Ser Asp Phe Ile His Ile Asp Ile Met Asp Gly His Phe Val Pro Asn
      35      40      45
Leu Thr Phe Gly Pro Gly Ile Ile Ala Ala Ile Asn Arg Ser Thr Asp
      50      55      60
Leu Phe Leu Glu Val His Ala Met Ile Tyr Asn Pro Phe Glu Phe Ile
      65      70      75      80
Glu Ser Phe Val Arg Ser Gly Ala Asp Arg Ile Ile Val His Phe Glu
      85      90      95
Ala Ser Glu Asp Ile Lys Glu Leu Leu Ser Tyr Ile Lys Lys Cys Gly
      100      105      110
Val Gln Ala Gly Leu Ala Phe Ser Pro Asp Thr Ser Ile Glu Phe Leu
      115      120      125
Pro Ser Phe Leu Pro Phe Cys Asp Val Val Val Leu Met Ser Val Tyr
      130      135      140
Pro Gly Phe Thr Gly Gln Ser Phe Leu Pro Asn Thr Ile Glu Lys Ile
      145      150      155      160
Ala Phe Ala Arg His Ala Ile Lys Thr Leu Gly Leu Lys Asp Ser Cys
      165      170      175
Leu Ile Glu Val Asp Gly Gly Ile Asp Gln Gln Ser Ala Pro Leu Cys
      180      185      190
Arg Asp Ala Gly Ala Asp Ile Leu Val Thr Ala Ser Tyr Leu Phe Glu
      195      200      205
Ala Asp Ser Leu Ala Met Glu Asp Lys Ile Leu Leu Leu Arg Gly Glu
      210      215      220
Asn Tyr Gly Val Lys
      225

```

&lt;210&gt;201

&lt;211&gt;397

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;201

```

Pro Ile Lys Asp Lys Ile Leu Met Ser Ser Pro Val Asn Asn Thr Pro
  1      5      10      15
Ser Ala Pro Asn Ile Pro Ile Pro Ala Pro Thr Thr Pro Gly Ile Pro
      20      25      30
Thr Thr Lys Pro Arg Ser Ser Phe Ile Glu Lys Val Ile Ile Val Ala

```

35 40 45  
 Lys Tyr Ile Leu Phe Ala Ile Ala Ala Thr Ser Gly Ala Leu Gly Thr  
 50 55 60  
 Ile Leu Gly Leu Ser Gly Ala Leu Thr Pro Gly Ile Gly Ile Ala Leu  
 65 70 75 80  
 Leu Val Ile Phe Phe Val Ser Met Val Leu Leu Gly Leu Ile Leu Lys  
 85 90 95  
 Asp Ser Ile Ser Gly Gly Glu Glu Arg Arg Leu Arg Glu Glu Val Ser  
 100 105 110  
 Arg Phe Thr Ser Glu Asn Gln Arg Leu Thr Val Ile Thr Thr Thr Leu  
 115 120 125  
 Glu Thr Glu Val Lys Asp Leu Lys Ala Ala Lys Asp Gln Leu Thr Leu  
 130 135 140  
 Glu Ile Glu Ala Phe Arg Asn Glu Asn Gly Asn Leu Lys Thr Thr Ala  
 145 150 155 160  
 Glu Asp Leu Glu Glu Gln Val Ser Lys Leu Ser Glu Gln Leu Glu Ala  
 165 170 175  
 Leu Glu Arg Ile Asn Gln Leu Ile Gln Ala Asn Ala Gly Asp Ala Gln  
 180 185 190  
 Glu Ile Ser Ser Glu Leu Lys Lys Leu Ile Ser Gly Trp Asp Ser Lys  
 195 200 205  
 Val Val Glu Gln Ile Asn Thr Ser Ile Gln Ala Leu Lys Val Leu Leu  
 210 215 220  
 Gly Gln Glu Trp Val Gln Glu Ala Gln Thr His Val Lys Ala Met Gln  
 225 230 235 240  
 Glu Gln Ile Gln Ala Leu Gln Ala Glu Ile Leu Gly Met His Asn Gln  
 245 250 255  
 Ser Thr Ala Leu Gln Lys Ser Val Glu Asn Leu Leu Val Gln Asp Gln  
 260 265 270  
 Ala Leu Thr Arg Val Val Gly Glu Leu Leu Glu Ser Glu Asn Lys Leu  
 275 280 285  
 Ser Gln Ala Cys Ser Ala Leu Arg Gln Glu Ile Glu Lys Leu Ala Gln  
 290 295 300  
 His Glu Thr Ser Leu Gln Gln Arg Ile Asp Ala Met Leu Ala Gln Glu  
 305 310 315 320  
 Gln Asn Leu Ala Glu Gln Val Thr Ala Leu Glu Lys Met Lys Gln Glu  
 325 330 335  
 Ala Gln Lys Ala Glu Ser Glu Phe Ile Ala Cys Val Arg Asp Arg Thr  
 340 345 350  
 Phe Gly Arg Arg Glu Thr Pro Pro Pro Thr Thr Pro Val Val Glu Gly  
 355 360 365  
 Asp Glu Ser Gln Glu Glu Asp Glu Gly Gly Thr Pro Pro Val Ser Gln  
 370 375 380  
 Pro Ser Ser Pro Val Asp Arg Ala Thr Gly Asp Gly Gln  
 385 390 395  
 <210>202  
 <211>118  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>202  
 Phe Ser Leu Val Asn Arg Glu Thr Ser Ser Leu Ser Leu Arg Ser Ser  
 1 5 10 15  
 Pro Pro Leu Ile Glu Ser Leu Arg Ile Lys Pro Lys Ser Thr Ile Glu  
 20 25 30  
 Thr Lys Lys Ile Thr Arg Arg Ala Ile Pro Ile Pro Gly Val Ser Ala  
 35 40 45  
 Pro Asp Arg Pro Arg Ile Val Pro Ser Ala Pro Asp Val Ala Ala Ile  
 50 55 60  
 Ala Asn Ser Met Tyr Leu Ala Thr Met Ile Thr Phe Ser Met Lys Leu  
 65 70 75 80  
 Glu Arg Gly Phe Val Val Gly Ile Pro Gly Val Val Gly Ala Gly Ile  
 85 90 95  
 Gly Met Phe Gly Ala Glu Gly Val Leu Phe Thr Gly Asp Asp Ile Arg  
 100 105 110

Ile Leu Ser Leu Ile Gly

115

&lt;210&gt;203

&lt;211&gt;217

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;203

Met His Ser Lys Phe Leu Ser Arg Arg Lys Lys Asn Ser Ser His Lys  
 1 5 10 15  
 Glu Glu Thr Ser Trp Asp Cys Ile Ala Ser Ser Tyr Asn Lys Ile Val  
 20 25 30  
 Gln Asp Lys Gly His Tyr Tyr His Arg Glu Thr Ile Leu Pro Gln Leu  
 35 40 45  
 Leu Pro Ser Leu Thr Leu Gly Ser Lys Ser Ser Val Leu Asp Ile Gly  
 50 55 60  
 Cys Gly Gln Gly Phe Leu Glu Arg Ala Leu Pro Lys Glu Cys Arg Tyr  
 65 70 75 80  
 Leu Gly Ile Asp Ile Ser Ser Arg Leu Ile Ala Leu Ala Lys Lys Met  
 85 90 95  
 Arg Ser Val Asn Ser His Gln Phe Lys Val Ala Asp Leu Ser Lys Arg  
 100 105 110  
 Leu Glu Phe Val Glu Pro Thr Leu Phe Ser His Ala Val Ala Ile Leu  
 115 120 125  
 Ser Leu Gln Asn Met Glu Phe Pro Gly Glu Ala Ile Arg Asn Thr Ala  
 130 135 140  
 Thr Leu Leu Glu Pro Leu Gly Gln Phe Phe Ile Val Leu Asn His Pro  
 145 150 155 160  
 Cys Phe Arg Ile Pro Arg Ala Ser Ser Trp His Tyr Asp Glu Asn Lys  
 165 170 175  
 Lys Ser Tyr Leu Ser Ser Tyr Arg Ser Leu Ser Leu Pro Asn Glu Asn  
 180 185 190  
 Pro Asn His Gly Ser Pro Arg Thr Lys Arg Phe Ala Phe Tyr Pro Leu  
 195 200 205  
 Leu Ser Leu Ser Ser Lys Leu Leu Val  
 210 215

&lt;210&gt;204

&lt;211&gt;437

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;204

Lys Thr Xaa Asn Ser Cys Ile Met Phe Arg Lys Leu Phe Pro Phe Ser  
 1 5 10 15  
 Lys Lys Lys Thr Gly Gln Lys Gln Arg Leu Arg Asn Asn Gly Leu Leu  
 20 25 30  
 Gln Ala Ile Ile Gln Ser Ile Lys Val Leu Leu His Asn Glu Ala Ser  
 35 40 45  
 Lys Glu Ala Cys Val Leu Ser Tyr Tyr Gly Leu Leu Thr Cys Val Pro  
 50 55 60  
 Ile Leu Val Phe Phe Leu Arg Leu Ser Gln His Leu Phe Thr Asn Leu  
 65 70 75 80  
 Asn Trp Lys Glu Trp Leu Ile Ile Lys Phe Pro Asp Tyr Lys Lys Pro  
 85 90 95  
 Ile Val Ala Ile Val Glu Ala Ala Tyr His Ala Thr Glu Ser Asn Ile  
 100 105 110  
 Gly Leu Val Leu Val Gly Ser Phe Phe Val Phe Cys Trp Ala Gly Ile  
 115 120 125  
 Leu Met Leu Leu Ser Leu Glu Asp Gly Leu Asn Lys Ile Phe Arg Thr  
 130 135 140  
 Ser Trp Thr Pro Ile Ser Leu Lys Arg Leu Val Ser Tyr Phe Val Ile  
 145 150 155 160  
 Thr Leu Val Ser Pro Met Ile Phe Ile Ile Val Cys Gly Ser Trp Ile  
 165 170 175  
 Tyr Ile Thr Gln Ile Met Pro Ile Gln Tyr Ala Lys Leu Phe Ser Leu  
 180 185 190



Ser His Ser Met Thr Ala Leu Tyr Phe Ile Ser Arg Phe Val Pro Tyr  
 195 200 205  
 Leu Leu Leu Tyr Leu Ala Leu Phe Cys Cys Tyr Ala Phe Leu Pro Arg  
 210 215 220  
 Val Ala Ile Gln Lys Thr Ser Ala Leu Ile Ser Thr Leu Ile Ile Gly  
 225 230 235 240  
 Ser Val Trp Ile Val Phe Gln Lys Ala Phe Phe Ser Leu Gln Val Ser  
 245 250 255  
 Ile Phe Asn Tyr Ser Phe Thr Tyr Gly Ala Leu Val Ala Leu Pro Ser  
 260 265 270  
 Phe Leu Leu Leu Leu Tyr Ile Tyr Thr Met Ile Tyr Leu Phe Gly Gly  
 275 280 285  
 Ala Leu Thr Phe Ile Ile Gln Asn Arg Gly Cys Thr Phe Ile Phe Leu  
 290 295 300  
 Gly Asp Lys Ile Leu Pro Ser Cys Tyr Leu Gln Leu Ile Thr Ser Thr  
 305 310 315 320  
 Tyr Ile Leu Ala Leu Thr Thr Arg Gln Phe Asn Glu Gly Leu Ser Pro  
 325 330 335  
 Leu Thr Ala Gln Phe Ile Ala Lys Gln Ser Lys Val Pro Ile Gly Glu  
 340 345 350  
 Val Ser Gln Cys Leu Asp Val Leu Glu Lys Glu Gly Phe Leu Phe Pro  
 355 360 365  
 Tyr Asn Asn Gly Tyr Gln Pro Val Phe Asn Phe Ser Glu Leu Thr Ile  
 370 375 380  
 Lys Asp Ile Ala Asp Lys Leu Leu His Arg Glu Ile Phe Lys Lys Phe  
 385 390 395 400  
 Asn Pro Asp Leu Gly Ile Thr Phe Ile Glu Asn Ser Phe Gln Asn Ile  
 405 410 415  
 Phe Asn Gln Ala Ser Lys Asn Lys Glu Asn Leu Thr Leu Ser Glu Ile  
 420 425 430  
 Ala Arg Arg Ile Lys  
 435  
 <210>205  
 <211>313  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>205  
 Ala Asn Gln Met Lys Arg Arg Ser Trp Leu Lys Ile Leu Gly Ile Cys  
 1 5 10 15  
 Leu Gly Ser Ser Ile Val Leu Gly Phe Leu Ile Phe Leu Pro Gln Leu  
 20 25 30  
 Leu Ser Thr Glu Ser Gly Lys Tyr Leu Val Phe Ser Leu Ile His Lys  
 35 40 45  
 Glu Ser Gly Leu Ser Cys Ser Ala Glu Glu Leu Lys Ile Ser Trp Phe  
 50 55 60  
 Gly Arg Gln Thr Ala Arg Lys Ile Lys Leu Thr Gly Glu Ala Lys Asp  
 65 70 75 80  
 Glu Val Xaa Ser Ala Glu Lys Phe Glu Leu Asp Gly Ser Leu Leu Arg  
 85 90 95  
 Leu Leu Ile Tyr Lys Lys Pro Lys Gly Ile Thr Leu Ser Gly Trp Ser  
 100 105 110  
 Leu Lys Ile Asn Glu Pro Ala Ser Ile Asp His Pro Ser Val Ser His  
 115 120 125  
 Leu Asp Pro Gly Ser Leu Leu Thr Tyr Leu Asn Asp Cys Lys Ile Ile  
 130 135 140  
 Ser Glu His Gly Phe Ile Thr Met Lys Thr Val Ser Gly Ser Ser Leu  
 145 150 155 160  
 Ser Val Ser Gly Xaa Tyr Leu Glu Xaa Ser Glu Lys Phe Met Thr  
 165 170 175  
 Lys Cys Val Val Ser Glu Asp Gln Gln Ser Gly Asn Ile Phe Ile Glu  
 180 185 190  
 Ser Val Leu Ser Pro Asp Val Ser Ile Ser Ala Gln Phe Ser Ser Val  
 195 200 205  
 Pro Val Ala Phe Phe Lys Ile Phe Ile Ala Ser Pro Phe Trp Asp His

210 215 220  
 Leu Leu Ser Tyr Glu Asp Ile Ile Asn Leu Ser Ala Glu Ala Thr His  
 225 230 235 240  
 Thr Asn Asp Gly Lys Ile Ser Met Thr Ala Ser Gly Glu Gly Asn Gln  
 245 250 255  
 Ile Gln Met Lys Leu Gln Gly His Ile His Lys Ser Thr Phe Tyr Ile  
 260 265 270  
 Val Glu Gly Ser Ser Ser Phe Ile Glu Leu Lys Pro Glu Leu Ala Ser  
 275 280 285  
 Ala Leu Cys Asn Gln Ile Ile Pro Leu Ser Thr Pro Ile Thr Ser Lys  
 290 295 300  
 Gln Ile Xaa Cys Tyr Gly Leu Leu Cys  
 305 310  
 <210>206  
 <211>275  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>206  
 Asn Leu Asn Leu Ser Ser Pro Gln Leu Phe Ala Thr Arg Ser Phe Arg  
 1 5 10 15  
 Cys Pro His Pro Leu Leu Val Ser Lys Ser Xaa Ala Thr Val Ser Tyr  
 20 25 30  
 Ala Lys Ile Pro Leu Asp Ile Thr Lys Trp Lys His Ile Glu Ile Thr  
 35 40 45  
 Ser Gln Ala Gln Leu Pro Glu Val Ala Ile His Pro Lys Asp Pro Asn  
 50 55 60  
 Leu Ala Leu Gln Leu Arg Asp Thr Lys Leu Gly Ile Lys Lys Thr Glu  
 65 70 75 80  
 Lys Xaa Ser Asp Ile Arg Tyr Ser Ser Ser Thr Val Leu Gly Gly Ala  
 85 90 95  
 Ser Pro Ser His Leu Asn Gly Leu Ile Ser Ile Asp Asn Lys Lys His  
 100 105 110  
 Leu Thr Lys Phe Arg Leu Gln Gln Ala Gln Leu Pro His Thr Tyr Leu  
 115 120 125  
 Arg Ala Ile Phe Pro Gln Pro Phe Val Ile Asn Val Pro Leu Asp Val  
 130 135 140  
 Ala Tyr Tyr Ser Leu Asn Ile Glu Gly Thr Tyr Lys Asn Ala His Leu  
 145 150 155 160  
 Glu Ala Asp Ala Ile Leu Asp Asn Pro Leu Leu Lys Leu Ser Cys Ser  
 165 170 175  
 Met Ser Gly Ala Trp Lys Asn Phe Leu Phe Lys Gly Gln Gly Thr Tyr  
 180 185 190  
 His Phe Asn Lys Lys Trp Gln Glu Ile Leu Ser Pro His Phe Ser Tyr  
 195 200 205  
 Ala Glu Ala Arg Phe Ser Gly Lys Ala Gln Ile Thr Asp Thr Asn Leu  
 210 215 220  
 Phe Phe Pro Lys Phe Ser Gly Lys Ile Thr Ala Arg Glu Asn Glu Leu  
 225 230 235 240  
 Leu Ile His Ala Lys Phe Gly Ser Pro Asn Glu Pro Ile Lys Pro Glu  
 245 250 255  
 Thr Thr Ser Ile Leu Ile His Gly Gln Phe Cys Ser Leu Pro Thr Gln  
 260 265 270  
 Pro Ser Phe  
 275  
 <210>207  
 <211>231  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>207  
 Asn Leu Lys Leu Pro Leu Tyr Ser Ser Thr Asp Asn Phe Val Leu Cys  
 1 5 10 15  
 Gln Leu Ser Leu Val Ser Asn His Leu Ala Pro Phe His Leu Lys Lys  
 20 25 30  
 Leu Thr Phe Ser Phe His Thr Asp Gly Gly Lys Phe Val Thr Lys Gly

```

      35      40      45
Asn Leu Gln Ala Leu Ile Glu Asn Pro Asp Tyr Pro Asp Leu Asn Asn
  50      55      60
Thr Arg Ile Leu Ile Pro Asp Leu Leu Leu Ser Leu Asp Glu Ser Ser
  65      70      75      80
Thr Ser Pro Ser Ser Lys Asp Leu Lys Ile Gln Gly Ser Gly Glu Ile
      85      90      95
Phe Ser Leu Pro Leu Asp Ser Ile Thr Lys Thr Tyr Gly Lys Gln Val
      100      105      110
Arg Leu Ser Pro Tyr Phe Gly Ser Ser Gly Asp Leu Asn Phe Val Val
      115      120      125
Asn Tyr Asn Pro Lys Asp Gln Asn Lys Leu Thr Leu Leu Ser Xaa Phe
      130      135      140
Lys Ser Glu Ala Leu Leu Gly Glu Leu Lys Leu Val Met Asp Phe Ser
      145      150      155      160
Met Lys Leu Ser Ser Gly Thr Gln Gly Thr Leu Gln Trp Glu Val Ser
      165      170      175
Pro Glu Arg Tyr Ala Ser Phe Phe Lys Asn Ala Ser Cys Ser Pro Thr
      180      185      190
Cys Leu Leu His Arg Thr Ala Asn Val Arg Leu Asp Ile Ser Lys Leu
      195      200      205
Ser Cys Pro Glu Glu Thr Lys Gly Leu Ser Cys Leu Thr Leu Leu Ala
      210      215      220
Ala Glu Asp Leu Lys Val His
      225      230
<210>208
<211>415
<212>PRT
<213>Chlamydia pneumoniae
<400>208
Asn Cys Lys Cys Thr Leu Arg His Leu Lys Thr Leu Leu Ser Arg Gly
  1      5      10      15
Asn Gln Arg Phe Ile Leu Ser His Ala Ser Cys Arg Arg Gly Leu Glu
      20      25      30
Gly Ser Leu Glu Ala Thr Pro Leu Ile Phe Tyr Asp Asn Val Ser Lys
      35      40      45
Glu Thr Phe Ile Ile Asn Asp Phe Xaa Gly Ser Leu Arg Ala Asn Asn
      50      55      60
Leu Asp Ala Lys Ile Glu Tyr Asp Leu Lys Gly Ser Cys Leu Ala Pro
      65      70      75      80
Arg Gln Asp Ser Lys Thr Leu Ala Glu Phe Ser Leu Glu Gly Gln Val
      85      90      95
Asp His Leu Phe Ser Pro Glu Ser Arg Glu Phe Lys Gln Thr Ala Asn
      100      105      110
Trp Ile His Ile Pro Ser Ser Phe Ile Ala Gly Ile Ile Pro Met Ser
      115      120      125
Pro Gly Leu Lys Ala Gln Ile Ser Ser Leu Ala Gly Pro Arg Ile Asn
      130      135      140
Val Ser Ile Lys Asn Ala Phe Arg Phe Gly Glu Gly Pro Val Asp Ile
      145      150      155      160
Met Val Asp Ser Glu Asn Leu Gln Ala Gln Ile Pro Leu Ile Leu Asn
      165      170      175
Glu Lys Ser Ile Leu Leu Arg Glu Asn Leu Thr Ala His Leu Ser Ile
      180      185      190
Asn Glu Asp Val Asn Lys Ala Phe Leu Gln Glu Phe Asn Pro Leu Leu
      195      200      205
Ala Gly Gly Ala Tyr Ser Gln Tyr Pro Val Thr Leu Glu Ile Asp Lys
      210      215      220
Gln Asn Phe Tyr Leu Pro Ile Arg Pro Tyr Ser Phe Glu Glu Phe Arg
      225      230      235      240
Ile Gln Ser Ala Thr Leu Asp Met Gly Lys Ile Ser Ile Ala Asn Thr
      245      250      255
Gly Thr Met Tyr Ala Leu Phe Gln Phe Leu Asp Ile Thr Asp Gln Lys
      260      265      270

```

Gln Phe Val Glu Ser Trp Phe Thr Pro Ile Phe Phe Ser Val Gln Lys  
 275 280 285  
 Gly Ser Ile Ile Cys Lys Arg Leu Asp Ala Leu Ile Asp Arg Arg Ile  
 290 295 300  
 Arg Leu Ala Leu Trp Gly Lys Thr Asp Ile Ala His Asp Arg Leu Phe  
 305 310 315 320  
 Met Thr Leu Gly Ile Asp Pro Glu Val Ile Lys Lys Tyr Phe His Asn  
 325 330 335  
 Thr Ser Leu Lys Thr Lys Asn Phe Phe Leu Ile Lys Ile Arg Gly Ser  
 340 345 350  
 Ile Ser Ser Pro Glu Val Asp Trp Ser Ser Ala Tyr Ala Arg Ile Ala  
 355 360 365  
 Leu Leu Lys Ser Tyr Ser Leu Gly Asn Pro Phe Ser Ser Leu Ala Asp  
 370 375 380  
 Lys Leu Phe Ser Ser Leu Gly Asp Ser Thr Pro Pro Pro Thr Val His  
 385 390 395 400  
 Pro Phe Pro Trp Glu Lys Ser Asn Phe Asp Ser Ile Glu Asn Lys  
 405 410 415

&lt;210&gt;209

&lt;211&gt;458

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;209

Leu Leu Gly Ile Lys Leu Met Arg Lys Arg His Ser Phe Asp Ser Thr  
 1 5 10 15  
 Ser Thr Lys Lys Glu Ala Val Ser Lys Ala Ile Gln Lys Ile Ile Lys  
 20 25 30  
 Ile Met Glu Thr Thr Asp Pro Ser Leu Asn Val Glu Thr Pro Asn Ala  
 35 40 45  
 Glu Ile Glu Ser Ile Leu Gln Glu Ile Lys Glu Ile Lys Gln Lys Leu  
 50 55 60  
 Ser Lys Gln Ala Glu Asp Leu Gly Leu Leu Glu Lys Tyr Cys Ser Gln  
 65 70 75 80  
 Glu Thr Leu Ser Asn Leu Glu Asn Thr Asn Ala Ser Leu Lys Leu Ser  
 85 90 95  
 Ile Gly Ser Val Ile Glu Glu Leu Ala Ser Leu Lys Gln Leu Val Glu  
 100 105 110  
 Glu Ser Ile Glu Glu Ser Leu Gly Gln Gln Asp Gln Leu Ile Gln Ser  
 115 120 125  
 Val Leu Ile Glu Ile Ser Asp Lys Phe Leu Ser Ser Ile Gly Glu Thr  
 130 135 140  
 Leu Ser Gly Asn Leu Asp Met Asn Gln Asn Val Ile Gln Gly Leu Leu  
 145 150 155 160  
 Ile Lys Glu Asn Pro Glu Lys Ser Glu Ala Ser Val Gly Tyr Val  
 165 170 175  
 Gln Thr Leu Leu Glu Pro Leu Ser Lys Arg Ile Gly Glu Thr His Lys  
 180 185 190  
 Lys Val Ala Thr His Asp Val Asn Ile Ser Ser Leu Gln Phe His Met  
 195 200 205  
 Met Ser Val Ala Gly Gly Arg Phe Arg Gly His Ile Asp Met Asn Gly  
 210 215 220  
 Tyr Arg Val Leu Gly Leu Gly Glu Pro Lys Asn Gly Glu Asp Ala Val  
 225 230 235 240  
 Ser Lys Asp Tyr Leu Glu Arg Tyr Val Ser Ser Gln Leu Thr Ile Asp  
 245 250 255  
 Lys Val Glu Asp Lys Pro Ile Thr Lys Pro Asn Lys Gly Lys Leu Leu  
 260 265 270  
 Tyr Ser Gln Gly Thr Ser Pro Lys Leu Glu Gly Pro Leu Pro Leu Gly  
 275 280 285  
 Leu Leu Thr Ser Gly Ile Ser Gly Phe Thr Trp Lys Ser Ala Ser Lys  
 290 295 300  
 Ser Asn Asp Gly Ser Phe Pro Phe Ser Ala Leu Arg His Lys Glu Thr  
 305 310 315 320  
 Glu Ser Asp Thr Asp Cys Phe Gln Ile Thr Ser Thr Thr Leu Ser Gly

```

      325      330      335
Asn Gln Ala Gly Thr Tyr Thr Trp Ser Leu Ser Leu Lys Val Leu Val
      340      345      350
Pro Ser Ile Phe Gln Ile Glu Lys Pro Glu Val Gln Leu Ser Leu Val
      355      360      365
Tyr Ser Tyr Glu Asp Trp Leu Pro Ile Asp Asn Ile Phe Asn Met Ser
      370      375      380
Gln Pro Arg Thr Ile Pro Leu Ala Leu Leu Gly Gln Thr Met Leu Ala
385      390      395      400
Gly Gln Lys Tyr Asp Ile Leu Glu Leu Ala Ala His Gln Thr Asn Gln
      405      410      415
Thr Leu Met Ile Ser Pro Asn Cys Ser Arg Phe Ser Leu Gln Leu Lys
      420      425      430
Gln Thr Asn Gln Phe Glu Asn Ser Pro Val Asp Phe Tyr Ile Val His
      435      440      445
Ala Ala His Ser Cys His Trp Ser Gly Phe
      450      455
<210>210
<211>226
<212>PRT
<213>Chlamydia pneumoniae
<400>210
Met Thr Ile Arg Val Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys
  1      5      10      15
Ile Leu Asp Gly Val Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu
      20      25      30
Phe Val Gly Lys Ser Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu
      35      40      45
Ala Gly Leu Val Gln Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu
      50      55      60
Ala Pro Ala Leu Val Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr
      65      70      75      80
Val Leu Gly Asn Cys Thr His Pro Gln Ile His Ile Lys Gly Arg Ser
      85      90      95
Thr Glu Glu Ala Arg Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp
      100      105      110
Ile Glu Glu Val Ala Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln
      115      120      125
Lys Gln Arg Val Ala Ile Val Arg Ser Leu Cys Met Asp Lys His Thr
      130      135      140
Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala
145      150      155      160
Ser Phe Arg His Leu Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val
      165      170      175
Gly Leu Thr Thr His Asp Met Gln Phe Val His Ser Cys Leu Asp Arg
      180      185      190
Ile Tyr Leu Ile Asp Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg
      195      200      205
Asp Gly Glu Leu Asp Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser
      210      215      220
Ala Gln
225
<210>211
<211>220
<212>PRT
<213>Chlamydia pneumoniae
<400>211
Glu Val Gly Val Asp His Trp Leu Ala Ile Ala Arg Leu Leu Leu Arg
  1      5      10      15
Gly Cys Gly Tyr Thr Leu Cys Val Ser Gly Ile Gly Ile Leu Cys Gly
      20      25      30
Ser Ile Leu Gly Leu Leu Ile Gly Thr Val Thr Ser Leu Tyr Phe Pro
      35      40      45
Ser Lys Leu Thr Lys Leu Leu Ala Asn Ser Tyr Val Thr Val Ile Arg

```

50 55 60  
 Gly Thr Pro Leu Phe Ile Gln Ile Leu Ile Ile Tyr Phe Gly Leu Pro  
 65 70 75 80  
 Glu Val Leu Pro Ile Glu Pro Thr Pro Leu Val Ala Gly Ile Ile Ala  
 85 90 95  
 Leu Ser Met Asn Ser Ala Ala Tyr Leu Ala Glu Asn Ile Arg Gly Gly  
 100 105 110  
 Ile Asn Ser Leu Ser Ile Gly Gln Trp Glu Ser Ala Met Val Leu Gly  
 115 120 125  
 Tyr Lys Lys Tyr Gln Ile Phe Val Tyr Ile Ile Tyr Pro Gln Val Phe  
 130 135 140  
 Lys Asn Ile Leu Pro Ser Leu Thr Asn Glu Phe Val Ser Leu Ile Lys  
 145 150 155 160  
 Glu Ser Ser Ile Leu Met Val Val Gly Val Pro Glu Leu Thr Lys Val  
 165 170 175  
 Thr Lys Asp Ile Val Ser Arg Glu Leu Asn Pro Met Glu Met Tyr Leu  
 180 185 190  
 Ile Cys Ala Gly Leu Tyr Phe Leu Met Thr Thr Ser Phe Ser Cys Ile  
 195 200 205  
 Ser Arg Leu Ser Glu Lys Arg Arg Ser Tyr Asp Asn  
 210 215 220

&lt;210&gt;212

&lt;211&gt;147

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;212

Met Lys Lys Lys Val Thr Ile Asp Glu Ala Leu Lys Glu Ile Leu Arg  
 1 5 10 15  
 Leu Glu Gly Ala Ala Thr Gln Glu Glu Leu Cys Ala Lys Leu Leu Ala  
 20 25 30  
 Gln Gly Phe Ala Thr Thr Gln Ser Ser Val Ser Arg Trp Leu Arg Lys  
 35 40 45  
 Ile Gln Ala Val Lys Val Ala Gly Glu Arg Gly Ala Arg Tyr Ser Leu  
 50 55 60  
 Pro Ser Ser Thr Glu Lys Thr Thr Thr Arg His Leu Val Leu Ser Ile  
 65 70 75 80  
 Arg His Asn Ala Ser Leu Ile Val Ile Arg Thr Val Pro Gly Ser Ala  
 85 90 95  
 Ser Trp Ile Ala Ala Leu Leu Asp Gln Gly Leu Lys Asp Glu Ile Leu  
 100 105 110  
 Gly Thr Leu Ala Gly Asp Asp Thr Ile Phe Val Thr Pro Ile Asp Glu  
 115 120 125  
 Gly Arg Leu Pro Leu Leu Met Val Ser Ile Ala Asn Leu Leu Gln Val  
 130 135 140  
 Phe Leu Asp  
 145

&lt;210&gt;213

&lt;211&gt;344

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;213

Met Leu Thr Leu Gly Leu Glu Ser Ser Cys Asp Glu Thr Ala Cys Ala  
 1 5 10 15  
 Ile Val Asn Glu Asp Lys Gln Ile Leu Ala Asn Ile Ile Ala Ser Gln  
 20 25 30  
 Asp Ile His Ala Ser Tyr Gly Gly Val Val Pro Glu Leu Ala Ser Arg  
 35 40 45  
 Ala His Leu His Ile Phe Pro Gln Val Ile Asn Lys Ala Leu Gln Gln  
 50 55 60  
 Ala Asn Leu Leu Ile Glu Asp Met Asp Leu Ile Ala Val Thr Gln Thr  
 65 70 75 80  
 Pro Gly Leu Ile Gly Ser Leu Ser Val Gly Val His Phe Gly Lys Gly  
 85 90 95  
 Ile Ala Ile Gly Ala Lys Lys Ser Leu Ile Gly Val Asn His Val Glu

100 105 110  
 Ala His Leu Tyr Ala Ala Tyr Met Ala Ala Gln Asn Val Gln Phe Pro  
 115 120 125  
 Ala Leu Gly Leu Val Val Ser Gly Ala His Thr Ala Ala Phe Phe Ile  
 130 135 140  
 Glu Asn Pro Thr Ser Tyr Lys Leu Ile Gly Lys Thr Arg Asp Asp Ala  
 145 150 155 160  
 Ile Gly Glu Thr Phe Asp Lys Val Gly Arg Phe Leu Gly Leu Pro Tyr  
 165 170 175  
 Pro Ala Gly Pro Leu Ile Glu Lys Leu Ala Leu Glu Gly Ser Glu Asp  
 180 185 190  
 Ser Tyr Pro Phe Ser Pro Ala Lys Val Pro Asn Tyr Asp Phe Ser Phe  
 195 200 205  
 Ser Gly Leu Lys Thr Ala Val Leu Tyr Ala Ile Lys Gly Asn Asn Ser  
 210 215 220  
 Ser Pro Arg Ser Pro Ala Pro Glu Ile Ser Leu Glu Lys Gln Arg Asp  
 225 230 235 240  
 Ile Ala Ala Ser Phe Gln Lys Ala Ala Cys Thr Thr Ile Ala Gln Lys  
 245 250 255  
 Leu Pro Thr Ile Ile Lys Glu Phe Ser Cys Arg Ser Ile Leu Ile Gly  
 260 265 270  
 Gly Gly Val Ala Ile Asn Glu Tyr Phe Arg Ser Ala Ile Gln Thr Ala  
 275 280 285  
 Cys Asn Leu Pro Val Tyr Phe Pro Pro Ala Lys Leu Cys Ser Asp Asn  
 290 295 300  
 Ala Ala Met Ile Ala Gly Leu Gly Gly Glu Asn Phe Gln Lys Asn Ser  
 305 310 315 320  
 Ser Ile Pro Glu Ile Arg Ile Cys Ala Arg Tyr Gln Trp Glu Ser Val  
 325 330 335  
 Ser Pro Phe Ser Leu Ala Ser Pro  
 340

&lt;210&gt;214

&lt;211&gt;514

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;214

Met Arg Lys Ile Ser Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu  
 1 5 10 15  
 Ser Val Val Leu Gln Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser  
 20 25 30  
 Arg Gly Glu Leu Ala Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp  
 35 40 45  
 Pro Arg Gln Val Arg Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile  
 50 55 60  
 Tyr Glu Gly Leu Val Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro  
 65 70 75 80  
 Ala Leu Ala Glu Asp Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr  
 85 90 95  
 Phe Lys Leu Lys Ser Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala  
 100 105 110  
 Glu Asp Phe Ile Glu Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser  
 115 120 125  
 Gly Ile Tyr Ala Phe Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile  
 130 135 140  
 Gln Glu Gly His Leu Ser Ile Asp His Phe Gly Val His Ser Pro Asn  
 145 150 155 160  
 Glu Ser Thr Leu Val Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu  
 165 170 175  
 Lys Leu Leu Ala Leu Pro Val Phe Phe Pro Val His Lys Ser Gln Arg  
 180 185 190  
 Thr Leu Gln Ser Lys Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro  
 195 200 205  
 Lys Asn Ile Lys Gln Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His  
 210 215 220

Tyr Tyr Asn Gln Ser Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe  
 225 230 235 240  
 Ile Pro Asp Ala Asn Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu  
 245 250 255  
 Asn Trp Gln Gly Pro Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu  
 260 265 270  
 Ser Asn Leu Gln Ser Lys Gly His Leu His Ser Phe Asp Val Ala Gly  
 275 280 285  
 Thr Ser Trp Leu Thr Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met  
 290 295 300  
 Lys Leu Arg Glu Ala Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val  
 305 310 315 320  
 Ser Thr Ile Phe Leu Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro  
 325 330 335  
 Thr Asn Ile His Ser Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln  
 340 345 350  
 Arg Gln Ala Tyr Ala Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu  
 355 360 365  
 Gln Ile Thr Ala Lys Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val  
 370 375 380  
 Ser Ser Ser Ala Ser Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp  
 385 390 395 400  
 Lys Glu Ser Leu Gly Phe Ala Ile Pro Ile Val Gly Lys Glu Phe Ala  
 405 410 415  
 Leu Leu Gln Ala Asp Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly  
 420 425 430  
 Gly Trp Phe Ala Asp Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe  
 435 440 445  
 Ala Tyr Pro Ser Gly Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe  
 450 455 460  
 Leu Glu Ile Leu Gln Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg  
 465 470 475 480  
 Ser Glu Leu Val Ser Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile  
 485 490 495  
 Ile Glu Pro Ile Tyr His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys  
 500 505 510  
 Leu Ser

&lt;210&gt;215

&lt;211&gt;494

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;215

Lys Glu Met Pro Arg Ser Leu Asp Pro Gly Lys Thr Arg Leu Ile Ala  
 1 5 10 15  
 Asp Gln Thr Leu Met Arg His Leu Tyr Glu Gly Leu Val Glu Glu His  
 20 25 30  
 Ser Gln Asn Gly Glu Ile Lys Pro Ala Leu Ala Glu Ser Tyr Thr Ile  
 35 40 45  
 Ser Glu Asp Gly Thr Arg Tyr Thr Phe Lys Ile Lys Asn Ile Leu Trp  
 50 55 60  
 Ser Asn Gly Asp Pro Leu Thr Ala Gln Asp Phe Val Ser Ser Trp Lys  
 65 70 75 80  
 Glu Ile Leu Lys Glu Asp Ala Ser Ser Val Tyr Leu Tyr Ala Phe Leu  
 85 90 95  
 Pro Ile Lys Asn Ala Arg Ala Ile Phe Asp Asp Thr Glu Ser Pro Glu  
 100 105 110  
 Asn Leu Gly Val Arg Ala Leu Asp Lys Arg His Leu Glu Ile Gln Leu  
 115 120 125  
 Glu Thr Pro Cys Ala His Phe Leu His Phe Leu Thr Leu Pro Ile Phe  
 130 135 140  
 Phe Pro Val His Glu Thr Leu Arg Asn Tyr Ser Thr Ser Phe Glu Glu  
 145 150 155 160  
 Met Pro Ile Thr Cys Gly Ala Phe Arg Pro Val Ser Leu Glu Lys Gly



```

      165      170      175
Leu Arg Leu His Leu Glu Lys Asn Pro Met Tyr His Asn Lys Ser Arg
      180      185      190
Val Lys Leu His Lys Ile Ile Val Gln Phe Ile Ser Asn Ala Asn Thr
      195      200      205
Ala Ala Ile Leu Phe Lys His Lys Lys Leu Asp Trp Gln Gly Pro Pro
      210      215      220
Trp Gly Glu Pro Ile Pro Pro Glu Ile Ser Ala Ser Leu His Gln Asp
      225      230      235      240
Asp Gln Leu Phe Ser Leu Pro Gly Ala Ser Thr Thr Trp Leu Leu Phe
      245      250      255
Asn Ile Gln Lys Lys Pro Trp Asn Asn Ala Lys Leu Arg Lys Ala Leu
      260      265      270
Ser Leu Ala Ile Asp Lys Asp Met Leu Thr Lys Val Val Tyr Gln Gly
      275      280      285
Leu Ala Glu Pro Thr Asp His Ile Leu His Pro Arg Leu Tyr Pro Gly
      290      295      300
Thr Tyr Pro Glu Arg Lys Arg Gln Asn Glu Arg Ile Leu Glu Ala Gln
      305      310      315      320
Gln Leu Phe Glu Glu Ala Leu Asp Glu Leu Gln Met Thr Arg Glu Asp
      325      330      335
Leu Glu Lys Glu Thr Leu Thr Phe Ser Thr Phe Ser Phe Ser Tyr Gly
      340      345      350
Arg Ile Cys Gln Met Leu Arg Glu Gln Trp Lys Lys Val Leu Lys Phe
      355      360      365
Thr Ile Pro Ile Val Gly Gln Glu Phe Phe Thr Ile Gln Lys Asn Phe
      370      375      380
Leu Glu Gly Asn Tyr Ser Leu Thr Val Asn Gln Trp Thr Ala Ala Phe
      385      390      395      400
Ile Asp Pro Met Ser Tyr Leu Met Ile Phe Ala Asn Pro Gly Gly Ile
      405      410      415
Ser Pro Tyr His Leu Gln Asp Ser His Phe Gln Thr Leu Leu Ile Lys
      420      425      430
Ile Thr Gln Glu His Lys Lys His Leu Arg Asn Gln Leu Ile Ile Glu
      435      440      445
Ala Leu Asp Tyr Leu Glu His Cys His Ile Leu Glu Pro Leu Cys His
      450      455      460
Pro Asn Leu Arg Ile Ala Leu Asn Lys Asn Ile Lys Asn Phe Asn Leu
      465      470      475      480
Phe Val Arg Arg Thr Ser Asp Phe Arg Phe Ile Glu Lys Leu
      485      490

```

&lt;210&gt;216

&lt;211&gt;448

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;216

```

Leu Lys Phe Asp Ser Lys Phe Ile Lys Val Ile Phe Lys Met Phe Ser
 1      5      10      15
Arg Trp Ile Thr Leu Phe Leu Leu Phe Ile Ser Leu Thr Gly Cys Ser
      20      25      30
Ser Tyr Ser Ser Lys His Lys Gln Ser Leu Ile Ile Pro Ile His Asp
      35      40      45
Asp Pro Val Ala Phe Ser Pro Glu Gln Ala Lys Arg Ala Met Asp Leu
      50      55      60
Ser Ile Ala Gln Leu Leu Phe Asp Gly Leu Thr Arg Glu Thr His Arg
      65      70      75      80
Glu Ser Asn Asp Leu Glu Leu Ala Ile Ala Ser Arg Tyr Thr Val Ser
      85      90      95
Glu Asp Phe Cys Ser Tyr Thr Phe Phe Ile Lys Asp Ser Ala Leu Trp
      100      105      110
Ser Asp Gly Thr Pro Ile Thr Ser Glu Asp Ile Arg Asn Ala Trp Glu
      115      120      125
Tyr Ala Gln Glu Asn Ser Pro His Ile Gln Ile Phe Gln Gly Leu Asn
      130      135      140

```

Phe Ser Thr Pro Ser Ser Asn Ala Ile Thr Ile His Leu Asp Ser Pro  
 145 150 155 160  
 Asn Pro Asp Phe Pro Lys Leu Leu Ala Phe Pro Ala Phe Ala Ile Phe  
 165 170 175  
 Lys Pro Glu Asn Pro Lys Leu Phe Ser Gly Pro Tyr Thr Leu Val Glu  
 180 185 190  
 Tyr Phe Pro Gly His Asn Ile His Leu Lys Lys Asn Pro Asn Tyr Tyr  
 195 200 205  
 Asp Tyr His Cys Val Ser Ile Asn Ser Ile Lys Leu Leu Ile Ile Pro  
 210 215 220  
 Asp Ile Tyr Thr Ala Ile His Leu Leu Asn Arg Gly Lys Val Asp Trp  
 225 230 235 240  
 Val Gly Gln Pro Trp His Gln Gly Ile Pro Trp Glu Leu His Lys Gln  
 245 250 255  
 Ser Gln Tyr His Tyr Tyr Thr Tyr Pro Val Glu Gly Ala Phe Trp Leu  
 260 265 270  
 Cys Leu Asn Thr Lys Ser Pro His Leu Asn Asp Leu Gln Asn Arg His  
 275 280 285  
 Arg Leu Ala Thr Cys Ile Asp Lys Arg Ser Ile Ile Glu Glu Ala Leu  
 290 295 300  
 Gln Gly Thr Gln Gln Pro Ala Glu Thr Leu Ser Arg Gly Ala Pro Gln  
 305 310 315 320  
 Pro Asn Gln Tyr Lys Lys Gln Lys Pro Leu Thr Pro Gln Glu Lys Leu  
 325 330 335  
 Val Leu Thr Tyr Pro Ser Asp Ile Leu Arg Cys Gln Arg Ile Ala Glu  
 340 345 350  
 Ile Leu Lys Glu Gln Trp Lys Ala Ala Gly Ile Asp Leu Ile Leu Glu  
 355 360 365  
 Gly Leu Glu Tyr His Leu Phe Val Asn Lys Arg Lys Val Gln Asp Tyr  
 370 375 380  
 Ala Ile Ala Thr Gln Thr Gly Val Ala Tyr Tyr Pro Gly Ala Asn Leu  
 385 390 395 400  
 Ile Ser Glu Glu Asp Lys Leu Leu Gln Asn Phe Glu Ile Ile Pro Ile  
 405 410 415  
 Tyr Tyr Leu Ser Tyr Asp Tyr Leu Thr Gln Asp Phe Ile Glu Gly Val  
 420 425 430  
 Ile Tyr Asn Ala Ser Gly Ala Val Asp Leu Lys Tyr Thr Tyr Phe Pro  
 435 440 445

&lt;210&gt;217

&lt;211&gt;534

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;217

Gln Ile Glu Tyr Tyr Ile Met Lys Met His Arg Leu Lys Pro Thr Leu  
 1 5 10 15  
 Lys Ser Leu Ile Pro Asn Leu Leu Phe Leu Leu Leu Thr Leu Ser Ser  
 20 25 30  
 Cys Ser Lys Gln Lys Gln Glu Pro Leu Gly Lys His Leu Val Ile Ala  
 35 40 45  
 Met Ser His Asp Leu Ala Asp Leu Asp Pro Arg Asn Ala Tyr Leu Ser  
 50 55 60  
 Arg Asp Ala Ser Leu Ala Lys Ala Leu Tyr Glu Gly Leu Thr Arg Glu  
 65 70 75 80  
 Thr Asp Gln Gly Ile Ala Leu Ala Leu Ala Glu Ser Tyr Thr Leu Ser  
 85 90 95  
 Lys Asp His Lys Val Tyr Thr Phe Lys Leu Arg Pro Ser Val Trp Ser  
 100 105 110  
 Asp Gly Thr Pro Leu Thr Ala Tyr Asp Phe Glu Lys Ser Ile Lys Gln  
 115 120 125  
 Leu Tyr Phe Glu Glu Phe Ser Pro Ser Ile His Thr Leu Leu Gly Val  
 130 135 140  
 Ile Lys Asn Ser Ser Ala Ile His Asn Ala Gln Lys Ser Leu Glu Thr  
 145 150 155 160  
 Leu Gly Ile Gln Ala Lys Asp Asp Leu Thr Leu Val Ile Thr Leu Glu

165 170 175  
 Gln Pro Phe Pro Tyr Phe Leu Thr Leu Ile Ala Arg Pro Val Phe Ser  
 180 185 190  
 Pro Val His His Thr Leu Arg Glu Ser Tyr Lys Lys Gly Thr Pro Pro  
 195 200 205  
 Ser Thr Tyr Ile Ser Asn Gly Pro Phe Val Leu Lys Lys His Xaa His  
 210 215 220  
 Gln Asn Tyr Leu Ile Leu Glu Lys Asn Pro His Tyr Tyr Asp His Glu  
 225 230 235 240  
 Ser Val Lys Leu Asp Arg Val Thr Leu Lys Ile Ile Pro Asp Ala Ser  
 245 250 255  
 Thr Ala Thr Lys Leu Phe Lys Ser Lys Ser Ile Asp Trp Ile Gly Ser  
 260 265 270  
 Pro Trp Ser Ala Pro Ile Ser Asn Glu Asp Gln Lys Val Leu Ser Gln  
 275 280 285  
 Glu Lys Ile Leu Thr Tyr Ser Val Ser Ser Thr Thr Leu Leu Ile Tyr  
 290 295 300  
 Asn Leu Gln Lys Pro Leu Ile Gln Asn Lys Ala Leu Arg Lys Ala Ile  
 305 310 315 320  
 Ala His Ala Ile Asp Arg Lys Ser Ile Leu Arg Leu Val Pro Ser Gly  
 325 330 335  
 Gln Glu Ala Val Thr Leu Val Pro Pro Asn Leu Ser Gln Leu Asn Leu  
 340 345 350  
 Gln Lys Glu Ile Ser Thr Glu Glu Arg Gln Thr Lys Ala Arg Ala Tyr  
 355 360 365  
 Phe Gln Glu Ala Lys Glu Thr Leu Ser Glu Lys Glu Leu Ala Glu Leu  
 370 375 380  
 Ser Ile Leu Tyr Pro Ile Asp Ser Ser Asn Ser Ser Ile Ile Ala Gln  
 385 390 395 400  
 Glu Ile Gln Arg Gln Leu Lys Asp Thr Leu Gly Leu Lys Ile Lys Ile  
 405 410 415  
 Gln Gly Met Glu Tyr His Cys Phe Leu Lys Lys Arg Arg Gln Gly Asp  
 420 425 430  
 Phe Phe Ile Ala Thr Gly Gly Trp Ile Ala Glu Tyr Val Ser Pro Val  
 435 440 445  
 Ala Phe Leu Ser Ile Leu Gly Asn Pro Arg Asp Leu Thr Gln Trp Arg  
 450 455 460  
 Asn Ser Asp Tyr Glu Lys Thr Leu Glu Lys Leu Tyr Leu Pro His Ala  
 465 470 475 480  
 Tyr Lys Glu Asn Leu Lys Arg Ala Glu Met Ile Ile Glu Glu Glu Thr  
 485 490 495  
 Pro Ile Ile Pro Leu Tyr His Gly Lys Tyr Ile Tyr Ala Ile His Pro  
 500 505 510  
 Lys Ile Gln Asn Thr Phe Gly Ser Leu Leu Gly His Thr Asp Leu Lys  
 515 520 525  
 Asn Ile Asp Ile Leu Ser  
 530  
 <210>218  
 <211>296  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>218  
 Leu Ser Leu Val Phe Ser Tyr Ile Lys Asn Arg Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ser Leu Trp Ile Val Leu Thr Leu Thr Phe Leu Val Met Lys Thr  
 20 25 30  
 Ile Pro Gly Asp Pro Phe Asn Asp Glu Gly Cys Asn Val Leu Ser Glu  
 35 40 45  
 Glu Val Leu Gln Thr Leu Lys Ser Arg Tyr Gly Leu Asp Lys Pro Leu  
 50 55 60  
 Tyr Gln Gln Tyr Thr Gln Tyr Leu His Ser Ile Ala Lys Leu Asp Phe  
 65 70 75 80  
 Gly Asn Ser Leu Val Tyr Lys Asp Arg Lys Val Thr Asn Ile Ile Ser  
 85 90 95

Thr Ala Phe Pro Ile Ser Ala Ile Leu Gly Leu Gln Ser Leu Phe Leu  
 100 105 110  
 Ser Ile Gly Gly Gly Ile Ala Leu Gly Thr Ile Ala Ala Leu Lys Lys  
 115 120 125  
 Lys Lys Gln Arg Arg Tyr Ile Leu Gly Ala Ser Ile Leu Gln Ile Ser  
 130 135 140  
 Ile Pro Ala Phe Ile Phe Ala Thr Leu Leu Gln Tyr Val Phe Ala Val  
 145 150 155 160  
 Lys Ile Pro Leu Leu Pro Ile Ala Cys Trp Gly Ser Phe Thr His Thr  
 165 170 175  
 Ile Leu Pro Thr Leu Ala Leu Ala Val Thr Pro Met Ala Phe Ile Ile  
 180 185 190  
 Gln Leu Thr Tyr Ser Ser Val Ser Ala Ala Leu Asn Lys Asp Tyr Val  
 195 200 205  
 Leu Leu Ala Tyr Ala Lys Gly Leu Ser Pro Leu Lys Val Val Ile Lys  
 210 215 220  
 His Ile Leu Pro Tyr Ala Ile Phe Pro Thr Ile Ser Tyr Ser Ala Phe  
 225 230 235 240  
 Leu Thr Thr Thr Val Ile Thr Gly Thr Phe Ala Ile Glu Asn Ile Phe  
 245 250 255  
 Cys Ile Pro Gly Leu Gly Lys Trp Phe Ile Cys Ser Ile Lys Gln Arg  
 260 265 270  
 Asp Tyr Pro Val Ala Leu Gly Leu Ser Val Phe Tyr Gly Thr Tyr Leu  
 275 280 285  
 Cys Ser Leu Leu Tyr Phe Leu Thr  
 290 295  
 <210>219  
 <211>284  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>219  
 Met Asp Asn Tyr Leu Leu Asn Ile Lys Asp Leu Thr Ile Thr Ser Thr  
 1 5 10 15  
 Asn Pro Lys Arg Thr Leu Ile Glu Asn Leu Ser Leu Gln Leu Lys Glu  
 20 25 30  
 Asn Arg Asn Leu Ala Leu Val Gly Glu Ser Gly Ser Gly Lys Thr Thr  
 35 40 45  
 Ile Thr Lys Ala Ile Leu Gly Phe Leu Pro Glu Asn Cys Leu Ile Lys  
 50 55 60  
 Thr Gly Ser Ile Leu Phe Glu Asp Ile Asp Ile Thr Lys Leu Ser Pro  
 65 70 75 80  
 Lys Glu Leu His Lys Ile Arg Gly Gln Lys Ile Ala Thr Ile Leu Gln  
 85 90 95  
 Asn Ala Met Gly Ser Leu Thr Pro Ser Met Arg Ile Gly Met Gln Ile  
 100 105 110  
 Ile Glu Thr Leu Arg Gln His His Lys Met Asn Lys Glu Glu Ala Tyr  
 115 120 125  
 Asn Lys Ala Met Gln Leu Leu Thr Asp Val Cys Ile Pro Asn Pro Lys  
 130 135 140  
 Tyr Ser Phe Ser Gln Tyr Pro Phe Glu Leu Ser Gly Gly Met Arg Gln  
 145 150 155 160  
 Arg Val Val Ile Ala Ile Ala Leu Ala Ser Gln Pro Lys Leu Ile Leu  
 165 170 175  
 Ala Asp Glu Pro Thr Thr Ala Leu Asp Ser Met Ser Gln Ala Gln Val  
 180 185 190  
 Leu Arg Ile Leu Arg Asn Ile Gln Gln Gln Lys Gln Ala Thr Ile Leu  
 195 200 205  
 Leu Val Thr His Asn Leu Ser Leu Val Lys Glu Leu Cys Asn Asp Ile  
 210 215 220  
 Cys Ile Ile Lys Asp Gly Lys Leu Ile Glu Thr Gly Thr Val Glu Glu  
 225 230 235 240  
 Ile Phe Leu Ser Pro Lys His Pro Tyr Thr Leu Lys Leu Leu Asn Ala  
 245 250 255  
 Val Ser Lys Ile Pro Ile Lys Lys Thr Ser Ser Pro Ile Leu Lys Asn

260 265 270  
 Lys Phe Gln Pro Leu Met Ser Met Gln Gly Gly Leu  
 275 280  
 <210>220  
 <211>293  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>220  
 Val Pro Thr Ser Asn Glu Tyr Ala Arg Trp Phe Met Thr Thr Leu Leu  
 1 5 10 15  
 Ser Ile Lys Asp Leu Ser Leu Thr Ile Arg Gly Lys Lys Ile Leu Asn  
 20 25 30  
 His Ile Asn Leu Asn Leu Ile Lys Gly Ser Tyr Leu Thr Ile Val Gly  
 35 40 45  
 Pro Ser Gly Ser Gly Lys Ser Ser Leu Ala Leu Thr Ile Leu Asp Leu  
 50 55 60  
 Leu Lys Pro Thr Thr Gly Thr Ile Thr Phe His Met Asp Pro Lys Ile  
 65 70 75 80  
 Pro Arg Ala Arg Lys Val Gln Val Ile Trp Gln Asp Ile Asp Ser Ser  
 85 90 95  
 Leu Asn Pro Cys Met Ser Ile Lys Gly Ile Ile Ser Glu Pro Leu Asn  
 100 105 110  
 Ile Ile Gly Thr Tyr Ser Lys Ala Glu Gln Asn Lys Glu Ile Tyr Asn  
 115 120 125  
 Val Leu Asp Leu Val Asn Leu Pro Lys Ser Val Leu His Leu Lys Pro  
 130 135 140  
 Tyr Lys Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Lys Ala  
 145 150 155 160  
 Leu Val Ser Lys Pro Glu Leu Leu Ile Cys Asp Glu Pro Leu Ser Ser  
 165 170 175  
 Leu Asp Thr Leu Asn Gln Ser Leu Ile Leu Asp Leu Phe Gln Thr Ile  
 180 185 190  
 Lys Lys Glu Tyr Gln Asn Thr Leu Leu Phe Ile Thr His Asp Met Ser  
 195 200 205  
 Ala Ala Tyr Tyr Ile Ala Asp Thr Ile Ala Val Met Asp Gln Gly Ser  
 210 215 220  
 Leu Val Glu His Ala Cys Arg Glu Lys Ile Phe Ser Thr Pro Lys His  
 225 230 235 240  
 Thr Thr Thr Gln Asp Leu Leu Asp Ala Ile Pro Ile Phe Ser Leu Ile  
 245 250 255  
 Ser Thr Glu Met Glu Pro Ser Glu Glu Tyr Glu Leu Gln Val Ala Ser  
 260 265 270  
 Lys Xaa Ile Asp Leu Glu Ile Thr Asn Ser Tyr Arg Lys Ile Arg Ile  
 275 280 285  
 Phe Asp Val Ser Gln  
 290  
 <210>221  
 <211>279  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>221  
 Ile Val Pro Leu Pro Gln Lys Asn Asn Lys Glu Thr Ser Cys Met Asn  
 1 5 10 15  
 Thr Tyr Thr Phe Ser Pro Thr Leu Gln Lys Ser Phe Ser Leu Phe Leu  
 20 25 30  
 Leu Glu Lys Leu Asp Ser Tyr Phe Phe Phe Gly Gly Thr Arg Thr Gln  
 35 40 45  
 Ile Leu Val Ile Thr Pro Thr Asn Ile Arg Leu Ala Ala Lys Lys Arg  
 50 55 60  
 Gly Cys Lys Val Ser Thr Ile Glu Lys Ile Ile Lys Ile Leu Ser Phe  
 65 70 75 80  
 Ile Leu Leu Pro Leu Val Ile Ile Ala Phe Ile Leu Arg Tyr Phe Leu  
 85 90 95  
 His Lys Lys Phe Asp Lys Gln Phe Leu Cys Ile Pro Lys Val Ile Ser

100 105 110  
 Asn Glu Asp Glu Ala Leu Leu Gly Ser Arg Pro Gln Ala Val Glu Lys  
 115 120 125  
 Ala Val Arg Glu Ile Ser Pro Ala Phe Phe Ser Ile Pro Arg Lys Tyr  
 130 135 140  
 Gln Leu Ile Arg Ile Asp Thr Pro Lys Asp Asp Ala Pro Ser Ile Leu  
 145 150 155 160  
 Phe Pro Ile Gly Ile Glu Ile Ile Leu Lys Asp Leu Cys Ile Asp Thr  
 165 170 175  
 Leu Lys Gln Ser Asn Leu Phe Leu Lys Arg Glu Met Asp Phe Leu Gly  
 180 185 190  
 His Pro Glu Glu Lys Ala Leu Phe Asp Ser Ile Cys Ser Ile Glu Lys  
 195 200 205  
 Asp Gln Glu Trp Met Ser Leu Glu Ser Lys Lys Leu Leu Ile Thr His  
 210 215 220  
 Phe Leu Lys Tyr Leu Phe Val Ser Gly Ile Glu Gln Leu Asn Pro Gly  
 225 230 235 240  
 Phe Asn Pro Glu Asn Gly Arg Gly Tyr Phe Ser Glu Ile Ser Thr Ala  
 245 250 255  
 Lys Ile His Phe His Gln His Gly Arg Tyr Gly Pro Ile Arg Ser Ser  
 260 265 270  
 Gly Pro Ile Met Lys Glu Ile  
 275

&lt;210&gt;222

&lt;211&gt;272

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;222

Ile Val Asp Arg Arg Ser Pro Ala Cys Tyr Asp Ser Ile Asn Ser Asp  
 1 5 10 15  
 Ala Ile Gly Val Ser Leu Leu Met Asp Ile Ser His Ile Leu Glu Asp  
 20 25 30  
 Leu Ala Tyr Asp Glu Gly Ile Leu Pro Arg Glu Ala Ile Glu Ala Ala  
 35 40 45  
 Ile Val Lys Gln Met Gln Ile Thr Pro Tyr Leu Leu His Ile Leu His  
 50 55 60  
 Asp Ala Thr Gln Arg Val Pro Glu Ile Val Asn Asp Gly Ser Tyr Gln  
 65 70 75 80  
 Gly His Leu Tyr Ala Met Tyr Leu Leu Ala Gln Phe Arg Glu Ser Arg  
 85 90 95  
 Ala Leu Pro Leu Ile Ile Lys Leu Phe Ala Phe Glu Asp Asp Thr Pro  
 100 105 110  
 His Ala Ile Ala Gly Asp Val Leu Thr Glu Asp Leu Pro Arg Ile Leu  
 115 120 125  
 Ala Ser Val Cys Asn Asp Asp Ser Leu Ile Lys Glu Leu Ile Glu Thr  
 130 135 140  
 Pro Lys Ile Asn Pro Tyr Val Lys Ala Ala Ala Ile Ser Gly Leu Val  
 145 150 155 160  
 Thr Leu Val Gly Ala Gly Lys Ile Pro Arg Asp Lys Val Ile Arg Xaa  
 165 170 175  
 Phe Ala Glu Leu Leu Asn Tyr Arg Leu Glu Lys Gln Pro Ser Phe Ala  
 180 185 190  
 Trp Asp Asn Leu Ile Ala Gly Ile Cys Thr Leu Tyr Pro Gly Glu Leu  
 195 200 205  
 Phe Tyr Pro Ile Ser Lys Ala Phe Asp Gly Gly Leu Val Asp Thr Ser  
 210 215 220  
 Phe Ile Ser Met Glu Asp Val Glu Asn Ile Ile His Glu Glu Thr Val  
 225 230 235 240  
 Glu Ser Cys Ile His Thr Leu Cys Ser Ser Thr Glu Leu Ile Asn Asp  
 245 250 255  
 Thr Leu Glu Glu Met Glu Lys Trp Leu Glu Asp Phe Pro Ile Glu Pro  
 260 265 270

&lt;210&gt;223

&lt;211&gt;246

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;223

Val Asn Lys Lys Lys Arg Phe Leu Ser Leu Leu Phe Leu Thr Ala Val  
 1 5 10 15  
 Leu Leu Gly Ile Trp Phe Ser Pro His Pro Ala Ser Ile Asn Ser Asn  
 20 25 30  
 Ala Trp Gln Leu Phe Ala Ile Phe Thr Thr Thr Ile Met Gly Ile Ile  
 35 40 45  
 Phe Gln Pro Val Pro Met Gly Ala Ile Ala Ile Ile Gly Ile Ser Thr  
 50 55 60  
 Leu Leu Leu Thr Gln Thr Leu Thr Leu Glu Gln Gly Leu Ser Gly Phe  
 65 70 75 80  
 His Asn Pro Ile Ala Trp Leu Val Phe Leu Ser Phe Ser Ile Ala Lys  
 85 90 95  
 Gly Ile Ile Lys Thr Gly Leu Gly Glu Arg Ile Ala Tyr Phe Phe Val  
 100 105 110  
 Ser Ala Leu Gly Lys Ser Pro Leu Gly Leu Ser Tyr Gly Leu Val Ile  
 115 120 125  
 Thr Asp Phe Phe Leu Ala Pro Ala Ile Pro Ser Val Thr Ala Arg Ala  
 130 135 140  
 Gly Gly Ile Leu Tyr Pro Val Val Thr Ser Leu Ser Asp Ser Phe Gly  
 145 150 155 160  
 Ser Ser Ala Glu Lys Gly Thr Gln Asp Leu Ile Gly Ser Phe Leu Ile  
 165 170 175  
 Lys Val Ala Tyr Gln Ser Ser Val Ile Thr Ser Ala Met Phe Leu Thr  
 180 185 190  
 Ala Met Ala Gly Asn Pro Leu Val Ala Ala Leu Ala Gly His Val Gly  
 195 200 205  
 Val Ser Leu Ser Trp Val Leu Trp Ala Lys Ala Ala Ile Ile Pro Gly  
 210 215 220  
 Leu Leu Ser Leu Phe Leu Met Pro Ile Ile Leu Tyr Lys Leu Tyr Pro  
 225 230 235 240  
 Pro Lys Asn His Ile Leu  
 245

&lt;210&gt;224

&lt;211&gt;123

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;224

Leu Ser Pro Arg Gly Leu Phe Pro Lys Ala Leu Thr Lys Lys Tyr Ala  
 1 5 10 15  
 Ile Arg Ser Pro Ser Pro Val Phe Met Ile Pro Phe Ala Ile Glu Lys  
 20 25 30  
 Glu Arg Lys Thr Asn His Ala Ile Gly Leu Trp Asn Pro Asp Asn Pro  
 35 40 45  
 Cys Ser Arg Val Asn Val Cys Val Ser Ser Ser Val Glu Ile Pro Ile  
 50 55 60  
 Met Ala Ile Ala Pro Met Gly Thr Gly Trp Lys Met Ile Pro Met Ile  
 65 70 75 80  
 Val Val Val Asn Ile Ala Lys Ser Cys Gln Ala Leu Glu Phe Ile Asp  
 85 90 95  
 Ala Gly Trp Gly Glu Asn Gln Met Pro Lys Ser Thr Ala Val Arg Lys  
 100 105 110  
 Arg Arg Asp Lys Lys Arg Phe Phe Leu Phe Thr  
 115 120

&lt;210&gt;225

&lt;211&gt;550

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;225

Met His Pro Leu Tyr Val Asp Leu Asp Thr Ile Ile Ser Ser Tyr Ser  
 1 5 10 15  
 Pro Pro Leu Pro Lys Glu Phe Gln Glu Ala Ala Ser Leu Ile Ala Val

488



530 535 540  
 Ile Pro Asp Thr Thr Tyr  
 545 550  
 <210>226  
 <211>322  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>226  
 Tyr Gln Lys Leu Trp Glu Arg Glu Arg Glu Tyr Phe Lys Thr Ile Arg  
 1 5 10 15  
 Glu Lys Glu His Ala Thr Ile Ser Thr Met Leu Val Glu Leu Glu Ala  
 20 25 30  
 Leu Lys Arg Glu Phe Ala His Leu Lys Asp Gln Lys Pro Thr Ser Asp  
 35 40 45  
 Gln Glu Ile Thr Ser Leu Tyr Gln Cys Leu Asp His Leu Glu Phe Val  
 50 55 60  
 Leu Leu Gly Leu Gly Gln Asp Lys Phe Leu Lys Ala Thr Glu Asp Glu  
 65 70 75 80  
 Asp Val Leu Phe Glu Ser Gln Lys Ala Ile Asp Ala Trp Asn Ala Leu  
 85 90 95  
 Leu Thr Lys Ala Arg Asp Val Leu Gly Leu Gly Asp Ile Gly Ala Ile  
 100 105 110  
 Tyr Gln Thr Ile Glu Phe Leu Gly Ala Tyr Leu Ser Lys Val Asn Arg  
 115 120 125  
 Arg Ala Phe Cys Ile Ala Ser Glu Ile His Phe Leu Lys Thr Ala Ile  
 130 135 140  
 Arg Asp Leu Asn Ala Tyr Tyr Leu Leu Asp Phe Arg Trp Pro Leu Cys  
 145 150 155 160  
 Lys Ile Glu Glu Phe Val Asp Trp Gly Asn Asp Cys Val Glu Ile Ala  
 165 170 175  
 Lys Arg Lys Leu Cys Thr Phe Glu Lys Glu Thr Lys Glu Leu Asn Glu  
 180 185 190  
 Ser Leu Leu Arg Glu Glu His Ala Met Glu Lys Cys Ser Ile Gln Asp  
 195 200 205  
 Leu Gln Arg Lys Leu Ser Asp Ile Ile Ile Glu Leu His Asp Val Ser  
 210 215 220  
 Leu Phe Cys Phe Ser Lys Thr Pro Ser Gln Glu Glu Tyr Gln Lys Asp  
 225 230 235 240  
 Cys Leu Tyr Gln Ser Arg Leu Arg Tyr Leu Leu Leu Leu Tyr Glu Tyr  
 245 250 255  
 Thr Leu Leu Cys Lys Thr Ser Thr Asp Phe Gln Glu Gln Ala Arg Ala  
 260 265 270  
 Lys Glu Glu Phe Ile Arg Glu Lys Phe Ser Leu Leu Glu Leu Glu Lys  
 275 280 285  
 Gly Ile Lys Gln Thr Lys Glu Leu Glu Phe Ala Ile Ala Lys Ser Lys  
 290 295 300  
 Leu Glu Arg Gly Cys Leu Val Met Arg Lys Tyr Glu Xaa Pro Leu Asn  
 305 310 315 320  
 Ile Val

<210>227  
 <211>101  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>227

Glu Cys Val Met Ser Tyr Pro Asp Ile Ser Asn Val Gln Ala Ser Ser  
 1 5 10 15  
 Ile Gln Ser Ala Leu Leu His Lys Thr Ser Asp Gln Ile Gln Gln Lys  
 20 25 30  
 Arg Cys Phe Lys Gln Ser Thr Phe Val Ile Leu Ala Val Ser Leu Val  
 35 40 45  
 Ile Ile Gly Ser Leu Phe Leu Leu Ala Gly Val Ala Ile Leu Thr Val  
 50 55 60  
 Phe Ser His Gly Val Leu Ser Leu Val Phe Gly Val Leu Gly Ile Val

65 70 75 80  
 Leu Gly Leu Leu Leu Leu Ala Gly Gly Val Gly Leu Leu Val Glu Glu  
 85 90 95  
 Ala Lys Ser Leu Leu  
 100  
 <210>228  
 <211>398  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>228  
 Glu Leu Ser Tyr Gly Val Val Val Ser Ile Tyr Ser Glu Ile Leu Ser  
 1 5 10 15  
 Phe Ser Glu Leu Thr Ser Cys Lys His Ser Leu Phe Pro Phe Gly Pro  
 20 25 30  
 Ile Glu Thr Ala Ser Ile Arg Ile His His Val Phe Asn Val Val Ile  
 35 40 45  
 Val Cys Leu Ile Ile Leu Gly Thr Leu Phe Val Cys Leu Gly Met Val  
 50 55 60  
 Phe Leu Gly Val Phe Ser Thr Tyr Leu Leu Gly Met Ser Ser Met Ile  
 65 70 75 80  
 Leu Gly Leu Leu Leu Ile Ser Ile Gly Leu Ala Leu Leu Lys Phe Lys  
 85 90 95  
 Glu Arg Tyr Gly Leu Glu Pro Lys Glu Leu Phe Gly Val Glu Gly Gly  
 100 105 110  
 Phe Asp Lys Lys Leu Pro Ser Glu Ile Ile Gln Met Gln Asp Gln Ile  
 115 120 125  
 Ala Asp Leu Ala Arg Glu Leu Asp Leu Glu Gln Lys Lys Asp Thr Leu  
 130 135 140  
 Ile Arg Gly Phe Ser Ala Arg Leu Asp Val Leu Glu Gly Ser Lys Thr  
 145 150 155 160  
 Glu Lys Lys Gln Ile Leu Lys Ile Gly Val Pro Arg Asn Leu Ser Glu  
 165 170 175  
 Ile Gln Glu Arg Ala Gln Glu Gln Asn Ser Ile Leu Glu Gln Cys Lys  
 180 185 190  
 Glu Ala Leu Leu Phe Arg Arg Lys Ser Ala Gln Glu Ile Phe Lys Lys  
 195 200 205  
 Leu Tyr Asp Arg Lys Ala Ala Phe Trp Arg Ser Tyr Arg Glu Asp Leu  
 210 215 220  
 Trp Cys Tyr Ser Glu Ile His Val Ser Lys Lys Ala Leu Ser Asn Leu  
 225 230 235 240  
 Tyr Ile Gly Asp Val Phe Glu Gly Thr Ala Pro His Phe Leu Met Glu  
 245 250 255  
 Ala Tyr Ala Met Cys Arg Thr Ala Lys Asn Leu Arg Asn Tyr Val Lys  
 260 265 270  
 Val Cys Val Glu Asp Met Arg Val Asn Glu Glu Lys Lys Arg Ala Lys  
 275 280 285  
 Gln Leu Ser Val Ser Glu Leu Leu Cys Cys Cys Thr Glu Ile Glu Thr  
 290 295 300  
 Asp Leu Glu Asn Glu Thr Asn Leu Phe Thr Ser Asp Ser Glu Asp Val  
 305 310 315 320  
 Leu Glu Glu Tyr Gln Ile His Cys Ile Arg Val Thr Met Leu His Ala  
 325 330 335  
 Leu Trp Ala Ile Tyr Asn Asp Glu Val Val Ser Arg Lys Pro Ile Asp  
 340 345 350  
 Thr Leu Asp Arg Val Arg Ala Arg Met Ala Val Glu Asp Cys Ile Glu  
 355 360 365  
 Thr Phe Glu Glu Leu Gln Met Cys Val Val His Thr Lys Thr Leu Glu  
 370 375 380  
 Leu Glu Ile Ala Gln Leu Tyr Val Asp Ile Leu Leu Glu Ala  
 385 390 395  
 <210>229  
 <211>413  
 <212>PRT  
 <213>Chlamydia pneumoniae

&lt;400&gt;229

Arg Met Tyr Phe Ser His Val Ser Thr Val Val Val Val Ala Leu Phe  
 1 5 10 15  
 Ile Leu Gly Ile Phe Phe Leu Ser Gly Ser Leu Ala Phe Leu Val His  
 20 25 30  
 Thr Ser Cys Gly Val Leu Leu Gly Ala Ala Leu Pro Ile Leu Cys Ile  
 35 40 45  
 Gly Leu Val Leu Leu Ala Val Ala Leu Ile Val Phe Leu Cys His Lys  
 50 55 60  
 His Lys Thr Arg Gln Asp Leu Asp Tyr Tyr Asp Gln Asp Leu Asp Ser  
 65 70 75 80  
 Leu Val Ile His Lys Lys Glu Ile Pro Asn Asp Ile Ser Glu Leu Arg  
 85 90 95  
 Val Thr Phe Glu Lys Leu Gln Asn Leu Phe Gln Phe His Thr Lys Asp  
 100 105 110  
 Phe Ser Asp Leu Ser Gln Glu Leu Gln Gly Lys Phe Ile Asn Cys Met  
 115 120 125  
 Glu Lys Trp Leu Thr Leu Glu Asp Glu Val Thr Lys Phe Leu Ile Val  
 130 135 140  
 Arg Asp Arg Phe Leu Glu Thr Arg Arg Asn Phe Thr Thr Phe Gly Glu  
 145 150 155 160  
 Gln Val Lys Gly Ile Gln Ser Asn Ile Phe Asp Leu His Glu Glu Lys  
 165 170 175  
 Ser Ser Leu Tyr Leu Glu Leu Tyr Arg Leu Arg Lys Asp Leu Gln Val  
 180 185 190  
 Leu Leu Asn Phe Phe Leu Leu Pro Pro Gly Ile Leu Lys Val Asp Tyr  
 195 200 205  
 Asp Glu Ile Glu Ala Ile Lys Gly Leu Phe Ile Arg Leu Thr Ser Arg  
 210 215 220  
 Leu Asp Lys Leu Asp Val Lys Ala Gln Glu Arg Lys Lys Phe Ile Asn  
 225 230 235 240  
 Glu Met Ser Arg Glu Phe Lys Glu Val Glu Lys Ala Phe Asp Ile Val  
 245 250 255  
 Asp Arg Ala Thr Lys Lys Leu Met Asp Arg Ala Lys Lys Glu Ser Pro  
 260 265 270  
 Ala Arg Leu Phe Met Gly Arg Thr Glu Ser Leu Leu Glu Met Lys Lys  
 275 280 285  
 Asn Glu Glu Ala Leu Lys Asn Gln Gly Leu Asp Pro Glu Asn Leu Ser  
 290 295 300  
 His Pro Glu Leu Phe Ser Pro Tyr Gln Gln Leu Leu Ile Leu Asn Tyr  
 305 310 315 320  
 Leu Asn Ser Glu Ile Val Leu His His Tyr Glu Phe Leu Ile Ser Gly  
 325 330 335  
 Thr Val Thr Ser Gly Leu Thr Leu Glu Cys Glu Asn Arg Met Arg  
 340 345 350  
 Ala Ala Ser Thr Gly Leu Asn Ala Leu Leu Val Arg Lys Leu Gln Phe  
 355 360 365  
 Arg Gly Ala Ile Lys Ser Ala Tyr Phe Glu Lys Leu Thr Glu Ile Glu  
 370 375 380  
 Lys Glu Leu Arg Ser Leu Gln Asp Val Ile Xaa Ser Leu Glu Leu Glu  
 385 390 395 400  
 Leu Ile His Lys Ile Lys Asp Ile Val Thr Glu Glu Thr  
 405 410

&lt;210&gt;230

&lt;211&gt;193

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;230

Ile Cys Phe Lys Arg Arg Lys Asp Arg Thr Gly Met Leu Ser Arg Gln  
 1 5 10 15  
 Lys Glu Ser Arg Glu Thr Gly Gly Val Ser Arg Ser Tyr Arg Arg Glu  
 20 25 30  
 Leu Leu Glu Val Leu Lys Thr Arg Leu Ser Val Glu Lys Glu Ile Gln  
 35 40 45

Leu Phe Glu Glu Val Val Ser Ala Phe Glu Glu Lys Leu Ala Ser Leu  
 50 55 60  
 His Arg Thr Val Phe Ser Glu Glu Glu Leu Gln Glu Ala Leu Asp Lys  
 65 70 75 80  
 Ala Lys Ala Glu Leu Asp Ile Gln Val Arg Lys Ser Val Val Glu  
 85 90 95  
 Asp Leu Ser Cys Glu Pro Thr Leu Ile Gln Tyr His Leu Leu Arg Leu  
 100 105 110  
 Tyr Glu Val Gln Cys Arg Ile Val Glu Gln Phe Leu Thr Gln Thr Phe  
 115 120 125  
 Ser Ser Glu Gln Glu Lys Val Leu Glu Glu Tyr Glu Ala Leu Lys Ala  
 130 135 140  
 Arg Ile Arg Lys Thr Leu Arg Val Lys Leu Asp Gln Val Arg Ala Asn  
 145 150 155 160  
 Val Ala Phe Val Ala Ser Thr Thr Asp Leu Leu Ser Glu Ser Glu Ser  
 165 170 175  
 Leu Asp Gly Asn Asp Ser Val Phe Glu Asp Ala His Asp Asp Phe Leu  
 180 185 190  
 Asp

&lt;210&gt;231

&lt;211&gt;267

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;231

Leu Thr Ser Ser Lys Lys Gln Val Met Ser Ser Ala Ile Ala Arg Asp  
 1 5 10 15  
 Cys Phe Pro Ser Pro Ser Pro Gln Pro Ser Ser Thr Leu Gly Val His  
 20 25 30  
 Pro Pro Lys Tyr Lys Ser Leu Ile Leu Ser Val Ser Leu Ile Val Leu  
 35 40 45  
 Gly Val Leu Leu Leu Cys Val Gly Met Leu Leu Leu Val Asn Ala Ile  
 50 55 60  
 Phe Ser Phe Ser Val Leu Thr Val Gly Leu Gly Gly Ala Gly Val Phe  
 65 70 75 80  
 Leu Gly Ser Leu Leu Leu Ile Leu Gly Leu Ile Phe Phe Val Ser Tyr  
 85 90 95  
 His Arg Lys Leu Ser Glu Ala Thr Arg Ser Leu Glu Gln Lys Ile Thr  
 100 105 110  
 Leu Glu Tyr Gln Pro Trp Ala Asp Leu Arg Lys Glu Leu Asn Glu Val  
 115 120 125  
 Gln Glu Trp Ser Asn Phe Leu Leu Asp Glu Trp Glu Asp Phe Lys Glu  
 130 135 140  
 Val Val Ala Gln His Lys Ser Gln Phe Ala Thr Phe Glu Gly Asp Leu  
 145 150 155 160  
 Leu Leu Phe Gly Arg Glu Val Glu Lys Tyr Glu Thr Ile Trp Lys Glu  
 165 170 175  
 Leu Asp Gly Arg Asp Val Ala Leu Leu Thr Glu Leu Lys Asn Ile Trp  
 180 185 190  
 Gly Pro Leu Glu Phe Leu Arg Lys Lys Gly Asp Arg Leu Gln Cys Glu  
 195 200 205  
 Ile Asp Lys Leu Arg Lys Glu Val Met Lys Val Gly Lys Ser Gly Leu  
 210 215 220  
 Lys Leu Ala Cys Glu Leu Thr Lys Phe Lys Ser Ala Leu Lys Asp Val  
 225 230 235 240  
 Lys Ile Glu Gln Glu Cys Tyr Arg Asp Lys Arg Lys Val Glu Lys Leu  
 245 250 255  
 Glu Val Phe Pro Glu Val Ile Gly Gly Asn Tyr  
 260 265

&lt;210&gt;232

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;232

Asn Lys Ala Arg Thr Met Asn Pro Val Thr Phe Asp Arg Ile Gln Val  
 1 5 10 15  
 Asp Phe Ile Pro Glu Asp Thr Ser Leu Arg Ile Asn Ser Tyr Ile Val  
 20 25 30  
 Ala Gly Gly Leu Leu Ile Leu Gly Val Val Leu Ser Ile Leu Ser Val  
 35 40 45  
 Ile Cys Leu Asp Ile Gly Leu Val Gly Leu Ser Ala Gly Ala Ala Phe  
 50 55 60  
 Thr Leu Gly Leu Gly Cys Leu Ile Phe Ala Leu Phe Leu Phe Ser Phe  
 65 70 75 80  
 Ser Leu Ile Leu Leu Leu Ser Gln Glu Lys Arg Val Pro Asp Val Leu  
 85 90 95  
 Ser Leu Tyr Leu Glu Lys Glu Val Pro Gln Tyr Glu Thr Pro Leu Tyr  
 100 105 110  
 Lys Glu Asp Leu Glu Ser Glu Arg Asp Met Ser Ala Ile Ser Glu Arg  
 115 120 125  
 Leu Gly Ile Ile Glu Glu Lys Leu Arg Ile Ala Glu Lys Phe Arg Tyr  
 130 135 140  
 Ser Asp Ser Val Phe Val  
 145 150  
 <210>233  
 <211>375  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>233  
 Gly Ser Ser Leu Ala Leu Lys Phe His Leu Ile His Gln Ser Lys Lys  
 1 5 10 15  
 Ser Gln Ala Arg Val Gly Gln Ile Glu Thr Ser His Gly Val Ile Asp  
 20 25 30  
 Thr Pro Ala Phe Val Pro Val Ala Thr His Gly Ala Leu Lys Gly Val  
 35 40 45  
 Ile Asp His Ser Asp Ile Pro Leu Leu Phe Cys Asn Thr Tyr His Leu  
 50 55 60  
 Leu Leu His Pro Gly Pro Glu Ala Val Ala Lys Leu Gly Gly Leu His  
 65 70 75 80  
 Gln Phe Met Gly Arg Gln Ala Pro Ile Ile Thr Asp Ser Gly Gly Phe  
 85 90 95  
 Gln Ile Phe Ser Leu Ala Tyr Gly Ser Val Ala Glu Glu Ile Lys Ser  
 100 105 110  
 Cys Gly Lys Lys Lys Gly Met Ser Ser Leu Val Lys Ile Thr Asp Glu  
 115 120 125  
 Gly Ala Trp Phe Lys Ser Tyr Arg Asp Gly Arg Lys Leu Phe Leu Ser  
 130 135 140  
 Pro Glu Leu Ser Val Gln Ala Gln Lys Asp Leu Gly Ala Asp Ile Ile  
 145 150 155 160  
 Ile Pro Leu Asp Glu Leu Leu Pro Phe His Thr Asp Gln Glu Tyr Phe  
 165 170 175  
 Leu Thr Ser Cys Ser Arg Thr Tyr Val Trp Glu Lys Arg Ser Leu Glu  
 180 185 190  
 Tyr His Arg Lys Asp Pro Arg His Gln Ser Met Tyr Gly Val Ile His  
 195 200 205  
 Gly Gly Leu Asp Pro Glu Gln Arg Arg Ile Gly Val Arg Phe Val Glu  
 210 215 220  
 Asp Glu Pro Phe Asp Gly Ser Ala Ile Gly Gly Ser Leu Gly Arg Asn  
 225 230 235 240  
 Leu Gln Glu Met Ser Glu Val Val Lys Ile Thr Thr Ser Phe Leu Ser  
 245 250 255  
 Lys Glu Arg Pro Val His Leu Leu Gly Ile Gly Asp Leu Pro Ser Ile  
 260 265 270  
 Tyr Ala Met Val Gly Phe Gly Ile Asp Ser Phe Asp Ser Ser Tyr Pro  
 275 280 285  
 Thr Lys Ala Ala Arg His Gly Leu Ile Leu Ser Lys Ala Gly Pro Ile  
 290 295 300  
 Lys Ile Gly Gln Gln Lys Tyr Ser Gln Asp Ser Ser Thr Ile Asp Pro

494

Ile Leu Gly Asn Ile Leu Gly Ala Gly Arg Leu Tyr Ser Val Trp Tyr  
 65 70 75 80  
 Thr Ser Asp Glu Asp Trp Lys Lys Gln Val Val  
 85 90

&lt;210&gt;237

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;237

Arg Gly Met Leu Pro Ala Trp Val Thr Pro Gly Phe Leu Thr Lys Leu  
 1 5 10 15  
 Ala Glu Gly Leu Lys Ile Asn Ser Gly Arg Ser Val Asn Pro Lys Gly  
 20 25 30  
 Leu Glu Gln Cys Ile Ala Ser Gly Gln Tyr Asn Glu Gln Ile Lys Lys  
 35 40 45  
 Asn Asn Leu Tyr Gly Ser Gln Val Leu Gly Gly Gln Leu Ala Thr Pro  
 50 55 60  
 Thr Ala Val Val Gly Asp Tyr Leu Ile Glu Asp Pro Thr Phe His Glu  
 65 70 75 80  
 Ile Glu Arg Ala Ile Gln His Ile Arg Gln Leu Gln Ala Val Glu Gly  
 85 90 95  
 Asp His Asp Asp  
 100

&lt;210&gt;238

&lt;211&gt;140

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;238

Gln Ile Leu Phe Thr Ser Pro Leu Asn Lys Lys Xaa Leu Val Leu Cys  
 1 5 10 15  
 Thr Ala Met Phe Phe Ile Val Cys Phe Gly Phe Leu Ile His Lys Lys  
 20 25 30  
 His Thr Ile Leu Pro Pro Lys Ala His Ile Pro Thr Asn Ala Lys His  
 35 40 45  
 Phe Pro Thr Ile Gly Asn Pro Tyr Ala Pro Ile Asn Ile Thr Val Phe  
 50 55 60  
 Glu Glu Pro Ser Cys Ser Ala Cys Ala Glu Phe Thr Thr Glu Val Phe  
 65 70 75 80  
 Pro Leu Leu Lys Lys His Tyr Ile Asp Thr Gly Glu Ile Ser Phe Thr  
 85 90 95  
 Leu Ile Pro Val Cys Phe Ile Arg Gly Ser Lys Pro Ala Ala Gln Ala  
 100 105 110  
 Leu Leu Cys Ile Tyr His His Asp Ser Thr Ser Gly Arg Tyr Arg Arg  
 115 120 125  
 Leu Tyr Gly Ile Phe Pro Ser Tyr Phe Asp Leu Ser  
 130 135 140

&lt;210&gt;239

&lt;211&gt;154

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;239

Leu Phe Thr Tyr Phe Leu Ser Tyr Cys Phe Pro Asn Gln Thr Phe Ser  
 1 5 10 15  
 Ser Leu Val Arg Ser Pro Thr Arg His Leu Gly Tyr Pro Phe Arg Leu  
 20 25 30  
 Arg Cys Arg Arg Ser Pro Thr Ile Phe Ala Asn Asp Thr Leu Ile Gly  
 35 40 45  
 Phe Ala Ile Leu Ala Val Val Cys Ile Ser Pro Thr Arg Pro Glu Ala  
 50 55 60  
 Leu Glu Val Gly Pro Thr Leu Pro Glu Gly Phe Ser Tyr Asn Pro Ser  
 65 70 75 80  
 Ala Gly Gly Arg Arg Ala Ala Val Leu Phe Leu Ser Leu Leu Gly Trp  
 85 90 95  
 Leu Glu Ala Arg Tyr Leu Thr Ala Ser Ser Leu Gly Ile Thr Ser Ser

100 105 110  
 Gln Ser Ser Asn Phe Leu Leu Leu Tyr Ser Ser Ile Met Thr Val Tyr  
 115 120 125  
 Ser Leu Leu Val Val Leu Ser Leu Ala Gly Ser Glu Arg Arg Trp His  
 130 135 140  
 Thr Arg Pro Lys Ile Val Ile Ala Thr Ala  
 145 150  
 <210>240  
 <211>94  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>240  
 Leu Leu Ala Met Leu Cys Leu Thr Ile Glu Pro Ala Leu Ala Val Val  
 1 5 10 15  
 Phe Ala Tyr Asp Glu Thr Arg Ala Thr Leu Arg Tyr Ile Ser Gln Phe  
 20 25 30  
 Leu Gly Asp Lys Arg Ala Leu Thr Arg Ala Ser Phe Phe Gly Ser Glu  
 35 40 45  
 Tyr Tyr Lys His Thr Leu Ser Trp Glu Glu Arg Thr Val Arg Pro Leu  
 50 55 60  
 Arg Lys Ala Tyr Lys Gln Ala Phe Glu Gly Ile Ser Phe Pro Ile Asn  
 65 70 75 80  
 Gln Leu Leu Ala Ile Leu Val Ala Ser Phe Cys Lys Ser Gln  
 85 90  
 <210>241  
 <211>234  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>241  
 Arg Phe Lys Lys Ala Leu Ile Tyr Met Ser Ser Gln Pro Leu Val Thr  
 1 5 10 15  
 Thr Ser Ser Ser Leu Ser Arg Tyr Val Val Leu Thr Gly Glu Glu Lys  
 20 25 30  
 Val Ala Cys Tyr Lys Lys Ala Phe Asn His Ile Trp His Gly Ala Pro  
 35 40 45  
 Ala Ile Ile Leu Ala Ala Ala Leu Leu Met Phe Cys Ile Phe Gly Phe  
 50 55 60  
 Val Leu Gly Ser Ile Leu Leu Gly Ala Pro Leu Glu Gly Ala Ser Ile  
 65 70 75 80  
 Leu Tyr Asp Val Ile Leu Pro Trp Leu Leu Pro Ser Ile Leu Val Phe  
 85 90 95  
 Val Leu Leu Val Leu Pro Leu Asn Ile Tyr Ala Tyr Ser His His Lys  
 100 105 110  
 Gln Val Leu Ala Leu His Glu Arg Ile Thr Gln Ser Asn Tyr Lys Glu  
 115 120 125  
 Ile Tyr Asp His Cys Glu Lys Glu Lys Lys Thr Pro Asn Lys Lys Ala  
 130 135 140  
 Leu Ser Leu Tyr Ile Glu Ser Gln Val Leu Val Pro Glu Tyr Ser Lys  
 145 150 155 160  
 Arg Phe Ser Ser Met Ile Leu Gly Lys Thr Leu Lys Ile Ile Pro Lys  
 165 170 175  
 Lys Asp Ser Pro Glu Ser Leu Lys His Asp Glu Leu Ile Gln Lys Ala  
 180 185 190  
 Leu Glu Arg Ala Lys Glu Asn Ile Tyr Met Asn Lys Asn Gln Arg Glu  
 195 200 205  
 Lys Arg Asp Glu Arg Glu Ala Lys Lys Glu Ala Lys Asn Ala Ser Lys  
 210 215 220  
 Thr Asn Pro Leu Trp Glu Gly Leu Gly Thr  
 225 230  
 <210>242  
 <211>235  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>242



Met Leu Gln Ala His Arg Leu Cys Tyr Ser Cys Asp Asn Gln Val Ile  
 1 5 10 15  
 Leu Lys Asp Ala Ser Phe Gln Ala Ser Pro Gly Thr Ile Thr Ile Ile  
 20 25 30  
 Leu Gly Ser Ser Gly Val Gly Lys Thr Thr Leu Phe Arg Leu Leu Ala  
 35 40 45  
 Gly Phe Leu Pro Leu Gln Glu Gly Glu Leu Leu Trp Asn Gly Ser Pro  
 50 55 60  
 Leu Asn Arg Lys Asp Val Ala Tyr Met Gln Gln Lys Glu Ala Leu Leu  
 65 70 75 80  
 Pro Trp Arg Thr Ala Leu Lys Asn Met Thr Leu Ser Thr Glu Leu Gly  
 85 90 95  
 Ile Asn Thr Ser His Asn Ala Leu Ser Asn Glu Arg Leu Glu Glu Ile  
 100 105 110  
 Ile His Asn Phe Asp Leu Gly Gln Leu Leu Asp Arg Tyr Pro Asp Glu  
 115 120 125  
 Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Gln Cys Leu  
 130 135 140  
 Ser Leu Lys Pro Ile Leu Leu Leu Asp Glu Pro Phe Ser Ser Leu Asp  
 145 150 155 160  
 Val Leu Leu Lys Glu Gln Leu Tyr Gln Asp Ile Val Ala Leu Ala Lys  
 165 170 175  
 Lys Glu Asn Lys Thr Val Leu Leu Val Thr His Asp Phe His Asp Val  
 180 185 190  
 Ser Cys Leu Gly Asp Val Leu Tyr Val Ile Lys Asn Lys Thr Leu Thr  
 195 200 205  
 Pro Val Pro Leu Asp Pro Ser Met Arg Pro Leu Asn Asn Gly Leu Cys  
 210 215 220  
 Phe Ile Lys Asp Leu Lys Lys His Leu Tyr Thr  
 225 230 235

&lt;210&gt;243

&lt;211&gt;301

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;243

Lys Lys Phe Leu Met Arg Arg Phe Leu Phe Leu Ile Leu Ser Ser Leu  
 1 5 10 15  
 Pro Leu Val Ala Phe Ser Ala Asp Asn Phe Thr Ile Leu Glu Glu Lys  
 20 25 30  
 Gln Ser Pro Leu Ser Arg Val Ser Ile Ile Phe Ala Leu Pro Gly Val  
 35 40 45  
 Thr Pro Val Ser Phe Asp Gly Asn Cys Ser Ile Pro Trp Phe Ser His  
 50 55 60  
 Ser Lys Lys Thr Leu Glu Gly Gln Arg Ile Tyr Tyr Ser Gly Asp Ser  
 65 70 75 80  
 Phe Gly Lys Tyr Phe Val Val Ser Ala Leu Trp Pro Asn Lys Val Ser  
 85 90 95  
 Ser Ala Val Val Ala Cys Asn Met Ile Leu Lys His Arg Val Asp Leu  
 100 105 110  
 Ile Leu Ile Ile Gly Ser Cys Tyr Ser Arg Ser Gln Asp Ser Arg Phe  
 115 120 125  
 Gly Ser Val Leu Val Ser Lys Gly Tyr Ile Asn Tyr Asp Ala Asp Val  
 130 135 140  
 Arg Pro Phe Phe Glu Arg Phe Glu Ile Pro Asp Ile Lys Lys Ser Val  
 145 150 155 160  
 Phe Ala Thr Ser Glu Val His Arg Glu Ala Ile Leu Arg Gly Gly Glu  
 165 170 175  
 Glu Phe Ile Ser Thr His Lys Gln Glu Ile Glu Glu Leu Leu Lys Thr  
 180 185 190  
 His Gly Tyr Leu Lys Ser Thr Thr Lys Thr Glu His Thr Leu Met Glu  
 195 200 205  
 Gly Leu Val Ala Thr Gly Glu Ser Phe Ala Met Ser Arg Asn Tyr Phe  
 210 215 220  
 Leu Ser Leu Gln Lys Leu Tyr Pro Glu Ile His Gly Phe Asp Ser Val

498

```

      115      120      125
Lys Leu Arg Ser Ser Pro Glu Ala Glu Leu Val Thr Pro Val Ala Leu
      130      135      140
Thr Thr Asp Arg Glu Glu Ile Leu Thr Glu Lys Lys Val Lys Cys Val
145      150      155      160
Phe Asp Ser Glu Gly Arg Ala Leu Tyr Phe Ser Arg Ser Pro Ile Pro
      165      170      175
Phe Ile Leu Lys Lys Ala Thr Pro Val Tyr Leu His Ile Gly Val Tyr
      180      185      190
Ala Phe Lys Arg Glu Ala Leu Phe Arg Tyr Leu Thr Ala Xaa Leu Xaa
      195      200      205
Ser Ser
      210
<210>246
<211>537
<212>PRT
<213>Chlamydia pneumoniae
<400>246
Met Pro Phe Lys Cys Ile Phe Leu Thr Gly Gly Val Val Ser Ser Leu
      1      5      10      15
Gly Lys Gly Leu Thr Ala Ala Ser Leu Ala Leu Ile Leu Glu Arg Gln
      20      25      30
Arg Leu Asn Val Ala Met Leu Lys Leu Asp Pro Tyr Leu Asn Val Asp
      35      40      45
Pro Gly Thr Met Asn Pro Phe Glu His Gly Glu Ile Tyr Val Thr Asp
      50      55      60
Asp Gly Val Glu Thr Asp Leu Asp Leu Gly His Tyr His Arg Phe Ser
      65      70      75      80
Ser Ala Ala Leu Ser Arg His Ser Ser Ala Thr Ser Gly Gln Ile Tyr
      85      90      95
Ala Arg Val Ile Lys Arg Glu Arg Glu Gly Asp Tyr Leu Gly Ser Thr
      100      105      110
Val Gln Val Ile Pro His Ile Thr Asn Glu Ile Ile Gln Val Ile Leu
      115      120      125
Asp Ala Ala Lys Glu His Ser Pro Asp Val Leu Ile Val Glu Ile Gly
      130      135      140
Gly Thr Ile Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Ala Ile Arg
145      150      155      160
Gln Phe Arg Tyr Asp His Ser Glu Asp Cys Leu Asn Ile His Met Thr
      165      170      175
Tyr Val Pro Tyr Leu Gln Ala Ala Asp Glu Val Lys Ser Lys Pro Thr
      180      185      190
Gln His Ser Val Gln Thr Leu Arg Gly Ile Gly Ile Ile Pro Asp Ala
      195      200      205
Ile Leu Cys Arg Ser Glu Lys Pro Leu Thr Gln Glu Val Lys Ser Lys
      210      215      220
Ile Ser Leu Phe Cys Asn Val Pro Asn Arg Ala Val Phe Asn Val Ile
225      230      235      240
Asp Val Lys His Thr Ile Tyr Glu Met Pro Leu Met Leu Ala Gln Glu
      245      250      255
Lys Ile Ala Asn Phe Ile Gly Glu Lys Leu Lys Leu Ala Thr Val Pro
      260      265      270
Glu Asn Leu Asp Asp Trp Arg Val Leu Val Asn Gln Leu Ser Gln Asp
      275      280      285
Leu Pro Lys Val Lys Ile Gly Val Val Gly Lys Tyr Val Gln His Arg
      290      295      300
Asp Ala Tyr Lys Ser Ile Phe Glu Ala Leu Thr His Ala Ala Leu Arg
305      310      315      320
Leu Gly His Ala Ala Glu Ile Ile Pro Ile Asp Ala Glu Asp Glu Asn
      325      330      335
Leu Thr Met Glu Leu Ser Gln Cys Asp Ala Cys Leu Val Pro Gly Gly
      340      345      350
Phe Gly Val Arg Gly Trp Glu Gly Lys Ile Ala Ala Ala Lys Phe Cys
      355      360      365

```

Arg Glu Gln Gly Ile Pro Tyr Phe Gly Ile Cys Leu Gly Met Gln Val  
 370 375 380  
 Leu Val Val Glu Tyr Ala Arg Asn Val Leu Asn Leu Asp Gln Ala Asn  
 385 390 395 400  
 Ser Leu Glu Met Asp Pro Asn Thr Pro His Pro Ile Val Tyr Val Met  
 405 410 415  
 Glu Gly Gln Asp Pro Leu Val Ala Thr Gly Gly Thr Met Arg Leu Gly  
 420 425 430  
 Ala Tyr Pro Cys Leu Leu Lys Pro Gly Ser Lys Ala His Lys Ala Tyr  
 435 440 445  
 Asn Glu Ser Ser Leu Ile Gln Glu Arg His Arg His Arg Tyr Glu Val  
 450 455 460  
 Asn Pro Asp Tyr Ile Gln Ser Leu Glu Asp His Gly Leu Arg Ile Val  
 465 470 475 480  
 Gly Thr Cys Pro Pro Gln Gly Leu Cys Glu Ile Ile Glu Val Ser Asp  
 485 490 495  
 His Pro Trp Met Ile Gly Val Gln Phe His Pro Glu Phe Val Ser Lys  
 500 505 510  
 Leu Ile Ser Pro His Pro Leu Phe Ile Ala Phe Ile Glu Ala Ala Leu  
 515 520 525  
 Val Tyr Ser Lys Asp Ala Ser His Val  
 530 535

&lt;210&gt;247

&lt;211&gt;154

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;247

Met Gln Ala Met Ser Lys Pro Ser Ser Cys Lys Ala Tyr Leu Gly Ile  
 1 5 10 15  
 Asp Tyr Gly Lys Lys Arg Ile Gly Leu Ala Tyr Ala Ala Glu Pro Leu  
 20 25 30  
 Leu Leu Thr Leu Pro Ile Gly Asn Ile Glu Ala Gly Lys Asn Leu Lys  
 35 40 45  
 Leu Ser Ala Glu Ala Leu His Lys Ile Ile Leu Ser Arg Asn Ile Thr  
 50 55 60  
 Cys Val Val Leu Gly Asn Pro Leu Pro Met Gln Lys Gly Leu Tyr Ser  
 65 70 75 80  
 Ser Leu Gln Glu Glu Val Ser Leu Leu Ala Glu Glu Leu Lys Lys Leu  
 85 90 95  
 Ser Thr Val Glu Ile Ile Leu Trp Asp Glu Arg Leu Ser Ser Val Gln  
 100 105 110  
 Ala Glu Arg Met Leu Lys Gln Asp Cys Gly Leu Ser Arg Lys Asp Arg  
 115 120 125  
 Lys Gly Lys Thr Asp Ser Leu Ala Ala Thr Leu Ile Leu Thr Ser Phe  
 130 135 140  
 Leu Asp Ser Leu Pro Lys Lys Leu Thr Leu  
 145 150

&lt;210&gt;248

&lt;211&gt;390

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;248

Met Thr Asn Val Val Gln Glu Thr Ile Gly Gly Leu Asn Ser Pro Arg  
 1 5 10 15  
 Thr Cys Pro Pro Cys Ile Leu Val Ile Phe Gly Ala Thr Gly Asp Leu  
 20 25 30  
 Thr Ala Arg Lys Leu Leu Pro Ala Leu Tyr His Leu Thr Lys Glu Gly  
 35 40 45  
 Arg Leu Ser Asp Gln Phe Val Cys Val Gly Phe Ala Arg Arg Glu Lys  
 50 55 60  
 Ser Asn Glu Leu Phe Arg Gln Glu Met Lys Gln Ala Val Ile Gln Phe  
 65 70 75 80  
 Ser Pro Ser Glu Leu Asp Ile Lys Val Trp Glu Asp Phe Gln Gln Arg  
 85 90 95

Leu Phe Tyr His Arg Ser Glu Phe Asp Asn Asn Met Gly Tyr Thr Ser  
 100 105 110  
 Leu Lys Asp Ser Leu Glu Asp Leu Asp Lys Thr Tyr Gly Thr Arg Gly  
 115 120 125  
 Asn Arg Leu Phe Tyr Leu Ser Thr Pro Pro Gln Tyr Phe Ser Arg Ile  
 130 135 140  
 Ile Glu Asn Leu Asn Lys His Lys Leu Phe Tyr Lys Asn Gln Asp Gln  
 145 150 155 160  
 Gly Lys Pro Trp Ser Arg Val Ile Ile Glu Lys Pro Phe Gly Arg Asp  
 165 170 175  
 Leu Asp Ser Ala Lys Gln Leu Gln Gln Cys Ile Asn Glu Asn Leu Asn  
 180 185 190  
 Glu Asn Ser Val Tyr His Ile Asp His Tyr Leu Gly Lys Glu Thr Val  
 195 200 205  
 Gln Asn Ile Leu Thr Thr Arg Phe Ala Asn Thr Ile Phe Glu Ser Cys  
 210 215 220  
 Trp Asn Ser Gln Tyr Ile Asp His Val Gln Ile Ser Leu Ser Glu Thr  
 225 230 235 240  
 Ile Gly Ile Gly Ser Arg Gly Asn Phe Phe Glu Lys Ser Gly Met Leu  
 245 250 255  
 Arg Asp Met Val Gln Asn His Met Met Gln Leu Leu Cys Leu Leu Thr  
 260 265 270  
 Met Glu Pro Pro Thr Thr Phe Asp Ala Asp Glu Ile Arg Lys Xaa Lys  
 275 280 285  
 Ile Lys Ile Leu Gln Arg Ile Ser Pro Phe Ser Glu Gly Ser Ser Ile  
 290 295 300  
 Val Arg Gly Gln Tyr Gly Pro Gly Thr Val Gln Gly Val Ser Val Leu  
 305 310 315 320  
 Gly Tyr Arg Glu Glu Glu Asn Val Asp Lys Asp Ser Arg Val Glu Thr  
 325 330 335  
 Tyr Val Ala Leu Lys Gln Ser Leu Ile Ile Pro Val Gly Leu Glu Phe  
 340 345 350  
 Leu Ser Ile Tyr Val Gln Glu Asn Asp Ser Pro Lys Asn Leu Gln Thr  
 355 360 365  
 Phe Leu Leu Phe Leu Lys Asn His Pro Thr Ile Tyr Leu Gln Pro Lys  
 370 375 380  
 Asn Val His Val Val Arg  
 385 390

&lt;210&gt;249

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;249

Gln Arg Phe Pro Ser Arg Asp Leu Arg Ser Phe Lys Thr Val Ile Asn  
 1 5 10 15  
 Asn Pro Arg Trp Leu Gly Val Pro Phe Tyr Leu Arg Ala Gly Lys Arg  
 20 25 30  
 Leu Ala Lys Lys Ser Thr Asp Ile Ser Ile Ile Phe Lys Lys Ser Pro  
 35 40 45  
 Tyr Asn Leu Phe Ala Ala Glu Glu Cys Ser Arg Cys Pro Ile Glu Asn  
 50 55 60  
 Asp Leu Leu Ile Ile Arg Ile Gln Pro Asp Glu Gly Val Ala Leu Lys  
 65 70 75 80  
 Phe Asn Cys Lys Val Pro Gly Thr Asn Asn Ile Val Arg Pro Val Lys  
 85 90 95  
 Met Asp Phe Arg Tyr Asp Ser Tyr Phe Gln Thr Thr Thr Pro Glu Ala  
 100 105 110  
 Tyr Glu Arg Leu Leu Cys Asp Cys Ile Ile Gly Asp Arg Thr Phe Ile  
 115 120 125  
 Tyr Gly Gly Gly  
 130

&lt;210&gt;250

&lt;211&gt;266

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;250

```

Met Thr Asn Ile Gly Ile Glu Thr Met Ala Thr Leu Ile Asn Phe Asn
 1           5           10           15
Asp Thr Asn Lys Leu Leu Leu Thr Lys Gln Pro Ser Leu Phe Ile Asp
           20           25           30
Leu Ala Ser Lys Asp Trp Ile Ala Ser Ala Asn Gln Ala Ile Lys Gln
           35           40           45
Arg Gly Ala Phe Tyr Val Ala Leu Ser Gly Gly Lys Thr Pro Leu Glu
           50           55           60
Ile Tyr Lys Asp Ile Val Ile Asn Lys Asp Lys Leu Ile Asp Pro Ser
           65           70           75           80
Lys Ile Phe Leu Phe Trp Gly Asp Glu Arg Leu Ala Pro Ile Thr Ser
           85           90           95
Ser Glu Ser Asn Tyr Gly Gln Ala Met Ser Ile Leu Arg Asp Leu Asn
           100          105          110
Ile Pro Asp Glu Gln Ile Phe Arg Met Glu Thr Glu Asn Pro Asp Gly
           115          120          125
Ala Lys Lys Tyr Gln Glu Leu Ile Glu Asn Lys Ile Pro Asp Ala Ser
           130          135          140
Phe Asp Met Ile Met Leu Gly Leu Gly Glu Asp Gly His Thr Leu Ser
           145          150          155          160
Leu Phe Ser Asn Thr Ser Ala Leu Glu Glu Glu Asn Asp Leu Val Val
           165          170          175
Phe Asn Ser Val Pro His Leu Glu Thr Glu Arg Met Thr Leu Thr Phe
           180          185          190
Pro Cys Val His Lys Gly Lys His Val Val Val Tyr Val Gln Gly Glu
           195          200          205
Asn Lys Lys Pro Ile Leu Lys Ser Val Phe Phe Ser Glu Gly Arg Glu
           210          215          220
Glu Lys Leu Tyr Pro Ile Glu Arg Val Gly Arg Asp Arg Ser Pro Leu
           225          230          235          240
Phe Trp Ile Ile Ser Pro Glu Ser Tyr Asp Ile Ala Asp Phe Asp Asn
           245          250          255
Ile Ser Ser Ile Tyr Lys Met Asp Ile Leu
           260          265

```

&lt;210&gt;251

&lt;211&gt;194

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;251

```

Leu Asn Ser Phe Phe Ser Phe Asn Ser Leu Asn Ser Trp His Cys Leu
 1           5           10           15
Ser Ile Ile Phe Cys Ser Ser Trp Ser Cys Ser Arg Asn Tyr Cys Gly
           20           25           30
Asn Asp Gly Val Cys Ala Ala Gly Gly Gly Ala Leu Leu Ile Ser Leu
           35           40           45
Leu Gly Leu Trp Ile Ala Ile Val Arg Lys Ala Lys His Gln Glu Ala
           50           55           60
Cys Val Gly His Leu Thr Asn Val Val Leu His Thr Ala Val Ser Glu
           65           70           75           80
Ala Leu Leu His Asp Pro Ser His Phe Gln Thr Asn Ala Leu Ala Arg
           85           90           95
Asp Leu Phe Leu Thr Asp Cys Leu Ser His Tyr Gly His Leu Phe Ser
           100          105          110
Asn Glu Glu Val Ala Gln Leu Val Gln Gly Gly Ala Pro Gly Gly Gly
           115          120          125
Ser Arg Pro Ser Gln His Tyr Gly Gly Ser Ser Asp Tyr Gln Asn Arg
           130          135          140
Arg Gly Gly Asn Gly Asn Phe Gly Gly Ser His Phe Gly Gly Gly Gly
           145          150          155          160
Gly Phe Ala Gly Ser His Phe Gly Ala Gly Tyr Pro Thr Ala Pro Thr
           165          170          175
Met Pro Ser Ala Pro Pro Pro Phe Pro Pro Pro Ala Tyr Asp Thr Ile

```

180 185 190

Tyr Gly

<210>252  
 <211>167  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>252

Xaa Ala Gln Asn Leu Gly Asn Leu Phe Asn Ser Phe Gly Ile Leu Ile  
 1 5 10 15  
 Met Cys Phe Ser Gln Cys Lys Ser Cys Gln Thr Pro Glu Lys Glu Thr  
 20 25 30  
 Ser Ala Ile Val Leu Gly Ala Thr Leu Leu Phe Phe Val Ile Ala Leu  
 35 40 45  
 Ile Leu Gly Pro Thr Leu Gly Ala Leu Val Tyr Cys Ala Tyr Lys Val  
 50 55 60  
 Tyr Thr Leu Gly Lys Met Ile Tyr Ser Leu Asn Lys Ala Lys Ala Lys  
 65 70 75 80  
 Val Leu Arg His Pro Ala Gln Asn Val Phe His Arg Ala Ala Gly Val  
 85 90 95  
 Ala Thr Ile Arg Ser Ser Glu Glu Ala Val Lys Ala Cys Lys Leu Tyr  
 100 105 110  
 Lys Ser Ala Met Ile Gly Ser Leu Val Val Ser Leu Ile Ala Ser Leu  
 115 120 125  
 Ala Leu Ile Ala Leu Thr Ala Gly Ile Val Leu Val Leu Phe Phe Val  
 130 135 140  
 Ala Pro Gly Ala Ala Pro Val Ile Thr Ala Ala Met Met Gly Ser Ala  
 145 150 155 160  
 Leu Gln Val Glu Ala Leu Cys  
 165

<210>253  
 <211>106  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>253

Lys Leu Ala Ile Ile Arg Arg Arg Arg Arg Arg Gly Lys Arg Arg Ile  
 1 5 10 15  
 Arg Arg Val Tyr Arg Arg Ile Gly Arg Trp Arg Phe Ser Arg Asn His  
 20 25 30  
 Val Ala Ala Thr Ile Ala Pro Leu Leu Met Lys Gln Ser Leu Val Thr  
 35 40 45  
 Trp Arg Trp Arg Arg Leu Thr Val Gln Gly Asp Phe Ala Leu Asp Ile  
 50 55 60  
 Ser Ile Leu Val Ile Thr Glu Glu Leu Leu Val Ser Ser Tyr Arg Leu  
 65 70 75 80  
 Ser Lys His Phe Phe Ser Ser Trp Ser Asp Arg Lys Val Gly His Leu  
 85 90 95  
 Asn Asn Cys Val Thr His Tyr Thr Thr Gln  
 100 105

<210>254  
 <211>390  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>254

Ile Phe Leu Val Lys Phe Met Ser Ala Met Ile Ser Leu Ser Ser Ser  
 1 5 10 15  
 His Glu Ala Ser Ile Ala Ser Asn Thr Gln Val Arg Asp Val Leu Val  
 20 25 30  
 Ser Leu Ala Met Asp Glu Phe Val Glu His Asn Thr Glu Ile Leu Pro  
 35 40 45  
 Ile Lys Val Phe Leu Ala Arg Gly Thr Leu Ser Ser Thr Ala Ile Ile  
 50 55 60  
 Asp Asp Leu Lys Asp Val Val Glu Thr Glu Gly Glu His His Phe Gln  
 65 70 75 80

Val Tyr Ser Asn Ile Ser Leu Lys Met Ile Tyr Gln Arg Phe Phe Glu  
 85 90 95  
 Lys Ile Phe Gly Ile Gly Cys Cys Pro Leu Leu Leu Val Thr Asp Ser  
 100 105 110  
 His His Thr Asp Pro Cys Gly Ala Leu Ile Thr Gly Ile Phe Ala Ala  
 115 120 125  
 Val Leu Phe Thr Val Leu Ala Ile Val Phe Gly Pro Thr Leu Gly Ile  
 130 135 140  
 Leu Cys Tyr Ser Ala Tyr Lys Ile Tyr Gln Leu Thr Lys Lys Ile Ser  
 145 150 155 160  
 Ser Leu Ser Arg Thr His Thr Glu Val Ile Asn Ser Val Gln Lys Ser  
 165 170 175  
 Asp Pro Phe Ile His Arg Ser Gly Ala Val Ala Ala Ala Ala Ala Ser  
 180 185 190  
 Gln Ser Thr Ile Lys Ala Cys Lys Val Phe Arg Gln Ser Thr Leu Ile  
 195 200 205  
 Phe Phe Val Leu Gly Leu Ile Ile Thr Ile Ser Leu Ala Ala Leu Ile  
 210 215 220  
 Val Gly Leu Val Phe Ala Leu Phe Phe Leu Asp Pro Gly Ala Pro Ala  
 225 230 235 240  
 Val Met Thr Ala Ala Met Ile Gly Cys Cys Ala Ala Gly Gly Thr Gly  
 245 250 255  
 Ile Leu Leu Ser Val Ile Gly Phe Leu Leu Ala Ser Val Tyr Ser Val  
 260 265 270  
 Gln Lys Ser Gln Glu Gly Val His His Met His Thr Ala Leu Leu Arg  
 275 280 285  
 Cys Ile Val Ser Asn Thr Ile Ile Gln Met Pro Tyr Leu Pro Ile Thr  
 290 295 300  
 Pro Gly Thr Lys Lys Val Leu Thr Gln Ser Ile Arg Arg Tyr Gln Gln  
 305 310 315 320  
 Phe Phe Ser Asp Asp Glu Tyr Arg Asp Ile Glu Ser Glu Val Pro Leu  
 325 330 335  
 Asn Arg Gln Thr Thr Pro Pro Pro Ser Tyr Glu Thr Leu Phe His Glu  
 340 345 350  
 Glu Gly Ser Asp Gly Ser Ser Asn Val Ile Pro Arg Glu Ser Pro Pro  
 355 360 365  
 Ala Tyr Ser Thr Ile Asp Ser Ser Asn Ser Pro Phe Pro Ser Ser Ser  
 370 375 380  
 Pro Pro Pro Tyr Tyr Arg  
 385 390

&lt;210&gt;255

&lt;211&gt;125

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;255

Thr Pro Ser Trp Leu Phe Cys Thr Leu Tyr Thr Glu Ala Ser Lys Lys  
 1 5 10 15  
 Pro Ile Thr Glu Arg Arg Ile Pro Val Pro Pro Ala Ala Gln His Pro  
 20 25 30  
 Ile Ile Ala Ala Val Ile Thr Ala Gly Ala Pro Gly Ser Lys Lys Asn  
 35 40 45  
 Arg Ala Lys Thr Arg Pro Thr Ile Lys Ala Ala Lys Asp Ile Val Ile  
 50 55 60  
 Ile Lys Pro Ser Thr Lys Lys Ile Asn Val Asp Cys Leu Asn Thr Leu  
 65 70 75 80  
 Gln Ala Leu Ile Val Asp Cys Glu Ala Ala Ala Ala Thr Ala Pro  
 85 90 95  
 Glu Arg Cys Ile Lys Gly Ser Asp Phe Cys Thr Glu Phe Met Thr Ser  
 100 105 110  
 Val Trp Val Leu Asp Lys Glu Asp Ile Phe Leu Val Ser  
 115 120 125

&lt;210&gt;256

&lt;211&gt;95

&lt;212&gt;PRT



&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;256

Arg His Leu Lys Cys Asp Pro Arg Leu Thr Leu Ser Pro Gly Lys Ala  
 1 5 10 15  
 Leu Asp Ala Leu His Asn Leu Asn Gly Asn Glu Arg Ser Arg Asn Arg  
 20 25 30  
 Thr Phe Lys Ile Asn Lys Thr Thr Leu Thr Thr Ala Gln Thr Thr Ala  
 35 40 45  
 Ile Thr Gly Tyr Asn Ile Val Ser Thr Thr Lys Gln Ala Val Phe Leu  
 50 55 60  
 Thr Gln Gly Phe Ile Ile Ile Ser Leu Arg His Ser Lys Lys Asn  
 65 70 75 80  
 Arg Thr Ser His Lys Asn Asn Arg Trp Phe Leu Arg Lys Leu Ile  
 85 90 95

&lt;210&gt;257

&lt;211&gt;291

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;257

Thr Cys Gln Lys Glu Ile Met Lys His Tyr Leu Ser Phe Ser Pro Ser  
 1 5 10 15  
 Ala Asp Phe Phe Ser Lys Gln Gly Ala Ile Glu Thr Gln Val Leu Phe  
 20 25 30  
 Gly Glu Arg Val Leu Val Lys Gly Ser Thr Cys Tyr Ala Tyr Ser Gln  
 35 40 45  
 Leu Phe His Asn Glu Leu Leu Trp Lys Pro Tyr Pro Gly His Ser Phe  
 50 55 60  
 Arg Ser Thr Leu Val Pro Cys Thr Pro Glu Phe His Ile His Pro Asn  
 65 70 75 80  
 Val Ser Val Val Ser Val Asp Ala Phe Leu Asp Pro Trp Gly Ile Pro  
 85 90 95  
 Leu Pro Phe Gly Thr Leu Leu His Val Asn Ser Gln Asn Thr Val Ile  
 100 105 110  
 Phe Pro Lys Asp Ile Leu Asn His Met Asn Thr Ile Trp Gly Ser Gly  
 115 120 125  
 Thr Pro Gln Cys Asp Pro Arg His Leu Arg Arg Leu Asn Tyr Asn Phe  
 130 135 140  
 Phe Ala Glu Leu Leu Ile Lys Asp Ala Asp Leu Leu Leu Asn Phe Pro  
 145 150 155 160  
 Tyr Val Trp Gly Gly Arg Ser Val His Glu Ser Leu Glu Lys Pro Gly  
 165 170 175  
 Val Asp Cys Ser Gly Phe Ile Asn Ile Leu Tyr Gln Ala Gln Gly Tyr  
 180 185 190  
 Asn Val Pro Arg Asn Ala Ala Asp Gln Tyr Ala Asp Cys His Trp Ile  
 195 200 205  
 Ser Ser Phe Glu Asn Leu Pro Ser Gly Gly Leu Ile Phe Leu Tyr Pro  
 210 215 220  
 Lys Glu Glu Lys Arg Ile Ser His Val Met Leu Lys Gln Asp Ser Ser  
 225 230 235 240  
 Thr Leu Ile His Ala Ser Gly Gly Gly Lys Lys Val Glu Tyr Phe Ile  
 245 250 255  
 Leu Glu Gln Asp Gly Lys Phe Leu Asp Ser Thr Tyr Leu Phe Phe Arg  
 260 265 270  
 Asn Asn Gln Arg Gly Arg Ala Phe Phe Gly Ile Pro Arg Lys Arg Lys  
 275 280 285  
 Ala Phe Leu  
 290

&lt;210&gt;258

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;258

Val Val Ala Lys Ser Thr Ile Gln Glu Ser Val Ala Thr Gly Arg Arg  
 1 5 10 15

Lys Gln Ala Val Ser Ser Val Arg Leu Arg Pro Gly Ser Gly Lys Ile  
                   20                  25                  30  
 Asp Val Asn Gly Lys Ser Phe Glu Asp Tyr Phe Pro Leu Glu Ile Gln  
                   35                  40                  45  
 Arg Thr Thr Ile Leu Ser Pro Leu Lys Lys Ile Thr Glu Asp Gln Ser  
                   50                  55                  60  
 Gln Tyr Asp Leu Ile Ile Arg Val Ser Gly Gly Gly Ile Gln Gly Gln  
                   65                  70                  75                  80  
 Val Ile Ala Thr Arg Leu Gly Leu Ala Arg Ala Leu Leu Lys Glu Asn  
                   85                  90                  95  
 Glu Glu Asn Arg Gln Asp Leu Lys Ser Cys Gly Phe Leu Leu Glu Ile  
                   100                  105                  110  
 Leu Glu Gly Lys Asn Val Lys Asn Thr Asp Ile Lys Lys Leu Val Lys  
                   115                  120                  125  
 Ala Ser Asn Ser Leu Ser Val Lys Ile Phe Thr Val Phe Arg Ile Val  
                   130                  135                  140  
 Phe Gly Lys Ser Leu Ser Tyr Tyr Arg Lys Ala Phe Leu Phe Leu Gly  
                   145                  150                  155                  160  
 Ile Pro Lys Asn Ala Arg Pro Leu  
                                   165

&lt;210&gt;259

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;259

Met Glu Lys Arg Lys Asp Thr Lys Thr Thr Ile Val Lys Ser Ser Glu  
   1                  5                  10                  15  
 Thr Thr Lys Ser Trp Tyr Val Val Asp Ala Ala Gly Lys Thr Leu Gly  
                   20                  25                  30  
 Arg Leu Ser Ser Glu Val Ala Lys Ile Leu Arg Gly Lys His Lys Val  
                   35                  40                  45  
 Thr Tyr Thr Pro His Val Ala Met Gly Asp Gly Val Ile Val Ile Asn  
                   50                  55                  60  
 Ala Glu Lys Val Arg Leu Thr Gly Ala Lys Lys Gly Gln Lys Ile Tyr  
                   65                  70                  75                  80  
 Arg Tyr Tyr Thr Gly Tyr Ile Ser Gly Met Arg Glu Ile Pro Phe Glu  
                   85                  90                  95  
 Asn Met Met Ala Arg Lys Pro Asn Tyr Ile Ile Glu His Ala Ile Lys  
                   100                  105                  110  
 Gly Met Met Pro Arg Thr Arg Leu Gly Lys Lys Gln Leu Lys Ser Leu  
                   115                  120                  125  
 Arg Ile Val Lys Gly Asp Ser Tyr Glu Thr Phe Glu Ser Gln Lys Pro  
                   130                  135                  140  
 Ile Leu Leu Asp Ile  
                   145

&lt;210&gt;260

&lt;211&gt;226

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;260

Met Ser Leu Leu Ile Glu Ala Lys Asn Leu Ser Lys Thr Ile Gln Gln  
   1                  5                  10                  15  
 Gln Asn Gln Asn Ile Ser Ile Leu Thr Asp Val Ser Leu Ser Leu His  
                   20                  25                  30  
 Ala Gly Glu Thr Ile Ser Ile Thr Gly Ala Ser Gly Asn Gly Lys Thr  
                   35                  40                  45  
 Thr Leu Leu His Leu Leu Gly Thr Leu Asp Val Pro Ser Ser Gly Ser  
                   50                  55                  60  
 Leu Arg Phe Phe Asp Lys Asp Leu Lys Asn Gln Asp Leu Ala Asn Phe  
                   65                  70                  75                  80  
 Arg Asn Gln His Ile Gly Phe Val Phe Gln Asn Phe Tyr Leu Leu Glu  
                   85                  90                  95  
 Asp Asp Thr Val Leu Lys Asn Val Leu Met Pro Ala Leu Ile Ala Arg  
                   100                  105                  110

Lys Asn Ile Ser Lys Gly Ser Pro Val Tyr Thr Arg Ala Leu Glu Leu  
 115 120 125  
 Leu Asp Leu Val Asn Leu Glu Asp Lys Val Arg Thr Arg Cys Ser Lys  
 130 135 140  
 Leu Ser Gly Gly Glu Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ile  
 145 150 155 160  
 Asn Glu Pro Ala Ile Leu Leu Ala Asp Glu Pro Ser Gly Asn Leu Asp  
 165 170 175  
 Glu Glu Thr Ser Glu Gln Ile His Asn Leu Leu Leu Glu Gln Ala Ser  
 180 185 190  
 Ala Leu Cys Gly Ile Leu Ile Val Thr His Asn Lys His Leu Ala Ser  
 195 200 205  
 Arg Cys Ser Arg Glu Gly Val Leu Ser Asn Gly Lys Leu Phe Phe His  
 210 215 220  
 Asn Ser  
 225  
 <210>261  
 <211>506  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>261  
 Leu Glu Val Met Lys Phe Glu Phe Ser Val Ala Leu Lys Tyr Leu Ile  
 1 5 10 15  
 Pro Gly Arg Gly Arg Leu Tyr Ser Ala Ile Val Ser Leu Phe Ser Val  
 20 25 30  
 Gly Ile Ile Ser Leu Val Val Trp Leu Ser Ile Val Phe Ile Ser Val  
 35 40 45  
 Ile His Gly Leu Glu Gln Arg Trp Ile Glu Asp Leu Ser Gln Leu His  
 50 55 60  
 Ser Pro Ile Thr Ile Leu Pro Ser Asp Thr Tyr Tyr Ser Ser Tyr Tyr  
 65 70 75 80  
 Tyr Gln Ile Asp Lys His Ser Ser Leu Ser Asn Tyr Thr Thr Lys Thr  
 85 90 95  
 Leu Gly Glu Lys Ile Ala Ser Pro Gln Val Asp Pro Tyr Asp Pro Glu  
 100 105 110  
 Ser Asp Tyr Leu Leu Pro Glu Thr Phe Pro Leu Lys Asp Cys Asp Leu  
 115 120 125  
 Gly Gly Gln Gln Lys Asp Pro Val Lys Met Thr Leu Glu Ser Leu Gly  
 130 135 140  
 Pro Tyr Leu Gln Ser Gln His Gly Lys Val Ile Glu Phe Glu Gln Gly  
 145 150 155 160  
 Val Gly Tyr Leu Asp Ile Lys Thr Ser Leu Lys Leu Gln Lys Pro Gln  
 165 170 175  
 Pro Arg Asn Leu Thr His Phe Leu Thr Tyr Pro Ser Lys Leu Ser Tyr  
 180 185 190  
 Glu Asp Lys Val Leu Pro Tyr Asp Glu Thr Asp Tyr Thr Ser Ala Glu  
 195 200 205  
 Leu Asn Pro Phe Asn Arg Ser Pro Ser Gly Trp Gln Gln Asp Phe His  
 210 215 220  
 His Leu Glu Glu Leu Tyr Arg Gly Ala Ser Ile Ile Leu Pro Ser Thr  
 225 230 235 240  
 Tyr Lys Asp Ser Gly Tyr Lys Val Gly Asp Thr Gly Val Phe Ser Thr  
 245 250 255  
 Tyr Ser Ile Glu Asn Glu Lys Glu Thr Gln Tyr Thr Val His Val Ile  
 260 265 270  
 Gly Phe Tyr Asn Pro Gly Leu Ser Pro Leu Gly Gly Arg Thr Val Phe  
 275 280 285  
 Ile Asp Pro Asp Leu Ala Arg Ser Ile Arg Ser Gln Ser Glu Gly Leu  
 290 295 300  
 Gly Met Ser Asn Gly Phe His Leu Phe Phe Pro Asn Thr Lys Arg Ile  
 305 310 315 320  
 Val Phe Val Lys Lys Gln Ile Glu Asn Ile Leu Thr Ser Leu Gly Val  
 325 330 335  
 Asp Asp Tyr Trp Glu Ile Ser Ser Leu His Asp Tyr Asp Tyr Phe Gln

340 345 350  
 Pro Ile Leu Asp Gln Leu Gln Ser Asp Gln Val Leu Phe Leu Phe Val  
 355 360 365  
 Cys Ile Leu Ile Leu Ile Val Ala Cys Ser Asn Ile Val Thr Met Ser  
 370 375 380  
 Met Leu Leu Val Asn Asn Lys Lys Lys Glu Ile Gly Ile Leu Lys Ala  
 385 390 395 400  
 Met Gly Thr Ser Ser Arg Ser Leu Lys Ile Ile Phe Ala Cys Cys Gly  
 405 410 415  
 Ala Phe Ser Gly Ala Cys Gly Val Val Ile Gly Thr Ile Phe Ala Ile  
 420 425 430  
 Ile Thr Leu Lys Asn Leu Gln Phe Ile Val Lys Ala Leu Asn Tyr Leu  
 435 440 445  
 Gln Gly Arg Glu Thr Phe Asn Thr Ala Phe Phe Gly Gln Asn Leu Pro  
 450 455 460  
 Asn Ser Val His Pro Gln Ala Ile Tyr Phe Leu Gly Leu Gly Thr Leu  
 465 470 475 480  
 Leu Leu Ala Ala Val Ser Gly Ala Leu Pro Ala Arg Lys Val Ala Lys  
 485 490 495  
 Met His Val Ser Glu Ile Leu Lys Ala Asp  
 500 505

&lt;210&gt;262

&lt;211&gt;84

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;262

Phe Ser Ala Phe Thr Met Asn Cys Lys Phe Phe Asn Val Ile Ile Ala  
 1 5 10 15  
 Asn Ile Val Pro Ile Thr Thr Pro Gln Ala Pro Glu Asn Ala Pro Gln  
 20 25 30  
 Gln Ala Lys Met Ile Phe Lys Leu Arg Asp Asp Val Pro Ile Ala Leu  
 35 40 45  
 Arg Met Pro Ile Ser Phe Phe Leu Leu Phe Thr Arg Ser Ile Asp Ile  
 50 55 60  
 Val Thr Met Leu Glu Gln Ala Thr Ile Arg Ile Ser Met His Thr Lys  
 65 70 75 80  
 Arg Lys Arg Thr

&lt;210&gt;263

&lt;211&gt;503

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;263

Leu Pro Trp Met Ser Pro Phe Lys Lys Ile Val Asn Arg Leu Leu Cys  
 1 5 10 15  
 Tyr Ile Ser Phe Gln Lys Glu Ser Arg Thr Leu Pro Ile Ile Ile Arg  
 20 25 30  
 Glu Pro Arg Met Thr Thr Lys Ser Leu Gly Ser Phe Asn Ser Val Ile  
 35 40 45  
 Ser Lys Asn Lys Ile His Phe Ile Ser Leu Gly Cys Ser Arg Asn Leu  
 50 55 60  
 Val Asp Ser Glu Val Met Leu Gly Ile Leu Leu Lys Ala Gly Tyr Glu  
 65 70 75 80  
 Ser Thr Asn Glu Ile Glu Asp Ala Asp Tyr Leu Ile Leu Asn Thr Cys  
 85 90 95  
 Ala Phe Leu Lys Ser Ala Arg Asp Glu Ala Lys Asp Tyr Leu Asp His  
 100 105 110  
 Leu Ile Asp Val Lys Lys Glu Asn Ala Lys Ile Ile Val Thr Gly Cys  
 115 120 125  
 Met Thr Ser Asn His Lys Asp Glu Leu Lys Pro Trp Met Ser His Ile  
 130 135 140  
 His Tyr Leu Leu Gly Ser Gly Asp Val Glu Asn Ile Leu Ser Ala Ile  
 145 150 155 160  
 Glu Ser Arg Glu Ser Gly Glu Lys Ile Ser Ala Lys Ser Tyr Ile Glu

165 170 175  
 Met Gly Glu Val Pro Arg Gln Leu Ser Thr Pro Lys His Tyr Ala Tyr  
 180 185 190  
 Leu Lys Val Ala Glu Gly Cys Arg Lys Arg Cys Ala Phe Cys Ile Ile  
 195 200 205  
 Pro Ser Ile Lys Gly Lys Leu Arg Ser Lys Pro Leu Asp Gln Ile Leu  
 210 215 220  
 Lys Glu Phe Arg Ile Leu Val Asn Lys Ser Val Lys Glu Ile Ile Leu  
 225 230 235 240  
 Ile Ala Gln Asp Leu Gly Asp Tyr Gly Lys Asp Leu Ser Thr Asp Arg  
 245 250 255  
 Ser Ser Gln Leu Glu Ser Leu Leu His Glu Leu Leu Lys Glu Pro Gly  
 260 265 270  
 Asp Tyr Trp Leu Arg Met Leu Tyr Leu Tyr Pro Asp Glu Val Ser Asp  
 275 280 285  
 Gly Ile Ile Asp Leu Met Gln Ser Asn Pro Lys Leu Leu Pro Tyr Val  
 290 295 300  
 Asp Ile Pro Leu Gln His Ile Asn Asp Arg Ile Leu Lys Gln Met Arg  
 305 310 315 320  
 Arg Thr Thr Ser Arg Glu Gln Ile Leu Gly Phe Leu Glu Lys Leu Arg  
 325 330 335  
 Ala Lys Val Pro Gln Val Tyr Ile Arg Ser Ser Val Ile Val Gly Phe  
 340 345 350  
 Pro Gly Glu Thr Gln Glu Glu Phe Gln Glu Leu Ala Asp Phe Ile Gly  
 355 360 365  
 Glu Gly Trp Ile Asp Asn Leu Gly Ile Phe Leu Tyr Ser Gln Glu Ala  
 370 375 380  
 Asn Thr Pro Ala Ala Glu Leu Pro Asp Gln Ile Pro Glu Lys Val Lys  
 385 390 395 400  
 Glu Ser Arg Leu Lys Ile Leu Ser Gln Ile Gln Lys Arg Asn Val Asp  
 405 410 415  
 Lys His Asn Gln Lys Leu Ile Gly Glu Lys Ile Glu Ala Val Ile Asp  
 420 425 430  
 Asn Tyr His Pro Glu Thr Asn Leu Leu Leu Thr Ala Arg Phe Tyr Gly  
 435 440 445  
 Gln Ala Pro Glu Val Asp Pro Cys Ile Ile Val Asn Glu Ala Lys Leu  
 450 455 460  
 Val Ser His Phe Gly Glu Arg Cys Phe Ile Glu Ile Thr Gly Thr Ala  
 465 470 475 480  
 Gly Tyr Asp Leu Val Gly Arg Val Val Lys Lys Ser Gln Asn Gln Ala  
 485 490 495  
 Leu Leu Lys Thr Ser Lys Ala  
 500

&lt;210&gt;264

&lt;211&gt;179

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;264

Ala Thr Ser Thr Val Cys Ala Leu Trp Ile Leu Gln Thr Tyr Gln Ser  
 1 5 10 15  
 His Asp Asp Ala Ala Ser Cys Ser Phe Arg Arg Ala Cys Arg Phe Gly  
 20 25 30  
 Arg Tyr Trp Leu Gly Gly Val Asn Val Pro Trp Asn Lys Phe Asn Gln  
 35 40 45  
 Thr Ser Thr Gln Ser Thr Val Ile Asn Ser Ala Ile Tyr Ile Asp Ser  
 50 55 60  
 Ser Gln Thr Trp Met Met Arg Phe Gln Ala Ser Ala Ser Ile Pro Arg  
 65 70 75 80  
 Leu Phe Arg Ile Ser Ile Phe Met Thr Lys His Gly Asp Trp Ile Asp  
 85 90 95  
 Asn Gly Thr Gly Gly Glu Leu Leu Leu Val Ala Tyr Glu Ala Asn Gln  
 100 105 110  
 Asn Pro Leu Phe Pro Asp Ile Arg Ile Glu Leu Ala Met Ser Thr Cys  
 115 120 125

Ser Gly Thr Ser Tyr Tyr Arg Ala Arg Pro Met Gln Trp Leu Cys Ser  
 130 135 140  
 Thr Tyr Tyr Ala Val Arg Pro Gly Tyr Phe Val Leu Glu Asn Arg Ser  
 145 150 155 160  
 Tyr Ser Phe Arg Val Gln Ser Phe Ser Trp Asn Ile Ala Thr Leu Pro  
 165 170 175  
 Phe Val Asn

&lt;210&gt;265

&lt;211&gt;175

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;265

Phe Cys Gly Gly Arg Leu Met Ser Ser Ser Ile Pro Thr Thr Gln Lys  
 1 5 10 15  
 Ile Thr Ile Ser Ile Pro Thr Phe Val Arg Phe Asn Ile Glu Ser Ile  
 20 25 30  
 Asn Leu Thr Asp Glu Gln Lys Lys Thr Ala Leu Thr Ile Gly Gln Asn  
 35 40 45  
 Ile Ala Thr Glu Asn Thr Gln Val Leu Gly Asn Phe Val Asp Ala Asp  
 50 55 60  
 Gly Gly Leu Ile Cys Gln Asn Asp Leu Ser Val Gly Gly Asn Ile Asn  
 65 70 75 80  
 Ile Thr Pro Gln Thr Phe Asn Thr Met Val Phe Asn Gly Arg Val Asn  
 85 90 95  
 Leu Ser Asn Ser Pro Phe Ser Tyr Gln Asp Ser Leu Gly Asn Lys Arg  
 100 105 110  
 Gln Asp Tyr Ala Asn Ile Asn Thr Glu Gln Pro Gln Gln Tyr Val Pro  
 115 120 125  
 Tyr Gly Tyr Tyr Lys Leu Thr Arg Val Met Met Met Gln Arg Ala Ala  
 130 135 140  
 Leu Ser Gly Gly His Val Gly Ser Gly Asp Ile Gly Trp Gly Glu Ser  
 145 150 155 160  
 Met Tyr Leu Gly Ile Ser Ser Ile Lys Arg Gln His Lys Val Gln  
 165 170 175

&lt;210&gt;266

&lt;211&gt;264

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;266

Ile Pro Met Lys Thr Leu Gly Val Lys Asp Gln Asn Leu Phe Ile Asp  
 1 5 10 15  
 Gln Ala Thr Leu Ser Val Glu Arg Asn Val Arg Ile Glu Asn Asn Leu  
 20 25 30  
 Glu Thr Arg Asp Leu Lys Val Leu Asp Thr Thr Thr Ser Pro Cys Glu  
 35 40 45  
 Phe Ile Val Lys Gly Asn Val Ser Ala Glu Gly Ser Gln Leu Asn Ala  
 50 55 60  
 Thr Thr Leu Ser Asp Gly Phe Asn Ile Tyr Ser Lys Thr Asp Val Ser  
 65 70 75 80  
 Gln Thr Pro Val Cys Asn Asn Ile Ser Asp Pro Gln Ser Ala Arg Asp  
 85 90 95  
 Ala Leu Thr Phe Ser Tyr Tyr Arg Lys Thr Gly Cys Gln Ala Ala Asn  
 100 105 110  
 Leu Tyr Thr Tyr Tyr Pro Gly Asn Gly Tyr Tyr Val Ala Pro Asn Thr  
 115 120 125  
 Thr Ile Glu Thr His Val Ala Ile Thr Ser Lys Ser Val Ser Arg  
 130 135 140  
 Asn Ala Thr Pro Asp Phe Ser Arg Tyr Ala Asp Ile Glu Pro Val Val  
 145 150 155 160  
 Lys Leu Lys Gln Val Gly Ile Tyr Gln Val Thr Met Gln Leu Thr Arg  
 165 170 175  
 Trp Ser Gly Gln His Asp Gly Asp Asn Ser Ala Thr Leu Ile Leu Asn  
 180 185 190

Phe Val Ser Gly Asn Asn Lys Thr Leu Leu Cys Thr Ser Asp Thr Arg  
 195 200 205  
 Gly Gly Tyr Ser Ser Asp Arg Thr Ser Val Ala Val Thr Ala Ile Phe  
 210 215 220  
 Ser Val Thr Glu Leu Val Ser Ser Pro Pro Tyr Asp Tyr Pro Trp Ile  
 225 230 235 240  
 Asn Leu Glu Ser Thr Ile Trp Met Asn Leu Met Ser Leu Ser Thr Cys  
 245 250 255  
 Gly His Leu Val Ser Ile Ser Ile  
 260

&lt;210&gt;267

&lt;211&gt;285

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;267

Thr Leu Leu Lys Val Ile Met Lys Asn Asn Ile Asn Asn Asn Glu Cys  
 1 5 10 15  
 Tyr Phe Lys Leu Asp Ser Thr Val Asp Gly Asp Leu Leu Ala Ala Asn  
 20 25 30  
 Leu Lys Thr Phe Asp Thr Gln Ala Gln Gly Ile Ser Ser Thr Glu Thr  
 35 40 45  
 Phe Ser Val Gln Gly Asn Ala Thr Phe Lys Asp Gln Val Ser Ala Thr  
 50 55 60  
 Gly Leu Thr Ser Gly Thr Thr Tyr Asn Leu Asn Ala Gln Asn Phe Thr  
 65 70 75 80  
 Ser Ser Gln Ile Ser Ile Asp Phe Lys Asn Asn Arg Leu Ser Asn Cys  
 85 90 95  
 Ala Leu Pro Lys Glu Asp Cys Asp Pro Val Pro Ala Asn Tyr Val Arg  
 100 105 110  
 Ser Pro Glu Tyr Phe Phe Cys Ser Lys Pro Leu Ile Gly Asp Phe Asp  
 115 120 125  
 Phe Asn Ser Gly Glu Ser Tyr Leu Pro Leu Thr Gly Ser Glu Tyr Thr  
 130 135 140  
 Leu Tyr Gln Ser Arg Asn Val Asn Ser Ile Phe Arg Phe Ile Gly Trp  
 145 150 155 160  
 Lys Gln Ser Thr Arg Glu Leu Thr Val Gly Gly Asn Thr Ala Ile Gln  
 165 170 175  
 Phe Leu Ala Ala Gly Thr Tyr Ile Val Ser Phe Thr Val Gly Lys Arg  
 180 185 190  
 Trp Gly Trp Asn Asn Gly Trp Gly Gly Ala Ile Tyr Ile Asn Asn Gly  
 195 200 205  
 Leu Gly Gln Val Gln Cys Glu Ser Thr Ile Tyr Ser Gly Gly Gly Tyr  
 210 215 220  
 Ala Thr Ile Gly Thr Leu Gly Thr Ser Ile Tyr Arg Ala Ser Val Asp  
 225 230 235 240  
 Val Ala Pro Asn Pro Asn Asp Pro Asn Ala Ser Asp Arg Tyr Arg Ala  
 245 250 255  
 Gly Ile Phe Tyr Leu Ser Asn Gly Gly Ser Ser Ala Gly Ile Gly Asn  
 260 265 270  
 Tyr Ser Phe Ser Leu Leu Tyr Tyr Pro Asp Asp Arg Gly  
 275 280 285

&lt;210&gt;268

&lt;211&gt;295

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;268

Phe Cys Gly Gly Arg Leu Met Ser Asn Pro Thr Pro Lys Thr Lys Ile  
 1 5 10 15  
 Ser Ile Pro Thr Phe Val Arg Phe Asn Ile Gln Ser Ile Asn Leu Thr  
 20 25 30  
 Glu Asp Gln Lys Lys Thr Thr Phe Thr Val Gly Gly Lys Val Thr Thr  
 35 40 45  
 Glu Asn Thr Val Val Arg Gly Asp Leu Thr Cys Thr Asp Gly Gly Leu  
 50 55 60

Thr Cys Gln Ser Asp Leu Thr Ile Gln Lys Asp Ile Asn Ile Arg Pro  
 65 70 75 80  
 Thr Ser Thr Asn Ser Met Val Phe Asp Gly Arg Leu Asn Leu Ser Asn  
 85 90 95  
 Ser Pro Leu Ser Tyr Lys Asn Ser Gln Gly Gln Asp Ile Thr Asp Tyr  
 100 105 110  
 Glu Lys Met Ser Ser Gly Lys Pro Gln Glu Tyr Val Pro Phe Gly Tyr  
 115 120 125  
 Tyr Lys Arg Thr Gln Ile Met Met Ala Gln Arg Ala Ala His Ser Ser  
 130 135 140  
 Gly Tyr Val Gly Gly Gly Ser Val Pro Ser Gly Ser Tyr Val Pro Trp  
 145 150 155 160  
 Asn Lys Phe Asp Gln Thr Ser Thr Gln Lys Thr Ser Gly Thr Glu Ile  
 165 170 175  
 Tyr Ile Asp Pro Asn Asp Ser Thr Lys Leu Val Phe Glu Val Asn Asn  
 180 185 190  
 Lys Val Pro Lys Leu Phe Arg Ile Ser Val Ile Met Ala Lys His Gly  
 195 200 205  
 Ser Trp Leu Asp Asn Gly Thr Gly Ala Asp Ile Leu Leu Ala Ala Asn  
 210 215 220  
 Glu Tyr Glu Gln Gly Gly Gly Arg Ile Asn Val Thr Asp Leu Ala Met  
 225 230 235 240  
 Thr Thr Ser Arg Gly Ser Ser Tyr Tyr Glu Thr Arg Pro Leu Gln Val  
 245 250 255  
 Val Cys Val Thr Tyr Tyr Ala Gln Asn Asn Gly Tyr Phe Thr Phe Gln  
 260 265 270  
 Asn Arg Ala Gly Gly Gly Leu Arg Val Ser Phe Phe Ser Trp Asn Ile  
 275 280 285  
 Val Ala Leu Pro Tyr Val Glu  
 290 295  
 <210>269  
 <211>290  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>269  
 Gly Val Val Met Lys Arg Arg Asn Leu Gln Lys Ile Leu Pro Asn Ala  
 1 5 10 15  
 Ser Thr Pro Ser Thr Asn Val Ala Glu Asn Thr Gly Ile Lys Asp Gln  
 20 25 30  
 Asn Leu Phe Leu Asp Gln Ala Thr Leu Asn Val Asp Gly Asn Val Asp  
 35 40 45  
 Ile Glu Asn Phe Leu Glu Thr Arg Asp Leu Lys Val Ala Asp Thr Ile  
 50 55 60  
 Thr Ser Pro Cys Glu Phe Thr Val Gly Gly Gly Leu Ser Ala Glu Ser  
 65 70 75 80  
 Ser Gln Phe Lys Ala Thr Thr Leu Ser Lys Gly Leu Glu Ile Thr Ser  
 85 90 95  
 Glu Asp Gln Asp Gly Arg Val Pro Lys Phe Thr Asn Val Ser Asp Pro  
 100 105 110  
 Gln Ser Pro Arg Asp Ala Leu Thr Tyr Asn Tyr Tyr Arg Asn Thr Gly  
 115 120 125  
 Cys Gln Ala Leu Asn Leu Tyr Thr Tyr Tyr Ser Ser Ser Gln Pro Thr  
 130 135 140  
 Thr Val Gly Lys Pro Ile Glu Thr Val Cys Gln Asn Pro Asn Pro Glu  
 145 150 155 160  
 Thr Tyr Arg Ile Ser Ala Ser Ala Lys Ile Tyr Asp Ala Val Thr Arg  
 165 170 175  
 Phe Pro Tyr Ile Gln Phe Lys Ala Pro Gly Ile Tyr Gln Val Thr Ile  
 180 185 190  
 Gln Ile Arg Arg Glu Ser Gly Gln His Ser Gly Leu Asp Asn Pro Asn  
 195 200 205  
 Leu Tyr Leu Asn Leu Met Ile Gly Asn Asn Lys Thr Leu Leu Cys Ala  
 210 215 220  
 Ser Asp Thr Arg Gly Tyr Ser Gly Gly His Arg Thr Ser Ile Ala Val



225 230 235 240  
 Thr Gly Thr Phe Thr Leu Thr Glu Ile Val Ala Thr Pro Pro His Asp  
 245 250 255  
 Tyr Pro Trp Leu Phe Leu Glu Thr Thr Ile Gly Leu Asp Ile Lys Ser  
 260 265 270  
 Met Ser Thr Cys Val Ile Trp Phe Pro Phe Gln Ala Asn Phe Ala Glu  
 275 280 285  
 Val Asp  
 290  
 <210>270  
 <211>134  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>270  
 Cys Phe Ser Phe Cys Arg Leu Gly Ser Lys Phe Glu Lys Ile Thr Leu  
 1 5 10 15  
 Gly Gly Asn Thr Ala Ile Gln Leu Leu Ala Ala Gly Thr Tyr Ile Leu  
 20 25 30  
 Thr Phe Thr Ile Gly Lys Arg Trp Gly Trp Asn Asn Gly Trp Gly Gly  
 35 40 45  
 Ser Ile Arg Leu Phe Glu Gly Lys Tyr Thr Gly Asp Gly Thr Met Leu  
 50 55 60  
 Cys Gly Ser Thr Val Tyr Ser Gly Gly Gly Tyr Ser Thr Ile Gly Tyr  
 65 70 75 80  
 Leu Ser Thr Ala Val Tyr Arg Asp His Ser Asp Ile Asp Pro Asp Pro  
 85 90 95  
 Asn Asn Pro Ser Asp Lys Tyr Met Asn Asn Phe Leu Phe Val Arg Asn  
 100 105 110  
 Gly Asp His Ser Ala Val Ile Gly Asn Tyr Ser Phe Thr Leu Leu Tyr  
 115 120 125  
 Phe Ala Gly Asp Lys Val  
 130  
 <210>271  
 <211>197  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>271  
 Ile Tyr Phe Val Phe Lys Arg Lys Thr Tyr Asn Tyr Phe Ile Glu Met  
 1 5 10 15  
 Thr Thr Thr Asn Asn Gln Asp Asn Asn Glu Cys Tyr Phe Lys Leu Asp  
 20 25 30  
 Ser Thr Val Asp Gly Asp Leu Leu Ala Ser Asn Ile Gln Thr Phe Asp  
 35 40 45  
 Lys Gln Ala Lys Gly Ile Ser Ser Thr Glu Thr Phe Ser Val Gln Gly  
 50 55 60  
 Asn Ala Thr Phe Lys Glu Lys Val Ser Ala Thr Gly Leu Thr Ser Ala  
 65 70 75 80  
 Ser Thr Tyr Lys Leu Asn Ala Thr Gly Pro Ala Pro Ser Ser Ile Thr  
 85 90 95  
 Ile Asp Met Lys Asn Asn Arg Leu Ser Asn Pro Ala Leu Pro Lys Asn  
 100 105 110  
 Pro Cys Asp Pro Val Pro Ala Asn Tyr Val Arg Ser Pro Gln Tyr Phe  
 115 120 125  
 Phe Cys Ala Lys Pro Ile Glu Gly Thr Phe Met Phe Asp Gly Ser Ser  
 130 135 140  
 Arg Tyr Leu Pro Ile Thr Gly Asp Gly Ser Asn Tyr Thr Leu Tyr Gln  
 145 150 155 160  
 Ser Ser Lys Ala Gly Asp Val Phe Arg Phe Val Asp Trp Asp Gln Asn  
 165 170 175  
 Ser Lys Lys Leu His Leu Gly Gly Thr Gln Pro Tyr Asn Phe Leu Leu  
 180 185 190  
 Gln Glu Pro Ile Ser  
 195  
 <210>272

&lt;211&gt;181

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;272

Ala Tyr Leu Asp Phe Ser Lys Arg Ser Cys Val Glu Glu Asp His Val  
 1 5 10 15  
 Ser Lys Lys Ile Asn Arg Asn Asp Leu Cys Pro Cys Gly Ser Asn Lys  
 20 25 30  
 Lys Tyr Lys Gln Cys Cys Leu Lys Lys Glu Glu Gln Thr Ala Arg Tyr  
 35 40 45  
 Thr Thr Glu Gly Lys Phe Lys Phe Ser Ala Glu Val Leu Ser Ala Ser  
 50 55 60  
 Glu Gln Gly Glu Ala Gly Asp Asn Cys Thr Lys Leu Phe Gln Arg Leu  
 65 70 75 80  
 Ser Gln Ser Leu Thr Ser Glu Gln Lys Ala Ala Val Gly Lys Phe His  
 85 90 95  
 Gln Ile Thr Lys Asn Lys Glu Val Met Ser Lys Lys Ala Leu Lys Lys  
 100 105 110  
 Ala Gln Ala Lys Glu Glu Lys Leu Val Thr Glu Lys Leu Gln Gln His  
 115 120 125  
 Asn Phe Glu Ile Leu Asn Thr Gly Glu Asn Leu Ala Pro Pro Met Glu  
 130 135 140  
 Ser Thr Ala Thr Leu Asn Gln Asp Thr Asn Phe Val Cys Glu Asp Phe  
 145 150 155 160  
 Ile Pro Thr Gln Glu Asp Phe Arg Ile Ser Glu Asn Ser Gln Lys Pro  
 165 170 175  
 Pro Val Glu Glu Asp  
 180

&lt;210&gt;273

&lt;211&gt;206

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;273

Met Ser Thr Leu Leu Leu Asn Pro Pro Trp Met Lys Ala Gly Lys Arg  
 1 5 10 15  
 Ile Glu Ser Leu Val Arg Lys Ala Leu Tyr Thr His Thr Met Leu Ala  
 20 25 30  
 Asn His Arg Lys Ile Val Val Ala Leu Ser Gly Gly Lys Asp Ser Leu  
 35 40 45  
 Thr Leu Leu Leu Met Leu Lys Ala Ile Ser Gly Arg Gly Phe Pro Asp  
 50 55 60  
 Leu Asp Leu His Ala Val Asn Ile Gly Gly Lys Tyr Ser Cys Gly Ala  
 65 70 75 80  
 Glu Val Asn Lys Pro Tyr Leu Thr Arg Ile Cys Asp Gln Leu Cys Ile  
 85 90 95  
 Pro Phe Arg Thr Ile Pro Ser Pro Tyr Ala Pro Glu Thr Pro Glu Cys  
 100 105 110  
 Tyr Pro Cys Ser Gln Ala Arg Arg Leu Leu Phe Gln Ala Ala Lys  
 115 120 125  
 Glu Ile Gly Ala Ser Ala Ile Ala Phe Gly His His Arg Asp Asp Leu  
 130 135 140  
 Val Gln Thr Ala Leu Leu Asn Leu Leu His Lys Ala Glu Phe Ala Gly  
 145 150 155 160  
 Met Leu Pro Val Leu Asp Met Val His Phe Gly Val Thr Ile Leu Arg  
 165 170 175  
 Pro Leu Ile Phe Thr Pro Glu Phe Trp Ile Arg Lys Phe Ala Lys Glu  
 180 185 190  
 Asn Ala Ser Gln Glu Ser Leu Ala Val Val Pro Trp Phe His  
 195 200 205

&lt;210&gt;274

&lt;211&gt;281

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;274

Leu Val Leu Met Asn Lys Arg Leu Lys Ile Ile Leu Thr Asn Asp Asp  
 1 5 10 15  
 Gly Ile Thr Ala Lys Gly Met Ser Cys Leu Val Ser Ala Leu Leu Glu  
 20 25 30  
 Ala Asn Ile Gly Asp Ile Tyr Ile Ala Ala Pro Gln Ala Glu Gln Ser  
 35 40 45  
 Gly Lys Ser Met Ala Ile Ser Leu Asn Gln Val Val Cys Ala Ser Pro  
 50 55 60  
 Tyr Ala Tyr Pro Gln Pro Val Lys Glu Ala Trp Ala Val Gly Gly Ser  
 65 70 75 80  
 Pro Thr Asp Cys Val Arg Leu Gly Leu Arg Thr Leu Phe Glu Ser Val  
 85 90 95  
 Ser Pro Asp Leu Val Ile Ser Gly Ile Asn Cys Gly Asn Asn Ile Cys  
 100 105 110  
 Lys Asn Ala Trp Tyr Ser Gly Thr Ile Gly Ala Ala Lys Gln Ala Leu  
 115 120 125  
 Val Asp Gly Ile Pro Ser Met Ala Leu Ser Gln Asp Asn His Ile Ser  
 130 135 140  
 Phe Phe Gln Gln Asp Lys Ala Pro Glu Ile Leu Lys Ala Leu Val Ile  
 145 150 155 160  
 Tyr Leu Leu Ser Gln Pro Phe Pro Cys Leu Thr Gly Leu Asn Ile Asn  
 165 170 175  
 Phe Pro Thr Ser Pro Gly Gly Ser Ser Trp Glu Gly Met Arg Leu Val  
 180 185 190  
 Pro Pro Gly Asp Glu Phe Phe Tyr Glu Glu Pro Gln Tyr Leu Gly Ser  
 195 200 205  
 Val Asn Lys Asn Gln Tyr Tyr Val Gly Lys Ile Ser Gly Val Arg Ile  
 210 215 220  
 Gly Glu His Pro Ser Glu Glu Leu Ala Cys Met Leu Glu Asn His Ile  
 225 230 235 240  
 Ser Val Ser Pro Ile Phe Ser Gln Asn Ser Pro Ile Gly Leu Met Thr  
 245 250 255  
 Leu Glu Glu Phe Gln Lys Thr Gln Glu Asn Phe Asn Ala Ser Leu Leu  
 260 265 270  
 Ser Ser Glu Leu Thr Thr Lys Ile Phe  
 275 280

&lt;210&gt;275

&lt;211&gt;313

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;275

Leu Arg Val Arg Pro Pro Ser Leu Ala Lys Tyr Ala Phe Arg Gly Phe  
 1 5 10 15  
 Arg Met Ser His Gly Pro Arg Pro Thr Lys Phe Ser Phe Pro Leu Tyr  
 20 25 30  
 Phe Ser Lys Thr Leu Ser Trp Phe Ile Leu Gly Gly Phe Leu Ala Ala  
 35 40 45  
 Cys Gly Val Gln Met Val Leu Val Pro Asn Glu Leu Ile Asp Gly Gly  
 50 55 60  
 Ile Val Gly Leu Ser Ile Ala Ser His Phe Leu Gly His Lys Ala  
 65 70 75 80  
 Leu Pro Phe Cys Leu Val Leu Phe Asn Leu Pro Phe Val Phe Leu Ala  
 85 90 95  
 Phe Lys Gln Ile Gly Lys Tyr Phe Val Ile Gln Met Leu Thr Ala Val  
 100 105 110  
 Ile Ile Phe Ser Cys Ser Leu Trp Leu Ile Asp Gln Leu Pro Ser Trp  
 115 120 125  
 Leu Gly Met Ser Pro Phe Val Phe Lys Gly Ser Glu Met Glu Thr Val  
 130 135 140  
 Val Leu Gly Gly Ala Ile Ile Gly Val Gly Cys Gly Leu Ile Ile Arg  
 145 150 155 160  
 His Gly Gly Ser Thr Asp Gly Thr Glu Ile Leu Gly Ile Ile Ile Asn  
 165 170 175  
 Lys Lys Lys Gly Tyr Thr Val Gly Gln Ile Ile Leu Phe Val Asn Phe

180 185 190  
 Phe Ile Phe Ala Leu Ser Gly Ile Val Tyr Lys Asn Trp His Thr Ala  
 195 200 205  
 Phe Val Ser Phe Leu Thr Tyr Gly Ile Ala Thr Lys Val Met Asp Met  
 210 215 220  
 Val Ile Leu Gly Leu Glu Asp Thr Lys Ser Val Thr Ile Ile Thr Ser  
 225 230 235 240  
 Ser Pro Arg Lys Leu Gly His Ile Leu Met Glu Thr Leu Gly Ile Gly  
 245 250 255  
 Leu Thr Tyr Ile His Ala Glu Gly Gly Tyr Ser Gly Glu Pro Arg Asn  
 260 265 270  
 Leu Leu Tyr Val Val Val Glu Arg Leu Gln Leu Ser Gln Leu Lys Glu  
 275 280 285  
 Ile Val His Arg Glu Asp Pro Ser Ala Phe Ile Ala Ile Glu Asn Leu  
 290 295 300  
 His Glu Val Ile Asn Gly Arg Arg Thr  
 305 310  
 <210>276  
 <211>192  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>276  
 Met Lys Arg Tyr Val Val Gly Ile Ser Gly Ala Ser Gly Val Ile Leu  
 1 5 10 15  
 Ala Val Lys Leu Ile Lys Glu Leu Val Asn Ala Lys His Gln Val Glu  
 20 25 30  
 Val Ile Ile Ser Pro Ser Gly Arg Lys Thr Leu Tyr Tyr Glu Leu Gly  
 35 40 45  
 Cys Gln Ser Phe Asp Ala Leu Phe Ser Glu Glu Asn Leu Glu Tyr Ile  
 50 55 60  
 His Thr His Ser Ile Gln Ala Ile Glu Ser Ser Leu Ala Ser Gly Ser  
 65 70 75 80  
 Cys Pro Val Glu Ala Thr Ile Ile Ile Pro Cys Ser Met Thr Thr Val  
 85 90 95  
 Ala Ala Ile Ser Ile Gly Leu Ala Asp Asn Leu Leu Arg Arg Val Ala  
 100 105 110  
 Asp Val Ala Leu Lys Glu Arg Arg Pro Leu Ile Leu Val Pro Arg Glu  
 115 120 125  
 Thr Pro Leu His Thr Ile His Leu Glu Asn Leu Leu Lys Leu Ser Lys  
 130 135 140  
 Ser Gly Ala Thr Ile Phe Pro Pro Met Pro Met Trp Tyr Phe Lys Pro  
 145 150 155 160  
 Gln Ser Val Glu Asp Leu Glu Asn Ala Leu Val Gly Lys Ile Leu Ala  
 165 170 175  
 Tyr Leu Asn Ile Pro Ser Asp Leu Thr Lys Gln Trp Ser Asn Pro Glu  
 180 185 190

&lt;210&gt;277

&lt;211&gt;296

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;277

Val Arg Leu Asn Tyr Phe Leu Asn Leu Val Asn Phe Lys Tyr Ser Ile  
 1 5 10 15  
 Phe Ser Ile Leu Phe Leu Ser Ala Ser Thr Val Phe Ala Leu Ser Ile  
 20 25 30  
 Asn Glu Ile Ser Gln Asn Leu Ser Phe Lys Glu Gly Phe Lys Ile Ser  
 35 40 45  
 Val Phe Gly Ala Ile Ala Phe Val Phe Ala Arg Thr Thr Gly Ile Val  
 50 55 60  
 Val Asn Gln Cys Ile Asp Arg Phe Ile Asp Lys Lys Asn Thr Arg Thr  
 65 70 75 80  
 Ser Lys Arg Val Leu Pro Ala Asn Leu Val Ser Leu Asn Phe Ala Trp  
 85 90 95  
 Val Leu Ser Leu Phe Cys Ser Phe Leu Phe Leu Phe Leu Cys Lys Ile

```

      100      105      110
Leu Arg Ile Phe Ser Leu Gly Ile Ala Ser Leu Thr Leu Met Ile Val
      115      120      125
Tyr Pro Tyr Met Lys Arg Val Thr Phe Phe Cys His Trp Gly Leu Gly
      130      135      140
Leu Val Tyr Thr Val Ala Ile Leu Met Asn Phe Cys Ala Phe Ala Glu
145      150      155      160
Ser Gly Leu Ser Met Arg Leu Cys Phe Leu Ala Leu Leu Trp Gly Gly
      165      170      175
Ser Val Gly Met Val Ile Ala Ala Asn Asp Ile Ile Tyr Ala Ile Glu
      180      185      190
Asp Thr Glu Phe Asp Arg Glu Glu Gly Leu Arg Ser Val Pro Ala His
      195      200      205
Tyr Gly Glu Lys Lys Ala Val Glu Ile Ala Lys Val Asn Leu Trp Val
      210      215      220
Ser Tyr Leu Ala Tyr Ile Phe Ser Gly Phe Val Gly Ser Leu Asp Lys
225      230      235      240
Glu Phe Tyr Phe Thr Ala Ile Ile Pro Leu Val Val Ile Leu Lys Val
      245      250      255
Val Arg Met Tyr Ser Asn Tyr Ser Lys Lys Asp Gln Glu Gly Glu Ser
      260      265      270
Gln Ile Leu Phe Ser Glu Tyr Cys Asp Cys Ser Ile Val Ser Cys Lys
      275      280      285
Tyr Asp Phe Val Leu Glu Phe Glu
      290      295

```

&lt;210&gt;278

&lt;211&gt;232

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;278

```

Ile Met Ala Leu Asp Glu Ile Asn Asn Gln Asn Asn Pro Ser Gln Gln
 1      5      10      15
Ile Ala Ser Ser Thr Ser Gln Thr Ser Lys Ile Asn Gln Asp Arg Lys
      20      25      30
Thr Phe Ala Cys Thr Val Thr Leu Leu Val Val Ala Thr Leu Met Ile
      35      40      45
Leu Ser Gly Ile Val Leu Leu Phe Thr Ile Gly Ser Leu Gly Leu Ser
      50      55      60
Val Pro Leu Ser Gly Ile Leu Gly Thr Phe Ala Val Thr Val Gly Ala
      65      70      75      80
Val Leu Phe Ile Thr Gly Leu Thr Ile Leu Val Arg Lys Ser Leu Gly
      85      90      95
Ile Glu Gln Lys Asn Glu Asp Leu Asn Phe Leu Lys Ile Lys Thr Pro
      100      105      110
Thr Pro Pro Ala Arg Pro Leu Met Ser Lys Phe Ser Val Thr Cys Ser
      115      120      125
Thr Thr Ser Ile Val Leu Gly Met Ala Leu Leu Ile Gly Ala Val Val
      130      135      140
Ser Val Phe Phe Leu Thr Gly Tyr Leu Gln Leu Gly Leu Cys Ala Gly
145      150      155      160
Leu Val Gly Leu Gly Thr Ala Leu Phe Val Ala Gly Leu Ala Arg Met
      165      170      175
Ser Pro Arg Ser Leu Ala Asp Gln Glu Gly Ser Gly Ser Ala Asp Ser
      180      185      190
Gln Ser Asn Ile Val Gly Ile Gly Glu Pro Lys Ala Ala Gln Glu Gln
      195      200      205
Lys Trp Tyr Lys Met Ala Val Arg Gly Glu Asp Gly Ile Pro Thr
      210      215      220
Ala Ile Arg Leu Thr Pro Glu Lys
225      230

```

&lt;210&gt;279

&lt;211&gt;263

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;279

Val Ser Ile Met Ser Leu Asn Lys Thr Asn Ala Leu Leu Asn Gln Pro  
 1 5 10 15  
 Glu Pro Ala Val Cys Leu Asn Ala Trp Asp Pro Lys Tyr Ile Asn Gln  
 20 25 30  
 Asp Arg Lys Thr Phe Ala Cys Thr Val Thr Leu Leu Val Ile Ala Thr  
 35 40 45  
 Leu Met Ile Leu Thr Thr Gly Val Ile Val Leu Leu Ala Met Gly Ser  
 50 55 60  
 Pro Gly Leu Ser Val Leu Val Ser Thr Ile Ile Gly Thr Ser Val Thr  
 65 70 75 80  
 Thr Leu Gly Thr Ala Leu Phe Ile Ile Gly Leu Val Lys Leu Ile Lys  
 85 90 95  
 Lys Ser Leu Ala Trp Ile Gln Tyr Gln Lys Tyr Phe Gln Glu Val Val  
 100 105 110  
 Lys Gln Lys Tyr Glu Pro Phe Ser Ile Pro Lys Asn Asp Asn Val His  
 115 120 125  
 Lys Leu Thr Ser Cys Leu Pro Ser Pro Leu Asp Ile Glu Ser Pro Ser  
 130 135 140  
 Pro Glu Ala Ser Thr Pro Val Ser Lys Leu Arg Ile Ala Cys Ser Gly  
 145 150 155 160  
 Val Ala Ile Val Leu Gly Val Thr Leu Leu Ile Gly Ala Val Val Ser  
 165 170 175  
 Val Phe Phe Cys Thr Gly Tyr Leu Gln Leu Ala Leu Cys Val Gly Phe  
 180 185 190  
 Ala Cys Leu Gly Thr Ala Leu Phe Val Gly Gly Leu Ala Gly Leu Arg  
 195 200 205  
 Thr His Ser Leu Ile Ala Gln Gly Ile Met Tyr Leu Tyr Leu Thr Tyr  
 210 215 220  
 Tyr Leu Ser Ser Ala Leu Glu Glu Arg Asn Glu Thr Val Lys Asp Gln  
 225 230 235 240  
 Arg Asn Glu Ile Asn Thr Tyr Leu Thr Glu Glu Cys Arg Gln Gln Lys  
 245 250 255  
 Arg Glu Lys Ala Leu Leu Glu  
 260

&lt;210&gt;280

&lt;211&gt;115

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;280

Asp Pro Cys Ser Ser Ser Trp Leu Phe Ser Ser Val Ser Gly Ser Arg  
 1 5 10 15  
 Ser Gly Ala Gly Arg Asp Val Gly Leu Asp Pro Glu Val Pro Gly Leu  
 20 25 30  
 Leu Ala Leu Phe Cys Ser Leu Gly Cys Pro Arg Arg Gly Leu Arg Ser  
 35 40 45  
 Ser Ile Pro Phe Ser Thr Phe Gly Val Asp Val Pro Gly Gly Leu Ala  
 50 55 60  
 Cys Ala Phe Ser Gly Ser Val Phe Gly Arg Thr Asn Gly Ser Tyr Ala  
 65 70 75 80  
 Asn Ile Asn Ser Ser Ser Glu Gly Ile Gly Asp Lys Gly Gly Val Gly  
 85 90 95  
 Phe Phe Gln Phe Gly Thr Lys Asp Phe Ile His Ser Gln Val Asp Val  
 100 105 110  
 Leu Leu Leu  
 115

&lt;210&gt;281

&lt;211&gt;331

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;281

Val Ala Phe Arg Cys Val Met Thr Ile Asp Met His Cys Asp Leu Leu  
 1 5 10 15  
 Ser His Pro His Phe Cys Arg Lys Asp Pro Ala Val Arg Cys Ser Pro

20 25 30  
 Glu Gln Leu Ser Gly Gly Val Arg Gln Gln Val Cys Ala Ile Phe  
 35 40 45  
 Val Pro His Ser Arg Gly Glu Pro Asn Cys Asp Lys Gln Asn Ser Leu  
 50 55 60  
 Phe Phe Ser Leu Pro Asn Gln Tyr Pro Asp Ile Gly Leu Leu Ser Tyr  
 65 70 75 80  
 Glu Glu Glu Glu Asn Gly Ser Ser Ser Gln Lys Lys Ser Leu Ser Leu  
 85 90 95  
 Ile Arg Ser Ile Glu Asn Ala Ser Ala Leu Gly Asp Asp Thr Ala Pro  
 100 105 110  
 Leu Gly Thr Leu Leu Ala Lys Leu Ile His Leu Thr Lys Gln Gly Pro  
 115 120 125  
 Leu Ala Tyr Leu Gly Ile Val Trp Lys Gly Asp Asn Arg Phe Gly Gly  
 130 135 140  
 Gly Thr Glu Ala Pro Lys Arg Leu Ser Asn Asp Gly Lys Val Leu Leu  
 145 150 155 160  
 Asp Ile Met Tyr Glu Leu Gly Val Pro Ile Asp Leu Ser His Cys Ser  
 165 170 175  
 Asp Lys Leu Ala Glu Asp Ile Leu Asp Tyr Thr Ala Asp Lys Leu Pro  
 180 185 190  
 Asn Leu Ala Val Ile Ala Ser His Ser Asn Phe Arg Ser Val Leu Asp  
 195 200 205  
 His Arg Arg Asn Leu Val Asp Ala His Ala Lys Glu Ile Val Arg Arg  
 210 215 220  
 Lys Gly Val Ile Gly Leu Asn Leu Val Arg Ser Tyr Val Gly Asp Ser  
 225 230 235 240  
 Leu Gly Asp Leu Glu Lys His Val Leu His Ala Glu Asn Leu Gly Ile  
 245 250 255  
 Leu Ser Ser Ile Val Leu Gly Ser Asp Phe Phe Tyr Ala Asn Glu Asp  
 260 265 270  
 Glu Asn Phe Phe Phe Asn Glu Cys Ser Ser Ala Glu Ala His Pro Val  
 275 280 285  
 Leu Asn Gln Leu Ile His Arg Ile Phe Ser Lys Gly Lys Ala Glu Ser  
 290 295 300  
 Ile Leu Ser Ser Arg Ala Glu Lys Phe Leu Lys Gln Val Ile Val Glu  
 305 310 315 320  
 Gln Val Asn Pro Lys Ile Thr Asp Val Lys Leu  
 325 330

&lt;210&gt;282

&lt;211&gt;218

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;282

Arg Ile Glu Asn Ile Ser Gly Tyr Pro Leu Ser Pro Thr Ala Lys Lys  
 1 5 10 15  
 Leu Ala Gln Leu Phe Pro Gly Ala Ile Thr Leu Val Val Lys His Arg  
 20 25 30  
 Asn Pro Arg Phe Pro Lys Glu Thr Leu Ala Phe Arg Ile Val Asp His  
 35 40 45  
 Ser Val Val Arg Glu Ile Val Asp His Cys Gly Thr Leu Ile Gly Thr  
 50 55 60  
 Ser Ala Asn Leu Ser Glu Phe Pro Ser Ala Leu Thr Ala Gln Glu Ile  
 65 70 75 80  
 Phe Ala Asp Phe Ala Asp His Asp Leu Cys Ile Phe Asp Gly Pro Cys  
 85 90 95  
 Ser His Gly Leu Glu Ser Thr Val Val Ala Ser Asp Pro Leu Tyr Ile  
 100 105 110  
 Tyr Arg Glu Gly Leu Ile Ser Arg Ser Val Ile Glu Asn Ile Ala Gly  
 115 120 125  
 Thr Glu Ala Lys Ile Phe His Arg Thr Ser His Ala Phe Ser Lys His  
 130 135 140  
 Ile Lys Ile Tyr Thr Val Lys Asn Gln Glu Gln Leu Val Ser Phe Leu  
 145 150 155 160

Ser Gly Ser Leu Asp Phe Lys Gly Val Val Cys Glu His Pro Lys Pro  
 165 170 175  
 Lys Asn Phe Tyr Thr Arg Leu Arg Glu Ala Leu Lys Lys Lys Thr Pro  
 180 185 190  
 Ser Ile Val Phe Ile Tyr Asp Ile Asn Thr Ser Asp Tyr Pro Glu Leu  
 195 200 205  
 Phe Pro Phe Leu Ser Pro Tyr Tyr Ile Glu  
 210 215

&lt;210&gt;283

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;283

Ser Ile Phe Gly Val Ile Val Pro Asp Lys Lys Ala Gln Ile Thr Phe  
 1 5 10 15  
 Ser Leu Pro Glu Val Met Ser Ala Ile His Gln Gly Lys Ile Val Ala  
 20 25 30  
 Leu Pro Thr Asp Thr Val Tyr Gly Phe Val Leu Ser Leu Tyr Ala Ser  
 35 40 45  
 Glu Ala Glu Glu Arg Leu Tyr Ala Leu Lys Asp Arg Glu Pro Ser Lys  
 50 55 60  
 Ala Phe Ala Leu Tyr Val Asn Ser Ile Glu Glu Ser Lys Thr Phe Leu  
 65 70 75 80  
 Val Ile Pro Tyr Leu Leu Gln Leu Arg Asn  
 85 90

&lt;210&gt;284

&lt;211&gt;243

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;284

Met Thr Asp Tyr Ser Phe Phe Arg Arg Lys Ile Gly Asn Ile Glu Ala  
 1 5 10 15  
 Ile Glu Cys Pro Gly Asn Pro Gln Asp Pro Ile Ile Ile Leu Cys His  
 20 25 30  
 Gly Tyr Gly Ser Leu Ala Asp Asn Leu Thr Phe Phe Pro Ser Ile Cys  
 35 40 45  
 Ser Phe Ser Lys Leu Arg Pro Thr Trp Ile Phe Pro Asn Gly Ile Leu  
 50 55 60  
 Pro Leu Glu Asn Asp Phe Arg Gly Ser Arg Ala Cys Phe Pro Leu Asn  
 65 70 75 80  
 Val Leu Leu Leu Gln Glu Leu Ser Arg Leu Tyr Ala Asn Gly Val Gly  
 85 90 95  
 Asn Leu Gln Glu Lys Tyr Asp Glu Leu Phe Asp Val Asp Leu Glu Thr  
 100 105 110  
 Pro Lys Glu Ala Leu Glu Glu Leu Ile Leu Asn Leu Asn Arg Pro Tyr  
 115 120 125  
 Asn Glu Ile Ile Ile Gly Gly Phe Ser Gln Gly Ala Ile Leu Ala Thr  
 130 135 140  
 His Leu Val Leu Thr Ser Gln Asn Pro Tyr Ala Gly Ala Leu Ile Phe  
 145 150 155 160  
 Ala Gly Ala Arg Leu Phe Asn Gln Gly Trp Glu Glu Gly Leu Lys Gln  
 165 170 175  
 Cys Ala Gln Val Pro Phe Leu Gln Ser His Gly Tyr Glu Asp Glu Ile  
 180 185 190  
 Leu Pro Tyr His Leu Gly Ala His Leu Asn Asp Leu Leu Leu Thr Lys  
 195 200 205  
 Leu Asn Gly Gln Phe Val Ser Phe His Gly Gly His Glu Ile Pro Ser  
 210 215 220  
 Val Val Phe Gln Lys Met Gln Val Thr Val Pro Asn Trp Ile Asp Pro  
 225 230 235 240  
 Ala Arg Gly

&lt;210&gt;285

&lt;211&gt;274



&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;285

Phe Asn Arg Gln Ser Asp Ala Thr Tyr Ala Thr Trp Val Met His Leu  
 1 5 10 15  
 Glu Glu Glu Asn Gln Gly Trp Glu Ala Leu Leu Arg Lys Val Tyr His  
 20 25 30  
 Gln Glu Val Pro Pro Ala Ile Leu Leu His Gly Phe Thr Leu Pro Val  
 35 40 45  
 Leu Gln Asp Lys Ala Glu Gln Leu Ala Ser Glu Ile Leu Leu Ser Ser  
 50 55 60  
 Ser Pro Gly Ser Glu His Lys Val Ser Gln Lys Ile His Pro Asp Ile  
 65 70 75 80  
 Tyr Gln Phe Phe Pro Glu Gly Lys Gly Arg Leu His Ser Ile Asp Leu  
 85 90 95  
 Pro Arg Gly Ile Lys Lys Gln Ile Tyr Ile Ser Pro Phe Glu Ala Asn  
 100 105 110  
 Tyr Lys Ile Tyr Ile Ile His Glu Ala Asp Arg Met Thr Leu Ala Ala  
 115 120 125  
 Ile Ser Ala Phe Leu Lys Val Phe Glu Glu Pro Pro Lys His Ala Val  
 130 135 140  
 Ile Ile Leu Thr Thr Ala Lys Val Gln Arg Leu Pro Lys Thr Ile Ile  
 145 150 155 160  
 Ser Arg Ser Leu Ser Ile Phe Ile Glu Arg Gly Glu Lys Ile Leu Cys  
 165 170 175  
 Ser Lys Glu Thr Phe Ser Tyr Leu Phe Arg Tyr Ala Gln Cys Glu Ile  
 180 185 190  
 Pro Val Thr Glu Val Ser Gln Ile Ile Lys Glu Ser Ser Glu Thr Asp  
 195 200 205  
 Lys Gln Val Leu Arg Asp Lys Val Gln Arg Phe Met Glu Val Leu Leu  
 210 215 220  
 Glu Leu Tyr Arg Asp Arg Tyr Thr Leu Asn Leu Gly Leu Lys Ala Ser  
 225 230 235 240  
 Ala Leu Asn Tyr Pro Glu His Val Lys Glu Ile Leu Gln Leu Pro Leu  
 245 250 255  
 Leu Pro Leu Asp Lys Val Leu Leu Ile Val Glu Ser Ala Trp Ser Val  
 260 265 270  
 Ile Glu

&lt;210&gt;286

&lt;211&gt;209

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;286

Gly Ser Ile Val Phe Ile Val Ile Glu Gly Gly Glu Gly Ser Gly Lys  
 1 5 10 15  
 Ser Ser Leu Ala Lys Ala Leu Gly Asp Gln Leu Val Ala Gln Asp Arg  
 20 25 30  
 Lys Val Leu Leu Thr Arg Glu Pro Gly Gly Cys Leu Ile Gly Glu Arg  
 35 40 45  
 Leu Arg Asp Leu Ile Leu Glu Pro Pro His Leu Glu Leu Ser Arg Cys  
 50 55 60  
 Cys Glu Leu Phe Leu Phe Leu Gly Ser Arg Ala Gln His Ile Gln Glu  
 65 70 75 80  
 Val Ile Ile Pro Ala Leu Arg Asp Gly Tyr Ile Val Ile Cys Glu Arg  
 85 90 95  
 Phe His Asp Ser Thr Ile Val Tyr Gln Gly Ile Ala Glu Gly Leu Gly  
 100 105 110  
 Ala Asp Phe Val Ala Asp Leu Cys Ser Lys Val Val Gly Pro Thr Pro  
 115 120 125  
 Phe Leu Pro Asn Phe Val Leu Leu Leu Asp Ile Pro Ala Asp Ile Gly  
 130 135 140  
 Leu Gln Arg Lys His Arg Gln Lys Val Phe Asp Lys Phe Glu Lys Lys  
 145 150 155 160

Pro Leu Ser Tyr His Asn Arg Ile Arg Glu Gly Phe Leu Ser Leu Ala  
 165 170 175  
 Ser Ala Asp Pro Ser Arg Tyr Leu Val Leu Asp Ala Arg Glu Ser Leu  
 180 185 190  
 Ala Ser Leu Ile Asp Lys Val Met Leu His Thr Gln Leu Gly Leu Cys  
 195 200 205  
 Thr

&lt;210&gt;287

&lt;211&gt;834

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;287

Met Phe Asn Lys Asp Glu Ile Ile Val Pro Lys Asn Leu Glu Glu Glu  
 1 5 10 15  
 Met Lys Glu Ser Tyr Leu Arg Tyr Ser Met Ser Val Ile Ile Ser Arg  
 20 25 30  
 Ala Leu Pro Asp Ile Arg Asp Gly Leu Lys Pro Ser Gln Arg Arg Val  
 35 40 45  
 Leu Tyr Ala Met Lys Gln Leu Ser Leu Ser Pro Gly Ala Lys His Arg  
 50 55 60  
 Lys Cys Ala Lys Ile Cys Gly Asp Thr Ser Gly Asp Tyr His Pro His  
 65 70 75 80  
 Gly Glu Ser Val Ile Tyr Pro Thr Leu Val Arg Met Ala Gln Asn Trp  
 85 90 95  
 Ala Met Arg Tyr Pro Leu Val Asp Gly Gln Gly Asn Phe Gly Ser Ile  
 100 105 110  
 Asp Gly Asp Pro Pro Ala Ala Met Arg Tyr Thr Glu Ala Arg Leu Thr  
 115 120 125  
 His Ser Ala Met Tyr Leu Met Glu Asp Leu Asp Lys Asp Thr Val Asp  
 130 135 140  
 Ile Val Pro Asn Tyr Asp Glu Thr Lys His Glu Pro Val Val Phe Pro  
 145 150 155 160  
 Ser Lys Phe Pro Asn Leu Leu Cys Asn Gly Ser Ser Gly Ile Ala Val  
 165 170 175  
 Gly Met Ala Thr Asn Ile Pro Pro His Asn Leu Gly Glu Leu Ile Glu  
 180 185 190  
 Ala Thr Leu Leu Leu Leu Ala Asn Pro Gln Ala Ser Val Asp Glu Ile  
 195 200 205  
 Leu Gln Val Met Pro Gly Pro Asp Phe Pro Thr Gly Gly Ile Ile Cys  
 210 215 220  
 Gly Ser Glu Gly Ile Arg Ser Thr Tyr Thr Thr Gly Arg Gly Lys Ile  
 225 230 235 240  
 Lys Val Arg Ala Arg Leu His Val Glu Glu Asn Glu Asp Lys His Arg  
 245 250 255  
 Glu Ser Ile Ile Ile Thr Glu Met Pro Tyr Asn Val Asn Lys Ser Arg  
 260 265 270  
 Leu Ile Glu Gln Ile Ala Asn Leu Val Asn Glu Lys Thr Leu Ala Gly  
 275 280 285  
 Ile Ser Asp Val Arg Asp Glu Ser Asp Lys Asp Gly Ile Arg Val Val  
 290 295 300  
 Leu Glu Ile Lys Lys Gly Glu Ser Ser Glu Ile Ile Ile Asn Arg Leu  
 305 310 315 320  
 Tyr Lys Phe Thr Asp Val Gln Val Thr Phe Gly Ala Asn Met Leu Ala  
 325 330 335  
 Leu Asp Lys Asn Leu Pro Arg Thr Met Ser Ile His Arg Met Ile Ser  
 340 345 350  
 Ala Trp Ile Arg His Arg Lys Glu Val Ile Arg Arg Arg Thr Arg Tyr  
 355 360 365  
 Glu Leu Asn Lys Ala Glu Thr Arg Ala His Val Leu Glu Gly Tyr Leu  
 370 375 380  
 Lys Ala Leu Ser Cys Leu Asp Ala Leu Val Lys Thr Ile Arg Glu Ser  
 385 390 395 400  
 Gly Asn Lys Glu His Ala Lys Glu Arg Ile Ile Glu Ser Phe Gly Phe

405 410 415  
 Thr Glu Pro Gln Ala Leu Ala Ile Leu Glu Leu Arg Leu Tyr Gln Leu  
 420 425 430  
 Thr Gly Leu Glu Ala Glu Lys Ile Gln Lys Glu Tyr Glu Glu Leu Leu  
 435 440 445  
 Asn Lys Ile Ala Tyr Tyr Lys Gln Val Leu Ser Asp Glu Gly Leu Val  
 450 455 460  
 Lys Asp Ile Ile Arg Asn Glu Leu Gln Asp Leu Lys His His Lys  
 465 470 475 480  
 Val Ala Arg Arg Thr Thr Ile Glu Phe Asp Ala Asp Asp Ile Arg Asp  
 485 490 495  
 Ile Glu Asp Ile Ile Thr Asn Glu Ser Val Ile Ile Thr Ile Ser Gly  
 500 505 510  
 Asp Asp Tyr Val Lys Arg Met Pro Val Lys Val Phe Lys Glu Gln Arg  
 515 520 525  
 Arg Gly Gly His Gly Val Thr Gly Phe Asp Met Lys Lys Gly Ala Gly  
 530 535 540  
 Phe Leu Lys Ala Val Tyr Ser Ala Phe Thr Lys Asp Tyr Leu Leu Ile  
 545 550 555 560  
 Phe Thr Asn Phe Gly Gln Cys Tyr Trp Leu Lys Val Trp Gln Leu Pro  
 565 570 575  
 Glu Gly Glu Arg Arg Ala Lys Gly Lys Pro Ile Ile Asn Phe Leu Glu  
 580 585 590  
 Gly Ile Arg Pro Gly Glu Glu Leu Ala Ala Ile Leu Asn Ile Lys Asn  
 595 600 605  
 Phe Asp Asn Ala Gly Phe Leu Phe Leu Ala Thr Lys Arg Gly Val Val  
 610 615 620  
 Lys Lys Val Ser Leu Asp Ala Phe Ser Asn Pro Arg Lys Lys Gly Ile  
 625 630 635 640  
 Arg Ala Leu Glu Ile Asp Glu Gly Asp Glu Leu Ile Ala Ala Cys His  
 645 650 655  
 Ile Val Ser Asp Glu Glu Lys Val Met Leu Phe Thr His Leu Gly Met  
 660 665 670  
 Ala Val Arg Phe Pro His Glu Lys Val Arg Pro Met Gly Arg Thr Ala  
 675 680 685  
 Arg Gly Val Arg Gly Val Ser Leu Lys Asn Glu Glu Asp Lys Val Val  
 690 695 700  
 Ser Cys Gln Ile Val Thr Glu Asn Gln Ser Val Leu Ile Val Cys Asp  
 705 710 715 720  
 Gln Gly Phe Gly Lys Arg Ser Leu Val Glu Asp Phe Arg Glu Thr Asn  
 725 730 735  
 Arg Gly Gly Val Gly Val Arg Ser Ile Leu Ile Asn Glu Arg Asn Gly  
 740 745 750  
 Asn Val Leu Gly Ala Ile Pro Val Thr Asp His Asp Ser Ile Leu Leu  
 755 760 765  
 Met Ser Ser Gln Gly Gln Ala Ile Arg Ile Asn Met Gln Asp Val Arg  
 770 775 780  
 Val Met Gly Arg Ser Thr Gln Gly Val Arg Leu Val His Leu Lys Glu  
 785 790 795 800  
 Gly Asp Ala Leu Val Ser Met Glu Lys Leu Ser Ser Asn Glu Asn Asp  
 805 810 815  
 Asp Glu Val Leu Ser Gly Ser Glu Glu Glu Cys Ser Asp Thr Val Ser  
 820 825 830  
 Leu Arg

&lt;210&gt;288

&lt;211&gt;789

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;288

Lys Gly Tyr Lys Leu Phe Val Ser Ala Pro Gly Cys Thr Leu Glu Ile  
 1 5 10 15  
 Arg Glu Ser Arg Val Phe Ile His Leu Val Tyr Glu Val Val Asp Asn  
 20 25 30

Ser Ile Asp Glu Ala Met Ala Gly Tyr Cys Ser Arg Ile Asp Val Arg  
 35 40 45  
 Ile Leu Glu Asp Gly Gly Ile Val Ile Val Asp Asn Gly Arg Gly Ile  
 50 55 60  
 Pro Ile Glu Val His Glu Arg Glu Ser Ala Lys Gln Gly Arg Glu Val  
 65 70 75 80  
 Ser Ala Leu Glu Val Val Leu Thr Val Leu His Ala Gly Gly Lys Phe  
 85 90 95  
 Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val  
 100 105 110  
 Ser Cys Val Asn Ala Leu Ser Glu Lys Leu Val Ala Thr Val Phe Lys  
 115 120 125  
 Asp Lys Lys Cys Tyr Gln Met Glu Phe Ser Arg Gly Ile Pro Val Thr  
 130 135 140  
 Pro Leu Gln Tyr Val Ser Val Ser Asp Arg Gln Gly Thr Glu Ile Val  
 145 150 155 160  
 Phe Tyr Pro Asp Pro Lys Ile Phe Ser Thr Cys Thr Phe Asp Arg Ser  
 165 170 175  
 Ile Leu Met Lys Arg Leu Arg Glu Leu Ala Phe Leu Asn Arg Gly Ile  
 180 185 190  
 Thr Ile Val Phe Glu Asp Asp Arg Asp Val Ser Phe Asp Lys Val Thr  
 195 200 205  
 Phe Phe Tyr Glu Gly Gly Ile Gln Ser Phe Val Ser Tyr Leu Asn Gln  
 210 215 220  
 Asn Lys Glu Ser Leu Phe Ser Glu Pro Ile Tyr Ile Cys Gly Thr Arg  
 225 230 235 240  
 Val Gly Asp Asp Gly Glu Ile Glu Phe Glu Ala Ala Leu Gln Trp Asn  
 245 250 255  
 Ser Gly Tyr Ser Glu Leu Val Tyr Ser Tyr Ala Asn Asn Ile Pro Thr  
 260 265 270  
 Arg Gln Gly Gly Thr His Leu Thr Gly Phe Ser Thr Ala Leu Thr Arg  
 275 280 285  
 Val Ile Asn Thr Tyr Ile Lys Ala His Asn Leu Ala Lys Asn Asn Lys  
 290 295 300  
 Leu Ala Leu Thr Gly Glu Asp Ile Arg Glu Gly Leu Thr Ala Val Ile  
 305 310 315 320  
 Ser Val Lys Val Pro Asn Pro Gln Phe Glu Gly Gln Thr Lys Gln Lys  
 325 330 335  
 Leu Gly Asn Ser Asp Val Ser Ser Val Ala Gln Gln Val Val Gly Glu  
 340 345 350  
 Ala Leu Thr Ile Phe Phe Glu Glu Asn Pro Gln Ile Ala Arg Met Ile  
 355 360 365  
 Val Asp Lys Val Phe Val Ala Ala Gln Ala Arg Glu Ala Ala Lys Lys  
 370 375 380  
 Ala Arg Glu Leu Thr Leu Arg Lys Ser Ala Leu Asp Ser Ala Arg Leu  
 385 390 395 400  
 Pro Gly Lys Leu Ile Asp Cys Leu Glu Lys Asp Pro Glu Lys Cys Glu  
 405 410 415  
 Met Tyr Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly  
 420 425 430  
 Arg Asp Arg Arg Phe Gln Ala Ile Leu Pro Ile Arg Gly Lys Ile Leu  
 435 440 445  
 Asn Val Glu Lys Ala Arg Leu Gln Lys Ile Phe Gln Asn Gln Glu Ile  
 450 455 460  
 Gly Thr Ile Ile Ala Ala Leu Gly Cys Gly Ile Gly Ala Asp Asn Phe  
 465 470 475 480  
 Asn Leu Ser Lys Leu Arg Tyr Arg Arg Ile Ile Met Thr Asp Ala  
 485 490 495  
 Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr  
 500 505 510  
 Arg His Met Thr Ala Leu Ile Glu Asn Glu Cys Val Tyr Ile Ala Gln  
 515 520 525  
 Pro Pro Leu Tyr Lys Val Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu  
 530 535 540

Ser Glu Lys Glu Met Asp Ser Tyr Leu Leu Met Leu Gly Thr Asn Glu  
 545 550 555 560  
 Ser Ser Ile Leu Phe Lys Ser Thr Glu Arg Glu Leu Arg Gly Glu Ala  
 565 570 575  
 Leu Glu Ser Phe Ile Asn Val Ile Leu Asp Val Glu Ser Phe Ile Asn  
 580 585 590  
 Thr Leu Glu Lys Lys Ala Ile Pro Phe Ser Glu Phe Leu Glu Met Tyr  
 595 600 605  
 Lys Glu Gly Ile Gly Tyr Pro Leu Tyr Tyr Leu Ala Pro Ala Thr Gly  
 610 615 620  
 Met Gln Gly Gly Arg Tyr Leu Tyr Ser Asp Glu Glu Lys Glu Glu Ala  
 625 630 635 640  
 Leu Ala Gln Glu Glu Thr His Lys Phe Lys Ile Ile Glu Leu Tyr Lys  
 645 650 655  
 Val Ala Val Phe Val Asp Ile Gln Asn Gln Leu Lys Glu Tyr Gly Leu  
 660 665 670  
 Asp Ile Ser Ser Tyr Leu Ile Pro Gln Lys Asn Glu Ile Val Ile Gly  
 675 680 685  
 Asn Glu Asp Ser Pro Ser Cys Asn Tyr Ser Cys Tyr Thr Leu Glu Glu  
 690 695 700  
 Val Ile Asn Tyr Leu Lys Asn Leu Gly Arg Lys Gly Ile Glu Ile Gln  
 705 710 715 720  
 Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Asp Gln Leu Trp Asp Thr  
 725 730 735  
 Thr Met Asn Pro Glu Gln Arg Thr Leu Ile His Val Ser Leu Lys Asp  
 740 745 750  
 Ala Val Glu Ala Asp His Ile Phe Thr Met Leu Met Gly Glu Glu Val  
 755 760 765  
 Pro Pro Arg Arg Glu Phe Ile Glu Ser His Ala Leu Ser Ile Arg Ile  
 770 775 780  
 Asn Asn Leu Asp Ile  
 785

&lt;210&gt;289

&lt;211&gt;116

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;289

Asp Met Phe Leu Lys Arg Lys Lys Arg Gly Gly Ser Gln Val Gln Asn  
 1 5 10 15  
 Lys Gly Thr Ala Ser Pro Ile Lys His Ala Lys His Tyr Leu His Asn  
 20 25 30  
 Tyr Leu Gln Glu Leu Gln Lys Ile Met Ala Ala Arg Pro His Asp Ala  
 35 40 45  
 Ile Asp Ala Trp Asn Gln Val Phe Arg Asp Lys Tyr Lys Gly Met Ser  
 50 55 60  
 Gln Ala Ile Gly Phe Arg Asp His Ile Leu Leu Val Lys Val Tyr Asn  
 65 70 75 80  
 Ser Ser Leu Tyr Ala Leu Leu Lys Gln Thr Pro Gln Asn Asp Leu Ile  
 85 90 95  
 Met Ser Leu Tyr Gln Val Ala Ser His Val Gln Ile Arg Glu Ile Gln  
 100 105 110  
 Phe Leu Leu Gly  
 115

&lt;210&gt;290

&lt;211&gt;200

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;290

Asn Ile Ser Ile Phe Tyr Pro Lys Tyr Phe Ile Glu Gly Lys Glu Val  
 1 5 10 15  
 Leu Ile Lys Asn Leu Pro Pro Leu Ile Phe Tyr Gly Val Ile Leu Met  
 20 25 30  
 Ile Ile Asn Val Arg Ala Pro Ala Phe Gly Ile Thr Ser Val Gln Gln  
 35 40 45

Phe Ser Thr Asn Phe Gln Ala Ala Ile Pro Ile Leu Asn Ile Val Ile  
 50 55 60  
 Gly Cys Ser Arg Ile Ser Ser Thr Tyr Ala Glu Asp Ile Glu Glu Val  
 65 70 75 80  
 Ala Gln Glu Lys Leu Glu Lys Ser Thr His Ser Lys Ser Ser Thr Ser  
 85 90 95  
 Val Asn Leu Trp Ala His Arg Val Arg Gly Val Val Glu Ile Leu Gly  
 100 105 110  
 Gly Gly Ile Val Ile Leu Ala Leu Glu Ile Thr Ala Leu Val Leu Gln  
 115 120 125  
 Val Ile Ile Lys Lys Leu Ile Lys Cys Leu Ile Asp Val Leu Cys Val Cys  
 130 135 140  
 Leu Phe Gly Leu Gly Val Cys Val Val Ala Ile Ile Gly Ala Ile Ala  
 145 150 155 160  
 Phe Cys Val Val Val Val Val Lys Tyr Leu Gly Phe Cys Ser Gln Gly  
 165 170 175  
 Glu Glu Leu Glu Pro Ile Glu Val Lys Thr Leu Ile Ser Pro Asp Lys  
 180 185 190  
 Pro Tyr Pro Thr Val Val Tyr Val  
 195 200

&lt;210&gt;291

&lt;211&gt;275

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;291

Arg Asp Ser Met Lys Lys Lys Leu Ser Leu Leu Val Gly Leu Ile Phe  
 1 5 10 15  
 Val Leu Ser Ser Cys His Lys Glu Asp Ala Gln Asn Lys Ile Arg Ile  
 20 25 30  
 Val Ala Ser Pro Thr Pro His Ala Glu Leu Leu Glu Ser Leu Gln Glu  
 35 40 45  
 Glu Ala Lys Asp Leu Gly Ile Lys Leu Lys Ile Leu Pro Val Asp Asp  
 50 55 60  
 Tyr Arg Ile Pro Asn Arg Leu Leu Leu Asp Lys Gln Val Asp Ala Asn  
 65 70 75 80  
 Tyr Phe Gln His Gln Ala Phe Leu Asp Asp Glu Cys Glu Arg Tyr Asp  
 85 90 95  
 Cys Lys Gly Glu Leu Val Val Ile Ala Lys Val His Leu Glu Pro Gln  
 100 105 110  
 Ala Ile Tyr Ser Lys Lys His Ser Ser Leu Glu Arg Leu Lys Ser Gln  
 115 120 125  
 Lys Lys Leu Thr Ile Ala Ile Pro Val Asp Arg Thr Asn Ala Gln Arg  
 130 135 140  
 Ala Leu His Leu Leu Glu Glu Cys Gly Leu Ile Val Cys Lys Gly Pro  
 145 150 155 160  
 Ala Asn Leu Asn Met Thr Ala Lys Asp Val Cys Gly Lys Glu Asn Arg  
 165 170 175  
 Ser Ile Asn Ile Leu Glu Val Ser Ala Pro Leu Leu Val Gly Ser Leu  
 180 185 190  
 Pro Asp Val Asp Ala Ala Val Ile Pro Gly Asn Phe Ala Ile Ala Ala  
 195 200 205  
 Asn Leu Ser Pro Lys Lys Asp Ser Leu Cys Leu Glu Asp Leu Ser Val  
 210 215 220  
 Ser Lys Tyr Thr Asn Leu Val Val Ile Arg Ser Glu Asp Val Gly Ser  
 225 230 235 240  
 Pro Lys Met Ile Lys Leu Gln Lys Leu Phe Gln Ser Pro Ser Val Gln  
 245 250 255  
 His Phe Phe Asp Thr Lys Tyr His Gly Asn Ile Leu Thr Met Thr Gln  
 260 265 270  
 Asp Asn Gly  
 275

&lt;210&gt;292

&lt;211&gt;221

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;292

```

Met Gln Ser Asp Leu Ile Gln Ile Leu Leu Lys Glu Thr Val Asn Thr
  1           5           10           15
Leu Tyr Met Val Ser Thr Ala Phe Phe Phe Ser Cys Ala Ile Gly Gly
          20           25           30
Met Leu Gly Leu Gly Leu Phe Cys Thr Ser Pro Lys Ser Leu Asn Pro
          35           40           45
Lys Lys Ser Leu Tyr Ala Thr Ile Ser Met Ile Leu Ser Phe Leu Thr
          50           55           60
Ala Ile Pro Phe Ala Ile Leu Ile Val Ile Leu Phe Pro Ile Thr Arg
          65           70           75           80
Trp Ile Val Gly Thr Ser Leu Gly Pro Thr Ala Ser Ile Val Pro Leu
          85           90           95
Thr Ile Gly Ala Ile Pro Phe Val Val Thr Ile Val Val Asp Ala Phe
          100          105          110
Arg Asn Ser Ala Leu Asn Tyr Leu Glu Ser Ala Val Ala Leu Gly Ile
          115          120          125
Pro Lys Arg Asn Ile Leu Phe Gly Ile Leu Leu Pro Glu Ser Tyr Pro
          130          135          140
Gln Leu Ile Phe Ser Leu Lys Ser Leu Val Val His Leu Ile Ser Cys
          145          150          155          160
Ser Thr Leu Ala Gly Phe Val Gly Gly Gly Gly Leu Gly Gln Leu Leu
          165          170          175
Leu Gln Tyr Gly Tyr Tyr Arg Phe Glu Trp Ser Val Thr Thr Ser Val
          180          185          190
Leu Val Ile Thr Leu Val Leu Ile Glu Ser Val Arg Ile Leu Gly Asp
          195          200          205
Phe Trp Gly Arg Arg Val Leu Lys Tyr Arg Gly Ile Leu
          210          215          220

```

&lt;210&gt;293

&lt;211&gt;341

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;293

```

Val Ser Glu Gln His Ser Pro Ile Ile Ser Val Gln Asp Val Ser Lys
  1           5           10           15
Lys Leu Gly Asp His Ile Leu Leu Ser Lys Val Ser Phe Ser Val Tyr
          20           25           30
Pro Gly Glu Val Phe Gly Ile Val Gly His Ser Gly Ser Gly Lys Thr
          35           40           45
Thr Leu Leu Arg Cys Leu Asp Phe Leu Asp Met Pro Thr Ser Gly Ser
          50           55           60
Ile Ser Val Ala Gly Phe Asp Asn Ser Leu Pro Thr Gln Lys Phe Ser
          65           70           75           80
Arg Arg Asn Phe Ser Lys Lys Val Ala Tyr Ile Ser Gln Asn Tyr Gly
          85           90           95
Leu Phe Ser Ser Lys Thr Val Phe Glu Asn Ile Ala Tyr Pro Leu Arg
          100          105          110
Ile His His Ser Glu Met Ser Lys Ser Glu Val Glu Glu Gln Val Tyr
          115          120          125
Asp Thr Leu Asn Phe Leu Asn Leu Tyr His Arg His Asp Ala Tyr Pro
          130          135          140
Gly Asn Leu Ser Gly Gly Gln Lys Gln Glu Val Ala Ile Ala Arg Ala
          145          150          155          160
Ile Val Cys Gln Pro Glu Val Val Leu Cys Asp Glu Ile Thr Ser Ala
          165          170          175
Leu Asp Pro Lys Ser Thr Glu Asn Ile Ile Glu Arg Leu Leu Gln Leu
          180          185          190
Asn Gln Glu Arg Gly Ile Thr Leu Val Leu Val Ser His Glu Ile Asp
          195          200          205
Val Val Lys Lys Ile Cys Ser His Val Leu Val Met His Gln Gly Ala
          210          215          220
Val Glu Glu Leu Gly Thr Thr Glu Glu Leu Phe Leu Asn Ser Glu Asn

```

225 230 235 240  
 Ser Ile Thr Asn Glu Leu Phe His Glu Asp Ile Asn Ile Ala Ala Leu  
 245 250 255  
 Ser Ser Cys Tyr Phe Ala Glu Asp Arg Glu Glu Val Leu Arg Leu Asn  
 260 265 270  
 Phe Ser Lys Glu Leu Ala Ile Gln Gly Ile Ile Ser Lys Val Ile Gln  
 275 280 285  
 Thr Gly Leu Val Ser Ile Asn Ile Leu Ser Gly Asn Ile Asn Leu Phe  
 290 295 300  
 Arg Lys Ser Pro Met Gly Phe Leu Ile Ile Val Leu Glu Gly Glu Val  
 305 310 315 320  
 Glu Gln Arg Lys Lys Ala Lys Glu Leu Leu Ile Glu Leu Gly Val Val  
 325 330 335  
 Ile Lys Glu Phe Tyr  
 340  
 <210>294  
 <211>357  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>294  
 Ile Ser Leu Arg Arg His Thr Leu Met Leu Asn Ile His Asp Ile Leu  
 1 5 10 15  
 Gly Asn Asp Asp Glu Asn Leu Leu Ser Tyr Gln Cys Lys His Ile Thr  
 20 25 30  
 Lys Asp Lys Leu Thr Leu Pro Ser His Asp Phe Val Asp Lys Val Phe  
 35 40 45  
 Gly Leu Ser Asp Arg Asn Asn Arg Val Leu Arg Ser Leu Gln Thr Met  
 50 55 60  
 Phe Ser His Gly Arg Leu Ala Asn Ser Gly Tyr Leu Ser Ile Leu Pro  
 65 70 75 80  
 Val Asp Gln Gly Ile Glu His Ser Ala Gly Ala Ser Phe Ala Ile Asn  
 85 90 95  
 Pro Ile Tyr Phe Asp Pro Glu Asn Ile Val Lys Leu Ala Ile Glu Ser  
 100 105 110  
 Gly Cys Ser Ala Val Ala Ser Thr Tyr Gly Thr Leu Ser Leu Leu Ser  
 115 120 125  
 Arg Lys Tyr Ala His Lys Ile Pro Phe Met Leu Lys Leu Asn His Asn  
 130 135 140  
 Glu Leu Leu Ser Tyr Pro Thr Lys Tyr His Gln Ile Phe Phe Thr Gln  
 145 150 155 160  
 Val Glu Ala Ala Tyr Ser Met Gly Ala Val Ala Val Gly Ala Thr Val  
 165 170 175  
 Tyr Phe Gly Ser Glu Thr Ser Asn Glu Glu Ile Val Ala Val Ser Asn  
 180 185 190  
 Ala Phe Ala Lys Ala Arg Ser Leu Gly Leu Ala Thr Val Leu Trp Cys  
 195 200 205  
 Tyr Leu Arg Asn Pro Ala Phe Val Ala Asn Gly Val Asp Tyr His Thr  
 210 215 220  
 Ala Ala Asp Leu Thr Gly Gln Ala Asp His Leu Gly Ala Thr Leu Gly  
 225 230 235 240  
 Ala Asp Ile Val Lys Gln Lys Leu Pro Thr Cys Gln Gly Gly Phe Lys  
 245 250 255  
 Ala Ile Asn Phe Gly Lys Thr Asp Glu Arg Val Tyr Ser Glu Leu Ser  
 260 265 270  
 Ser Asn His Pro Ile Asp Leu Cys Arg Tyr Gln Val Leu Asn Ser Tyr  
 275 280 285  
 Cys Gly Lys Val Gly Leu Ile Asn Ser Gly Gly Pro Ser Gly Lys Asn  
 290 295 300  
 Asp Phe Thr Glu Ala Ala Arg Thr Ala Val Ile Asn Lys Arg Ala Gly  
 305 310 315 320  
 Gly Met Gly Leu Ile Leu Gly Arg Lys Ala Phe Gln Arg Pro Leu Ser  
 325 330 335  
 Glu Gly Ile Gln Leu Leu Asn Leu Val Gln Asp Ile Tyr Leu Asp Pro  
 340 345 350



Asn Ile Thr Ile Ala

355

&lt;210&gt;295

&lt;211&gt;468

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;295

```

Met His Ser His Ser Lys Pro Thr Lys Pro Leu Gly Thr Phe Thr Val
  1      5      10      15
Gly Met Leu Ser Leu Ala Val Val Ile Ser Leu Arg Asn Leu Pro Leu
      20      25      30
Thr Ala Lys His Gly Leu Ser Thr Leu Phe Phe Tyr Gly Leu Ala Val
      35      40      45
Ile Cys Phe Met Ile Pro Tyr Ala Leu Ile Ser Ala Glu Leu Ala Ser
      50      55      60
Phe Lys Pro Gln Gly Ile Tyr Ile Trp Ala Arg Asp Ala Leu Gly Lys
      65      70      75      80
Trp Trp Gly Phe Phe Ala Ile Trp Met Gln Trp Phe His Asn Met Thr
      85      90      95
Trp Tyr Pro Ala Val Leu Ala Phe Ile Ala Ser Thr Ile Val Tyr Lys
      100      105      110
Ile Asn Pro Glu Leu Ala His Asn Lys Val Tyr Ile Ala Thr Val Ile
      115      120      125
Leu Ala Gly Phe Trp Ile Leu Thr Phe Phe Asn Phe Leu Gly Ile Thr
      130      135      140
Ser Ser Ala Leu Phe Ser Ser Ile Cys Val Ile Ile Gly Thr Leu Ile
      145      150      155      160
Pro Gly Val Ile Leu Val Ser Leu Ala Leu Phe Trp Ile Phe Ser Gly
      165      170      175
Asn Pro Ile Ala Ile Ser Leu Ser Trp Gly Asn Leu Leu Pro Asn Phe
      180      185      190
Ser Asn Val Ser Ser Leu Val Leu Leu Ala Gly Met Leu Leu Ala Leu
      195      200      205
Cys Gly Leu Glu Ala Asn Ala Asn Leu Ala Ser Asp Met Val Asn Pro
      210      215      220
Arg Lys Asn Tyr Pro Lys Ala Val Phe Ile Gly Ala Ile Ala Thr Leu
      225      230      235      240
Thr Ile Leu Val Leu Gly Ser Leu Ser Ile Ala Ile Val Ile Pro Lys
      245      250      255
Glu Glu Ile Ser Leu Val Ser Gly Leu Val Lys Thr Phe Thr Leu Phe
      260      265      270
Phe Asp Lys Tyr Asn Leu Ser Trp Met Thr Gly Ile Val Val Val Met
      275      280      285
Thr Ile Ala Gly Ser Leu Gly Glu Leu Asn Ala Trp Met Phe Ala Gly
      290      295      300
Thr Lys Gly Leu Phe Ile Ser Thr Gln Asn Asp Cys Leu Pro Arg Leu
      305      310      315      320
Phe Lys Lys Val Asn Ser Lys Asn Val Pro Thr Asn Leu Met Leu Phe
      325      330      335
Gln Gly Ile Val Val Thr Ile Phe Thr Leu Leu Phe Leu Cys Leu Asp
      340      345      350
Ser Ala Asp Leu Val Tyr Trp Ile Leu Thr Ala Leu Ser Val Gln Met
      355      360      365
Tyr Leu Ala Met Tyr Ile Cys Leu Phe Leu Ala Gly Pro Ile Leu Arg
      370      375      380
Ile Lys Glu Pro Arg Ala Gln Arg Leu Tyr Ser Val Pro Gly Lys Phe
      385      390      395      400
Leu Gly Ile Cys Thr Met Ser Ile Leu Gly Ile Leu Ser Cys Ala Phe
      405      410      415
Ala Leu Trp Val Ser Phe Leu Pro Pro Arg Glu Leu Ala Gln Ile Ser
      420      425      430
Glu Gly Ser Lys Ile Gly Tyr Thr Thr Phe Leu Leu Leu Ala Phe Ser
      435      440      445
Leu Asn Cys Leu Ile Pro Phe Gly Ile Tyr Phe Thr His Lys Arg Leu

```

```

<210>297
<211>168
<212>PRT
<213>Chlamydia pneumoniae
<400>297
Phe Leu Asp Met Asn Ile Pro Ala Pro Gln Val Pro Val Ile Asp Glu
  1              5              10              15
Pro Val Val Asn Asn Thr Ser Ser Tyr Gly Leu Ser Leu Lys Ser Ser
          20              25              30
Leu Arg Pro Ile Thr Tyr Leu Ile Leu Ala Ile Leu Ala Ile Ala Thr
      35              40              45
Leu Met Ser Val Leu Tyr Phe Cys Gly Ile Ile Ser Val Gly Thr Phe
      50              55              60
Val Leu Gly Met Leu Ile Pro Leu Ser Val Cys Ser Val Leu Cys Val
      65              70              75              80
Ala Tyr Leu Phe Tyr Gln Gln Ser Ser Ile Glu Lys Thr Lys Val Phe
          85              90              95
Ser Ile Thr Ser Pro Ser Val Phe Phe Ser Asp Glu Asp Leu Asn Leu
      100              105
Leu Leu Gly Arg Glu Glu Asp Ser Val Ser Ala Ile Asp Glu Leu Leu
      115              120              125
Lys Asn Phe Pro Ala Asp Asp Phe Arg Arg Pro Lys Met Leu Pro Tyr
      130              135              140
Ser Asn Phe Leu Asp Glu Gln Gly Arg Pro Asn Glu Ser Arg Glu Glu
      145              150              155              160
Asp Ser His Thr Ser Lys Ile Leu
          165
<210>298

```

&lt;211&gt;517

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;298

Lys Glu Leu Phe Asn Leu Phe Phe Phe Thr Ala Asn Lys Glu Thr Thr  
 1 5 10 15  
 Ala Ser His Glu Leu Ile Tyr Arg Lys Asn Gln Ser Phe Ser Leu Ser  
 20 25 30  
 Pro Val Thr Ile Leu Cys Leu Leu Ala Ile Ser Val Leu Leu Leu  
 35 40 45  
 Gly Val Val Phe Ala Leu Val Gly Cys His Val Leu Ala Ala Pro Leu  
 50 55 60  
 Gly Leu Leu Val Trp Gly Cys Ala Ala Ser Val Cys Ser Met Met Ala  
 65 70 75 80  
 Ile Val Ser Leu Met Cys Leu Tyr Lys Gly Gly Lys Pro Leu Ile Glu  
 85 90 95  
 Pro Ser Asn Glu Lys Ile Asp Pro Thr Lys Asp Leu Glu Ile Lys  
 100 105 110  
 Asp Pro Glu Ser Leu Lys Pro Val Pro Val Glu Gly Gln Ser Leu Pro  
 115 120 125  
 Lys Glu Arg Lys Thr Val Ser Phe Lys Ala Lys Ile Pro Ser Ile Val  
 130 135 140  
 Glu Asp Asp Phe Lys Pro Tyr Val Ile Gln Ser Thr Phe Tyr His Gln  
 145 150 155 160  
 Asn Lys Val Tyr Ser Lys Pro Ile Ala Glu Arg Met Gln Ser Leu Glu  
 165 170 175  
 Lys Glu Ile Thr Thr Leu Ile Val Asp Phe Pro Arg Ala Leu Glu Glu  
 180 185 190  
 Ser Ser Lys Ser Ser Gly Ser Leu Leu Arg Gly Val Ile Ser Glu Ile  
 195 200 205  
 Lys Asn Leu Phe Leu Pro Arg Phe Leu Ser Arg Lys Val Lys Tyr Ser  
 210 215 220  
 Leu Thr Ala Cys Leu Arg Arg Leu Gly Ser Ile Val Glu Glu Tyr Ala  
 225 230 235 240  
 Ser Ser Asp Leu Leu Ile Leu Leu Leu Thr Lys Pro Glu Pro Leu Asn  
 245 250 255  
 Met Val Thr Gln Gln Leu Ile Ala His Leu Asn Ser Leu Lys Thr Glu  
 260 265 270  
 Lys Arg Lys Leu Thr Pro His Met Gln Lys Leu Val Leu Ser Ile Asn  
 275 280 285  
 Phe Trp Phe Tyr Gly Trp Ser Leu Glu Glu Lys Cys Ile Glu Lys Ile  
 290 295 300  
 Val Ala Tyr Asp Pro Asn Leu Leu Thr Asp Glu Leu Lys Ala His Leu  
 305 310 315 320  
 Glu Ala Gly Asn Ile Val Gln Phe Leu Leu Ser Phe Gln Ser Ser Glu  
 325 330 335  
 Met Gln Arg Glu Phe Arg Ala Leu Phe Pro Ser Asp Ala Gln Glu Leu  
 340 345 350  
 Pro Ser Ala Lys Asp Gly Ser Asn Tyr Val Pro Ala Ile Asn Ser Ser  
 355 360 365  
 Glu Tyr Met Tyr Asp Phe Lys Asp Leu Ser Val Leu Lys Lys Ser Leu  
 370 375 380  
 Ser Glu Arg Leu Ala Phe Cys Glu Lys Ile Pro Ser Pro Ser Ser Trp  
 385 390 395 400  
 Asn Phe Thr Ser Ser Val Ala Ser His Tyr Lys Asp Phe Ser Leu Leu  
 405 410 415  
 Phe Thr Phe Phe Ser Asn Gln Gln Ser Val Ile Leu Gln Asn Pro Phe  
 420 425 430  
 Leu Leu Ile Glu Leu Leu His Glu Asn Pro Lys Cys Gln Thr Phe Leu  
 435 440 445  
 Lys Gly Leu Leu Glu Lys Ala Met Pro Met Ser Asn Trp Ala Ala Leu  
 450 455 460  
 Phe Arg Pro Met Leu Met Gly Met Leu Cys Ser Gly Ile Ala Arg Lys  
 465 470 475 480

532

420 425 430  
 Gln Leu Gly Val Thr Val Ala Thr Gly Val Leu Gly Ala Ser Leu Thr  
 435 440 445  
 Ala Thr Thr Leu Gly Val Leu Ser Pro Phe Phe Phe Ala Lys Leu Gly  
 450 455 460  
 Val Asp Pro Ala Leu Ala Ser Gly Pro Ile Val Thr Ala Leu Asn Asp  
 465 470 475 480  
 Ile Met Ser Met Ile Ile Phe Phe Leu Ile Ala Gly Gly Ile Asn Phe  
 485 490 495  
 Leu Phe Phe Asn  
 500  
 <210>300  
 <211>714  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>300  
 Arg Arg Cys Met Ile Arg Ser Pro Leu Pro Phe Ile Ser Ser Lys Arg  
 1 5 10 15  
 Ala Leu Asn Met Leu Gly Leu Gln Asp Glu Phe Ser Cys Pro Glu Asp  
 20 25 30  
 Val Val Asp Phe Leu Phe Ser Glu Ile Glu Leu Leu Ala Gln Gln Asp  
 35 40 45  
 Glu Pro Ser Glu Gly Tyr Leu Ala Leu Ser Arg Ser Leu Leu Met Met  
 50 55 60  
 Thr His Asn His Pro Lys Val Val Lys Arg Val Ile Phe Tyr Gly Val  
 65 70 75 80  
 Ser Tyr Gly Leu Lys His Lys Ser Met Ser Ile Phe Ile Asp Val Leu  
 85 90 95  
 Thr Tyr Ile Asp Phe Leu Phe Glu Lys Leu Gly Ile Ser Ala Ser Asp  
 100 105 110  
 Arg Leu Ser Leu Cys Ser Ala Arg Thr Cys Ile Asn Phe Glu Leu Tyr  
 115 120 125  
 Ser Gln Thr Gly Glu Met Lys Phe Leu Ser Glu Val Val Asp Asn Phe  
 130 135 140  
 Arg Leu Ile Glu Gln Leu Leu Lys Met His Pro Gln Leu Lys Asn Arg  
 145 150 155 160  
 Phe Gly Trp Glu His Phe Arg Ile Gly Ala Lys Gln Glu Glu Val Ser  
 165 170 175  
 Leu Val Ala Ser Ala Ser Val Tyr Gln Ala Val Gly Arg Ser Phe Ile  
 180 185 190  
 Glu Leu Tyr His Lys His Leu Glu Leu Ser Asp Leu Ala Cys Gly Met  
 195 200 205  
 Lys Cys Leu Ala Leu Ala Leu Asp Leu Ser Pro Asn Asn Ala His Ile  
 210 215 220  
 His Ala Asp Tyr Ala Lys Gly Leu Val Val Leu Gly Thr Arg Gln Gly  
 225 230 235 240  
 Lys Ser Leu Leu Ile Glu Arg Gly Met Glu His Phe Ser Lys Ala Ile  
 245 250 255  
 Phe Leu Ser Phe Ser Arg Asp Gly Asp Thr Leu Ala Tyr Gln Asn Tyr  
 260 265 270  
 Arg Tyr Ser Tyr Ala Leu Ala Ser Val Lys Leu Phe Asp Leu Thr Tyr  
 275 280 285  
 Lys Lys Glu His Phe Asp Gln Ala Met Asn Ile Leu Tyr Gln Thr Val  
 290 295 300  
 Gln Ala Phe Pro Asn Leu Ser Gly Leu Trp Met Val Trp Gly Glu Leu  
 305 310 315 320  
 Leu Ile Arg Ser Gly Trp Leu Asn Ser Asn Met Lys Tyr Ile Glu Val  
 325 330 335  
 Gly Leu Glu Lys Leu Ala Ser Leu Gln Lys Lys Thr Asn Asp Pro Ile  
 340 345 350  
 Ala Leu Ser Gly Leu Leu Ala Thr Gly Ile Ala Ile Leu Gly Leu Tyr  
 355 360 365  
 Leu Glu Glu Pro Asn Leu Phe Lys Asp Ser Arg His Arg Leu Ile Ser  
 370 375 380

Ala Met Arg Met Phe Pro Gly Asn Ser Ala Leu Val His Ala Leu Gly  
 385 390 395 400  
 Val Val Gln Leu Cys Ser Ala Leu Tyr Phe Asn Glu Asp Ser His Phe  
 405 410 415  
 Ala Ser Ala Ile Ser Cys Phe Gln Ser Cys Leu Glu Trp Asp Leu Asp  
 420 425 430  
 Ala Thr Gly Met Trp Gln Lys Leu Phe Asp Ala Tyr Phe Ser Trp Gly  
 435 440 445  
 Ile Lys Lys Lys Ser Ala Arg Leu Leu Arg Lys Ala Val Asp Val Ala  
 450 455 460  
 Ser Arg Leu Cys Ser Leu Arg Pro Glu Ala Phe Leu Phe Trp Ser Asp  
 465 470 475 480  
 Arg Gly Leu Ala Leu Lys Cys Leu Ala Glu Ala Thr Ile Asp Glu Ala  
 485 490 495  
 Tyr Lys Glu Ile Phe Leu Ser Glu Ser Leu Leu His Tyr Gln Arg Ala  
 500 505 510  
 Trp Asp Leu Ser Gly Arg Leu Glu Ile Leu Glu Leu Trp Gly Gln Ser  
 515 520 525  
 His Tyr Leu Leu Ala Glu Leu Gln Gln Ser Leu Phe His Tyr Asp Glu  
 530 535 540  
 Ala Tyr Thr Leu Leu Thr Lys Val Asp Leu Thr Leu Ser Ser Ser Arg  
 545 550 555 560  
 Val Lys Leu Ile Leu Ala Ala Val Leu Leu Gly Lys Gly Arg Leu Leu  
 565 570 575  
 Gln Asp Thr Asp Pro Ala Glu Glu Ala Arg Glu Ile Leu Glu Pro Leu  
 580 585 590  
 Val Glu Val Tyr Leu Glu Asp Glu Asn Phe Leu Leu Leu Gly Lys  
 595 600 605  
 Val Tyr Leu Phe Leu Phe Trp Lys Asn Lys Asn Val Cys Leu Gly Lys  
 610 615 620  
 Leu Ala Arg Thr Tyr Leu Glu Lys Ala Thr Ser Leu Gly Cys Pro Glu  
 625 630 635 640  
 Ala Tyr Tyr Thr Leu Gly Lys Phe Tyr Ala Val Ile Lys Asp Val Asn  
 645 650 655  
 Lys Ala Trp Gly Met Val Ile Arg Ser Ala Gln Tyr Gly Val Arg Ile  
 660 665 670  
 Thr Glu Ala Lys Trp Leu Asn Asp Pro Tyr Leu Ala Asn Leu Arg Glu  
 675 680 685  
 Ile His Ala Phe Arg Glu Val Val Glu Asn Gln Lys Gly Arg Leu Trp  
 690 695 700  
 Leu Gly Asn Lys Thr Glu Met Lys Arg Asn  
 705 710

&lt;210&gt;301

&lt;211&gt;405

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;301

Ile Ser Ile Thr Ile Arg Glu Phe Leu Phe Phe Gly Phe Glu Cys Arg  
 1 5 10 15  
 Ala Lys Phe Tyr Asn Val Ile Met Ser Cys Phe Asn Leu Thr Ser Thr  
 20 25 30  
 Asn Glu Ser Leu Arg Pro Ile Ser Pro Lys Ala Ser Phe Pro Lys Gln  
 35 40 45  
 Gly Trp Gln Ser Tyr Phe Arg Ser Ala Leu Arg Lys His Arg Ser Asp  
 50 55 60  
 Thr Leu Ser Val Ser Val Cys Lys Val Asn Lys Tyr Asp Ala Asn Leu  
 65 70 75 80  
 Phe Val Arg Leu Thr Val Ile Ala Leu Ala Val Val Gly Val Leu Ile  
 85 90 95  
 Leu Phe Ser Ile Met Leu Ala Ser Ile Gln Gly Thr Leu Val Ile Thr  
 100 105 110  
 Ser Trp Pro Leu Val Thr Ala Ala Ile Leu Ile Pro Thr Ile Leu Leu  
 115 120 125  
 Thr Gly Gly Met Tyr Ile Leu His Arg Leu Gly Lys Lys Val Asp Val

130 135 140  
 Ile Ser Gly Val Cys Ile Pro Pro Phe Ser Arg Arg Cys Trp Val Pro  
 145 150 155 160  
 Ile Ser Ser Ser His Thr Leu Glu Lys Phe Asp Glu Lys His Val Ser  
 165 170 175  
 Ala Cys Ser Tyr Leu Asp Ile Ser Thr Leu Ser Ala Asp Gly Ser Gly  
 180 185 190  
 Ile Ala Ala Val Tyr Gln Cys Pro Pro Leu Leu Phe Arg Ala Phe Pro  
 195 200 205  
 Cys Phe Gly Ile Pro Cys Ala Met Pro Phe Val Ala Leu Leu Arg Met  
 210 215 220  
 Ile Tyr Asn Leu Ile Arg Phe Leu Val Val Pro Phe Tyr Ile Ile Phe  
 225 230 235 240  
 Arg Met Ile Tyr Glu His Phe Phe Cys Lys His Leu Pro Glu Asp Asp  
 245 250 255  
 Arg Phe Ile Tyr Lys Asp Val Ala Arg Glu Met Gly Arg Ser Leu Ala  
 260 265 270  
 Ala Phe Leu Lys Ala Pro Phe Tyr Ala Ser Ala Cys Met Ile Gly Ala  
 275 280 285  
 Phe Tyr Ser Leu Leu Asp Pro Leu Ala Gly Arg Val Leu Met Gly Ser  
 290 295 300  
 Val Glu Arg Asp Trp Asn Asp Asn Val Ile Leu Ala Arg Ser Val Ser  
 305 310 315 320  
 Leu Ala Asn Glu Ala His Ser Leu Phe Arg Phe Glu Gly Gly Gly Gly  
 325 330 335  
 Arg Lys Gly Leu Gly Gln His Ala Phe Tyr Leu Met Leu Cys Cys Gln  
 340 345 350  
 Pro Gln Ser Val Phe Leu Phe Asp Lys Gly Glu Ile Val Ser Gly Ala  
 355 360 365  
 His Pro Ser Ile Gln Leu Pro Glu Arg Arg Gly Leu Asp Thr Ser Gly  
 370 375 380  
 Arg Tyr Pro His Ile Ser Val Ile Pro Asp Ser Gly Asn Asp Ser Ala  
 385 390 395 400  
 Lys Asn Phe Ile Val  
 405

&lt;210&gt;302

&lt;211&gt;400

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;302

Asn Phe Asn Arg Leu Met Lys Lys Gln Arg Ser His Tyr Thr Lys Asn  
 1 5 10 15  
 Asn Leu Leu Leu Leu Leu Ser Ile Leu Val Gly Leu Gly Leu Gly Ser  
 20 25 30  
 Val Gln Ser Pro Trp Ile Val Tyr Ser Ala Glu Cys Ile Ala Asn Thr  
 35 40 45  
 Phe Leu Lys Phe Leu Arg Leu Leu Ser Ile Pro Leu Val Phe Cys Ala  
 50 55 60  
 Leu Gly Ser Thr Ile Thr Ser Ile Gln Asn Phe Asn Thr Met Val Thr  
 65 70 75 80  
 Leu Gly Lys Arg Ile Leu Tyr Tyr Thr Leu Leu Thr Thr Val Ile Ala  
 85 90 95  
 Ala Ser Ile Gly Leu Leu Leu Phe Phe Leu Leu Arg Pro Gln Met Ile  
 100 105 110  
 Thr Gln Asp Ala Leu Ala Thr Thr Lys Cys Asn Pro Leu Gly Tyr  
 115 120 125  
 Leu Asp Val Leu Ser Asp Thr Leu Pro Glu Asn Ile Phe Lys Pro Phe  
 130 135 140  
 Leu Gln Gly Asn Val Ile Ser Ala Ala Cys Leu Ala Val Leu Leu Gly  
 145 150 155 160  
 Thr Ala Ser Leu Phe Leu Gln Glu Lys Glu Lys His Phe Val Asn Gln  
 165 170 175  
 Phe Phe Asn Ser Phe Phe Ser Ile Phe Leu Asn Leu Ala Arg Gly Gly  
 180 185 190

Leu Lys Leu Leu Pro Ile Ala Met Leu Gly Phe Ser Val Ile Leu Phe  
 195 200 205  
 Lys Glu Leu Lys Asp Gln Ser Asn Leu Thr Met Phe Ala Glu Tyr Leu  
 210 215 220  
 Leu Cys Val Ile Gly Ala Asn Leu Ala Gln Gly Phe Ile Val Leu Pro  
 225 230 235 240  
 Ile Leu Leu Lys Ile Asn Lys Val Ser Pro Leu Lys Val Ala Lys Ala  
 245 250 255  
 Met Ser Pro Ala Leu Val Thr Ala Phe Phe Ser Lys Ser Ser Ala Ala  
 260 265 270  
 Thr Leu Pro Leu Thr Met Glu Leu Ala Glu Asp Asp Leu Lys Ile Asn  
 275 280 285  
 Lys Asn Leu Ser Arg Phe Ser Phe Pro Leu Cys Ser Val Ile Asn Met  
 290 295 300  
 Asn Gly Cys Ala Ala Phe Ile Leu Ile Thr Val Leu Phe Val Ala Thr  
 305 310 315 320  
 Ser Asn Gly Met Ile Ile Ser Pro Leu Met Ser Leu Gly Trp Ile Phe  
 325 330 335  
 Ile Ala Thr Leu Ala Ala Ile Gly Asn Ala Gly Val Pro Met Gly Cys  
 340 345 350  
 Tyr Phe Leu Thr Leu Ser Leu Leu Thr Ser Met Asn Val Pro Leu Ser  
 355 360 365  
 Ile Leu Gly Leu Ile Leu Pro Phe Tyr Thr Val Ile Asp Met Ile Glu  
 370 375 380  
 Thr Ser Leu Asn Val Trp Ser Asp Cys Cys Val Ser Leu Ala Asn  
 385 390 395 400  
 <210>303  
 <211>234  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>303  
 Ser Trp Gly Ile Ile Ile Phe Ser Thr Cys Ala Ser Leu Asp Ile Leu  
 1 5 10 15  
 Gly Thr Thr Gln Leu Gln Asp Gly Ala Gly Ala Ser Ser Ile Gly Ile  
 20 25 30  
 Thr Phe Ile Tyr Leu Pro Glu Leu Phe Thr Arg Leu Pro Gly Gly Ile  
 35 40 45  
 Tyr Leu Thr Thr Leu Phe Ser Ser Ile Phe Phe Leu Ala Phe Ser Met  
 50 55 60  
 Ala Ala Leu Ser Ser Met Ile Ser Met Leu Phe Leu Leu Ser Gln Thr  
 65 70 75 80  
 Leu Ala Glu Phe Gly Ile Lys Pro Tyr Ile Ser Glu Thr Leu Ala Thr  
 85 90 95  
 Ile Ile Ala Phe Val Leu Gly Ile Pro Ser Ala Leu Ser Leu Thr Phe  
 100 105 110  
 Phe Ser Asn Gln Asp Thr Val Trp Gly Val Ala Leu Ile Val Asn Gly  
 115 120 125  
 Leu Ile Phe Ile Tyr Ala Ala Leu Val Tyr Gly Phe Pro Lys Leu Lys  
 130 135 140  
 Lys Glu Val Ile Asn Ala Ala Pro Gly Asp Leu Arg Leu Asn Lys Ala  
 145 150 155 160  
 Phe Asp Tyr Ile Ile Lys Tyr Leu Leu Leu Ile Glu Gly Ile Leu Leu  
 165 170 175  
 Leu Gly Trp Tyr Phe Tyr Glu Gly Leu Phe Pro Glu Asn Gly Gln Trp  
 180 185 190  
 Trp Asn Pro Ile Ser Leu Tyr Ser Leu Gly Ser Leu Val Leu Gln Trp  
 195 200 205  
 Ser Leu Gly Leu Ile Ile Leu Trp Lys Phe Asn Lys Gln Leu Tyr Leu  
 210 215 220  
 Arg Phe Ser Arg Tyr Asn His Glu Ile Leu  
 225 230  
 <210>304  
 <211>179  
 <212>PRT



&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;304

Glu Lys His Met Ser Ala Pro Ile Pro Thr Pro Gln Glu Leu Ser Asp  
 1 5 10 15  
 Gln Ile Thr Cys Leu Asn Val Gln Tyr Gln Gln Val Ser Glu Leu Ala  
 20 25 30  
 Arg Glu Asn Lys Gly Asp Ile Glu Gly Leu Lys Thr Leu Thr Ala Ala  
 35 40 45  
 Leu Thr Ala Asp Ala Gly Ile Gln Pro Ser Ala Asp Glu Ile Tyr Ser  
 50 55 60  
 Leu Gln Thr Ala Ala Ala Leu Ile Leu Ser Ala Ser Glu Lys Pro Gly  
 65 70 75 80  
 Ser Gly Pro Ser Gly Ser Thr Glu Gly Ser Val Thr Val Gln Ser Pro  
 85 90 95  
 Cys Lys Phe Lys Lys Val Leu Ala Val Val Leu Thr Ile Ile Ala Leu  
 100 105 110  
 Ile Ala Ile Ala Val Leu Ile Ala Cys Ile Ile Ala Ala Cys Gly Gly  
 115 120 125  
 Phe Pro Leu Leu Leu Ser Ala Leu Asn Leu Tyr Thr Ile Gly Ala Cys  
 130 135 140  
 Val Ser Leu Pro Ile Ile Ala Ser Thr Ser Val Ala Leu Ile Cys Leu  
 145 150 155 160  
 Cys Thr Phe Val Ala Asn Ser Leu Ile Lys Pro Val Ile Thr Val Arg  
 165 170 175  
 Thr Thr Arg

&lt;210&gt;305

&lt;211&gt;212

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;305

Val Lys Asn Thr Lys Asn Ser Asp Phe Met Thr Ser Pro Ile Pro Phe  
 1 5 10 15  
 Gln Ser Ser Gly Asp Ala Ser Phe Leu Ala Glu Gln Pro Gln Gln Leu  
 20 25 30  
 Pro Ser Thr Ser Glu Ser Gln Leu Val Thr Gln Leu Leu Thr Met Met  
 35 40 45  
 Lys His Thr Gln Ala Leu Ser Glu Thr Val Leu Gln Gln Gln Arg Asp  
 50 55 60  
 Arg Leu Xaa Thr Ala Ser Ile Ile Leu Gln Val Gly Gly Ala Pro Thr  
 65 70 75 80  
 Gly Gly Ala Gly Ala Pro Phe Gln Pro Gly Pro Ala Asp Asp His His  
 85 90 95  
 His Pro Ile Pro Pro Pro Val Val Pro Ala Gln Ile Glu Thr Glu Ile  
 100 105 110  
 Thr Thr Ile Arg Ser Glu Leu Gln Leu Met Arg Ser Thr Leu Gln Gln  
 115 120 125  
 Ser Thr Lys Gly Ala Arg Thr Gly Val Leu Val Val Thr Ala Ile Leu  
 130 135 140  
 Met Thr Ile Ser Leu Leu Ala Ile Ile Ile Ile Leu Ala Val Leu  
 145 150 155 160  
 Gly Phe Thr Gly Val Leu Pro Gln Val Ala Leu Leu Met Gln Gly Glu  
 165 170 175  
 Thr Asn Leu Ile Trp Ala Met Val Ser Gly Ser Ile Ile Cys Phe Ile  
 180 185 190  
 Ala Leu Ile Gly Thr Leu Gly Leu Ile Leu Thr Asn Lys Asn Thr Pro  
 195 200 205  
 Leu Pro Ala Ser

210

&lt;210&gt;306

&lt;211&gt;907

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;306

Val	Trp	Ser	Met	Gln	Arg	Val	Leu	Arg	Leu	Leu	Phe	Asn	Leu	His	His
1				5					10					15	
Gly	Glu	Glu	Lys	Arg	Ala	Phe	Leu	Phe	Phe	Leu	Leu	Gly	Leu	Val	Trp
			20					25					30		
Gly	Ile	Gly	Cys	Tyr	Gly	Thr	Leu	Ser	Leu	Ala	Glu	Gly	Leu	Phe	Ile
		35					40					45			
Glu	Lys	Leu	Gly	Ser	Ala	Glu	Leu	Pro	Lys	Ile	Tyr	Leu	Gly	Ser	Ser
	50					55					60				
Leu	Ile	Leu	Cys	Val	Leu	Ser	Ser	Leu	Ile	Leu	Tyr	Asn	Leu	Phe	Lys
65					70					75					80
Lys	His	Ile	Ser	Ala	Thr	Ala	Leu	Phe	Leu	Ile	Pro	Val	Ser	Leu	Ser
				85					90					95	
Ile	Leu	Cys	Asn	Phe	Tyr	Leu	Ile	Leu	Ser	Ser	Ile	Phe	Ala	Ile	Asp
			100					105					110		
Pro	Pro	Arg	Ser	Pro	Leu	Phe	Phe	Tyr	Arg	Ile	Val	Ile	Trp	Ser	Leu
		115					120					125			
Thr	Ile	Leu	Ser	Tyr	Thr	Ser	Phe	Trp	Gly	Phe	Val	Asp	Gln	Phe	Phe
130						135					140				
Asn	Leu	Gln	Asp	Gly	Lys	Arg	His	Phe	Cys	Ile	Phe	Asn	Ala	Ile	Ile
145					150					155					160
Phe	Leu	Gly	Asp	Ala	Ile	Gly	Ser	Gly	Ile	Ile	Ala	Ser	Leu	Val	His
			165					170						175	
Thr	Ile	Gly	Ile	Gln	Gly	Ile	Leu	Ile	Leu	Phe	Thr	Ala	Ala	Leu	Val
			180					185					190		
Leu	Thr	Phe	Pro	Ile	Val	Phe	Tyr	Val	Ser	Lys	Ser	Leu	Lys	Ser	Leu
	195						200					205			
Ser	Asp	Asp	His	Asp	Leu	Phe	Ile	Asp	Thr	Gly	His	Pro	Pro	Pro	Leu
	210					215					220				
Ser	Lys	Ala	Leu	Lys	Leu	Cys	Phe	Tyr	Asp	Lys	Tyr	Thr	Phe	Tyr	Leu
225					230					235					240
Leu	Cys	Phe	Tyr	Phe	Leu	Met	Gln	Leu	Leu	Ala	Ile	Ala	Thr	Glu	Phe
				245					250					255	
Asn	Tyr	Leu	Lys	Ile	Phe	Glu	Ile	Gln	Phe	Ala	Ser	Lys	Glu	Glu	Phe
		260						265					270		
Glu	Leu	Val	Ala	His	Ile	Gly	Lys	Cys	Ser	Leu	Trp	Ile	Ser	Leu	Gly
		275					280					285			
Asn	Met	Cys	Phe	Ala	Leu	Phe	Ala	Tyr	Ser	Arg	Ile	Val	Lys	Arg	Leu
	290					295					300				
Gly	Val	Asn	Asn	Ile	Ile	Leu	Phe	Ala	Pro	Leu	Cys	Phe	Leu	Ser	Leu
305					310					315					320
Phe	Leu	Phe	Trp	Thr	Phe	Lys	Thr	Thr	Leu	Ser	Ile	Ala	Val	Leu	Ala
				325					330					335	
Met	Val	Val	Arg	Glu	Gly	Val	Thr	Tyr	Ala	Leu	Asp	Asp	Asn	Asn	Leu
			340					345					350		
Gln	Leu	Leu	Ile	Tyr	Gly	Val	Pro	Asn	Lys	Ile	Arg	Asn	Gln	Ile	Arg
		355					360					365			
Ile	Val	Val	Glu	Ser	Phe	Ile	Glu	Pro	Ile	Gly	Met	Leu	Val	Trp	Ser
	370					375					380				
Leu	Val	Cys	Phe	Leu	Ser	Ser	Gln	Gln	Tyr	Val	Phe	Cys	Leu	Ile	Ile
385					390					395					400
Ser	Leu	Ile	Ala	Thr	Ile	Leu	Val	Cys	Leu	Val	Arg	Ser	Tyr	Tyr	Ala
			405						410				415		
Lys	Ala	Ile	Leu	Lys	Asn	Leu	Ser	Ala	Gln	Ala	Leu	Gln	Leu	Thr	Arg
			420					425					430		
Ser	Met	Gln	Asp	Trp	Ile	Lys	Ser	Met	Thr	Val	Lys	Gln	Lys	Arg	Gln
		435					440					445			
Val	Glu	Leu	Phe	Leu	Leu	Ala	His	Leu	Lys	His	Pro	Ser	Glu	Arg	His
	450					455					460				
Gln	Thr	Phe	Ala	Phe	Gln	His	Leu	Leu	Asn	Leu	Ala	Ser	Arg	Ser	Val
465					470					475					480
Leu	Pro	Ser	Leu	Leu	Ala	His	Met	Asn	Lys	Leu	Ser	Leu	Pro	Asn	Lys
				485					490					495	
Leu	Lys	Thr	Ile	Glu	Met	Val	Lys	Ser	Ser	Leu	Trp	Ala	Lys	Asp	Phe
				500				505					510		

Leu Thr Leu Glu Leu Leu Lys Arg Trp Thr Ser Ile Phe Pro His Pro  
 515 520 525  
 Ala Ile Ala Ser Ala Ile His Leu Tyr Phe Ala Glu His Asp Leu Leu  
 530 535 540  
 His Ile Thr His Ile Ala Glu Asp Leu Tyr Asp Thr Val Gly Asp Arg  
 545 550 555 560  
 Leu Leu Ala Ala Ile Leu Thr Val Arg Arg Gln Glu Ala Tyr Gly Pro  
 565 570 575  
 Tyr Arg Asp Leu Ala Asp Lys Arg Leu Lys Glu Leu Leu Asn Ser Asp  
 580 585 590  
 Gln Pro Glu Asp Ile Val Met Gly Leu Thr Ile Leu Lys Leu Glu Lys  
 595 600 605  
 Asn Pro Gln Asn Phe Pro Ile Leu Leu Asp Phe Leu Asn Thr Lys Asn  
 610 615 620  
 Glu Asp Ile Leu Ile Val Thr Cys Lys Ala Leu His Thr Ser Val Arg  
 625 630 635 640  
 Ala Asn His Lys Pro Tyr Cys Pro Glu Leu Lys Arg Leu Arg Gln  
 645 650 655  
 Cys Ser His Asn Asp Glu Ala Ser Gln Tyr Leu Leu Lys Thr Ile Ser  
 660 665 670  
 Ile Ala Leu Asp Ile Ser Phe Val Lys Asp Leu Leu Met Thr Thr Ser  
 675 680 685  
 Gln Leu Lys Asn Thr Ser Arg Lys Tyr Ala Glu Ala Met Ile Gly Glu  
 690 695 700  
 Leu Asp Lys Glu Val Ala Pro Ala Phe Leu Gln Val Leu Thr Asp Glu  
 705 710 715 720  
 Gly Thr His Asn Arg Cys Arg Ile Leu Ala Ala Lys Ala Leu Cys Lys  
 725 730 735  
 Ile Asp Asn Trp Leu Leu Lys Lys His Ala Tyr Lys Ile Val Lys Ser  
 740 745 750  
 Lys Ala Ser Lys Ala Leu Phe Tyr Ser Tyr His Gly His Tyr Ile Gln  
 755 760 765  
 Lys Lys Tyr Pro Thr Tyr Asn Leu Ser Leu Leu Ala Asn Thr Leu Asn  
 770 775 780  
 Ser Asn Tyr Tyr Ala Glu Val Asn Phe Met Leu Ser Leu Leu Gly Ile  
 785 790 795 800  
 Leu Gly Ser Met Glu His Ser Gly Val Leu Ile Arg Ala Leu Thr Ser  
 805 810 815  
 Lys Asn Gln Lys Ile Lys Ala Gln Ala Leu Glu Ser Leu Glu Lys Asn  
 820 825 830  
 Cys Asp Ser His Leu Phe Ser Leu Leu Glu Pro Phe Val Asn Gln Pro  
 835 840 845  
 Gly Met Cys Tyr Ser Glu Lys Tyr Tyr Phe Lys Cys Gly Val Ile Pro  
 850 855 860  
 Leu Thr Leu Lys Glu Leu Leu Asn Met Met Glu Asn Ser Pro Ser Ser  
 865 870 875 880  
 Leu Asn Lys Leu Thr Ala Gln Gln Leu Lys Glu Glu Leu Ser Tyr Cys  
 885 890 895  
 Asp Pro Asp Phe Pro Ile Cys Lys Tyr Asn Leu  
 900 905

&lt;210&gt;307

&lt;211&gt;142

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;307

Ile Arg Asn Phe Phe Met Asn Leu Ile Asp Arg Ala Phe Leu Leu Lys  
 1 5 10 15  
 Lys Thr Ile Ile Phe Gln Ser Leu Asp Met Asp Leu Leu Leu Thr Ile  
 20 25 30  
 Ala Asp Lys Thr Glu Thr Ile Ile Phe Lys Pro Gly Ser Asn Val Phe  
 35 40 45  
 Ser Ile Gly Gln Pro Gly Phe Ser Phe Tyr Ile Ile Val Glu Gly Tyr  
 50 55 60  
 Ile Thr Ile Ser Lys Glu Lys Leu Glu Ser Pro Leu Asn Leu Lys Pro

```

      65              70              75              80
Leu Asp Cys Phe Gly Glu Glu Ser Leu Phe Asn Asn Lys Pro Arg Glu
      85              90              95
Tyr Asn Ala Ser Ala Asn Thr Gln Val Arg Met Leu Val Leu Ser Lys
      100             105             110
Gly Gln Ile Leu Asn Ile Val Glu Glu Cys Pro Ser Val Ala Leu Ser
      115             120             125
Phe Leu Glu Leu Tyr Ala Lys Gln Ile Lys Phe Arg Glu Pro
      130             135             140
<210>308
<211>79
<212>PRT
<213>Chlamydia pneumoniae
<400>308
Met Ser Leu Glu Asp Asp Val Ile Ala Ile Ile Val Glu Gln Leu Gly
  1              5              10              15
Val Asp Pro Lys Glu Val Asn Glu Asn Ser Ser Phe Ile Glu Asp Leu
      20              25              30
Asn Ala Asp Ser Leu Asp Leu Thr Glu Leu Ile Met Thr Leu Glu Glu
      35              40              45
Lys Phe Ala Phe Glu Ile Ser Glu Glu Asp Ala Glu Lys Leu Arg Thr
      50              55              60
Val Gly Asp Val Phe Thr Tyr Ile Lys Lys Arg Gln Ala Glu Gln
      65              70              75
<210>309
<211>251
<212>PRT
<213>Chlamydia pneumoniae
<400>309
Met Ile Cys Met Asp Ile Thr Leu Val Gly Lys Lys Val Ile Val Thr
  1              5              10              15
Gly Gly Ser Arg Gly Ile Gly Leu Gly Ile Val Lys Leu Phe Leu Glu
      20              25              30
Asn Gly Ala Asp Val Glu Ile Trp Gly Leu Asn Glu Glu Arg Gly Gln
      35              40              45
Ala Val Ile Glu Ser Leu Thr Gly Leu Gly Gly Glu Val Ser Phe Ala
      50              55              60
Arg Val Asp Val Ser His Asn Gly Gly Val Lys Asp Cys Val Gln Lys
      65              70              75              80
Phe Leu Asp Lys His Asn Lys Ile Asp Ile Leu Val Asn Asn Ala Gly
      85              90              95
Ile Thr Arg Asp Asn Leu Leu Met Arg Met Ser Glu Asp Asp Trp Gln
      100             105             110
Ser Val Ile Ser Thr Asn Leu Thr Ser Leu Tyr Tyr Thr Cys Ser Ser
      115             120             125
Val Ile Arg His Met Ile Lys Ala Arg Ser Gly Ser Ile Ile Asn Val
      130             135             140
Ala Ser Ile Val Ala Lys Ile Gly Ser Ala Gly Gln Thr Asn Tyr Ala
      145             150             155             160
Ala Ala Lys Ala Gly Ile Ile Ala Phe Thr Lys Ser Leu Ala Lys Glu
      165             170             175
Val Ala Ala Arg Asn Ile Arg Val Asn Cys Leu Ala Pro Gly Phe Ile
      180             185             190
Glu Thr Asp Met Thr Ser Val Leu Asn Asp Asn Leu Lys Ala Glu Trp
      195             200             205
Leu Lys Ser Ile Pro Leu Gly Arg Ala Gly Thr Pro Glu Asp Val Ala
      210             215             220
Arg Val Ala Leu Phe Leu Ala Ser Gln Leu Ser Ser Tyr Met Thr Ala
      225             230             235             240
Gln Thr Leu Val Val Asp Gly Gly Leu Thr Tyr
      245             250
<210>310
<211>308
<212>PRT

```

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;310

Met Lys Lys Arg Tyr Ala Phe Leu Phe Pro Gly Gln Gly Ser Gln Tyr  
 1 5 10 15  
 Val Gly Met Gly Gln Asp Leu Tyr Met Glu Tyr Pro Glu Val Arg Glu  
 20 25 30  
 Leu Phe Asp Phe Ala Asn Glu Arg Leu Gly Phe Ser Leu Thr Ser Ile  
 35 40 45  
 Met Phe Glu Gly Pro Glu Asp Leu Leu Met Glu Thr Val His Ser Gln  
 50 55 60  
 Leu Ala Ile Tyr Leu His Ser Met Ala Val Val Lys Val Leu Ser Gln  
 65 70 75 80  
 Arg Ser Ser Ile Gln Pro Ser Leu Val Ser Gly Leu Ser Leu Gly Glu  
 85 90 95  
 Tyr Thr Ala Leu Val Ala Ser Asp Arg Ile Ser Val Leu Asp Gly Leu  
 100 105 110  
 Glu Leu Val Arg Lys Arg Gly Gln Leu Met Asn Glu Ala Cys Asn Gln  
 115 120 125  
 Ser Pro Gly Ala Met Ala Ala Leu Leu Gly Leu Pro Ser Glu Val Ile  
 130 135 140  
 Glu Glu Asn Ile Thr Ser Leu Gly Gln Gly Ile Trp Ile Ala Asn Tyr  
 145 150 155 160  
 Asn Ala Pro Lys Gln Leu Val Val Ala Gly Ile Ala Glu Lys Val Asp  
 165 170 175  
 Gln Ala Ile Glu Leu Phe Arg Asp Leu Gly Cys Lys Lys Ala Val Arg  
 180 185 190  
 Leu Lys Val Ser Gly Ala Phe His Thr Pro Leu Met Gln Val Ala Gln  
 195 200 205  
 Asp Gly Leu Ala Pro Asp Ile Tyr Ala Leu Cys Met Lys Asp Ser Ser  
 210 215 220  
 Leu Pro Leu Val Ser His Val Val Gly Lys Ser Leu Val Asn Thr Glu  
 225 230 235 240  
 Glu Met Arg Glu Cys Leu Ala Arg Gln Met Thr Ser Pro Thr Leu Trp  
 245 250 255  
 Tyr Gln Ser Cys Tyr His Ile Glu Ser Glu Val Asp Glu Phe Leu Glu  
 260 265 270  
 Leu Gly Pro Gly Lys Val Leu Ala Gly Leu Asn Arg Ser Ile Gly Ile  
 275 280 285  
 Ser Lys Pro Ile Thr Ser Leu Gly Thr Phe Ala Gln Ile Glu Lys Phe  
 290 295 300  
 Leu Ser Glu Val  
 305

&lt;210&gt;311

&lt;211&gt;116

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;311

Leu Tyr His Phe Leu Asp Ser Ser Thr Arg Leu Tyr Phe Pro Ile Lys  
 1 5 10 15  
 Arg Ser Leu Ala Gln Ala His Leu Gly Ile Glu Asp Val Pro Thr Phe  
 20 25 30  
 Asp Cys Gln Ala Ala Cys Thr Gly Tyr Leu Tyr Gly Leu Ser Val Ala  
 35 40 45  
 Lys Ala Tyr Val Glu Ser Gly Thr Tyr Asn His Val Leu Leu Ile Ala  
 50 55 60  
 Ala Asp Lys Leu Ser Ser Phe Val Asp Tyr Thr Asp Arg Asn Thr Cys  
 65 70 75 80  
 Val Leu Phe Gly Asp Gly Gly Ala Ala Cys Val Ile Gly Glu Ser Arg  
 85 90 95  
 Pro Gly Ser Leu Glu Ile Asn Arg Leu Ser Leu Gly Ala Asp Gly Lys  
 100 105 110  
 Leu Gly Glu Tyr  
 115  
 <210>312

&lt;211&gt;105

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;312

```

Met Trp Phe Ser Val Asn Lys Asn Lys Lys Ala Ala Ile Trp Ala Thr
 1           5           10           15
Gly Ser Tyr Leu Pro Glu Lys Val Leu Ser Asn Ala Asp Leu Glu Lys
           20           25           30
Met Val Asp Thr Ser Asp Glu Trp Ile Val Thr Arg Thr Gly Ile Lys
           35           40           45
Glu Arg Arg Ile Ala Gly Pro Gln Glu Tyr Thr Ser Leu Met Gly Ala
           50           55           60
Ile Ala Ala Glu Lys Ala Ile Ala Asn Ala Gly Leu Ser Lys Asp Gln
           65           70           75           80
Ile Asp Cys Ile Ile Phe Ser Thr Ala Ala Pro Asp Tyr Ile Phe Pro
           85           90           95
Ser Ser Gly Val Leu Leu Lys His Ile
           100           105

```

&lt;210&gt;313

&lt;211&gt;230

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;313

```

Arg Lys Lys Leu Val Tyr Tyr Ser Glu Ser Leu Tyr Ser Asn Leu Asn
 1           5           10           15
Leu Gly Pro Arg Pro Glu Cys Lys Asn Lys Ile His Ile Thr Met Thr
           20           25           30
Arg Tyr Pro Asp Tyr Leu Ser Lys Leu Ile Phe Phe Leu Arg Lys Leu
           35           40           45
Pro Gly Ile Gly Phe Lys Thr Ala Glu Lys Leu Ala Phe Glu Leu Ile
           50           55           60
Ser Trp Asp Ser Glu Gln Leu Lys Ile Leu Gly Asn Ala Phe His Asn
           65           70           75           80
Val Ala Ser Glu Arg Ser His Cys Pro Leu Cys Phe Thr Leu Lys Glu
           85           90           95
Ser Lys Glu Ala Asp Cys His Phe Cys Arg Glu Glu Arg Asp Asn Gln
           100           105           110
Ser Leu Cys Ile Val Ala Ser Pro Lys Asp Val Phe Phe Leu Glu Arg
           115           120           125
Ser Lys Val Phe Lys Gly Arg Tyr His Val Leu Gly Ser Leu Leu Ser
           130           135           140
Pro Ile Thr Gly Lys His Ile Glu Asn Glu Arg Leu Ser Ile Leu Lys
           145           150           155           160
Ser Arg Ile Glu Thr Leu Cys Pro Lys Glu Ile Ile Leu Ala Ile Asp
           165           170           175
Ala Thr Leu Glu Gly Asp Ala Thr Ala Leu Phe Leu Lys Gln Glu Leu
           180           185           190
Gln His Phe Ser Val Asn Ile Ser Arg Leu Ala Leu Gly Leu Pro Ile
           195           200           205
Gly Leu Ser Phe Asp Tyr Val Asp Ser Gly Thr Leu Ala Arg Ala Phe
           210           215           220
Ser Gly Arg His Ser Tyr
           225           230

```

&lt;210&gt;314

&lt;211&gt;795

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;314

```

Gly Arg Leu Leu Gly Met Leu Ile Met Arg Asn Lys Val Ile Leu Gln
 1           5           10           15
Ile Ser Ile Leu Ala Leu Ile Gln Thr Pro Leu Thr Leu Phe Ser Thr
           20           25           30
Glu Lys Val Lys Glu Gly His Val Val Val Asp Ser Ile Thr Ile Ile
           35           40           45

```

Thr Glu Gly Glu Asn Ala Ser Asn Lys His Pro Leu Pro Lys Leu Lys  
 50 55 60  
 Thr Arg Ser Gly Ala Leu Phe Ser Gln Leu Asp Phe Asp Glu Asp Leu  
 65 70 75 80  
 Arg Ile Leu Ala Lys Glu Tyr Asp Ser Val Glu Pro Lys Val Glu Phe  
 85 90 95  
 Ser Glu Gly Lys Thr Asn Ile Ala Leu His Leu Ile Ala Lys Pro Ser  
 100 105 110  
 Ile Arg Asn Ile His Ile Ser Gly Asn Gln Val Val Pro Glu His Lys  
 115 120 125  
 Ile Leu Lys Thr Leu Gln Ile Tyr Arg Asn Asp Leu Phe Glu Arg Glu  
 130 135 140  
 Lys Phe Leu Lys Gly Leu Asp Asp Leu Arg Thr Tyr Tyr Leu Lys Arg  
 145 150 155 160  
 Gly Tyr Phe Ala Ser Ser Val Asp Tyr Ser Leu Glu His Asn Gln Glu  
 165 170 175  
 Lys Gly His Ile Asp Val Leu Ile Lys Ile Asn Glu Gly Pro Cys Gly  
 180 185 190  
 Lys Ile Lys Gln Leu Thr Phe Ser Gly Ile Ser Arg Ser Glu Lys Ser  
 195 200 205  
 Asp Ile Gln Glu Phe Ile Gln Thr Lys Gln His Ser Thr Thr Thr Ser  
 210 215 220  
 Trp Phe Thr Gly Ala Gly Leu Tyr His Pro Asp Ile Val Glu Gln Asp  
 225 230 235 240  
 Ser Leu Ala Ile Thr Asn Tyr Leu His Asn Asn Gly Tyr Ala Asp Ala  
 245 250 255  
 Ile Val Asn Ser His Tyr Asp Leu Asp Asp Lys Gly Asn Ile Leu Leu  
 260 265 270  
 Tyr Met Asp Ile Asp Arg Gly Ser Arg Tyr Thr Leu Gly His Val His  
 275 280 285  
 Ile Gln Gly Phe Glu Val Leu Pro Lys Arg Leu Ile Glu Lys Gln Ser  
 290 295 300  
 Gln Val Gly Pro Asn Asp Leu Tyr Cys Pro Asp Lys Ile Trp Asp Gly  
 305 310 315 320  
 Ala His Lys Ile Lys Gln Thr Tyr Ala Lys Tyr Gly Tyr Ile Asn Thr  
 325 330 335  
 Asn Val Asp Val Leu Phe Ile Pro His Ala Thr Arg Pro Ile Tyr Asp  
 340 345 350  
 Val Thr Tyr Glu Val Ser Glu Gly Ser Pro Tyr Lys Val Gly Leu Ile  
 355 360 365  
 Lys Ile Thr Gly Asn Thr His Thr Lys Ser Asp Val Ile Leu His Glu  
 370 375 380  
 Thr Ser Leu Phe Pro Gly Asp Thr Phe Asn Arg Leu Lys Leu Glu Asp  
 385 390 395 400  
 Thr Glu Gln Arg Leu Arg Asn Thr Gly Tyr Phe Gln Ser Val Ser Val  
 405 410 415  
 Tyr Thr Val Arg Ser Gln Leu Asp Pro Met Gly Asn Ala Asp Gln Tyr  
 420 425 430  
 Arg Asp Ile Phe Val Glu Val Lys Glu Thr Thr Thr Gly Asn Leu Gly  
 435 440 445  
 Leu Phe Leu Gly Phe Ser Ser Leu Asp Asn Leu Phe Gly Gly Ile Glu  
 450 455 460  
 Leu Ser Glu Ser Asn Phe Asp Leu Phe Gly Ala Arg Asn Ile Phe Ser  
 465 470 475 480  
 Lys Gly Phe Arg Cys Leu Arg Gly Gly Gly Glu His Leu Phe Leu Lys  
 485 490 495  
 Ala Asn Phe Gly Asp Lys Val Thr Asp Tyr Thr Leu Lys Trp Thr Lys  
 500 505 510  
 Pro His Phe Leu Asn Thr Pro Trp Ile Leu Gly Ile Glu Leu Asp Lys  
 515 520 525  
 Ser Ile Asn Arg Ala Leu Ser Lys Asp Tyr Ala Val Gln Thr Tyr Gly  
 530 535 540  
 Gly Asn Val Ser Thr Thr Tyr Ile Leu Asn Glu His Leu Lys Tyr Gly  
 545 550 555 560

Leu Phe Tyr Arg Gly Ser Gln Thr Ser Leu His Glu Lys Arg Lys Phe  
 565 570 575  
 Leu Leu Gly Pro Asn Ile Asp Ser Asn Lys Gly Phe Val Ser Ala Ala  
 580 585 590  
 Gly Val Asn Leu Asn Tyr Asp Ser Val Asp Ser Pro Arg Thr Pro Thr  
 595 600 605  
 Thr Gly Ile Arg Gly Gly Val Thr Phe Glu Val Ser Gly Leu Gly Gly  
 610 615 620  
 Thr Tyr His Phe Thr Lys Leu Ser Leu Asn Ser Ser Ile Tyr Arg Lys  
 625 630 635 640  
 Leu Thr Arg Lys Gly Ile Leu Lys Ile Lys Gly Glu Ala Gln Phe Ile  
 645 650 655  
 Lys Pro Tyr Ser Asn Thr Thr Ala Glu Gly Val Pro Val Ser Glu Arg  
 660 665 670  
 Phe Phe Leu Gly Gly Glu Thr Thr Val Arg Gly Tyr Lys Ser Phe Ile  
 675 680 685  
 Ile Gly Pro Lys Tyr Ser Ala Thr Glu Pro Gln Gly Gly Leu Ser Ser  
 690 695 700  
 Leu Leu Ile Ser Glu Glu Phe Gln Tyr Pro Leu Ile Arg Gln Pro Asn  
 705 710 715 720  
 Ile Ser Ala Phe Val Phe Leu Asp Ser Gly Phe Val Gly Leu Gln Glu  
 725 730 735  
 Tyr Lys Ile Ser Leu Lys Asp Leu Arg Ser Ser Ala Gly Phe Gly Leu  
 740 745 750  
 Arg Phe Asp Val Met Asn Asn Val Pro Val Met Leu Gly Phe Gly Trp  
 755 760 765  
 Pro Phe Arg Pro Thr Glu Thr Leu Asn Gly Glu Lys Ile Asp Val Ser  
 770 775 780  
 Gln Arg Phe Phe Phe Ala Leu Gly Gly Met Phe  
 785 790 795

&lt;210&gt;315

&lt;211&gt;158

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;315

Asp Gln Gln Ala Gln Leu Asn Ala Asn Leu Gly Tyr Val Asn Leu Lys  
 1 5 10 15  
 Arg Cys Leu Glu Glu Ser Asp Leu Gly Lys Lys Glu Thr Glu Glu Leu  
 20 25 30  
 Glu Ala Xaa Lys Gln Gln Phe Val Lys Asn Ala Glu Lys Ile Glu Glu  
 35 40 45  
 Glu Leu Thr Ser Ile Tyr Asn Lys Leu Gln Asp Glu Asp Tyr Met Glu  
 50 55 60  
 Ser Leu Ser Asp Ser Ala Ser Glu Glu Leu Arg Lys Lys Phe Glu Asp  
 65 70 75 80  
 Leu Ser Gly Glu Tyr Asn Ala Tyr Gln Ser Gln Tyr Tyr Gln Ser Ile  
 85 90 95  
 Asn Gln Ser Asn Val Lys Arg Ile Gln Lys Leu Ile Gln Glu Val Lys  
 100 105 110  
 Ile Ala Ala Glu Ser Val Arg Ser Lys Glu Lys Leu Glu Ala Ile Leu  
 115 120 125  
 Asn Glu Glu Ala Val Leu Ala Ile Ala Pro Gly Thr Asp Lys Thr Thr  
 130 135 140  
 Glu Ile Ile Ala Ile Leu Asn Glu Ser Phe Lys Lys Gln Asn  
 145 150 155

&lt;210&gt;316

&lt;211&gt;367

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;316

Ser Lys Phe Lys Glu Phe Ser Met Ser Glu Ala Pro Val Tyr Thr Leu  
 1 5 10 15  
 Lys Gln Leu Ala Glu Leu Leu Gln Val Glu Val Gln Gly Asn Ile Glu  
 20 25 30



Thr Pro Ile Ser Gly Val Glu Asp Ile Ser Gln Ala Gln Pro His His  
 35 40 45  
 Ile Ala Phe Leu Asp Asn Glu Lys Tyr Ser Ser Phe Leu Lys Asn Thr  
 50 55 60  
 Lys Ala Gly Ala Ile Ile Leu Ser Arg Ser Gln Ala Met Gln His Ala  
 65 70 75 80  
 His Leu Lys Lys Asn Phe Leu Ile Thr Asn Glu Ser Pro Ser Leu Thr  
 85 90 95  
 Phe Gln Lys Cys Ile Glu Leu Phe Ile Glu Pro Val Thr Ser Gly Phe  
 100 105 110  
 Pro Gly Ile His Pro Thr Ala Val Ile His Pro Thr Ala Arg Ile Glu  
 115 120 125  
 Lys Asn Val Thr Ile Glu Pro Tyr Val Val Ile Ser Gln His Ala His  
 130 135 140  
 Ile Gly Ser Asp Thr Tyr Ile Gly Ala Gly Ser Val Ile Gly Ala His  
 145 150 155 160  
 Ser Val Leu Gly Ala Asn Cys Leu Ile His Pro Lys Val Val Ile Arg  
 165 170 175  
 Glu Arg Val Leu Met Gly Asn Arg Val Val Val Gln Pro Gly Ala Val  
 180 185 190  
 Leu Gly Ser Cys Gly Phe Gly Tyr Ile Thr Asn Ala Phe Gly His His  
 195 200 205  
 Lys Pro Leu Lys His Leu Gly Tyr Val Ile Val Gly Asp Asp Val Glu  
 210 215 220  
 Ile Gly Ala Asn Thr Thr Ile Asp Arg Gly Arg Phe Lys Asn Thr Val  
 225 230 235 240  
 Ile His Glu Gly Thr Lys Ile Asp Asn Gln Val Gln Val Ala His His  
 245 250 255  
 Val Glu Ile Gly Lys His Ser Ile Ile Val Ala Gln Ala Gly Ile Ala  
 260 265 270  
 Gly Ser Thr Lys Ile Gly Glu His Val Ile Ile Gly Gly Gln Thr Gly  
 275 280 285  
 Ile Thr Gly His Ile Ser Ile Ala Asp His Val Ile Met Ile Ala Gln  
 290 295 300  
 Thr Gly Val Thr Lys Ser Ile Thr Ser Pro Gly Ile Tyr Gly Gly Ala  
 305 310 315 320  
 Pro Ala Arg Pro Tyr Gln Glu Thr His Arg Leu Ile Ala Lys Ile Arg  
 325 330 335  
 Asn Leu Pro Lys Thr Glu Glu Arg Leu Ser Lys Leu Glu Lys Gln Val  
 340 345 350  
 Arg Asp Leu Ser Thr Pro Ser Leu Ala Glu Ile Pro Ser Glu Ile  
 355 360 365

&lt;210&gt;317

&lt;211&gt;354

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;317

Arg Glu Gln Lys Gly Leu His His Met Asp Val Ser Arg Lys Ile Asn.  
 1 5 10 15  
 Arg His Thr Gln Phe Tyr Val Asp Ser Ile Asp Gly Val Ile Lys Asn  
 20 25 30  
 Phe Asp His Lys Pro Ser Glu Asp Lys Ser Arg Asp His Glu Glu Leu  
 35 40 45  
 Glu Glu Lys Leu Leu Thr Ile Thr Lys Arg Ile Val Ala Ser Ala Gln  
 50 55 60  
 Glu Phe Gln Asn Arg Lys Thr Asp Ser Lys Asn Tyr Tyr Leu Lys Lys  
 65 70 75 80  
 Thr Gln Trp Leu Pro Phe Lys Asn Glu Glu Leu Glu Gln Thr Lys Glu  
 85 90 95  
 Leu Phe Ala Met Leu Thr Ser Met Asp Lys Lys Ile Ala Gln Leu Phe  
 100 105 110  
 Phe Tyr Ser Pro Gly Cys Ser Ser Asp Trp Val Glu Phe Thr Glu Val  
 115 120 125  
 Ile Cys His Leu Asn Asp Ser Ile Gly Leu Gly Gly Val Leu Leu Cys

130 135 140  
 Cys Gly Leu Phe Glu Gln Gln Cys Glu His Val Val Thr Val Asn Lys  
 145 150 155 160  
 Lys Leu Asp Leu Pro Leu Leu Leu Gly Thr Thr Val Val Asn Ser Leu  
 165 170 175  
 Arg Tyr Tyr Leu Thr Tyr Arg Asn Ile Ser Leu Leu Asn Cys Gln Ser  
 180 185 190  
 Met Ser Glu Leu Gly Lys Glu Leu Gly Asp Val Leu Lys Gln His Gly  
 195 200 205  
 Val Ala Phe Thr Leu Ile Phe Lys Glu Ile Val Asp Ile Asp Leu Leu  
 210 215 220  
 Asn Tyr Val Lys Leu Ile Gln Gly Leu Lys Arg Ser Gly Asn Ile Gln  
 225 230 235 240  
 Ala Arg Ile Tyr Asp Asn Asp Val Pro Thr Leu Pro Ser Val Ser Ser  
 245 250 255  
 Ser Pro Ile Ala Leu Arg Tyr Ser Leu Ala Asn Thr Ile Arg Gly Leu  
 260 265 270  
 Ala Leu His Val Asp Phe Ser Ser Leu Lys Phe Ile Ser Pro Ser Ile  
 275 280 285  
 Leu Ser Asn Thr Glu His Thr Ala Lys Ala Leu Asn Ser Gly Gly Glu  
 290 295 300  
 Cys Phe Ile Phe Ser Asn Leu Asp Glu Phe Asn Leu Gly Met Lys Ile  
 305 310 315 320  
 Val Met Gln Leu Leu Arg Thr Gly Lys Ile Ser Pro Glu Ile Leu Asn  
 325 330 335  
 Lys Asn Ile Met Lys Ile Leu Met Ile Lys Arg Arg Val Arg Ser Leu  
 340 345 350  
 Tyr Ile

&lt;210&gt;318

&lt;211&gt;342

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;318

Met Asp Ser Ser Ala Pro Tyr Asn Ile Ala Ser Gln Gly Thr Glu Lys  
 1 5 10 15  
 Ser Thr Val Glu Arg Ile Leu Asp Leu Tyr Gly Pro Ala Ser Cys Ile  
 20 25 30  
 Lys Phe Leu Lys Gln Met Val Leu Ile Arg Glu Phe Glu Ala Arg Gly  
 35 40 45  
 Glu Glu Ala Tyr Leu Glu Gly Leu Val Gly Gly Phe Tyr His Ser Tyr  
 50 55 60  
 Ala Gly Gln Glu Ala Val Ala Thr Ala Ala Ile Ala Asn Thr Gly Leu  
 65 70 75 80  
 Asp Pro Trp Val Phe Ser Ser Tyr Arg Cys His Ala Leu Ala Ile Leu  
 85 90 95  
 Leu Asn Ile Pro Leu Gln Glu Ile Ala Ala Glu Leu Leu Gly Lys Glu  
 100 105 110  
 Thr Gly Cys Ala Leu Gly Arg Gly Gly Ser Met His Met Cys Gly Pro  
 115 120 125  
 Asn Phe Pro Gly Gly Phe Gly Ile Val Gly Gly Gln Ile Pro Leu Ala  
 130 135 140  
 Ala Gly Ala Ala Phe Thr Ile Lys Tyr Gln Glu Gln Lys Asn Arg Val  
 145 150 155 160  
 Ser Leu Cys Phe Ile Gly Asp Gly Ala Val Ala Gln Gly Val Phe His  
 165 170 175  
 Glu Thr Leu Asn Phe Val Ser Leu His Gln Leu Pro Leu Met Leu Ile  
 180 185 190  
 Ile Glu Asn Asn Gly Trp Ser Met Gly Thr Ser Leu Asn Arg Ala Val  
 195 200 205  
 Ala Lys Gln Pro Ile Ala Glu Ser Gln Gly Ser Ser Tyr Asp Ile Arg  
 210 215 220  
 Ala Val Thr Val Asn Gly Phe Asp Leu Phe Asn Ser Leu Leu Gly Phe  
 225 230 235 240

Arg Glu Ala Tyr Arg Tyr Met Val Asp Thr Glu Ser Pro Val Leu Val  
 245 250 255  
 Glu Cys Leu Cys Ser Arg Phe Arg Gly His Ser Ile Ser Asp Pro Asn  
 260 265 270  
 Leu Tyr Arg Ser Lys Glu Glu Met Gln Cys Leu Phe Lys Lys Asp Pro  
 275 280 285  
 Ile Val Leu Ala Lys Asp Trp Leu Ile Arg Leu Glu Val Leu Thr Glu  
 290 295 300  
 Glu Glu Phe Gln Asn Ile Arg Gln Glu Cys Lys Thr Ala Val Leu Glu  
 305 310 315 320  
 Ala Phe Ser Asn Ala Lys Leu Ser Ser Asp Pro Ser Val Thr Thr Leu  
 325 330 335  
 Glu Glu Gly Val Tyr Ala  
 340

&lt;210&gt;319

&lt;211&gt;161

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;319

Arg Lys Glu Ser Met Pro Lys His Lys Thr Leu Glu Ile Arg Glu Ala  
 1 5 10 15  
 Leu Arg Glu Ala Ile Asp Glu Glu Met Ser Arg Asp Pro Asn Val Cys  
 20 25 30  
 Ile Leu Gly Glu Glu Val Gly Asp Tyr Asn Gly Ala Tyr Lys Val Thr  
 35 40 45  
 Lys Gly Leu Leu Asp Lys Trp Gly Pro Lys Arg Val Ile Asp Ala Pro  
 50 55 60  
 Ile Ser Glu Ala Ala Phe Ser Gly Ile Gly Ile Gly Ala Ala Leu Ser  
 65 70 75 80  
 Gly Leu Arg Pro Ile Ile Glu Phe Met Ser Trp Asn Phe Ser Phe Val  
 85 90 95  
 Ala Leu Asp Gln Ile Ile Ser His Ala Ala Lys Met His Phe Met Thr  
 100 105 110  
 Gly Gly Lys Phe Ser Val Pro Ile Val Phe Arg Gly Pro Asn Gly Ala  
 115 120 125  
 Ala Ala Gln Val Ser Cys Gln His Ser His Cys Val Glu Ser Leu Tyr  
 130 135 140  
 Ala Asn Ile Pro Gly Leu Asn Tyr Tyr Ser Pro Phe Glu Pro Leu Arg  
 145 150 155 160  
 Arg

&lt;210&gt;320

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;320

Asn Ile Thr Leu Lys Gly Glu Val Pro Thr Glu Glu Tyr Leu Val Pro  
 1 5 10 15  
 Ile Gly Lys Ala His Arg Val Gln Glu Gly Asn Asp Leu Thr Ile Ile  
 20 25 30  
 Thr Tyr Ser Arg Met Val Ser Ile Thr Lys Glu Ala Cys Ser Leu Ala  
 35 40 45  
 Lys Lys Arg Trp Gly Leu Ser Ile Glu Ile Ile Asp Leu Arg Thr Ile  
 50 55 60  
 Lys Pro Leu Asp Ile Ser Thr Ile Leu Ser Ser Val Arg Lys Thr Ser  
 65 70 75 80  
 Arg Cys Ile Val Ile Glu Glu Gly His Tyr Phe Ala Gly Ile Ser Ser  
 85 90 95  
 Glu Ile Ile Ala Leu Ile Thr Glu His Val Phe Asp Ser Leu Asp Ala  
 100 105 110  
 Pro Pro Leu Arg Val Cys Gln Lys Glu Thr Pro Met Pro Tyr Ser Lys  
 115 120 125  
 Ile Leu Glu Gln Ala Thr Leu Pro Asn Val Asn Arg Ile Leu Asp Thr  
 130 135 140

Ile Glu Lys Val Met Arg

145 150

&lt;210&gt;321

&lt;211&gt;432

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;321

Gly Lys Phe Val Ile Ser Leu Leu Lys Met Pro Lys Leu Ser Pro Thr  
 1 5 10 15  
 Met Glu Val Gly Thr Ile Val Lys Trp His Lys Lys Ser Asn Asp Gln  
 20 25 30  
 Val Ser Phe Gly Asp Val Ile Val Glu Ile Ser Thr Asp Lys Ala Ile  
 35 40 45  
 Leu Glu His Thr Ala Asn Glu Asp Gly Trp Ile Arg Glu Ile Leu Arg  
 50 55 60  
 His Glu Gly Glu Lys Ile Val Ile Gly Thr Pro Ile Ala Val Leu Ser  
 65 70 75 80  
 Thr Glu Ala Asn Glu Pro Phe Asn Leu Glu Leu Leu Pro Lys Thr  
 85 90 95  
 Glu Pro Ser Asn Leu Glu Ala Ser Pro Lys Gly Ser Ser Glu Glu Val  
 100 105 110  
 Ser Pro Ala Thr Thr Pro Gln Ala Ala Ser Ala Thr Phe Thr Ala Val  
 115 120 125  
 Thr Phe Lys Pro Glu Pro Pro Leu Ser Ser Pro Leu Val Phe Lys His  
 130 135 140  
 Val Gly Thr Thr Asn Asn Leu Ser Pro Leu Ala Arg Gln Leu Ala Lys  
 145 150 155 160  
 Glu Lys Asn Ile Asp Val Ser Ser Ile Gln Gly Ser Gly Pro Gly Gly  
 165 170 175  
 Arg Ile Val Lys Lys Asp Leu Glu Lys Ala Pro Pro Lys Ser Ile Ala  
 180 185 190  
 Gly Phe Gly Tyr Pro Glu Ser Pro Glu Val Pro Pro Gly Ser Tyr His  
 195 200 205  
 Glu Glu Asn Leu Ser Pro Ile Arg Glu Val Ile Ala Ala Arg Leu Gln  
 210 215 220  
 Ala Ala Lys Ile Ser Ile Pro His Phe Tyr Val Arg Gln Gln Val Tyr  
 225 230 235 240  
 Ala Ser Pro Leu Leu Asn Leu Leu Lys Glu Leu Gln Ala Gln Gly Ile  
 245 250 255  
 Lys Leu Ser Ile Asn Asp Cys Ile Val Arg Ala Cys Ala Leu Ala Leu  
 260 265 270  
 Lys Glu Phe Pro Ser Ile Asn Ser Gly Phe Asn Ser Val Asp Asn Lys  
 275 280 285  
 Ile Val Arg Phe Asp Thr Ile Asp Ile Ser Ile Ala Val Ala Ile Pro  
 290 295 300  
 Asp Gly Ile Ile Thr Pro Ile Ile Arg Cys Ala Asp Arg Lys Asn Leu  
 305 310 315 320  
 Gly Met Ile Ser Ala Glu Ile Lys Ser Leu Ala Leu Lys Ala Arg Asn  
 325 330 335  
 Gln Ser Leu Gln Asp Thr Glu Tyr Lys Gly Gly Ser Phe Cys Val Ser  
 340 345 350  
 Asn Leu Gly Met Thr Gly Ile Thr Glu Phe Thr Ala Ile Val Asn Pro  
 355 360 365  
 Pro Gln Ala Ala Ile Leu Ala Val Gly Ser Val Thr Glu Gln Ala Leu  
 370 375 380  
 Val Leu Asp Gly Glu Ile Thr Ile Gly Ser Thr Cys Asn Leu Thr Leu  
 385 390 395 400  
 Ser Val Asp His Arg Val Ile Asp Gly Tyr Pro Ala Ala Met Phe Met  
 405 410 415  
 Lys Arg Leu Gln Lys Ile Leu Glu Ala Pro Ala Val Leu Leu Leu Asn  
 420 425 430

&lt;210&gt;322

&lt;211&gt;104

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;322

Ile Asp Glu Thr Ser Met Phe Phe Ser Phe Ala Ser Cys Leu Ala Asn  
 1 5 10 15  
 Gly Glu Arg Leu Phe Val Val Pro Thr Cys Leu Lys Thr Lys Gly Glu  
 20 25 30  
 Glu Arg Gly Gly Ser Gly Leu Lys Val Thr Ala Val Asn Val Ala Glu  
 35 40 45  
 Ala Ala Cys Gly Val Val Ala Gly Glu Thr Ser Ser Glu Glu Pro Phe  
 50 55 60  
 Gly Asp Ala Ser Arg Leu Glu Gly Ser Val Leu Gly Arg Ser Ser Ser  
 65 70 75 80  
 Arg Leu Lys Gly Ser Leu Ala Ser Val Glu Ser Thr Ala Ile Gly Val  
 85 90 95  
 Pro Ile Thr Ile Phe Ser Pro Ser  
 100

&lt;210&gt;323

&lt;211&gt;828

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;323

Asn Gly Cys Ile Val Glu Asp Phe Ser Ser Phe Asp Lys Asn Lys Val  
 1 5 10 15  
 Ser Val Asp Ser Met Lys Arg Ala Ile Leu Asp Arg Leu Tyr Leu Ser  
 20 25 30  
 Val Val Gln Ser Pro Glu Ser Ala Ser Pro Arg Asp Ile Phe Thr Ala  
 35 40 45  
 Val Ala Lys Thr Val Met Glu Trp Leu Ala Lys Gly Trp Leu Lys Thr  
 50 55 60  
 Gln Asn Gly Tyr Tyr Lys Asn Asp Val Lys Arg Val Tyr Tyr Leu Ser  
 65 70 75 80  
 Met Glu Phe Leu Leu Gly Arg Ser Leu Thr Ser Asn Leu Leu Asn Leu  
 85 90 95  
 Gly Ile Leu Asp Leu Val Arg Lys Ala Leu Lys Thr Leu Asn Tyr Asp  
 100 105 110  
 Phe Asp His Leu Val Glu Met Glu Ser Asp Ala Gly Leu Gly Asn Gly  
 115 120 125  
 Gly Leu Gly Arg Leu Ala Ala Cys Tyr Leu Asp Ser Met Ala Thr Leu  
 130 135 140  
 Ala Val Pro Ala Tyr Gly Tyr Gly Ile Arg Tyr Asp Tyr Gly Ile Phe  
 145 150 155 160  
 Asp Gln Arg Ile Val Asn Gly Tyr Gln Glu Glu Ala Pro Asp Glu Trp  
 165 170 175  
 Leu Arg Tyr Gly Asn Pro Trp Glu Ile Cys Arg Gly Glu Tyr Leu Tyr  
 180 185 190  
 Pro Val Arg Phe Tyr Gly Arg Val Ile His Tyr Thr Asp Ser Arg Gly  
 195 200 205  
 Lys Gln Val Ala Asp Leu Val Asp Thr Gln Glu Val Leu Ala Met Ala  
 210 215 220  
 Tyr Asp Ile Pro Ile Pro Gly Tyr Gly Asn Asp Thr Val Asn Ser Leu  
 225 230 235 240  
 Arg Leu Trp Gln Ala Gln Ser Pro Arg Gly Phe Glu Phe Ser Tyr Phe  
 245 250 255  
 Asn His Gly Asn Tyr Ile Gln Ala Ile Glu Asp Ile Ala Leu Ile Glu  
 260 265 270  
 Asn Ile Ser Arg Val Leu Tyr Pro Asn Asp Ser Ile Thr Glu Gly Gln  
 275 280 285  
 Glu Leu Arg Leu Lys Gln Glu Tyr Phe Leu Val Ser Ala Thr Ile Gln  
 290 295 300  
 Asp Ile Ile Arg Arg Tyr Thr Lys Thr His Ile Cys Leu Asp Asn Leu  
 305 310 315 320  
 Ala Asp Lys Val Val Val Gln Leu Asn Asp Thr His Pro Ala Leu Gly  
 325 330 335  
 Ile Ala Glu Met Met His Ile Leu Val Asp Arg Glu Glu Leu Pro Trp

340 345 350  
 Asp Lys Ala Trp Glu Met Thr Thr Val Ile Phe Asn Tyr Thr Asn His  
 355 360 365  
 Thr Ile Leu Pro Glu Ala Leu Glu Arg Trp Pro Leu Asp Leu Phe Ser  
 370 375 380  
 Lys Leu Leu Pro Arg His Leu Glu Ile Ile Tyr Glu Ile Asn Ser Arg  
 385 390 395 400  
 Trp Leu Glu Lys Val Gly Ser Arg Tyr Pro Lys Asn Asp Asp Lys Arg  
 405 410 415  
 Arg Ser Leu Ser Ile Val Glu Glu Gly Tyr Gln Lys Arg Ile Asn Met  
 420 425 430  
 Ala Asn Leu Ala Val Val Gly Ser Ala Lys Val Asn Gly Val Ser Ser  
 435 440 445  
 Phe His Ser Gln Leu Ile Lys Asp Thr Leu Phe Lys Glu Phe Tyr Glu  
 450 455 460  
 Phe Phe Pro Glu Lys Phe Ile Asn Val Thr Asn Gly Val Thr Pro Arg  
 465 470 475 480  
 Arg Trp Ile Ala Leu Cys Asn Pro Arg Leu Ser Lys Leu Leu Asn Glu  
 485 490 495  
 Thr Ile Gly Asp Arg Tyr Ile Ile Asp Leu Ser His Leu Ser Leu Ile  
 500 505 510  
 Arg Ser Phe Ala Glu Asp Ser Gly Phe Arg Asp His Trp Lys Gly Val  
 515 520 525  
 Lys Leu Lys Asn Lys Gln Asp Leu Thr Ser Arg Ile Tyr Asn Glu Val  
 530 535 540  
 Gly Glu Ile Val Asp Pro Asn Ser Leu Phe Asp Cys His Ile Lys Arg  
 545 550 555 560  
 Ile His Glu Tyr Lys Arg Gln Leu Met Asn Ile Leu Arg Val Ile Tyr  
 565 570 575  
 Val Tyr Asn Asp Leu Lys Glu Asn Pro Asn Gln Asp Val Val Pro Thr  
 580 585 590  
 Thr Val Ile Phe Ser Gly Lys Ala Ala Pro Gly Tyr Val Met Ala Lys  
 595 600 605  
 Leu Ile Ile Lys Leu Ile Asn Ser Val Ala Asp Val Val Asn Gln Asp  
 610 615 620  
 Ser Arg Val Asn Asp Lys Leu Lys Val Leu Phe Leu Pro Asn Tyr Arg  
 625 630 635 640  
 Val Ser Met Ala Glu His Ile Ile Pro Gly Thr Asp Leu Ser Glu Gln  
 645 650 655  
 Ile Ser Thr Ala Gly Met Glu Ala Ser Gly Thr Gly Asn Met Lys Phe  
 660 665 670  
 Ala Leu Asn Gly Ala Leu Thr Ile Gly Thr Met Asp Gly Ala Asn Ile  
 675 680 685  
 Glu Met Ala Glu His Ile Gly Lys Glu Asn Met Phe Ile Phe Gly Leu  
 690 695 700  
 Leu Glu Glu Gln Ile Val Gln Leu Arg Arg Glu Tyr Cys Pro Gln Thr  
 705 710 715 720  
 Ile Cys Asp Lys Asn Pro Lys Ile Arg Gln Val Leu Asp Leu Leu Glu  
 725 730 735  
 Gln Gly Phe Phe Asn Ser Asn Asp Lys Asp Leu Phe Lys Pro Ile Val  
 740 745 750  
 His Arg Leu Leu His Glu Gly Asp Pro Phe Phe Val Leu Ala Asp Leu  
 755 760 765  
 Glu Ser Tyr Ile Ala Ala His Glu Asn Val Asn Lys Leu Phe Lys Glu  
 770 775 780  
 Pro Asp Ser Trp Thr Lys Ile Ser Ile Tyr Asn Thr Ala Gly Met Gly  
 785 790 795 800  
 Phe Phe Ser Ser Asp Arg Ala Ile Gln Asp Tyr Ala Arg Asp Ile Trp  
 805 810 815  
 His Val Pro Thr Lys Ser Cys Ser Gly Glu Gly Asn  
 820 825

&lt;210&gt;324

&lt;211&gt;86

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;324

Val Phe Ser His Pro Leu Ala Asn His Ser Ile Thr Val Phe Ala Thr  
 1 5 10 15  
 Ala Val Lys Ile Ser Leu Gly Asp Ala Asp Ser Gly Asp Cys Thr Thr  
 20 25 30  
 Leu Lys Tyr Arg Arg Ser Lys Ile Ala Arg Phe Ile Glu Ser Thr Leu  
 35 40 45  
 Thr Leu Phe Leu Ser Lys Leu Glu Lys Ser Ser Thr Met Gln Pro Phe  
 50 55 60  
 Gln Ile Pro Ser Arg Thr Leu His Met Arg Asn Leu Lys Lys Lys Lys  
 65 70 75 80  
 Glu Leu Arg Leu Gly Lys  
 85

&lt;210&gt;325

&lt;211&gt;128

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;325

Phe Phe Thr Gln Glu Asn Asn Met Ala Thr Val Ala Gln Thr Pro Gln  
 1 5 10 15  
 Thr Thr Gln Pro Gln Pro Ser Val Ser His Lys Ala Thr His Arg Tyr  
 20 25 30  
 Cys Ser Trp Val Phe Phe Lys Pro Ile Leu Val Ser Leu Gly Leu Leu  
 35 40 45  
 Leu Ala Ser Leu Thr Thr Leu Gly Leu Val Ile Ala Ser Gly Val Thr  
 50 55 60  
 Leu Ser Leu Gly Ile Gly His Cys Ser Cys Tyr Thr Asp Ser Thr Ala  
 65 70 75 80  
 Gly Ile Ala Leu Val Leu Ala Phe Asn His Ile Arg Gln Phe Lys Gln  
 85 90 95  
 Ala Arg Thr Ala Glu Leu Asn Ser Met Lys Met Ile Ser Ala Pro Ala  
 100 105 110  
 Ala Ala Thr Val Gln Lys Gln Lys Leu Glu Asp Arg Tyr Ser Ser Lys  
 115 120 125

&lt;210&gt;326

&lt;211&gt;448

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;326

Phe Met Arg Ala Trp Glu Glu Phe Leu Leu Leu Gln Glu Lys Glu Ile  
 1 5 10 15  
 Gly Thr Asn Thr Val Asp Lys Trp Leu Arg Ser Leu Lys Val Leu Cys  
 20 25 30  
 Phe Asp Ala Cys Asn Leu Tyr Leu Glu Ala Gln Asp Ser Phe Gln Ile  
 35 40 45  
 Thr Trp Phe Glu Glu His Ile Arg His Lys Val Lys Ser Gly Leu Val  
 50 55 60  
 Asn Asn Asn Asn Lys Pro Ile Arg Val His Val Thr Ser Val Asp Lys  
 65 70 75 80  
 Ala Ala Pro Phe Tyr Lys Glu Lys Gln Met Gln Gln Glu Lys Thr Ala  
 85 90 95  
 Tyr Phe Thr Met His Tyr Gly Ser Val Asn Pro Glu Met Thr Phe Ser  
 100 105 110  
 Asn Phe Leu Val Thr Pro Glu Asn Asp Leu Pro Phe Arg Val Leu Gln  
 115 120 125  
 Glu Phe Thr Lys Ser Pro Asp Glu Asn Gly Gly Val Thr Phe Asn Pro  
 130 135 140  
 Ile Tyr Leu Phe Gly Pro Glu Gly Ser Gly Lys Thr His Leu Met Gln  
 145 150 155 160  
 Ser Ala Ile Ser Val Leu Arg Glu Ser Gly Gly Lys Ile Leu Tyr Val  
 165 170 175  
 Ser Ser Asp Leu Phe Thr Glu His Leu Val Ser Ala Ile Arg Ser Gly  
 180 185 190

Glu Met Gln Lys Phe Arg Ser Phe Tyr Arg Asn Ile Asp Ala Leu Phe  
 195 200 205  
 Ile Glu Asp Ile Glu Val Phe Ser Gly Lys Ser Ala Thr Gln Glu Glu  
 210 215 220  
 Phe Phe His Thr Phe Asn Ser Leu His Ser Glu Gly Lys Leu Ile Val  
 225 230 235 240  
 Val Ser Ser Ser Tyr Ala Pro Val Asp Leu Val Ala Val Glu Asp Arg  
 245 250 255  
 Leu Ile Ser Arg Phe Glu Trp Gly Val Ala Ile Pro Ile His Pro Leu  
 260 265 270  
 Val Gln Glu Gly Leu Arg Ser Phe Leu Met Arg Gln Val Glu Arg Leu  
 275 280 285  
 Ser Ile Arg Ile Gln Glu Thr Ala Leu Asp Phe Leu Ile Tyr Ala Leu  
 290 295 300  
 Ser Ser Asn Val Lys Thr Leu Leu His Ala Leu Asn Leu Leu Ala Lys  
 305 310 315 320  
 Arg Val Met Tyr Lys Lys Leu Ser His Gln Leu Leu Tyr Glu Asp Asp  
 325 330 335  
 Val Lys Thr Leu Leu Lys Asp Val Leu Glu Ala Ala Gly Ser Val Arg  
 340 345 350  
 Leu Thr Pro Leu Lys Ile Ile Arg Asn Val Ala Gln Tyr Tyr Gly Val  
 355 360 365  
 Ser Gln Glu Ser Ile Leu Gly Arg Ser Gln Ser Arg Glu Tyr Val Leu  
 370 375 380  
 Pro Arg Gln Val Ala Met Tyr Phe Cys Arg Gln Lys Leu Ser Leu Ser  
 385 390 395 400  
 Tyr Val Arg Ile Gly Asp Val Phe Ser Arg Asp His Ser Thr Val Ile  
 405 410 415  
 Ser Ser Ile Arg Leu Ile Glu Gln Lys Ile Glu Glu Asn Ser His Asp  
 420 425 430  
 Ile His Met Ala Ile Gln Asp Ile Ser Xaa Glu Phe Lys Phe Leu Ala  
 435 440 445

&lt;210&gt;327

&lt;211&gt;808

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;327

Tyr Phe Asp Leu Leu Ser Leu Ile Phe Arg Val Tyr Gln Met Asn Lys  
 1 5 10 15  
 Arg Thr Leu Leu Phe Val Ser Leu Ile Gly Ile Ala Phe Val Gly Cys  
 20 25 30  
 Gln Ile Phe Phe Gly Tyr Asn Glu Phe Arg Ser Cys Lys Asn Leu Ala  
 35 40 45  
 Glu Lys Gln Arg Lys Ile Ser Glu Gln Thr Leu Ala Ala Val Glu Ser  
 50 55 60  
 Val Gly Leu Ser Val Ala Ser Trp Asp Thr Asp Val Asn Gly Glu Glu  
 65 70 75 80  
 His Lys Asn Asn Tyr Ala Val Arg Val Gly Asp Lys Leu Phe Leu Leu  
 85 90 95  
 His Asn Gly Glu Ala Ala Gln Ser Val Tyr Ser Ser Gly Glu Ser Trp  
 100 105 110  
 Ser Phe Val Asp His Lys Cys Gly Phe Asp Asn Ile His Leu Ala Leu  
 115 120 125  
 Tyr Arg Gln Gln Gly Ser Ser Phe Asn Pro Thr Asn Thr Gly Lys Val  
 130 135 140  
 Phe Leu Pro Thr Asn His Glu Gly Leu Pro Val Leu Val Val Glu Phe  
 145 150 155 160  
 Arg Asn Asn Lys Glu Pro Leu Val Phe Leu Gly Glu Tyr Ala Gln Gly  
 165 170 175  
 Arg Ile Ser Asn Lys Asp Ser Thr Ile Phe Gly Thr Ala Leu Val Phe  
 180 185 190  
 Trp Arg Ser Gly Ser Asp Tyr Ile Pro Leu Gly Leu Tyr Asp Ser Arg  
 195 200 205  
 Glu Glu Lys Leu Val Ser Leu Asp Leu Pro Ile Thr Arg Ala Val Ile



553

725 730 735  
 Lys Gly Pro Val Thr Asp Gln Gln Lys Gln Gln Gln Val Met Gly Asn  
 740 745 750  
 Met Met Ala Ile Leu Phe Thr Ala Met Phe Tyr Asn Phe Pro Ser Gly  
 755 760 765  
 Leu Asn Ile Tyr Trp Leu Ser Ser Met Ile Leu Gly Val Val Gln Gln  
 770 775 780  
 Trp Ile Thr Asn Lys Ile Leu Asp Ser Lys His Leu Lys Asn Glu Val  
 785 790 795 800  
 Val Leu Asn Asn Lys Lys His Arg  
 805

&lt;210&gt;328

&lt;211&gt;203

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;328

Phe Phe Met Asp Gly Val Phe Thr Tyr Asn Ile Leu Lys Arg Ser Phe  
 1 5 10 15  
 Lys Tyr Gly Thr Glu Ala Cys Arg Val Met Glu Ala Phe Phe Gly Phe  
 20 25 30  
 Leu Leu Trp Ala Ala Ile Phe Ser Trp Ile Tyr Lys Lys Lys Ile Ser  
 35 40 45  
 Lys Leu Thr Phe Leu Phe Leu Thr Asp Leu Cys Gly Ser Val Phe Gly  
 50 55 60  
 Ile Ala Ala Phe Phe Ile Arg Leu Gly Asn Phe Trp Asn Gln Glu Ile  
 65 70 75 80  
 Val Gly Thr Pro Thr Ser Leu Pro Trp Gly Val Val Phe Ser Asp Pro  
 85 90 95  
 Met Gln Gly Val Gln Gly Val Pro Val His Pro Val Gln Leu Tyr Glu  
 100 105 110  
 Gly Ile Ser Tyr Leu Val Val Ser Gly Ile Leu Tyr Phe Leu Ser Tyr  
 115 120 125  
 Lys Arg Tyr Leu His Leu Gly Lys Gly Tyr Val Thr Ser Ile Ala Cys  
 130 135 140  
 Ile Ser Val Ala Phe Ile Arg Phe Phe Ala Glu Tyr Val Lys Ser His  
 145 150 155 160  
 Gln Gly Lys Val Leu Ala Glu Asp Cys Leu Leu Thr Ile Gly Gln Ile  
 165 170 175  
 Leu Ser Ile Pro Leu Phe Leu Phe Gly Val Ala Leu Leu Ile Ile Cys  
 180 185 190  
 Ser Leu Lys Ala Arg Arg His Arg Ser His Ile  
 195 200

&lt;210&gt;329

&lt;211&gt;153

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;329

Cys Thr Met Ala Arg Asn Ile Lys Tyr Phe Leu Ile Leu Phe Pro Gly  
 1 5 10 15  
 Ile Leu Trp Ile Ser Ala Gly Met Lys Leu Leu Lys Ala Thr Ala  
 20 25 30  
 Ile Ala Leu Asp Pro Leu Ser Ser Phe Phe Thr Tyr Cys Leu Leu Ser  
 35 40 45  
 Met Val Ser Trp Gly Leu Ala Ser Leu Lys His Arg Tyr Leu Leu Ser  
 50 55 60  
 Lys Thr Ile Arg Lys Gln Leu Ser Leu Ser Ser Glu Phe Phe Ser Gln  
 65 70 75 80  
 Lys Ile Thr Trp Ile Ala Tyr Ile Lys Gln Thr Phe Ile Ser Arg Arg  
 85 90 95  
 Phe Leu Ile Met Val Ile Met Ile Ala Phe Ser Leu Val Leu Arg Arg  
 100 105 110  
 Tyr Ile Ser Asn Pro Gln Ala Leu Phe Val Ile Arg Ala Thr Val Gly  
 115 120 125  
 Tyr Ala Leu Ile Lys Thr Ala Ile Ala Tyr Phe Ser Lys Leu Gln Asn

130 135 140  
 Ala Leu Met Glu Asn Pro Glu Gly Asn  
 145 150  
 <210>330  
 <211>122  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>330  
 Met Glu Ile Ile His Ile Gly Thr Asp Ile Ile Glu Ile Ser Arg Ile  
 1 5 10 15  
 Arg Glu Ala Ile Ala Thr His Gly Asn Arg Leu Leu Asn Arg Ile Phe  
 20 25 30  
 Thr Glu Ala Glu Gln Lys Tyr Cys Leu Glu Lys Thr Asp Pro Ile Pro  
 35 40 45  
 Ser Phe Ala Gly Arg Phe Ala Gly Lys Glu Ala Val Ala Lys Ala Leu  
 50 55 60  
 Gly Thr Gly Ile Gly Ser Val Val Ala Trp Lys Asp Ile Glu Val Phe  
 65 70 75 80  
 Lys Val Ser His Gly Pro Glu Val Leu Leu Pro Ser His Val Tyr Ala  
 85 90 95  
 Lys Ile Gly Ile Ser Lys Val Ile Leu Ser Ile Ser His Cys Lys Glu  
 100 105 110  
 Tyr Ala Thr Ala Thr Ala Ile Ala Leu Ala  
 115 120  
 <210>331  
 <211>311  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>331  
 Met Ile His Ser Arg Leu Ile Ile Ile Gly Ser Gly Pro Ser Gly Tyr  
 1 5 10 15  
 Thr Ala Ala Ile Tyr Ala Ser Arg Ala Leu Leu His Pro Leu Leu Phe  
 20 25 30  
 Glu Gly Phe Phe Ser Gly Ile Ser Gly Gly Gln Leu Met Thr Thr Thr  
 35 40 45  
 Glu Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu Gly Pro Lys  
 50 55 60  
 Leu Met Asn Asn Met Lys Glu Gln Ala Val Arg Phe Gly Thr Lys Thr  
 65 70 75 80  
 Leu Ala Gln Asp Ile Ile Ser Val Asp Phe Ser Val Arg Pro Phe Ile  
 85 90 95  
 Leu Lys Ser Lys Glu Glu Thr Tyr Ser Cys Asp Ala Cys Ile Ile Ala  
 100 105 110  
 Thr Gly Ala Ser Ala Lys Arg Leu Glu Ile Pro Gly Ala Gly Asn Asp  
 115 120 125  
 Glu Phe Trp Gln Lys Gly Val Thr Ala Cys Ala Val Cys Asp Gly Ala  
 130 135 140  
 Ser Pro Ile Phe Lys Asn Lys Asp Leu Tyr Val Ile Gly Gly Gly Asp  
 145 150 155 160  
 Ser Ala Leu Glu Glu Ala Leu Tyr Leu Thr Arg Tyr Gly Ser His Val  
 165 170 175  
 Tyr Val Val His Arg Arg Asp Lys Leu Arg Ala Ser Lys Ala Met Glu  
 180 185 190  
 Ala Arg Ala Gln Asn Asn Glu Lys Ile Thr Phe Leu Trp Asn Ser Glu  
 195 200 205  
 Ile Val Lys Ile Ser Gly Asp Ser Ile Val Arg Ser Val Asp Ile Lys  
 210 215 220  
 Asn Val Gln Thr Gln Glu Ile Thr Thr Arg Glu Ala Ala Gly Val Phe  
 225 230 235 240  
 Phe Ala Ile Gly His Lys Pro Asn Thr Asp Phe Leu Gly Gly Gln Leu  
 245 250 255  
 Thr Leu Asp Glu Ser Gly Tyr Ile Val Thr Glu Lys Gly Thr Ser Lys  
 260 265 270  
 Thr Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Tyr

275 280 285  
 Tyr Arg Gln Ala Val Thr Ser Ala Gly Gly Gly Cys Ile Ala Ala Leu  
 290 295 300  
 Asp Ala Glu Arg Phe Leu Gly  
 305 310  
 <210>332  
 <211>580  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>332  
 Met Pro Lys Gln Ala Glu Tyr Thr Trp Gly Ser Lys Lys Ile Leu Asp  
 1 5 10 15  
 Asn Ile Glu Cys Leu Thr Glu Asp Val Ala Glu Phe Lys Asp Leu Leu  
 20 25 30  
 Tyr Thr Ala His Arg Ile Thr Ser Ser Glu Glu Glu Ser Asp Asn Glu  
 35 40 45  
 Ile Gln Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Asn Lys  
 50 55 60  
 Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro  
 65 70 75 80  
 Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Val Leu Gly Ala Glu  
 85 90 95  
 Val Glu Val Tyr Leu Asp Gln Ala Glu Asp Glu Glu Gly Lys Val Val  
 100 105 110  
 Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu  
 115 120 125  
 Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys  
 130 135 140  
 Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro  
 145 150 155 160  
 Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val  
 165 170 175  
 Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Glu Arg Arg  
 180 185 190  
 Asn Ile Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser  
 195 200 205  
 Lys Lys Ala Glu Leu Ile Glu Gln Ile Ser Ile Gly Glu Tyr Arg Lys  
 210 215 220  
 Gly Val Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp  
 225 230 235 240  
 Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile  
 245 250 255  
 Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile  
 260 265 270  
 Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys  
 275 280 285  
 Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro  
 290 295 300  
 Gly Lys Arg Val Leu Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala  
 305 310 315 320  
 Phe Ile Glu Ile Glu Gly Ile Glu Gly Leu Ile His Ile Ser Glu  
 325 330 335  
 Met Ser Trp Val Lys Asn Ile Val Asp Pro Ser Glu Val Val Asn Lys  
 340 345 350  
 Gly Asp Glu Val Glu Ala Ile Val Leu Ser Ile Gln Lys Asp Glu Gly  
 355 360 365  
 Lys Ile Ser Leu Gly Leu Lys Gln Thr Glu Arg Asn Pro Trp Asp Asn  
 370 375 380  
 Ile Glu Glu Lys Tyr Pro Ile Gly Leu His Val Asn Ala Glu Ile Lys  
 385 390 395 400  
 Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu  
 405 410 415  
 Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His  
 420 425 430

Pro Ser Glu Leu Phe Lys Lys Gly Asn Ser Val Glu Ala Val Ile Leu  
 435 440 445  
 Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu  
 450 455 460  
 Ser Ser Asn Pro Trp Asn Glu Ile Glu Ala Met Phe Pro Ala Gly Thr  
 465 470 475 480  
 Val Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val  
 485 490 495  
 Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser  
 500 505 510  
 Asp Lys Pro Phe Ala Lys Ile Glu Asp Ile Ile Ser Ile Gly Glu Asn  
 515 520 525  
 Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser  
 530 535 540  
 Leu Ser Val Lys Glu Tyr Leu Ala Asp Asn Ala Tyr Asp Gln Asp Ser  
 545 550 555 560  
 Arg Thr Glu Leu Asp Phe Lys Asp Ser Gln Gly Pro Lys Glu Arg Lys  
 565 570 575  
 Lys Lys Gly Lys  
 580

&lt;210&gt;333

&lt;211&gt;225

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;333

Met Asn Lys Asn Leu Val Ala Ile Phe Asp Tyr Met Glu Lys Glu Lys  
 1 5 10 15  
 Gly Ile Gln Arg Ser Thr Ile Ile Gly Ala Ile Glu Ser Ala Leu Lys  
 20 25 30  
 Ile Ala Ala Lys Lys Thr Leu Arg Asp Asp Ala Asn Ile Ser Val Asn  
 35 40 45  
 Ile Asn Ser Arg Thr Gly Asp Ile Glu Val Phe Cys Glu Lys Glu Ile  
 50 55 60  
 Val Glu Ile Cys Gln Asn Pro Ser Lys Glu Ile Pro Leu Asp Lys Ala  
 65 70 75 80  
 Arg Glu Tyr Asp Pro Asp Cys Gln Ile Gly Gln Tyr Met Asp Val Pro  
 85 90 95  
 Phe Val Ser Asp Asn Phe Gly Arg Ile Ala Ala His Ala Arg Gln  
 100 105 110  
 Ile Ile Gly Gln Lys Leu Arg His Ala Glu Arg Asp Val Ile Tyr Glu  
 115 120 125  
 Glu Tyr Arg His Arg Val Asn Glu Thr Leu Ser Gly Val Val Lys Arg  
 130 135 140  
 Phe Ala Lys Gly Ser Asn Leu Ile Ile Asp Leu Gly Lys Val Glu Ala  
 145 150 155 160  
 Ile Leu Pro Thr Arg Phe Tyr Pro Lys Thr Glu Lys His Lys Ile Gly  
 165 170 175  
 Asp Lys Ile Tyr Ala Leu Leu Tyr Glu Val Gln Glu Ser Glu Asn Gly  
 180 185 190  
 Gly Ala Glu Val Ile Leu Ser Arg Ser His Ala Glu Phe Val Lys Gln  
 195 200 205  
 Leu Phe Ile Ser Arg Ser Pro Arg Thr Arg Arg Arg Phe Cys Gly Asp  
 210 215 220

Cys

225

&lt;210&gt;334

&lt;211&gt;174

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;334

Lys Ile Ser Phe Arg Glu Leu Asn Asp Glu Lys Ile Asp Ile Val Asn  
 1 5 10 15  
 Tyr Ser Pro Val Ser Thr Glu Leu Leu Gln Asn Leu Leu Tyr Pro Ile  
 20 25 30

Glu Ile Gln Lys Ile Ala Ile Leu Glu Asp Asp Lys Val Ile Ala Ile  
           35                  40                  45  
 Val Val Asn Asp Ala Asp Tyr Ala Thr Val Ile Gly Lys Arg Gly Ile  
           50                  55                  60  
 Asn Ala Arg Leu Ile Ser His Ile Leu Asp Tyr Glu Leu Glu Val Gln  
           65                  70                  75                  80  
 Arg Met Ser Glu Tyr Asn Lys Leu Leu Glu Ile Gln Arg Leu Gln Leu  
                   85                  90                  95  
 Ala Glu Phe Asp Ser Pro His Leu Asp Gln Pro Leu Glu Met Glu Gly  
                   100                  105                  110  
 Ile Ser Lys Leu Val Ile Gln Asn Leu Glu His Ala Gly Tyr Asp Thr  
           115                  120                  125  
 Ile Arg Arg Val Leu Leu Ala Ser Ala Asn Asp Leu Ala Ser Val Pro  
           130                  135                  140  
 Gly Ile Ser Leu Glu Leu Ala Tyr Lys Ile Leu Glu Gln Val Ser Lys  
           145                  150                  155                  160  
 Tyr Gly Glu Ser Lys Val Asp Glu Lys Pro Glu Ile Glu Asp  
                   165                  170

&lt;210&gt;335

&lt;211&gt;761

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;335

Leu Leu Ile Arg Ser Leu Ser Lys Ser Ala Asn Met Glu Lys Val Lys  
   1                  5                  10                  15  
 Leu Thr Lys Asn Leu Lys Leu Lys Ile Lys Asn Ala Gln Leu Thr Lys  
           20                  25                  30  
 Ala Ala Gly Leu Asp Lys Leu Lys Gln Lys Leu Ala Gln Ala Gly Ser  
           35                  40                  45  
 Ser Glu Ala Lys Ser Ser Ser Glu Lys Pro Ser Ala Lys Glu Lys Ser  
           50                  55                  60  
 Val Lys Val Ala Leu Ala Ala Thr Ser Thr Pro Thr Ala Ser Ala Glu  
           65                  70                  75                  80  
 Gln Ala Ser Pro Glu Ser Thr Ser Arg Arg Ile Arg Ala Lys Asn Arg  
                   85                  90                  95  
 Ser Ser Phe Ser Ser Ser Glu Glu Glu Ser Ser Ala His Ile Pro Val  
           100                  105                  110  
 Asp Thr Ser Glu Pro Ala Pro Val Ser Ile Ala Asp Pro Glu Pro Glu  
           115                  120                  125  
 Leu Glu Val Val Asp Glu Val Cys Asp Glu Ser Pro Glu Val His Pro  
           130                  135                  140  
 Val Ala Glu Val Leu Pro Glu Gln Pro Val Leu Pro Glu Thr Pro Pro  
           145                  150                  155                  160  
 Gln Glu Lys Glu Leu Glu Pro Lys Pro Val Lys Pro Ala Glu Pro Lys  
                   165                  170                  175  
 Ser Val Val Met Ile Lys Ser Lys Phe Gly Pro Thr Gly Lys His Ile  
                   180                  185                  190  
 Asn His Leu Leu Ala Lys Thr Phe Lys Ala Pro Ala Lys Glu Glu Lys  
           195                  200                  205  
 Val Val Ala Gly Ser Lys Ser Thr Lys Pro Val Ala Ser Asp Lys Thr  
           210                  215                  220  
 Gly Lys Pro Gly Thr Ser Glu Gly Gly Glu Gln Asn Asn Arg Glu Lys  
           225                  230                  235                  240  
 Gln Phe Asn Pro Ala Asn Arg Ser Pro Ala Ser Gly Pro Lys Arg Asp  
                   245                  250                  255  
 Ala Gly Lys Lys Asn Leu Thr Asp Phe Arg Asp Arg Ser Lys Lys Ser  
           260                  265                  270  
 Asp Glu Ser Leu Lys Ala Phe Thr Gly Arg Asp Arg Tyr Gly Leu Asn  
           275                  280                  285  
 Glu Gly Gly Glu Glu Asp Arg Trp Arg Lys Lys Arg Val Tyr Lys Pro  
           290                  295                  300  
 Lys Lys His Tyr Asp Glu Ala Ser Ile Gln Arg Pro Thr His Ile Lys  
           305                  310                  315                  320  
 Ile Ser Leu Pro Ile Thr Val Lys Asp Leu Ala Thr Glu Met Lys Leu

325 330 335  
 Lys Ala Ser Glu Val Ile Gln Lys Leu Phe Ile His Gly Met Thr Tyr  
 340 345 350  
 Val Val Asn Asp Ile Leu Asp Ser Glu Thr Ala Val Gln Phe Ile Gly  
 355 360 365  
 Leu Glu Phe Gly Cys Thr Ile Asp Ile Asp Tyr Ser Glu Gln Asp Lys  
 370 375 380  
 Leu Cys Leu Ser Asn Asp Thr Val Arg Asp Glu Ile Gln Ser Thr Asp  
 385 390 400  
 Pro Ser Lys Leu Val Ile Arg Ser Pro Ile Val Ala Phe Met Gly His  
 405 410 415  
 Val Asp His Gly Lys Thr Thr Leu Ile Asp Ser Leu Arg Lys Ser Asn  
 420 425 430  
 Val Ala Ala Thr Glu Ala Gly Ala Ile Thr Gln His Met Gly Ala Phe  
 435 440 445  
 Cys Cys Ser Thr Pro Val Gly Asp Ile Thr Ile Leu Asp Thr Pro Gly  
 450 455 460  
 His Glu Ala Phe Ser Ala Met Arg Ala Arg Gly Ala Glu Val Cys Asp  
 465 470 475 480  
 Ile Val Val Leu Val Val Ala Gly Asp Glu Gly Ile Lys Xaa Gln Thr  
 485 490 495  
 Leu Glu Ala Ile Glu His Ala Lys Ala Ala Asp Ile Ala Ile Val Val  
 500 505 510  
 Ala Ile Asn Lys Cys Asp Lys Pro Asn Phe Asn Ser Glu Thr Ile Tyr  
 515 520 525  
 Arg Gln Leu Ser Glu Ile Asn Leu Leu Pro Glu Ala Trp Gly Gly Ser  
 530 535 540  
 Thr Val Thr Val Asn Thr Ser Ala Lys Thr Gly Glu Gly Leu Ser Glu  
 545 550 555 560  
 Leu Leu Glu Met Leu Ala Leu Gln Ala Glu Val Leu Glu Leu Lys Ala  
 565 570 575  
 Asp Pro Ser Ala Arg Ala Arg Gly Leu Val Ile Glu Ser Glu Leu His  
 580 585 590  
 Lys Gly Leu Gly Pro Val Ala Thr Val Leu Ile Gln Asn Gly Ser Leu  
 595 600 605  
 Lys Leu Gly Glu Ala Leu Val Phe Asn Asp Cys Tyr Gly Lys Val Lys  
 610 615 620  
 Thr Met His Asn Glu His Asn Glu Leu Met Lys Glu Ala Gly Pro Ser  
 625 630 635 640  
 Ile Pro Val Leu Ile Thr Gly Leu Ser Asp Ile Pro Lys Ala Gly Asp  
 645 650 655  
 Pro Phe Phe Val Val Lys Asn Glu Lys Thr Ala Arg Asp Ile Ile Glu  
 660 665 670  
 Ala Arg Ser Ala Gly Gln Gln Arg Phe Ala Leu Gln Gln Lys Lys Arg  
 675 680 685  
 Pro Asn Phe Asp Ser Met Leu Gln Asn Lys Lys Thr Leu Lys Leu Met  
 690 695 700  
 Ile Lys Ala Asp Val Gln Gly Ser Ile Glu Ala Leu Val Ser Ser Ile  
 705 710 715 720  
 Ser Lys Ile Lys Ser Glu Lys Val Asp Val Glu Ile Leu Thr Asn Ser  
 725 730 735  
 Val Gly Glu Ile Ser Glu Ser Asp Ile Arg Leu Leu Pro Pro Leu Lys  
 740 745 750  
 Gln Phe Ser Ser Val Ser Ile Gln Glu  
 755 760  
 <210>336  
 <211>170  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>336  
 Asn Phe Asn Lys Gln Cys Arg Arg Asn Phe Arg Ile Arg His Ser Phe  
 1 5 10 15  
 Thr Ala Ala Ser Lys Ala Val Leu Ile Gly Phe His Thr Gly Ile Glu  
 20 25 30

Ser His Ala Glu Pro Leu Ile Lys Ser Leu Gly Val Arg Val Glu Leu  
 35 40 45  
 Phe Thr Val Ile Tyr His Ala Ile Asp Ala Ile Lys Glu Ile Met Thr  
 50 55 60  
 Ser Leu Leu Asp Pro Ile Ala Glu Glu Lys Asp Glu Gly Ser Ala Glu  
 65 70 75 80  
 Ile Lys Glu Ile Phe Arg Ser Ser Gln Val Gly Ser Ile Tyr Gly Cys  
 85 90 95  
 Ile Val Thr Glu Gly Ile Met Thr Arg Asn His Lys Val Arg Val Leu  
 100 105 110  
 Arg Asn Lys Glu Ile Leu Trp Lys Gly Thr Leu Ser Ser Leu Lys Arg  
 115 120 125  
 Val Lys Glu Asp Val Lys Glu Val Arg Lys Gly Leu Glu Cys Gly Ile  
 130 135 140  
 Leu Leu Glu Gly Tyr Gln Gln Ala Gln Ile Gly Asp Val Leu Gln Cys  
 145 150 155 160  
 Tyr Glu Val Ile Tyr His Pro Gln Lys Leu  
 165 170

&lt;210&gt;337

&lt;211&gt;141

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;337

Val Met Ser Tyr Asn Val Met Lys Leu Ser Ile Ile His Lys Asn Tyr  
 1 5 10 15  
 Asn Leu Lys Tyr Cys Met Thr Glu Asn Arg Arg Ile Lys Arg Val Asn  
 20 25 30  
 Ala Leu Leu Gln Glu Ala Ile Ala Lys Val Ile Leu Lys Asp Val Lys  
 35 40 45  
 His Pro Lys Ile Ser Asn Leu Trp Ile Thr Val Thr Arg Val Ser Leu  
 50 55 60  
 Ser Lys Asp Leu His Ser Ala Arg Val Tyr Val Ser Val Met Pro His  
 65 70 75 80  
 Glu Asn Thr Lys Glu Glu Ala Leu Glu Ala Leu Lys Val Ser Ala Gly  
 85 90 95  
 Phe Ile Ala His Arg Ala Ser Lys Asn Val Val Leu Lys Tyr Phe Pro  
 100 105 110  
 Glu Leu His Phe Tyr Leu Asp Asp Ile Phe Ser Pro Gln Asp Tyr Ile  
 115 120 125  
 Glu Asn Leu Leu Trp Gln Ile Gln Glu Lys Glu Lys Ser  
 130 135 140

&lt;210&gt;338

&lt;211&gt;243

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;338

Leu Asn Thr Ile Lys Asp Met Thr Met Asp Leu Ala Val Glu Leu Lys  
 1 5 10 15  
 Glu Gly Ile Leu Leu Val Asp Lys Pro Gln Gly Arg Thr Ser Phe Ser  
 20 25 30  
 Leu Ile Arg Ala Leu Thr Lys Leu Ile Gly Val Lys Lys Ile Gly His  
 35 40 45  
 Ala Gly Thr Leu Asp Pro Phe Ala Thr Gly Val Met Val Met Leu Ile  
 50 55 60  
 Gly Arg Lys Phe Thr Arg Leu Ser Asp Ile Leu Leu Phe Glu Asp Lys  
 65 70 75 80  
 Glu Tyr Glu Ala Ile Ala His Leu Gly Thr Thr Asp Ser Tyr Asp  
 85 90 95  
 Cys Asp Gly Lys Val Val Gly Arg Ser Lys Lys Ile Pro Ser Leu Glu  
 100 105 110  
 Glu Val Leu Ser Ala Ala Glu Tyr Phe Gln Gly Glu Ile Gln Gln Leu  
 115 120 125  
 Pro Pro Met Phe Ser Ala Lys Lys Val Gln Gly Lys Lys Leu Tyr Glu  
 130 135 140



Tyr Ala Arg Lys Gly Leu Ser Ile Glu Arg His His Ser Thr Val Gln  
 145 150 155 160  
 Val His Leu Gln Ile Thr Lys Tyr Glu Tyr Pro Leu Leu His Phe Val  
 165 170 175  
 Val Ser Cys Ser Lys Gly Thr Tyr Ile Arg Ser Ile Ala His Glu Leu  
 180 185 190  
 Gly Thr Met Leu Gly Cys Gly Ala Tyr Leu Glu Gln Leu Arg Arg Leu  
 195 200 205  
 Arg Ser Gly Arg Phe Ser Ile Asp Glu Cys Ile Asp Gly Asn Leu Leu  
 210 215 220  
 Asp His Pro Asp Phe Asp Ile Ser Pro Tyr Leu Arg Asp Ala His Gly  
 225 230 235 240  
 Asn Ser Leu

&lt;210&gt;339

&lt;211&gt;308

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;339

Met Pro Met Glu Ile Ala Tyr Ser Leu Thr Ser Ser Phe Ser Val Asp  
 1 5 10 15  
 Ser Val Thr Val Gly Phe Phe Asp Gly Cys His Leu Gly His Ser Asn  
 20 25 30  
 Leu Leu Ser Ile Leu Thr Ser Tyr Ser Gly Ser Ser Gly Val Ile Thr  
 35 40 45  
 Phe Asp Ser His Pro Gln Thr Val Leu Ser Leu Asn His Thr Lys Leu  
 50 55 60  
 Ile Asn Thr Lys Glu Glu Arg Leu Gln Leu Leu Gln Thr Phe Pro Ile  
 65 70 75 80  
 Asp Trp Leu Gly Val Leu Thr Phe Asp Leu Asn Phe Ala Asn Gln Ser  
 85 90 95  
 Ala Glu Glu Phe Leu Thr Leu Leu His Arg Asn Leu Lys Cys Lys Arg  
 100 105 110  
 Leu Ile Leu Gly Tyr Asp Ser Cys Ile Gly Lys Glu Gln Gln Ser Asn  
 115 120 125  
 Thr Glu Ala Leu Asp Thr Ile Gly Lys Pro Leu Gly Ile Glu Val Ile  
 130 135 140  
 Lys Ile Pro Pro Tyr Arg Met Asp Asn Ile Val Val Ser Ser Lys Ala  
 145 150 155 160  
 Ile Arg Gln Phe Leu Ser Ala Gly Asn Leu Glu Cys Ala His Arg Phe  
 165 170 175  
 Leu Gly His Pro Tyr Ala Ile Ser Gly Lys Ile Thr Glu Gly Ser Gly  
 180 185 190  
 Ile Gly Gly Ser Leu Gly Phe Ala Thr Ile Asn Leu Pro Arg Glu Glu  
 195 200 205  
 Ser Leu Ile Pro Leu Gly Val Tyr Ala Cys Glu Ile Arg Tyr Asp Ser  
 210 215 220  
 Thr Thr Cys Gln Gly Val Met Asn Leu Gly Thr Ala Pro Thr Phe Gly  
 225 230 235 240  
 Arg Glu Ser Leu Tyr Ala Glu Ala His Ile Phe Ser Phe Ala Glu Asn  
 245 250 255  
 Leu Tyr Gly Lys Glu Val Ser Ile Ile Pro Arg Lys Phe Leu Arg Glu  
 260 265 270  
 Glu Lys Lys Phe Gln Ser Lys Glu Thr Leu Ile Arg Ala Ile Glu Lys  
 275 280 285  
 Asp Ile Leu Asp Ala Gln Asp Trp Phe Ala Lys Gly Ser Phe Asn Tyr  
 290 295 300  
 Glu Gly Thr Ala  
 305

&lt;210&gt;340

&lt;211&gt;198

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;340

Tyr Asn Tyr Cys Ser Leu Arg Lys Gly Leu Pro Leu Arg Thr Leu Glu  
 1 5 10 15  
 Leu Thr Pro Glu Ile Val Ala Leu Lys Pro Tyr Pro Phe Leu Thr  
 20 25 30  
 Met Lys Pro Met Phe Tyr Ile Ala Asn Val Asp Glu Ser Ser Leu Pro  
 35 40 45  
 Asp Met Asp Asn Asp Tyr Val Ala Ala Val Arg Glu Val Ala Ala Lys  
 50 55 60  
 Glu Asn Ser Lys Val Val Pro Ile Cys Val Arg Ile Glu Glu Glu Ile  
 65 70 75 80  
 Val Ser Leu Pro Ile Glu Glu Arg Leu Glu Phe Leu Met Ser Leu Gly  
 85 90 95  
 Leu Glu Lys Ser Gly Leu His Arg Leu Val Arg Ala Ala Tyr Asp Thr  
 100 105 110  
 Leu Gly Leu Ile Ser Tyr Phe Thr Thr Gly Pro Gln Glu Ser Arg Ala  
 115 120 125  
 Trp Thr Val Val Arg Gly Ser Ser Ala Trp Glu Ala Ala Gly Glu Ile  
 130 135 140  
 His Thr Asp Ile Gln Lys Gly Phe Ile Arg Ala Glu Val Ile Thr Phe  
 145 150 155 160  
 Glu Asp Met Ile Glu Cys Gln Gly Arg Ala Ala Ala Arg Glu Leu Gly  
 165 170 175  
 Lys Leu His Ile Glu Gly Arg Asp Tyr Ile Val Gln Asp Gly Asp Thr  
 180 185 190  
 Met Leu Phe Leu His Asn  
 195

&lt;210&gt;341

&lt;211&gt;180

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;341

Met Ser His Thr Glu Cys Gly Ile Val Gly Leu Pro Asn Val Gly Lys  
 1 5 10 15  
 Ser Gly Leu Phe Asn Ala Leu Thr Gly Ala Gln Val Ala Ser Cys Asn  
 20 25 30  
 Tyr Pro Phe Cys Thr Ile Asp Pro Asn Val Gly Ile Val Pro Val Ile  
 35 40 45  
 Asp Glu Arg Leu Glu Ala Leu Ala Lys Ile Ser Asn Ser Gln Lys Ile  
 50 55 60  
 Ile Tyr Ala Asp Met Lys Phe Val Asp Ile Ala Gly Leu Val Lys Gly  
 65 70 75 80  
 Ala Ser Asp Gly Ala Gly Leu Gly Asn Arg Phe Leu Ser His Ile Arg  
 85 90 95  
 Glu Thr His Ala Ile Ala His Val Val Arg Cys Phe Asp Asp Pro Asp  
 100 105 110  
 Val Thr His Val Ser Gly Lys Val Asn Pro Val Glu Asp Ile Glu Val  
 115 120 125  
 Ile Asn Leu Glu Leu Ile Phe Ser Asp Phe Ser Ser Ala Lys Asn Ile  
 130 135 140  
 His Ser Lys Leu Glu Lys Leu Ala Lys Gly Lys Arg Glu Val Gly Ala  
 145 150 155 160  
 Leu Leu Pro Leu Phe Asp Thr Ile Ile Ala His Leu Glu Lys Gly Cys  
 165 170 175  
 Arg Tyr Val Leu  
 180

&lt;210&gt;342

&lt;211&gt;360

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;342

Met Gly Glu Lys Thr Glu Lys Ala Thr Pro Lys Arg Leu Arg Asp Ala  
 1 5 10 15  
 Arg Lys Lys Gly Gln Val Ala Lys Ser Gln Asp Phe Pro Ser Ala Val  
 20 25 30

Thr Phe Ile Val Ser Met Phe Thr Ala Phe Ser Leu Ser Thr Phe Phe  
 35 40 45  
 Phe Lys His Leu Gly Gly Phe Leu Val Ser Met Leu Ser Gln Ala Pro  
 50 55 60  
 Thr Arg His Asp Pro Val Ile Thr Leu Phe Tyr Leu Lys Asn Cys Leu  
 65 70 75 80  
 Met Leu Ile Leu Thr Ala Ser Leu Pro Leu Leu Gly Ala Val Ala Val  
 85 90 95  
 Val Gly Val Ile Val Gly Phe Leu Ile Val Gly Pro Thr Phe Ser Thr  
 100 105 110  
 Glu Val Phe Lys Pro Asp Ile Lys Lys Phe Asn Pro Ile Glu Asn Ile  
 115 120 125  
 Lys Gln Lys Phe Lys Ile Lys Thr Leu Ile Glu Leu Ile Lys Ser Ile  
 130 135 140  
 Leu Lys Ile Phe Gly Ala Ala Leu Ile Leu Tyr Ile Thr Leu Lys Ser  
 145 150 155 160  
 Lys Val Ser Leu Ile Ile Glu Thr Ala Gly Val Ser Pro Ile Ile Thr  
 165 170 175  
 Ala Gln Ile Phe Lys Glu Ile Phe Tyr Lys Ala Val Thr Ser Ile Gly  
 180 185 190  
 Ile Phe Phe Leu Ile Val Ala Ile Leu Asp Leu Val Tyr Gln Arg His  
 195 200 205  
 Asn Phe Ala Lys Glu Leu Lys Met Glu Lys Phe Glu Val Lys Gln Glu  
 210 215 220  
 Phe Lys Asp Thr Glu Gly Asn Pro Glu Ile Lys Gly Arg Arg Arg Gln  
 225 230 235 240  
 Ile Ala Gln Glu Ile Ala Tyr Glu Asp Ser Ser Ser Gln Val Lys His  
 245 250 255  
 Ala Ser Thr Val Val Ser Asn Pro Lys Asp Ile Ala Val Ala Ile Gly  
 260 265 270  
 Tyr Met Pro Glu Lys Tyr Lys Ala Pro Trp Ile Ile Ala Met Gly Ile  
 275 280 285  
 Asn Leu Arg Ala Lys Arg Ile Leu Asp Glu Ala Glu Lys Tyr Gly Ile  
 290 295 300  
 Pro Ile Met Arg Asn Val Pro Leu Ala His Gln Leu Leu Asp Glu Gly  
 305 310 315 320  
 Lys Glu Leu Lys Phe Ile Pro Glu Ser Thr Tyr Glu Ala Ile Gly Glu  
 325 330 335  
 Ile Leu Leu Tyr Ile Thr Ser Leu Asn Ala Gln Asn Pro Asn Asn Lys  
 340 345 350  
 Asn Thr Asn Gln Pro Asp His Leu  
 355 360

&lt;210&gt;343

&lt;211&gt;606

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;343

Ser Val Cys Gly Ser Cys His Ser Gly Phe Gly Asp Phe Val Val Gly  
 1 5 10 15  
 Gly Asn Tyr Val Val Gly Phe Ile Ile Phe Leu Ile Ile Thr Ile Ile  
 20 25 30  
 Gln Phe Ile Val Val Thr Lys Gly Ala Glu Arg Val Ala Glu Val Ala  
 35 40 45  
 Ala Arg Phe Arg Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp  
 50 55 60  
 Ala Asp Leu Arg Ala Gly Met Ile Asp Ala Thr Gln Ala Arg Asp Lys  
 65 70 75 80  
 Arg Ala Gln Ile Gln Lys Glu Ser Glu Leu Tyr Gly Ala Met Asp Gly  
 85 90 95  
 Ala Met Lys Phe Ile Lys Gly Asp Val Ile Ala Gly Ile Val Ile Ser  
 100 105 110  
 Leu Ile Asn Ile Val Gly Gly Leu Thr Ile Gly Val Ala Met His Gly  
 115 120 125  
 Met Asp Leu Ala Gln Ala Ala His Val Tyr Thr Leu Leu Ser Ile Gly

130 135 140  
 Asp Gly Leu Val Ser Gln Ile Pro Ser Leu Leu Ile Ala Leu Thr Ala  
 145 150 155 160  
 Gly Ile Val Thr Thr Arg Val Ser Ser Asp Lys Asn Thr Asn Leu Gly  
 165 170 175  
 Lys Glu Ile Ser Thr Gln Leu Val Lys Glu Pro Arg Ala Leu Leu Leu  
 180 185 190  
 Ala Gly Ala Ala Thr Leu Gly Val Gly Phe Phe Lys Gly Phe Pro Leu  
 195 200 205  
 Trp Ser Phe Ser Ile Leu Ala Leu Ile Phe Val Ala Leu Gly Ile Leu  
 210 215 220  
 Leu Leu Thr Lys Lys Ser Ala Ala Gly Lys Lys Gly Gly Gly Ser Gly  
 225 230 235 240  
 Ala Ser Thr Thr Val Gly Ala Ala Gly Asp Gly Ala Ala Thr Val Gly  
 245 250 255  
 Asp Asn Pro Asp Asp Tyr Ser Leu Thr Leu Pro Val Ile Leu Glu Leu  
 260 265 270  
 Gly Lys Asp Leu Ser Lys Leu Ile Gln His Lys Thr Lys Ser Gly Gln  
 275 280 285  
 Ser Phe Val Asp Asp Met Ile Pro Lys Met Arg Gln Ala Leu Tyr Gln  
 290 295 300  
 Asp Ile Gly Ile Arg Tyr Pro Gly Ile His Val Arg Thr Asp Ser Pro  
 305 310 315 320  
 Ser Leu Glu Gly Tyr Asp Tyr Met Ile Leu Leu Asn Glu Val Pro Tyr  
 325 330 335  
 Val Arg Gly Lys Ile Pro Pro His His Val Leu Thr Asn Glu Val Glu  
 340 345 350  
 Asp Asn Leu Ser Arg Tyr Asn Leu Pro Phe Ile Thr Tyr Lys Asn Ala  
 355 360 365  
 Ala Gly Leu Pro Ser Ala Trp Val Ser Glu Asp Ala Lys Ala Ile Leu  
 370 375 380  
 Glu Lys Ala Ala Ile Lys Tyr Trp Thr Pro Leu Glu Val Ile Ile Leu  
 385 390 395 400  
 His Leu Ser Tyr Phe Phe His Lys Ser Ser Gln Glu Phe Leu Gly Ile  
 405 410 415  
 Gln Glu Val Arg Ser Met Ile Glu Phe Met Glu Arg Ser Phe Pro Asp  
 420 425 430  
 Leu Val Lys Glu Val Thr Arg Leu Ile Pro Leu Gln Lys Leu Thr Glu  
 435 440 445  
 Ile Phe Lys Arg Leu Val Gln Glu Gln Ile Ser Ile Lys Asp Leu Arg  
 450 455 460  
 Thr Ile Leu Glu Ser Leu Ser Glu Trp Ala Gln Thr Glu Lys Asp Thr  
 465 470 475 480  
 Val Leu Leu Thr Glu Tyr Val Arg Ser Ser Leu Lys Leu Tyr Ile Ser  
 485 490 495  
 Phe Lys Phe Ser Gln Gly Gln Ser Ala Ile Ser Val Tyr Leu Leu Asp  
 500 505 510  
 Pro Glu Ile Glu Glu Met Ile Arg Gly Ala Ile Lys Gln Thr Ser Ala  
 515 520 525  
 Gly Ser Tyr Leu Ala Leu Asp Pro Asp Ser Val Asn Leu Ile Leu Lys  
 530 535 540  
 Ser Met Arg Asn Thr Ile Thr Pro Thr Pro Ala Gly Gly Gln Pro Pro  
 545 550 555 560  
 Val Leu Leu Thr Ala Ile Asp Val Arg Arg Tyr Val Arg Lys Leu Ile  
 565 570 575  
 Glu Thr Glu Phe Pro Asp Ile Ala Val Ile Ser Tyr Gln Glu Ile Leu  
 580 585 590  
 Pro Glu Ile Arg Ile Gln Pro Leu Gly Arg Ile Gln Ile Phe  
 595 600 605

&lt;210&gt;344

&lt;211&gt;215

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;344

Tyr Val Val Ala His Arg Arg His Met Ala Ala Ser Gly Gly Thr Gly  
 1 5 10 15  
 Gly Leu Gly Gly Thr Gln Gly Val Asn Leu Ala Ala Val Glu Ala Ala  
 20 25 30  
 Ala Ala Lys Ala Asp Ala Ala Glu Val Val Ala Ser Gln Glu Gly Ser  
 35 40 45  
 Glu Met Asn Met Ile Gln Gln Ser Gln Asp Leu Thr Asn Pro Ala Ala  
 50 55 60  
 Ala Thr Arg Thr Lys Lys Lys Glu Glu Lys Phe Gln Thr Leu Glu Ser  
 65 70 75 80  
 Arg Lys Lys Gly Glu Ala Gly Lys Ala Glu Lys Lys Ser Glu Ser Thr  
 85 90 95  
 Glu Glu Lys Pro Asp Thr Asp Leu Ala Asp Lys Tyr Ala Ser Gly Asn  
 100 105 110  
 Ser Glu Ile Ser Gly Gln Glu Leu Arg Gly Leu Arg Asp Ala Ile Gly  
 115 120 125  
 Asp Asp Ala Ser Pro Glu Asp Ile Leu Ala Leu Val Gln Glu Lys Ile  
 130 135 140  
 Lys Asp Pro Ala Leu Gln Ser Thr Ala Leu Asp Tyr Leu Val Gln Thr  
 145 150 155 160  
 Thr Pro Pro Ser Gln Gly Lys Leu Lys Glu Ala Leu Ile Gln Ala Arg  
 165 170 175  
 Asn Thr His Thr Glu Gln Phe Gly Arg Thr Ala Ile Gly Ala Lys Asn  
 180 185 190  
 Ile Leu Phe Ala Ser Gln Glu Tyr Ala Asp Gln Leu Asn Val Ser Pro  
 195 200 205  
 Ser Gly Phe Ala Leu Cys Thr  
 210 215  
 <210>345  
 <211>240  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>345  
 Ile Lys Arg Ser Ala Tyr Pro Ser Lys Glu Tyr Ser Tyr Gly Ala Ile  
 1 5 10 15  
 Arg Thr Asn Cys Tyr Trp Cys Glu Lys His Leu Ile Cys Leu Ser Arg  
 20 25 30  
 Ile Cys Arg Pro Thr Glu Cys Phe Ser Phe Arg Xaa Arg Ser Leu Tyr  
 35 40 45  
 Leu Glu Val Thr Gly Asp Thr His Thr Cys Asp Gln Leu Leu Ser Met  
 50 55 60  
 Leu Gln Asp Arg Tyr Thr Tyr Gln Asp Met Ala Ile Val Ser Ser Phe  
 65 70 75 80  
 Leu Met Lys Gly Met Ala Thr Glu Leu Lys Arg Gln Gly Pro Tyr Val  
 85 90 95  
 Pro Ser Ala Gln Leu Gln Val Leu Met Thr Glu Thr Arg Asn Leu Gln  
 100 105 110  
 Ala Val Leu Thr Ser Tyr Asp Tyr Phe Glu Ser Arg Val Pro Ile Leu  
 115 120 125  
 Leu Asp Ser Leu Lys Ala Glu Gly Ile Gln Thr Pro Ser Asp Leu Asn  
 130 135 140  
 Phe Val Lys Ile Ala Glu Ser Tyr His Lys Ile Ile Asn Asp Lys Phe  
 145 150 155 160  
 Pro Thr Ala Ser Lys Val Glu Arg Glu Val Arg Asn Leu Ile Gly Asp  
 165 170 175  
 Asp Val Asp Ser Val Thr Gly Val Leu Asn Leu Phe Phe Ser Ala Leu  
 180 185 190  
 Arg Gln Thr Ser Ser Arg Leu Phe Ser Ser Ala Asp Lys Arg Gln Gln  
 195 200 205  
 Leu Gly Ala Met Ile Ala Asn Ala Leu Asp Ala Val Asn Ile Asn Asn  
 210 215 220  
 Glu Asp Tyr Pro Lys Ala Ser Asp Phe Pro Lys Pro Tyr Pro Trp Ser  
 225 230 235 240  
 <210>346

&lt;211&gt;151

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;346

Lys Arg Ile Ala Met Gln Asn Gln Tyr Glu Gln Leu Leu Glu Ser Leu  
 1 5 10 15  
 Ala Pro Leu Leu Asn Thr Thr Leu Ala Pro Asp Lys Asn Asn Ser Cys  
 20 25 30  
 Leu Ile Arg Phe Ser Asp Thr His Val Pro Val Gln Ile Glu Glu Asp  
 35 40 45  
 Gly Asn Ser Gly Asp Leu Ala Val Ser Thr Leu Leu Gly Thr Leu Pro  
 50 55 60  
 Glu Asn Val Phe Arg Glu Arg Ile Phe Lys Ala Ala Leu Ser Val Asn  
 65 70 75 80  
 Gly Ser Phe Gln Ser Ser Ile Lys Gly Ile Leu Gly Tyr Gly Glu Val  
 85 90 95  
 Thr Gln Gln Leu Tyr Leu Ser Asp Ile Leu Ser Met Asn Tyr Leu Asn  
 100 105 110  
 Gly Glu Lys Leu Phe Glu Tyr Leu Lys Leu Phe Ser Leu His Ala Lys  
 115 120 125  
 Ile Trp Met Glu Ser Leu Arg Thr Gly Asn Leu Pro Asp Leu His Val  
 130 135 140  
 Leu Gly Ile Tyr Tyr Val Ala  
 145 150

&lt;210&gt;347

&lt;211&gt;526

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;347

Val Asn Val Leu Lys Tyr Thr Lys His Ser Pro Ser Ala His Ala Trp  
 1 5 10 15  
 Lys Leu Ile Gly Thr Ser Pro Lys His Gly Ile Tyr Leu Pro Leu Phe  
 20 25 30  
 Ser Ile His Thr Lys Asn Ser Cys Gly Ile Gly Glu Phe Leu Asp Leu  
 35 40 45  
 Ile Pro Leu Ile Ser Trp Cys Gln Lys Gln Gly Phe Ser Val Ile Gln  
 50 55 60  
 Leu Leu Pro Leu Asn Asp Thr Gly Glu Asp Thr Ser Pro Tyr Asn Ser  
 65 70 75 80  
 Ile Ser Ser Val Ala Leu Asn Pro Leu Phe Leu Ser Leu Ser Ser Leu  
 85 90 95  
 Pro Asn Ile Asp Thr Ile Pro Glu Val Ala Lys Lys Leu Gln Asp Met  
 100 105 110  
 His Glu Leu Cys Ser Thr Pro Ser Val Ser Tyr Thr Gln Val Lys Glu  
 115 120 125  
 Lys Lys Trp Ala Phe Leu Arg Glu Tyr Tyr Gln Lys Cys Cys Lys Ser  
 130 135 140  
 Ser Leu Glu Gly Asn Ser Asn Phe Ser Glu Phe Leu Glu Ser Glu Arg  
 145 150 155 160  
 Tyr Trp Leu Tyr Pro Tyr Gly Thr Phe Arg Ala Ile Lys His His Met  
 165 170 175  
 His Gly Glu Pro Ile Asn Asn Trp Pro Lys Ser Leu Thr Asp Gln Glu  
 180 185 190  
 Asn Phe Pro Asp Leu Thr Lys Lys Phe His Asp Glu Val Leu Phe Phe  
 195 200 205  
 Ser Tyr Leu Gln Phe Leu Cys Tyr Gln Gln Leu Cys Glu Val Lys Ala  
 210 215 220  
 Tyr Ala Asp Gln His His Val Leu Leu Lys Gly Asp Leu Pro Ile Leu  
 225 230 235 240  
 Ile Ser Lys Asp Ser Cys Asp Val Trp Tyr Phe Arg Asp Tyr Phe Ser  
 245 250 255  
 Ser Ser Arg Ser Val Gly Ala Pro Pro Asp Leu Tyr Asn Ser Glu Gly  
 260 265 270  
 Gln Asn Trp His Leu Pro Ile Tyr Asn Phe Ser Gln Leu Ala Lys Asp

275 280 285  
 Asp Tyr Ile Trp Trp Lys Glu Arg Leu Arg Tyr Ala Gln Asn Phe Tyr  
 290 295 300  
 Ser Val Tyr Arg Leu Asp His Ile Ile Gly Phe Phe Arg Leu Trp Ile  
 305 310 315 320  
 Trp Asp Ser Ser Gly Arg Gly Arg Phe Ile Pro Asp Asn Pro Lys Asp  
 325 330 335  
 Tyr Ile Lys Gln Gly Thr Glu Ile Leu Ser Thr Met Leu Gly Ala Ser  
 340 345 350  
 Ser Met Leu Pro Ile Gly Glu Asp Leu Gly Ile Ile Pro Gln Asp Val  
 355 360 365  
 Lys Thr Thr Leu Thr His Leu Gly Ile Cys Gly Thr Arg Ile Pro Arg  
 370 375 380  
 Trp Glu Arg Asn Trp Glu Ser Asp Ser Ala Phe Ile Pro Leu Lys Asp  
 385 390 395 400  
 Tyr Asn Pro Leu Ser Val Thr Thr Leu Ser Thr His Asp Ser Asp Thr  
 405 410 415  
 Phe Ala Gln Trp Trp Leu Asn Ser Pro Lys Glu Ala Lys Gln Phe Ala  
 420 425 430  
 Lys Phe Leu His Leu Pro Phe Gln Lys Thr Leu Thr Thr Glu Thr Gln  
 435 440 445  
 Ile Asp Ile Leu Lys Leu Ser His Glu Ser Ala Ser Ile Phe His Ile  
 450 455 460  
 Asn Leu Phe Asn Asp Tyr Leu Ala Leu Cys Pro Asp Leu Val Ser Lys  
 465 470 475 480  
 Asn Leu Gln Arg Glu Arg Ile Asn Thr Pro Gly Thr Ile Ser Lys Lys  
 485 490 495  
 Asn Trp Ser Tyr Arg Val Arg Pro Ser Leu Glu Glu Leu Ala Ile His  
 500 505 510  
 Lys Lys Phe Asn Gly Tyr Ile Glu Lys Ile Leu Thr Gly Leu  
 515 520 525

&lt;210&gt;348

&lt;211&gt;89

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;348

Met Ser Arg Lys Cys Pro Leu Thr Gly Lys Arg Pro Arg Arg Gly Tyr  
 1 5 10 15  
 Ser Tyr Thr Leu Arg Gly Ile Ala Lys Lys Lys Gly Ile Gly Leu  
 20 25 30  
 Lys Val Thr Gly Lys Thr Lys Arg Arg Phe Phe Pro Asn Met Leu Thr  
 35 40 45  
 Lys Arg Leu Trp Ser Thr Glu Glu Asn Arg Phe Leu Lys Leu Lys Ile  
 50 55 60  
 Ser Ala Ser Ala Leu Arg His Ile Asp Lys Leu Gly Leu Glu Lys Val  
 65 70 75 80  
 Leu Glu Arg Ala Lys Ser Lys Asn Phe  
 85

&lt;210&gt;349

&lt;211&gt;584

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;349

Met Ser Phe Leu Arg Arg His Ile Ser Leu Phe Arg Ser Gln Lys Gln  
 1 5 10 15  
 Leu Ile Asp Val Phe Ala Pro Val Ser Pro Asn Leu Glu Leu Ala Glu  
 20 25 30  
 Ile His Arg Arg Val Ile Glu Asp Gln Gly Pro Ala Leu Leu Phe His  
 35 40 45  
 Asn Val Ile Gly Ser Ser Phe Pro Val Leu Thr Asn Leu Phe Gly Thr  
 50 55 60  
 Lys His Arg Val Asp Gln Leu Phe Ser Gln Ala Pro Asp Asn Leu Ile  
 65 70 75 80  
 Ala Arg Val Ala His Leu Ile Ser Ser Thr Pro Lys Leu Ser Ser Leu

<210>350



&lt;211&gt;354

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;350

Lys Met Asn Lys Arg Gln Lys Asp Lys Leu Lys Ile Cys Val Ile Ile  
 1 5 10 15  
 Ser Thr Leu Ile Leu Val Gly Ile Phe Ala Arg Ala Pro Arg Gly Asp  
 20 25 30  
 Thr Phe Lys Thr Phe Leu Lys Ser Glu Glu Ala Ile Ile Tyr Ser Asn  
 35 40 45  
 Gln Cys Asn Glu Asp Met Arg Lys Ile Leu Cys Asp Ala Ile Glu His  
 50 55 60  
 Ala Asp Glu Glu Ile Phe Leu Arg Ile Tyr Asn Leu Ser Glu Pro Lys  
 65 70 75 80  
 Ile Gln Gln Ser Leu Thr Arg Gln Ala Gln Ala Lys Asn Lys Val Thr  
 85 90 95  
 Ile Tyr Tyr Gln Lys Phe Lys Ile Pro Gln Ile Leu Lys Gln Ala Ser  
 100 105 110  
 Asn Val Thr Leu Val Glu Gln Pro Pro Ala Gly Arg Lys Leu Met His  
 115 120 125  
 Gln Lys Ala Leu Ser Ile Asp Lys Lys Asp Ala Trp Leu Gly Ser Ala  
 130 135 140  
 Asn Tyr Thr Asn Leu Ser Leu Arg Leu Asp Asn Asn Leu Ile Leu Gly  
 145 150 155 160  
 Met His Ser Ser Glu Leu Cys Asp Leu Ile Ile Thr Asn Thr Ser Gly  
 165 170 175  
 Asp Phe Ser Ile Lys Asp Gln Thr Gly Lys Tyr Phe Val Leu Pro Gln  
 180 185 190  
 Asp Arg Lys Ile Ala Ile Gln Ala Val Leu Glu Lys Ile Gln Thr Ala  
 195 200 205  
 Gln Lys Thr Ile Gln Val Ala Met Phe Ala Leu Thr His Ser Glu Ile  
 210 215 220  
 Ile Gln Ala Leu His Gln Ala Lys Gln Arg Gly Ile His Val Asp Ile  
 225 230 235 240  
 Ile Ile Asp Arg Ser His Ser Lys Leu Thr Phe Lys Gln Leu Arg Gln  
 245 250 255  
 Leu Asn Ile Asn Lys Asp Phe Val Ser Ile Asn Thr Ala Pro Cys Thr  
 260 265 270  
 Leu His His Lys Phe Ala Val Ile Asp Asn Lys Thr Leu Leu Ala Gly  
 275 280 285  
 Ser Ile Asn Trp Ser Lys Gly Arg Phe Ser Leu Asn Asp Glu Ser Leu  
 290 295 300  
 Ile Ile Leu Glu Asn Leu Thr Lys Gln Gln Asn Gln Lys Leu Arg Met  
 305 310 315 320  
 Ile Trp Lys Asp Leu Ala Lys His Ser Glu His Pro Thr Val Asp Asp  
 325 330 335  
 Glu Glu Lys Glu Ile Ile Glu Lys Ser Leu Pro Val Glu Glu Gln Glu  
 340 345 350  
 Ala Ala

&lt;210&gt;351

&lt;211&gt;243

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;351

Phe Ile Ser Ile Glu Met Leu Leu Leu Ser Arg Gln Leu Phe Ser Val  
 1 5 10 15  
 Leu Pro Ser Arg Phe Gln Asp Leu His Val Tyr Arg Phe Lys Glu Ser  
 20 25 30  
 Leu Lys Leu Leu Gln Phe Met Thr Met Val Gly Gly Glu Ile Val Val  
 35 40 45  
 Val Leu Ala Glu Ile Lys Glu Glu Asp Leu Arg Ala Arg Lys Leu Pro  
 50 55 60  
 Val Arg Lys Arg Arg Glu Lys Asn Tyr Leu Arg Ile Phe Arg Val Leu

```

      65      70      75      80
Ser Arg Phe Asp Val Met Arg Ile Ile Arg Phe Asp Pro Tyr Gly Ala
      85      90      95
Leu Ser Ala Gln Ser Ile Ala Lys Asp Ser Arg Gln Asn Ser Pro Leu
      100      105      110
Val Glu Lys Ile Ser Glu Glu Ile Ala Thr Asn Glu Ala Ile Arg Leu
      115      120      125
Ala Leu Leu Ala Ile Gly Asp Arg Glu Gln Glu Glu Lys Lys Gln Arg
      130      135      140
His Arg Tyr Lys Leu Leu Gly Gln Lys Gln Ala Lys Val Leu Leu Ser
      145      150      155      160
Gln Leu Arg His Val His Leu Asp Phe Lys Lys Leu Tyr Cys Asp Ser
      165      170      175
Lys Lys Lys Glu Asp Gln Glu Lys Asp Glu Lys Asn Lys Gln Lys Arg
      180      185      190
Ser Ile Lys Val Thr Lys Lys Lys Lys Gly Ile Ser Leu Gly Ala Ala
      195      200      205
Ala Ser Gln Ala Ile Ala Ala Ala Glu Ala Trp Val Ile Ala Arg
      210      215      220
Asn Lys Gly Val Leu Glu Thr Ala Ser Thr Leu Phe Tyr Gln Lys Asp
      225      230      235      240
Glu Glu Ala

```

&lt;210&gt;352

&lt;211&gt;584

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;352

```

Ile Gln Arg Ile Ile Met Ala Val Ser Gly Gly Gly Gly Val Gln Pro
  1      5      10      15
Ser Ser Asp Pro Gly Lys Trp Asn Pro Ala Leu Gln Gly Glu Gln Ala
      20      25      30
Glu Gly Pro Ser Pro Leu Lys Glu Ser Ile Phe Ser Glu Thr Lys Gln
      35      40      45
Ala Ser Ser Ala Ala Lys Gln Glu Ser Leu Val Arg Ser Gly Ser Thr
      50      55      60
Gly Met Tyr Ala Thr Glu Ser Gln Ile Asn Lys Ala Lys Tyr Arg Lys
      65      70      75      80
Ala Gln Asp Arg Ser Ser Thr Ser Pro Lys Ser Lys Leu Lys Gly Thr
      85      90      95
Phe Ser Lys Met Arg Ala Ser Val Gln Gly Phe Met Ser Gly Phe Gly
      100      105      110
Ser Arg Ala Ser Arg Val Ser Ala Lys Arg Ala Ser Asp Ser Gly Glu
      115      120      125
Gly Thr Ser Leu Leu Pro Thr Glu Met Asp Val Ala Leu Lys Lys Gly
      130      135      140
Asn Arg Ile Ser Pro Glu Met Gln Gly Phe Phe Leu Asp Ala Ser Gly
      145      150      155      160
Met Gly Gly Ser Ser Ser Asp Ile Ser Gln Leu Ser Leu Glu Ala Leu
      165      170      175
Lys Ser Ser Ala Phe Ser Gly Ala Arg Ser Leu Ser Leu Ser Ser Ser
      180      185      190
Glu Ser Ser Ser Val Ala Ser Phe Gly Ser Phe Gln Lys Ala Ile Glu
      195      200      205
Pro Met Ser Glu Glu Lys Val Asn Ala Trp Thr Val Ala Arg Leu Gly
      210      215      220
Gly Glu Met Val Ser Ser Leu Leu Asp Pro Asn Val Glu Thr Ser Ser
      225      230      235      240
Leu Val Arg Arg Ala Met Ala Thr Gly Asn Glu Gly Met Ile Asp Leu
      245      250      255
Ser Asp Leu Gly Gln Glu Glu Xaa Ser Thr Ala Met Thr Ser Pro Arg
      260      265      270
Ala Val Glu Gly Lys Val Lys Val Ser Ser Ser Asp Ser Pro Glu Ala
      275      280      285

```

Asn Pro Thr Gly Ile Pro Asn Ser Asn Thr Leu Glu Arg Ala Glu Lys  
 290 295 300  
 Glu Ala Glu Lys Gln Glu Ser Arg Glu Gln Leu Ser Glu Asp Gln Met  
 305 310 315 320  
 Met Leu Ala Arg Ala Met Ala Gly Leu Leu Thr Gly Ala Ala Pro Gln  
 325 330 335  
 Glu Val Leu Ser Asn Ser Val Trp Ser Gly Pro Ser Thr Val Phe Pro  
 340 345 350  
 Pro Pro Lys Phe Ser Gly Thr Leu Pro Thr Gln Arg Ser Gly Asp Lys  
 355 360 365  
 Ser Lys His Lys Ser Pro Gly Ile Glu Lys Ser Thr Asn His Thr Asn  
 370 375 380  
 Phe Ser Pro Leu Arg Glu Gly Thr Val Lys Ser Ala Glu Val Lys Ser  
 385 390 395 400  
 Leu Pro His Pro Glu Ser Met Tyr Arg Phe Pro Lys Asp Ser Ile Val  
 405 410 415  
 Ser Arg Glu Glu Pro Glu Ala Val Val Lys Glu Ser Thr Ala Phe Lys  
 420 425 430  
 Asn Pro Glu Asn Ser Ser Gln Asn Phe Leu Pro Ile Ala Val Glu Ser  
 435 440 445  
 Val Phe Pro Lys Glu Ser Gly Thr Gly Gly Ala Leu Gly Ser Asp Ala  
 450 455 460  
 Val Ser Ser Ser Tyr His Phe Leu Ala Gln Arg Gly Val Ser Leu Leu  
 465 470 475 480  
 Ala Pro Leu Pro Arg Ala Thr Asp Asp Tyr Lys Glu Lys Leu Glu Ala  
 485 490 495  
 His Lys Gly Pro Gly Gly Pro Pro Asp Pro Leu Ile Tyr Gln Tyr Arg  
 500 505 510  
 Asn Val Ala Val Glu Pro Pro Ile Val Leu Arg Ser Pro Gln Pro Phe  
 515 520 525  
 Ser Gly Ser Ser Arg Leu Ser Val Gln Gly Lys Pro Glu Ala Ala Ser  
 530 535 540  
 Val His Asp Asp Gly Gly Gly Asn Ser Gly Gly Phe Ser Gly Asp  
 545 550 555 560  
 Gln Arg Arg Gly Ser Ser Gly Gln Lys Ala Ser Arg Gln Glu Lys Lys  
 565 570 575  
 Gly Lys Lys Leu Ser Thr Asp Ile  
 580

&lt;210&gt;353

&lt;211&gt;271

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;353

Glu Ile Gly Met Leu Leu Arg Gly Ile Pro Ala Ala Glu Lys Ile Leu  
 1 5 10 15  
 Gln Arg Leu Lys Glu Glu Ile Ser Gln Ser Pro Thr Ser Pro Gly Leu  
 20 25 30  
 Ala Val Val Leu Ile Gly Asn Asp Pro Ala Ser Glu Val Tyr Val Gly  
 35 40 45  
 Met Lys Val Lys Lys Ala Thr Glu Ile Gly Ile Ile Ser Lys Ala His  
 50 55 60  
 Lys Leu Pro Ser Asp Ser Thr Leu Ser Ser Val Leu Lys Leu Ile Glu  
 65 70 75 80  
 Arg Leu Asn Gln Asp Pro Ser Ile His Gly Ile Leu Val Gln Leu Pro  
 85 90 95  
 Leu Pro Lys His Leu Asp Ser Glu Val Ile Leu Gln Ala Ile Ser Pro  
 100 105 110  
 Asp Lys Asp Val Asp Gly Leu His Pro Val Asn Met Gly Lys Leu Leu  
 115 120 125  
 Leu Gly Asn Phe Asp Gly Leu Leu Pro Cys Thr Pro Ala Gly Ile Ile  
 130 135 140  
 Glu Leu Leu Asn Tyr Tyr Glu Ile Pro Leu Arg Gly Arg His Ala Ala  
 145 150 155 160  
 Ile Val Gly Arg Ser Asn Ile Val Gly Lys Pro Leu Ala Ala Leu Met

165 170 175  
 Met Gln Lys His Pro Gln Thr Asn Cys Thr Val Thr Val Leu His Ser  
 180 185 190  
 Gln Ser Glu Asn Leu Pro Glu Ile Leu Lys Thr Ala Asp Ile Ile Ile  
 195 200 205  
 Ala Ala Leu Gly Ala Pro Leu Phe Ile Lys Glu Thr Met Val Ala Pro  
 210 215 220  
 His Ala Val Ile Val Asp Val Gly Thr Thr Arg Val Pro Ala Asp Asn  
 225 230 235 240  
 Ala Lys Gly Tyr Thr Leu Leu Gly Asp Val Asp Phe Asn Asn Val Val  
 245 250 255  
 Thr Lys Cys Ala Glu Ser Leu Gln Phe Leu Glu Ala Leu Val Pro  
 260 265 270

&lt;210&gt;354

&lt;211&gt;300

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;354

Arg Arg Trp Ser His Asp Cys Arg Tyr Ala His Glu Gln Tyr Met Ala  
 1 5 10 15  
 Met Leu Pro Lys Phe Phe Leu Val Leu Leu Cys Leu Gly Leu Cys Ser  
 20 25 30  
 Cys Ser Gln Lys Thr Thr Thr Ile Glu Gly Glu Gln Met Thr Ile Phe  
 35 40 45  
 Tyr Arg Ile Val Leu Gly Thr Ser Leu Ser Ala Lys Glu Lys Ala Ser  
 50 55 60  
 Leu Ser Gln Gln Ile Asp Arg Cys Phe His Lys Ile Asp Ser Ile Tyr  
 65 70 75 80  
 Asn Asn Trp Asn Pro Tyr Ser Glu Leu Ser Ile Ile Asn Arg Ala Pro  
 85 90 95  
 Ala Asp Val Pro Ile Thr Leu Ser Val Glu Leu Ser Glu Phe Leu Asp  
 100 105 110  
 Gln Val Asp Thr Leu Tyr Lys Leu Ser Glu Gly Arg Phe Asp Pro Thr  
 115 120 125  
 Val Gly Pro Leu Lys Thr Leu Trp Leu Leu His Leu Lys Ser Gln Thr  
 130 135 140  
 Leu Pro Pro Lys Asp Val Trp Glu Gln His Tyr Lys Asp Met Gly Trp  
 145 150 155 160  
 Gln His Leu Glu Phe Gln Ser Asn Thr Lys Thr Leu Ile Lys Lys Asn  
 165 170 175  
 Pro His Val Gln Ile Asp Leu Cys Gly Val Val Lys Gly Tyr Ala Val  
 180 185 190  
 Asp Cys Leu Asn Glu Ile Cys Asn Thr Phe Cys Pro Asn Asn Tyr Val  
 195 200 205  
 Glu Trp Gly Gly Glu Ile Lys Thr Ser Gly His His Pro Ser Gly Arg  
 210 215 220  
 Pro Trp Arg Ile Phe Ser Glu Ala Ala Gly Thr Ile Leu Asp Ile Asp  
 225 230 235 240  
 Asp Met Ala Ile Ala Thr Ser Gly Asn His Ile Gln Lys Trp Cys Val  
 245 250 255  
 Glu Gly Lys Ile Tyr Thr His Ile Leu Asp Thr Arg Thr Gly Lys Pro  
 260 265 270  
 Leu Glu Leu Ser Ser Tyr Pro Ile Gln Ser Val Ser Val Val His Pro  
 275 280 285  
 Thr Ala His Thr Pro Thr Leu Leu Pro Gln Ser Ser  
 290 295 300

&lt;210&gt;355

&lt;211&gt;165

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;355

Leu Leu Tyr Trp Phe Leu Ser Pro Ile Met Gly Glu Asp Leu Met Ala  
 1 5 10 15  
 Gln Lys Glu Ile Val Ser Asn Arg Lys Ala Leu Arg Asn Tyr Glu Val

20 25 30  
 Ile Glu Thr Leu Glu Ala Gly Ile Val Leu Thr Gly Thr Glu Ile Lys  
 35 40 45  
 Ser Leu Arg Asp His Gly Gly Asn Leu Gly Asp Ala Tyr Val Ile Val  
 50 55 60  
 Ser Lys Gly Glu Gly Trp Leu Leu Asn Ala Ser Ile Ala Pro Tyr Arg  
 65 70 75 80  
 Phe Gly Asn Ile Tyr Asn His Glu Glu Arg Arg Lys Arg Lys Leu Leu  
 85 90 95  
 Leu His Arg Tyr Glu Leu Arg Lys Leu Glu Gly Lys Ile Ala Gln Lys  
 100 105 110  
 Gly Met Thr Leu Ile Pro Leu Gly Met Phe Leu Ser Arg Gly Tyr Val  
 115 120 125  
 Lys Val Arg Leu Gly Cys Cys Arg Gly Lys Lys Ala Tyr Asp Lys Arg  
 130 135 140  
 Arg Thr Ile Ile Glu Arg Glu Lys Glu Arg Glu Val Ala Ala Ala Met  
 145 150 155 160  
 Lys Arg Arg His His  
 165

&lt;210&gt;356

&lt;211&gt;135

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;356

Glu Asn Met Lys Phe Val Val Ser Arg Asn Glu Leu Gly Asn Leu Ile  
 1 5 10 15  
 Lys Lys Ile Gln Ser Val Val Pro Gln Asn Thr Pro Ile Pro Val Leu  
 20 25 30  
 Thr His Val Leu Ile Glu Thr Tyr Asn Asp Glu Leu Val Phe Thr Ala  
 35 40 45  
 Thr Asp Leu Thr Val Ser Thr Arg Cys Val Thr Lys Ala Lys Val Tyr  
 50 55 60  
 Glu Lys Gly Ala Ile Ser Ile Pro Ser Lys Arg Phe Phe Gln Leu Val  
 65 70 75 80  
 Lys Glu Leu Thr Glu Ala Asn Leu Glu Ile Ser Ser Ser Ala Gly Glu  
 85 90 95  
 Met Ala Gln Ile Thr Ser Gly Ser Ser Tyr Phe Ala Tyr Ser Ala Trp  
 100 105 110  
 Lys Lys Lys Thr Ser Pro Cys Ser Leu Ile Tyr Lys Met Leu Cys Val  
 115 120 125  
 Phe Pro Cys Leu Gln Ser Ser  
 130 135

&lt;210&gt;357

&lt;211&gt;303

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;357

Glu Arg Arg Tyr Phe His Ser Leu Gln Glu Ile Phe Ser Ile Ser Lys  
 1 5 10 15  
 Arg Ile Asn Arg Gly Lys Phe Arg Asn Phe Leu Phe Ser Arg Gly Asn  
 20 25 30  
 Gly Thr Asn His Leu Gly Ile Phe Ile Phe Arg Leu Leu Ser Met Glu  
 35 40 45  
 Lys Glu Asp Phe Pro Met Leu Pro Asp Ile Gln Asn Ala Leu Arg Phe  
 50 55 60  
 Ser Leu Pro Ala Glu Gln Leu Lys Thr Met Leu Gln Arg Thr Ser Phe  
 65 70 75 80  
 Ala Val Ser Arg Glu Ser Arg Tyr Val Leu Thr Gly Val Leu Leu  
 85 90 95  
 Ala Ile Ala Asn Gly Val Ala Thr Ile Val Gly Thr Asp Gly Lys Arg  
 100 105 110  
 Leu Ala Lys Ile Asp Ala Glu Val Thr Leu Asp Lys Ser Phe Ser Gly  
 115 120 125  
 Glu Tyr Ile Ile Pro Ile Lys Ala Val Glu Glu Ile Ile Lys Met Cys

130 135 140  
 Ser Asp Glu Gly Glu Ala Thr Ile Phe Leu Asp Gln Asp Lys Ile Ala  
 145 150 155 160  
 Val Glu Cys Asp Asn Thr Leu Leu Ile Thr Lys Leu Leu Ser Gly Glu  
 165 170 175  
 Phe Pro Asp Phe Ser Pro Val Ile Ser Thr Glu Ser Asn Val Lys Leu  
 180 185 190  
 Asp Leu His Arg Glu Glu Leu Ile Thr Leu Leu Lys Gln Val Ala Leu  
 195 200 205  
 Phe Thr Asn Glu Ser Ser His Ser Val Lys Phe Ser Phe Leu Pro Gly  
 210 215 220  
 Glu Leu Thr Leu Thr Ala Asn Cys Thr Lys Val Gly Glu Gly Lys Val  
 225 230 235 240  
 Ser Met Ala Val Asn Tyr Ser Gly Glu Leu Leu Glu Ile Ala Phe Asn  
 245 250 255  
 Pro Phe Phe Phe Leu Asp Ile Leu Lys His Ser Lys Asp Glu Leu Val  
 260 265 270  
 Ser Leu Gly Ile Ser Asp Ser Tyr Asn Pro Gly Ile Ile Thr Asp Ser  
 275 280 285  
 Ala Ser Gly Leu Phe Val Ile Met Pro Met Arg Leu His Asp Asp  
 290 295 300  
 <210>358  
 <211>218  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>358  
 Pro Leu Tyr Pro Leu Leu Ile Val Leu Ser Ser Arg Ser Ser Ala Glu  
 1 5 10 15  
 Lys Cys Ser Leu Lys Lys Gln Ala Asn Leu Asn Arg Gly Leu Trp Asp  
 20 25 30  
 Glu Gln Leu Val Lys His Gly Thr Tyr Leu Ser Ile Gln Arg Phe Leu  
 35 40 45  
 Cys Ser Gln Lys Leu Ser Asp Leu Ser Lys Glu Leu Trp Ser Asn Asn  
 50 55 60  
 Leu Lys Glu Gln Leu Ala Leu Lys Phe Lys Ser Ser Leu Ile Lys Asn  
 65 70 75 80  
 Ser Asp Ile Ser Glu Thr Ala Val Ala Glu Glu Phe His Lys Gln Leu  
 85 90 95  
 Ser Ile Ser Leu Pro Arg Asp Leu Glu Trp Gly Ser Thr Ser Val Gly  
 100 105 110  
 Pro His Arg Glu Asp Phe Leu Leu Thr Met Asn Gln Met Pro Val Ser  
 115 120 125  
 Gln Phe Ser Ser Glu Gly Gln Lys His Ser Leu Leu Ala Ile Leu Arg  
 130 135 140  
 Leu Ala Glu Cys Leu Tyr Leu Lys Gln Ser His His Val Ser Pro Leu  
 145 150 155 160  
 Val Cys Leu Asp Asp Ile His Ala Gly Leu Asp Asn Glu Arg Val Gly  
 165 170 175  
 Gln Leu Leu Asp Pro Ala Pro Thr Leu Gly Gln Thr Leu Ile Thr Ser  
 180 185 190  
 Thr His Met His Gly Glu Leu Pro Lys Thr Ser Leu Val Leu Ser Ile  
 195 200 205  
 Glu Asn Ala Gln Val Ser Glu Gln Ile Ile  
 210 215  
 <210>359  
 <211>127  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>359  
 His Met Lys Lys Phe Leu Leu Thr Ile Leu Phe Leu Ala Val Gly Asn  
 1 5 10 15  
 Pro Leu Phe Ser Glu Thr Ser Val Ile Gln Thr Leu Pro Ser Gly Ile  
 20 25 30  
 Gly Gly Leu Lys Glu Thr Ser Lys Gln Lys Glu Ser Val Val Cys Val

35 40 45  
 His Ala Phe Leu Arg Ser Tyr Thr Ser Leu Lys Pro Ile Ala Arg Val  
 50 55 60  
 Leu Glu Lys Glu His Tyr Asp Val Phe Ile Trp Asn Tyr Glu Thr Arg  
 65 70 75 80  
 Lys Phe Thr Leu Glu Lys His Ala Glu His Leu Asn Arg Leu Leu Lys  
 85 90 95  
 Lys Ile Ala Glu Leu Lys Pro Gly Val Pro Ile Asn Phe Val Thr His  
 100 105 110  
 Ser Ile Gly Gly Val Ile Val Arg Ala Leu Ala Glu Lys Asn Ser  
 115 120 125

&lt;210&gt;360

&lt;211&gt;244

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;360

Leu Ile Leu Leu Glu Glu Ser Leu Phe Val Arg Leu Leu Lys Lys Ile  
 1 5 10 15  
 Ala Glu Leu Lys Pro Gly Val Pro Ile Asn Phe Val Thr His Ser Ile  
 20 25 30  
 Gly Gly Val Ile Val Arg Val Ala Leu Ala His Pro Asp Cys Pro Glu  
 35 40 45  
 Glu Ala Lys Lys Gly Lys Ala Ile Leu Met Ala Pro Pro Asn Ala Gly  
 50 55 60  
 Ser Thr Leu Ala Arg Arg Tyr Arg Cys Val Lys Phe Val Gln Phe Val  
 65 70 75 80  
 Phe Gly Gly Lys Leu Gly Arg Gln Leu Leu Thr Tyr Cys Pro Thr Lys  
 85 90 95  
 Met Leu Asn Val Gly Lys Leu Pro Ser Ser Leu Asp Val Leu Ile Leu  
 100 105 110  
 Ser Gly Asn Arg His Ser Lys Phe Leu Pro Phe Arg Leu Pro Tyr Glu  
 115 120 125  
 Asn Asp Gly Lys Val Cys Thr Ile Glu Thr Lys Leu Asp Thr Pro His  
 130 135 140  
 Lys Ala Tyr Val Ile His Thr Ser His Thr Tyr Ile Ile Thr Asn Arg  
 145 150 155 160  
 Lys Ser Leu Tyr Leu Met Lys Glu Phe Leu Lys Glu Gly Asn Thr Thr  
 165 170 175  
 Pro Ile Ile Glu His Val Pro Glu Ala Ala Leu Glu Gln Thr Val Met  
 180 185 190  
 Glu Asp Lys Gln Lys Asn Ser Arg Leu Lys Pro Tyr Pro Asn Gln Asp  
 195 200 205  
 Ile Tyr Val Ile His Cys Phe Gly Ser Arg Pro Tyr Asn Leu Tyr Gly  
 210 215 220  
 Phe Pro Lys Lys Trp Ser Leu Asn Gln Lys Asn Glu Ile Asn Pro Glu  
 225 230 235 240  
 Lys Leu Glu Lys

&lt;210&gt;361

&lt;211&gt;621

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;361

Met Thr Ile Ile Tyr Phe Ile Leu Ala Ala Leu Ala Leu Gly Ile Leu  
 1 5 10 15  
 Val Leu Ile His Glu Leu Gly His Leu Val Val Ala Lys Ala Val Gly  
 20 25 30  
 Met Ala Val Glu Ser Phe Ser Ile Gly Phe Gly Pro Ala Leu Phe Lys  
 35 40 45  
 Lys Arg Ile Gly Gly Ile Glu Tyr Arg Ile Gly Cys Ile Pro Phe Gly  
 50 55 60  
 Gly Tyr Val Arg Ile Arg Gly Met Glu Arg Thr Lys Glu Lys Gly Glu  
 65 70 75 80  
 Lys Gly Lys Ile Asp Ser Val Tyr Asp Ile Pro Gln Gly Phe Phe Ser

576



595 600 605  
 Ile Phe Leu Thr Phe Gln Asp Leu Phe Arg Phe Phe Gly  
 610 615 620  
 <210>362  
 <211>340  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>362  
 Ser Lys Val Ile Phe Gln Gln Leu Gln Glu Phe Ala Pro Leu Ala Ala  
 1 5 10 15  
 Ala Val Tyr Asn Glu Glu Val Tyr Asn Glu Ala Cys Gln Arg Phe Pro  
 20 25 30  
 His Met Gln Phe Phe Leu Gly Gln Glu Gly Leu Thr Gln Leu Cys Ile  
 35 40 45  
 Met Asp Thr Val Thr Thr Val Val Ala Ala Ser Ser Gly Ile Glu Ala  
 50 55 60  
 Leu Pro Ala Ile Leu Glu Ser Met Lys Lys Gly Lys Ala Leu Ala Leu  
 65 70 75 80  
 Ala Asn Lys Glu Ile Leu Val Cys Ala Gly Glu Leu Val Ser Lys Thr  
 85 90 95  
 Ala Lys Glu Asn Gly Ile Lys Val Leu Pro Ile Asp Ser Glu His Asn  
 100 105 110  
 Ala Leu Tyr Gln Cys Leu Glu Gly Arg Thr Ile Glu Gly Ile Lys Lys  
 115 120 125  
 Leu Ile Leu Thr Ala Ser Gly Gly Pro Leu Leu Asn Lys Ser Leu Glu  
 130 135 140  
 Glu Leu Ser Cys Val Thr Lys Gln Asp Val Leu Asn His Pro Ile Trp  
 145 150 155 160  
 Asn Met Gly Ser Lys Val Thr Val Asp Ser Ser Thr Leu Val Asn Lys  
 165 170 175  
 Gly Leu Glu Ile Ile Glu Ala Tyr Trp Leu Phe Gly Leu Glu Asn Val  
 180 185 190  
 Glu Ile Leu Ala Val Ile His Pro Gln Ser Leu Ile His Gly Met Val  
 195 200 205  
 Glu Phe Leu Asp Gly Ser Val Ile Ser Ile Met Asn Pro Pro Asp Met  
 210 215 220  
 Leu Phe Pro Ile Gln Tyr Ala Leu Thr Ala Pro Glu Arg Phe Ala Ser  
 225 230 235 240  
 Pro Arg Asp Gly Met Asp Phe Ser Lys Lys Gln Thr Leu Glu Phe Phe  
 245 250 255  
 Pro Val Asp Glu Glu Arg Phe Pro Ser Ile Arg Leu Ala Gln Gln Val  
 260 265 270  
 Leu Glu Lys Gln Gly Ser Ser Gly Ser Phe Phe Asn Ala Ala Asn Glu  
 275 280 285  
 Val Leu Val Arg Arg Phe Leu Cys Glu Glu Ile Ser Trp Cys Asp Ile  
 290 295 300  
 Leu Arg Lys Leu Thr Thr Leu Met Glu Cys His Lys Val Tyr Ala Cys  
 305 310 315 320  
 His Ser Leu Glu Asp Ile Leu Glu Val Asp Gly Glu Ala Arg Ala Leu  
 325 330 335  
 Ala Gln Glu Ile  
 340  
 <210>363  
 <211>329  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>363  
 Lys Lys Gly Ser Leu Met Ala Leu Gly Pro Ser Pro Tyr Tyr Gly Val  
 1 5 10 15  
 Ser Phe Phe Gln Phe Phe Ser Val Phe Phe Ser Arg Leu Phe Ser Gly  
 20 25 30  
 Ser Leu Phe Thr Gly Ser Leu Tyr Ile Asp Asp Ile Gln Ile Ile Val  
 35 40 45  
 Phe Leu Ala Ile Ser Cys Ser Gly Ala Phe Ala Gly Thr Phe Leu Val

50 55 60  
 Leu Arg Lys Met Ala Met Tyr Ala Asn Ala Val Ser His Thr Val Leu  
 65 70 75 80  
 Phe Gly Leu Val Cys Val Cys Leu Phe Thr His Gln Leu Thr Thr Leu  
 85 90 95  
 Ser Leu Gly Thr Leu Thr Leu Ala Ala Met Ala Thr Ala Met Leu Thr  
 100 105 110  
 Gly Phe Leu Ile Tyr Phe Ile Arg Asn Thr Phe Lys Val Ser Glu Glu  
 115 120 125  
 Ser Ser Thr Ala Leu Val Phe Ser Leu Leu Phe Ser Leu Ser Leu Val  
 130 135 140  
 Leu Leu Val Phe Met Thr Lys Asn Ala His Ile Gly Thr Glu Leu Val  
 145 150 155 160  
 Leu Gly Asn Ala Asp Ser Leu Thr Lys Glu Asp Ile Phe Pro Val Thr  
 165 170 175  
 Ile Val Ile Leu Ala Asn Ala Val Ile Thr Ile Phe Ala Phe Arg Ser  
 180 185 190  
 Leu Val Cys Ser Ser Phe Asp Ser Val Phe Ala Ser Ser Leu Gly Ile  
 195 200 205  
 Pro Ile Arg Leu Val Asp Tyr Leu Ile Ile Phe Gln Leu Ser Ala Cys  
 210 215 220  
 Leu Val Gly Ala Phe Lys Ala Val Gly Val Leu Met Ala Leu Ala Phe  
 225 230 235 240  
 Leu Ile Ile Pro Ser Leu Ile Ala Lys Val Ile Ala Lys Ser Ile Arg  
 245 250 255  
 Ser Leu Met Ala Trp Ser Leu Val Phe Ser Ile Xaa Thr Ala Phe Leu  
 260 265 270  
 Ala Pro Ala Ser Ser Arg Ala Ile Leu Ser Ala Tyr Asp Leu Gly Leu  
 275 280 285  
 Ser Thr Ser Gly Ile Ser Val Val Phe Leu Thr Met Met Tyr Ile Val  
 290 295 300  
 Val Lys Phe Ile Ser Tyr Phe Arg Gly Tyr Phe Ser Lys Asn Phe Glu  
 305 310 315 320  
 Lys Ile Ser Glu Lys Ser Ser Gln Tyr  
 325

&lt;210&gt;364

&lt;211&gt;391

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;364

Trp Arg Asn Met Phe Ser His Cys Lys Leu Leu Phe Phe Gly Leu Cys  
 1 5 10 15  
 Cys Leu Gly Val Leu Leu Arg Tyr Leu Val Met Gly Ile Ile Val Phe  
 20 25 30  
 Leu Gly Lys Val Cys Lys Leu His Lys Asp Ser Ala Leu Cys Phe Val  
 35 40 45  
 Leu Val Val Phe Phe Ala Ile Gly Val Ile Leu Ala Ser Tyr Val Lys  
 50 55 60  
 Glu Ser Ser Pro Thr Leu Tyr Asn Arg Ile Asn Ala Tyr Leu Tyr Gly  
 65 70 75 80  
 Gln Ala Ala Thr Leu Gly Phe Leu Glu Ala Thr Leu Ala Ala Ile Val  
 85 90 95  
 Phe Cys Ala Ser Leu Phe Ala Leu Trp Trp Trp Tyr Arg Gln Ile Val  
 100 105 110  
 Val Thr Thr Phe Asp Lys Asp Phe Ala Val Thr Cys Gly Leu Lys Thr  
 115 120 125  
 Val Leu Tyr Glu Ala Leu Ser Leu Ile Phe Ile Ser Leu Val Ile Val  
 130 135 140  
 Ser Gly Val Arg Ser Val Gly Ile Val Leu Ile Ser Ala Met Phe Val  
 145 150 155 160  
 Ala Pro Ser Leu Gly Ala Arg Gln Leu Ser Asp Arg Leu Ser Thr Ile  
 165 170 175  
 Leu Ile Leu Ser Ala Phe Phe Gly Gly Ile Ser Gly Ala Leu Gly Ser  
 180 185 190

Tyr Ile Ser Val Ala Phe Thr Cys Arg Ala Ile Ile Gly Gln Gln Ala  
 195 200 205  
 Val Pro Val Thr Leu Pro Thr Gly Pro Leu Val Val Ile Cys Ala Gly  
 210 215 220  
 Leu Leu Ala Gly Leu Cys Leu Leu Phe Ser Pro Lys Ser Gly Trp Val  
 225 230 235 240  
 Ile Arg Phe Val Arg Arg Lys His Phe Ser Phe Ser Lys Asp Gln Glu  
 245 250 255  
 His Leu Leu Lys Val Phe Trp His Ile Ser His Asn Arg Leu Glu Asn  
 260 265 270  
 Ile Ser Val Arg Asp Phe Val Cys Ser Tyr Lys Tyr Gln Glu Tyr Phe  
 275 280 285  
 Gly Pro Lys Pro Phe Pro Arg Trp Arg Val Gln Ile Leu Glu Trp Arg  
 290 295 300  
 Gly Tyr Val Lys Lys Glu Gln Asp Tyr Tyr Arg Leu Thr Lys Lys Gly  
 305 310 315 320  
 Arg Ser Glu Ala Leu Arg Leu Val Arg Ala His Arg Leu Trp Glu Ser  
 325 330 335  
 Tyr Leu Val Asn Ser Leu Asp Phe Ser Lys Glu Ser Val His Glu Leu  
 340 345 350  
 Ala Glu Glu Ile Glu His Val Leu Thr Glu Glu Leu Asp His Thr Leu  
 355 360 365  
 Thr Glu Ile Leu Asn Asp Pro Cys Tyr Asp Pro His Arg Gln Ile Ile  
 370 375 380  
 Pro Asn Lys Lys Lys Glu Val  
 385 390

&lt;210&gt;365

&lt;211&gt;113

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;365

Thr Phe Gly Thr Asn Pro Glu Ala Leu Ser Arg Lys Thr Ile Trp Ile  
 1 5 10 15  
 Val Leu Ile Met Leu Ser Cys Val Phe Ser Asp Thr Ile Phe Leu Ser  
 20 25 30  
 Ser Phe Leu Ala Val Thr Leu Ile Cys Met Thr Thr Ala Leu Trp Gly  
 35 40 45  
 Thr Ile Leu Leu Ile Ser Lys Gln Pro Leu Leu Ser Glu Ser Leu Ser  
 50 55 60  
 His Ala Ser Tyr Pro Gly Leu Leu Val Gly Ala Leu Met Ala Gln Tyr  
 65 70 75 80  
 Val Phe Ser Leu Gln Ala Ser Ile Phe Trp Ile Val Leu Phe Gly Cys  
 85 90 95  
 Ala Ala Ser Val Phe Gly Tyr Gly Asp His Cys Phe Leu Arg Glu Ser  
 100 105 110

Met

&lt;210&gt;366

&lt;211&gt;259

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;366

Leu Asn Val Lys Asp Glu Thr Phe Trp Ser Val His Asn Leu Cys Val  
 1 5 10 15  
 Asn Tyr Glu His Ala Ala Val Leu Tyr His Ile Ser Phe Ser Leu Gly  
 20 25 30  
 Lys Gly Ser Leu Thr Ala Ile Leu Gly Pro Asn Gly Ala Gly Lys Ser  
 35 40 45  
 Thr Leu Leu Lys Ala Ser Leu Gly Leu Ile Lys Pro Ser Ser Gly Thr  
 50 55 60  
 Val Tyr Phe Phe Asn Gln Lys Phe Lys Lys Val Arg Gln Arg Ile Ala  
 65 70 75 80  
 Tyr Met Pro Gln Arg Ala Ser Val Asp Trp Asp Phe Pro Met Thr Val  
 85 90 95

Leu Asp Leu Ala Leu Met Gly Cys Tyr Ser Tyr Lys Gly Met Trp Gly  
 100 105 110  
 Arg Ile Ser Ser Asp Asp Arg Arg Glu Ala Phe His Ile Leu Glu Arg  
 115 120 125  
 Val Gly Leu Glu Ser Val Ala Asp Arg Gln Ile Gly Gln Leu Ser Gly  
 130 135 140  
 Gly Gln Gln Gln Arg Ala Phe Leu Ala Arg Ala Leu Met Gln Lys Ala  
 145 150 155 160  
 Asp Leu Tyr Leu Met Asp Glu Leu Phe Ser Ala Ile Asp Met Ala Ser  
 165 170 175  
 Phe Lys Thr Ser Val Gly Val Leu Gln Glu Leu Arg Asp Gln Gly Lys  
 180 185 190  
 Thr Ile Val Val Val His His Asp Leu Ser His Val Arg Gln Leu Phe  
 195 200 205  
 Asp His Val Val Leu Leu Asn Lys Arg Leu Ile Cys Cys Gly Pro Thr  
 210 215 220  
 Asp Glu Cys Leu Asn Gly Asp Thr Ile Phe Gln Thr Tyr Gly Cys Glu  
 225 230 235 240  
 Ile Glu Leu Leu Glu Gln Thr Leu Lys Leu Ser Arg Gly Lys Gln Phe  
 245 250 255  
 Gly Ser Cys

&lt;210&gt;367

&lt;211&gt;336

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;367

Trp Ile Leu Lys Asn Ala Ser Arg Glu Met Asp Ala Lys Met Gly Tyr  
 1 5 10 15  
 Ile Phe Lys Val Met Arg Trp Ile Phe Cys Phe Val Ala Cys Gly Ile  
 20 25 30  
 Thr Phe Gly Cys Thr Asn Ser Gly Phe Gln Asn Ala Asn Ser Arg Pro  
 35 40 45  
 Cys Ile Leu Ser Met Asn Arg Met Ile His Asp Cys Val Glu Arg Val  
 50 55 60  
 Val Gly Asn Arg Leu Ala Thr Ala Val Leu Ile Lys Gly Ser Leu Asp  
 65 70 75 80  
 Pro His Ala Tyr Glu Met Val Lys Gly Asp Lys Asp Lys Ile Ala Gly  
 85 90 95  
 Ser Ala Val Ile Phe Cys Asn Gly Leu Gly Leu Glu His Thr Leu Ser  
 100 105 110  
 Leu Arg Lys His Leu Glu Asn Asn Pro Asn Ser Val Lys Leu Gly Glu  
 115 120 125  
 Arg Leu Ile Ala Arg Gly Ala Phe Val Pro Leu Glu Glu Asp Gly Ile  
 130 135 140  
 Cys Asp Pro His Ile Trp Met Asp Leu Ser Ile Trp Lys Glu Ala Val  
 145 150 155 160  
 Ile Glu Ile Thr Glu Val Leu Ile Glu Lys Phe Pro Glu Trp Ser Ala  
 165 170 175  
 Glu Phe Lys Ala Asn Ser Glu Glu Leu Val Cys Glu Met Ser Ile Leu  
 180 185 190  
 Asp Ser Trp Ala Lys Gln Cys Leu Ser Thr Ile Pro Glu Asn Leu Arg  
 195 200 205  
 Tyr Leu Val Ser Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr  
 210 215 220  
 Leu Ala Thr Pro Glu Glu Val Ala Ser Gly Ala Trp Arg Ser Arg Cys  
 225 230 235 240  
 Ile Ser Pro Glu Gly Leu Ser Pro Glu Ala Gln Ile Ser Val Arg Asp  
 245 250 255  
 Ile Met Ala Val Val Asp Tyr Ile Asn Glu His Asp Val Ser Val Val  
 260 265 270  
 Phe Pro Glu Asp Thr Leu Asn Gln Asp Ala Leu Lys Lys Ile Val Ser  
 275 280 285  
 Ser Leu Lys Lys Ser His Leu Val Arg Leu Ala Gln Lys Pro Leu Tyr

290 295 300  
 Ser Asp Asn Val Asp Asp Asn Tyr Phe Ser Thr Phe Lys His Asn Val  
 305 310 315 320  
 Cys Leu Ile Thr Glu Glu Leu Gly Gly Val Ala Leu Glu Cys Gln Arg  
 325 330 335

&lt;210&gt;368

&lt;211&gt;172

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;368

Lys Val Gly Phe Met Ala Val Glu Gln Ser His Ile Lys Glu Glu Ile  
 1 5 10 15  
 Glu Lys Leu Ile Gly Lys Ala Ile Lys Arg Val Cys Gly Asn Lys Glu  
 20 25 30  
 Asn Asp Leu Cys Arg Tyr Leu Pro Gly Pro Ser Gly Gly Tyr Met His  
 35 40 45  
 His Phe Thr Leu Lys Lys Met Lys Ser Ala Ala Pro Glu Gln Leu Leu  
 50 55 60  
 Lys Met Leu Lys Thr Phe Ile Leu Glu Ser Glu Thr Pro Arg Thr Ile  
 65 70 75 80  
 Asn Pro Lys Pro Arg Ala Pro Arg Gly Ser Lys Lys Arg Arg Asp Phe  
 85 90 95  
 Ile Asn Phe Thr Lys Thr Asp Ile Glu Arg Val Leu Glu Leu Ala Arg  
 100 105 110  
 Gln Val Gly Asp Lys Asp Leu Leu Ala Arg Phe Ser Pro Lys Lys Pro  
 115 120 125  
 Leu Thr Ser Leu Lys Arg Glu Leu Ile Arg Ser Ile Arg Asn Gly Ile  
 130 135 140  
 Val Ser Val Glu Leu Trp Asn Ala Tyr Val Glu Ala Val Lys Ala Val  
 145 150 155 160  
 Ser Ser Pro Asn Leu Glu Val Thr Ser Pro Phe Val  
 165 170

&lt;210&gt;369

&lt;211&gt;524

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;369

Lys Ile Lys Val Phe Gln Arg Val Asn Met Thr Lys Thr Glu Glu Lys  
 1 5 10 15  
 Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro Ile His Thr His Glu  
 20 25 30  
 Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe Phe Cys Ile Thr Phe  
 35 40 45  
 Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr Leu Ile Val Gly Ala  
 50 55 60  
 Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile Lys Phe Trp Leu Val  
 65 70 75 80  
 Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr Ala Lys Leu Ser Asn  
 85 90 95  
 Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val Gly Thr Pro Phe Leu  
 100 105 110  
 Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr Pro Leu Arg Asp Val  
 115 120 125  
 Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln Ala Ile Leu Pro Pro  
 130 135 140  
 Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn Trp Thr Phe Ala Ala  
 145 150 155 160  
 Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val Met Leu Ser Leu Met  
 165 170 175  
 Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile His Glu Ala Lys Arg  
 180 185 190  
 Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile Ser Leu Leu Ala Ser  
 195 200 205  
 Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg Ala Ser Val Ser Glu

210 215 220  
 Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu Leu Met Ala Met Thr  
 225 230 235 240  
 Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr Trp Trp Ile Asn Lys  
 245 250 255  
 Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro Glu Glu Met Gln Lys  
 260 265 270  
 Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met Lys Asp Ser Phe Leu  
 275 280 285  
 Tyr Leu Ala Arg Ser Pro Tyr Ile Leu Leu Leu Ala Leu Leu Val Ile  
 290 295 300  
 Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val Thr Trp Lys Ser Gln  
 305 310 315 320  
 Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr Ser Glu Phe Met Gly  
 325 330 335  
 Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val Leu Ile Met Leu Phe  
 340 345 350  
 Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp Leu Thr Gly Ala Leu  
 355 360 365  
 Val Thr Pro Val Met Val Leu Thr Gly Ile Val Phe Phe Ala Leu  
 370 375 380  
 Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val Ala Met Phe Gly Thr  
 385 390 395 400  
 Thr Pro Leu Met Leu Ala Val Val Val Gly Ala Ile Gln Asn Ile Leu  
 405 410 415  
 Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser Thr Lys Glu Met Ala  
 420 425 430  
 Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys Gly Lys Ala Ala Ile  
 435 440 445  
 Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly Gly Ala Leu Ile Gln  
 450 455 460  
 Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly Ala Met Thr Pro Tyr  
 465 470 475 480  
 Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile Trp Leu Val Ser Ala  
 485 490 495  
 Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser Ala Leu Lys Glu Gln  
 500 505 510  
 Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser Ser  
 515 520

&lt;210&gt;370

&lt;211&gt;448

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;370

Leu Pro Phe His Glu Phe Val Arg Phe Phe Gln Ser Lys Lys Val Ile  
 1 5 10 15  
 Ile Thr Val Arg His Ser Gly Cys Thr Met Lys Cys Ser Pro Leu Thr  
 20 25 30  
 Leu Val Pro His Ile Phe Leu Lys Asn Asp Cys Glu Cys His Arg Ser  
 35 40 45  
 Cys Ser Leu Lys Ile Arg Thr Ile Ala Arg Leu Ile Leu Gly Leu Val  
 50 55 60  
 Leu Ala Leu Val Ser Ala Leu Ser Phe Val Phe Leu Ala Ala Pro Ile  
 65 70 75 80  
 Ser Tyr Ala Ile Gly Gly Thr Leu Ala Leu Ala Ala Ile Val Ile Leu  
 85 90 95  
 Ile Ile Thr Leu Val Val Ala Leu Leu Ala Lys Ser Lys Val Leu Pro  
 100 105 110  
 Ile Pro Asn Glu Leu Gln Lys Ile Tyr Asn Arg Tyr Pro Lys Glu  
 115 120 125  
 Val Phe Tyr Phe Val Lys Thr His Ser Leu Thr Val Asn Glu Leu Lys  
 130 135 140  
 Ile Phe Ile Asn Cys Trp Lys Ser Gly Thr Asp Leu Pro Pro Asn Leu  
 145 150 155 160

His Lys Lys Ala Glu Ala Phe Gly Ile Asp Ile Leu Lys Ser Ile Asp  
 165 170 175  
 Leu Thr Leu Phe Pro Glu Phe Glu Glu Ile Leu Leu Gln Asn Cys Pro  
 180 185 190  
 Leu Tyr Trp Leu Ser His Phe Ile Asp Lys Thr Glu Ser Val Ala Gly  
 195 200 205  
 Glu Ile Gly Leu Asn Lys Thr Gln Lys Val Tyr Gly Leu Leu Gly Pro  
 210 215 220  
 Leu Ala Phe His Lys Gly Tyr Thr Thr Ile Phe His Ser Tyr Thr Arg  
 225 230 235 240  
 Pro Leu Leu Thr Leu Ile Ser Glu Ser Gln Tyr Lys Phe Leu Tyr Ser  
 245 250 255  
 Lys Ala Ser Lys Asn Gln Trp Asp Ser Pro Ser Val Lys Lys Thr Cys  
 260 265 270  
 Glu Glu Ile Phe Lys Glu Leu Pro His Asn Met Ile Phe Arg Lys Asp  
 275 280 285  
 Val Gln Gly Ile Ser Gln Phe Leu Phe Leu Phe Phe Ser His Gly Ile  
 290 295 300  
 Thr Trp Glu Gln Ala Gln Met Ile Gln Leu Ile Asn Pro Asp Asn Trp  
 305 310 315 320  
 Lys Met Leu Cys Gln Phe Asp Lys Ala Gly Gly His Cys Ser Met Ala  
 325 330 335  
 Thr Phe Gly Gly Phe Leu Asn Thr Glu Thr Asn Met Phe Asp Pro Val  
 340 345 350  
 Ser Ser Asn Tyr Glu Pro Thr Val Asn Phe Met Thr Trp Lys Glu Leu  
 355 360 365  
 Lys Val Leu Leu Glu Lys Val Lys Glu Ser Pro Met His Pro Ala Ser  
 370 375 380  
 Ala Leu Val Gln Lys Ile Cys Val Asn Thr Thr His His Gln Asn Leu  
 385 390 395 400  
 Leu Lys Arg Trp Gln Phe Val Arg Asn Thr Ser Ser Gln Trp Thr Ser  
 405 410 415  
 Ser Leu Pro Gln Tyr Ala Phe His Ala Gln Thr Tyr Lys Leu Glu Lys  
 420 425 430  
 Lys Asn Arg Lys Gln Ser Pro Tyr Thr Ile Phe Pro Ile Arg Gly Val  
 435 440 445  
 <210>371  
 <211>365  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>371  
 Ile Lys Glu Phe Asn His Tyr Ser Tyr Cys Tyr Gln Cys His Leu Thr  
 1 5 10 15  
 Leu Arg Thr Leu Ile Ala Phe Leu Cys Val Ala Ala Pro Val Ser Tyr  
 20 25 30  
 Ile Leu Ser Gly Ala Leu Leu Gly Leu Gly Leu Leu Ile Ala Leu Ile  
 35 40 45  
 Gly Val Ile Leu Gly Ile Lys Lys Ile Thr Pro Met Ile Ser Ser Lys  
 50 55 60  
 Glu Gln Val Phe Pro Gln Glu Leu Val Asn Arg Ile Arg Ala His Tyr  
 65 70 75 80  
 Pro Lys Phe Val Ser Asp Phe Val Ser Glu Ala Lys Pro Asn Leu Lys  
 85 90 95  
 Asp Leu Ile Ser Phe Ile Asp Leu Leu Asn Gln Leu His Ser Glu Val  
 100 105 110  
 Gly Ser Ser Thr Asn Tyr Asn Val Ser Glu Glu Leu Gln Gln Lys Ile  
 115 120 125  
 Asp Thr Phe Glu Gly Ile Ala Arg Leu Lys Asn Glu Val Arg Thr Ala  
 130 135 140  
 Ser Leu Lys Arg Leu Glu Ser Ala Ala Ser Ser Arg Pro Leu Phe Pro  
 145 150 155 160  
 Ser Leu Pro Lys Ile Leu Gln Lys Val Phe Pro Phe Phe Trp Leu Gly  
 165 170 175  
 Glu Phe Ile Ser Ala Gly Ser Lys Val Val Glu Leu His Arg Val Lys

180 185 190  
 Lys Ile Gly Gly Ser Leu Glu Glu Asp Leu Ser Asp Tyr Ile Lys Pro  
 195 200 205  
 Glu Met Leu Pro Thr Tyr Trp Leu Ile Pro Leu Asp Phe Arg Pro Thr  
 210 215 220  
 Asn Ser Ser Ile Leu Asn Leu His Thr Leu Val Leu Ala Arg Val Leu  
 225 230 235 240  
 Thr Arg Asp Val Phe Gln His Leu Lys Tyr Ala Ala Leu Asn Gly Glu  
 245 250 255  
 Trp Asn Leu Asn His Ser Asp Leu Asn Thr Met Lys Gln Gln Leu Phe  
 260 265 270  
 Ala Lys Tyr His Ala Ala Tyr Gln Ser Tyr Lys His Leu Ser Gln Pro  
 275 280 285  
 Ser Leu Gln Glu Asp Glu Phe Tyr Asn Leu Leu Leu Cys Ile Phe Lys  
 290 295 300  
 His Arg Tyr Ser Trp Lys Gln Met Ser Leu Ile Lys Thr Val Pro Ala  
 305 310 315 320  
 Asp Leu Trp Glu Asn Leu Cys Cys Leu Thr Leu Asp His Thr Gly Arg  
 325 330 335  
 Pro Gln Asp Met Glu Phe Ala Ser Leu Ile Gly Thr Leu Tyr Thr Gln  
 340 345 350  
 Gly Leu Ile His Lys Glu Ser Glu His Phe Phe Leu His  
 355 360 365  
 <210>372  
 <211>455  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>372  
 Ile Arg Asp Phe Tyr Leu His Ile Ile Tyr Thr Ala Phe Asn Arg Ser  
 1 5 10 15  
 Ile Ser Lys Glu Leu Ala Met Ser Met Thr Ile Val Pro His Ala Leu  
 20 25 30  
 Phe Lys Asn His Cys Glu Cys His Ser Thr Phe Pro Leu Ser Ser Arg  
 35 40 45  
 Thr Ile Val Arg Ile Ala Ile Ala Ser Leu Phe Cys Ile Gly Ala Leu  
 50 55 60  
 Ala Ala Leu Gly Cys Leu Ala Pro Pro Val Ser Tyr Ile Val Gly Ser  
 65 70 75 80  
 Val Leu Ala Phe Ile Ala Phe Val Ile Leu Ser Leu Val Ile Leu Ala  
 85 90 95  
 Leu Ile Phe Gly Glu Lys Lys Leu Pro Pro Thr Pro Arg Ile Ile Pro  
 100 105 110  
 Asp Arg Phe Thr His Val Ile Asp Glu Ala Tyr Gly Leu Ser Ile Ser  
 115 120 125  
 Ala Phe Val Arg Glu Gln Gln Val Thr Leu Ala Glu Phe Arg Gln Phe  
 130 135 140  
 Ser Thr Ala Leu Leu Cys Asn Ile Ser Pro Glu Glu Lys Ile Lys Gln  
 145 150 155 160  
 Leu Pro Ser Glu Leu Arg Ser Lys Val Glu Ser Phe Gly Ile Ser Arg  
 165 170 175  
 Leu Ala Gly Asp Leu Glu Lys Asn Asn Trp Pro Ile Phe Glu Asp Leu  
 180 185 190  
 Leu Ser Gln Thr Cys Pro Leu Tyr Trp Leu Gln Lys Phe Ile Ser Ala  
 195 200 205  
 Gly Asp Pro Gln Val Cys Arg Asp Leu Gly Val Pro Arg Glu Cys Tyr  
 210 215 220  
 Gly Tyr Tyr Trp Leu Gly Pro Leu Gly Tyr Ser Thr Ala Lys Ala Thr  
 225 230 235 240  
 Ile Phe Cys Lys Glu Thr His His Ile Leu Gln Gln Leu Thr Lys Glu  
 245 250 255  
 Asp Val Leu Leu Lys Asn Lys Ala Leu Gln Glu Lys Trp Asp Thr  
 260 265 270  
 Asp Glu Val Lys Ala Ile Val Glu Arg Ile Tyr Thr Thr Tyr Thr Ala  
 275 280 285



Arg Gly Thr Leu Lys Thr Glu Ala Gly Gly Leu Thr Lys Glu Thr Ile  
 290 295 300  
 Ser Lys Glu Leu Leu Leu Ser Leu His Gly Tyr Ser Phe Asp Gln  
 305 310 315 320  
 Leu Gln Leu Ile Thr Gln Leu Pro Arg Asp Ala Trp Asp Trp Leu Cys  
 325 330 335  
 Phe Val Asp Asn Ser Thr Ala Tyr Asn Leu Gln Leu Cys Ala Leu Val  
 340 345 350  
 Gly Ala Leu Ser Ser Gln Asn Leu Asp Glu Ser Ser Ile Asp Phe  
 355 360 365  
 Asp Val Asn Leu Gly Leu Tyr Val Ile Gln Asp Leu Lys Glu Ala Val  
 370 375 380  
 Gln Ala Phe Ser Ala Ser Asp Glu Pro Lys Lys Glu Leu Gly Lys Phe  
 385 390 395 400  
 Leu Leu Arg His Leu Ser Ser Val Ser Lys Arg Leu Glu Ser Val Leu  
 405 410 415  
 Arg Gln Gly Leu His Arg Ile Ala Leu Glu His Gly Asn Ala Arg Ala  
 420 425 430  
 Arg Val Tyr Asp Val Asn Phe Val Thr Gly Ala Arg Ile His Arg Lys  
 435 440 445  
 Thr Ser Ile Phe Phe Lys Asp  
 450 455  
 <210>373  
 <211>291  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>373  
 Tyr Ser Ser His Asn Gly Ala Ser Met Val Asn Ile Gln Pro Val Tyr  
 1 5 10 15  
 Arg Asn Thr Gln Val Asn Tyr Ser Gln Ala Thr Gln Phe Ser Val Cys  
 20 25 30  
 Gln Pro Ala Leu Ser Leu Ile Ile Val Ser Val Val Ala Ala Val Leu  
 35 40 45  
 Ala Ile Val Ala Leu Val Cys Ser Gln Ser Leu Leu Ser Ile Glu Leu  
 50 55 60  
 Gly Thr Ala Leu Val Leu Val Ser Leu Ile Leu Phe Ala Ser Ala Met  
 65 70 75 80  
 Phe Met Ile Tyr Lys Met Arg Gln Glu Pro Lys Glu Leu Leu Ile Pro  
 85 90 95  
 Lys Lys Ile Met Glu Leu Ile Gln Glu His Tyr Pro Ser Ile Val Val  
 100 105 110  
 Asp Phe Ile Arg Asp Gln Glu Val Ser Ile Tyr Glu Ile His His Leu  
 115 120 125  
 Ile Ser Ile Leu Asn Lys Thr Asn Val Phe Asp Lys Ala Pro Val Tyr  
 130 135 140  
 Leu Gln Glu Lys Leu Leu Gln Phe Gly Ile Glu Lys Phe Lys Asp Val  
 145 150 155 160  
 His Pro Ser Lys Leu Pro Asn Phe Glu Glu Ile Leu Leu Gln His Cys  
 165 170 175  
 Pro Leu His Trp Leu Gly Arg Leu Val Tyr Pro Met Val Ser Asp Val  
 180 185 190  
 Thr Pro Gly Thr Tyr Gly Tyr Tyr Trp Cys Gly Pro Leu Gly Leu Tyr  
 195 200 205  
 Glu Asn Ala Pro Ser Leu Phe Glu Arg Arg Ser Leu Leu Leu Leu Lys  
 210 215 220  
 Lys Ile Ser Phe Gly Glu Phe Ala Leu Leu Glu Asp Gly Leu Lys Lys  
 225 230 235 240  
 Asn Thr Trp Ser Ser Ser Glu Leu Val Gln Ile Arg Gln Asn Leu Phe  
 245 250 255  
 Thr Arg Tyr Tyr Ala Asp Lys Glu Glu Val Asp Glu Ala Glu Leu Asn  
 260 265 270  
 Ala Asp Tyr Glu Gln Phe Asp Ser Leu Leu His Leu Ile Phe Ser His  
 275 280 285  
 Lys Leu Ser

290  
 <210>374  
 <211>607  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>374  
 Thr Leu Gln Tyr Ile Leu Lys Glu Tyr Lys Ile Glu Asn Ile Arg Asn  
 1 5 10 15  
 Phe Ser Ile Ile Ala His Ile Asp His Gly Lys Ser Thr Ile Ala Asp  
 20 25 30  
 Arg Leu Leu Glu Ser Thr Ser Thr Val Glu Glu Arg Glu Met Arg Glu  
 35 40 45  
 Gln Leu Leu Asp Ser Met Asp Leu Glu Arg Glu Arg Gly Ile Thr Ile  
 50 55 60  
 Lys Ala His Pro Val Thr Met Thr Tyr Leu Tyr Glu Gly Glu Val Tyr  
 65 70 75 80  
 Gln Leu Asn Leu Ile Asp Thr Pro Gly His Val Asp Phe Ser Tyr Glu  
 85 90 95  
 Val Ser Arg Ser Leu Ser Ala Cys Glu Gly Ala Leu Leu Ile Val Asp  
 100 105 110  
 Ala Ala Gln Gly Val Gln Ala Gln Ser Leu Ala Asn Val Tyr Leu Ala  
 115 120 125  
 Leu Glu Arg Asp Leu Glu Ile Ile Pro Val Leu Asn Lys Ile Asp Leu  
 130 135 140  
 Pro Ala Ala Asp Pro Val Arg Ile Ala Gln Gln Ile Glu Asp Tyr Ile  
 145 150 155 160  
 Gly Leu Asp Thr Thr Asn Ile Ile Ala Cys Ser Ala Lys Thr Gly Gln  
 165 170 175  
 Gly Ile Pro Ala Ile Leu Lys Ala Ile Ile Asp Leu Val Pro Pro Pro  
 180 185 190  
 Lys Ala Pro Ala Glu Thr Glu Leu Lys Ala Leu Val Phe Asp Ser His  
 195 200 205  
 Tyr Asp Pro Tyr Val Gly Ile Met Val Tyr Val Arg Ile Ile Ser Gly  
 210 215 220  
 Glu Leu Lys Lys Gly Asp Arg Ile Thr Phe Met Ala Ala Lys Gly Ser  
 225 230 235 240  
 Ser Phe Glu Val Leu Gly Ile Gly Ala Phe Leu Pro Lys Ala Thr Phe  
 245 250 255  
 Ile Glu Gly Ser Leu Arg Pro Gly Gln Val Gly Phe Phe Ile Ala Asn  
 260 265 270  
 Leu Lys Lys Val Lys Asp Val Lys Ile Gly Asp Thr Val Thr Lys Thr  
 275 280 285  
 Lys His Pro Ala Lys Thr Pro Leu Glu Gly Phe Lys Glu Ile Asn Pro  
 290 295 300  
 Val Val Phe Ala Gly Ile Tyr Pro Ile Asp Ser Ser Asp Phe Asp Thr  
 305 310 315 320  
 Leu Lys Asp Ala Leu Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr  
 325 330 335  
 Ile Glu Gln Glu Ser Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly  
 340 345 350  
 Phe Leu Gly Leu Leu His Leu Glu Ile Ile Phe Glu Arg Ile Ile Arg  
 355 360 365  
 Glu Phe Asp Leu Asp Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys  
 370 375 380  
 Val Val Leu Lys Asn Gly Lys Val Leu Asp Ile Asp Asn Pro Ser Gly  
 385 390 395 400  
 Tyr Pro Asp Pro Ala Ile Ile Glu His Val Glu Glu Pro Trp Val His  
 405 410 415  
 Val Asn Ile Ile Thr Pro Gln Glu Tyr Leu Ser Asn Ile Met Asn Leu  
 420 425 430  
 Cys Leu Asp Lys Arg Gly Ile Cys Val Lys Thr Glu Met Leu Asp Gln  
 435 440 445  
 His Arg Leu Val Leu Ala Tyr Glu Leu Pro Leu Asn Glu Ile Val Ser  
 450 455 460

Asp Phe Asn Asp Lys Leu Lys Ser Val Thr Lys Gly Tyr Gly Ser Phe  
 465 470 475 480  
 Asp Tyr Arg Leu Gly Asp Tyr Arg Lys Gly Ser Ile Ile Lys Leu Glu  
 485 490 495  
 Val Leu Ile Asn Glu Glu Pro Ile Asp Ala Phe Ser Cys Leu Val His  
 500 505 510  
 Arg Asp Lys Ala Glu Ser Arg Gly Arg Ser Ile Cys Glu Lys Leu Val  
 515 520 525  
 Asp Val Ile Pro Gln Gln Leu Phe Lys Ile Pro Ile Gln Ala Ala Ile  
 530 535 540  
 Asn Lys Lys Val Ile Ala Arg Glu Thr Ile Arg Ala Leu Ser Lys Asn  
 545 550 555 560  
 Val Thr Ala Lys Cys Tyr Gly Gly Asp Ile Thr Arg Lys Arg Lys Leu  
 565 570 575  
 Trp Glu Lys Gln Lys Lys Gly Lys Lys Arg Met Lys Glu Phe Gly Lys  
 580 585 590  
 Val Ser Ile Pro Asn Thr Ala Phe Ile Glu Val Leu Lys Leu Asp  
 595 600 605  
 <210>375  
 <211>332  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>375  
 Gly Val Ala Ile Ser Gly Ser Tyr Phe Ser Ile Asn Ser Ser Lys Ser  
 1 5 10 15  
 Thr Gly Pro Ser Leu Leu Phe Leu Gly Arg Asn Trp Arg Cys Arg Pro  
 20 25 30  
 Leu Cys Lys Gly Cys Ser Gln Trp Tyr Arg Ile Arg Arg Tyr Pro Val  
 35 40 45  
 Asp Met Arg Thr Tyr Gly Ile Leu Arg Asp Phe Leu Lys Leu Ser Ala  
 50 55 60  
 Thr Ala Val Ala Thr Ile Leu Lys Glu Trp Asn Thr Leu Glu Leu Glu  
 65 70 75 80  
 Ser Tyr Leu Ile Arg Ile Ala Ser Glu Val Leu Ala Leu Lys Asp Pro  
 85 90 95  
 Glu Gly Ile Pro Val Ile Asp Thr Ile Leu Asp Val Val Gly Gln Lys  
 100 105 110  
 Gly Thr Gly Lys Trp Thr Ala Ile Asp Ala Leu Asn Ser Gly Val Pro  
 115 120 125  
 Leu Ser Leu Ile Ile Gly Ala Val Leu Ala Arg Phe Leu Ser Ser Trp  
 130 135 140  
 Lys Glu Ile Arg Glu Gln Ala Ala Arg Asn Tyr Pro Gly Thr Pro Leu  
 145 150 155 160  
 Ile Phe Glu Met Pro His Asp Pro Ser Val Phe Ile Gln Asp Val Phe  
 165 170 175  
 His Ala Leu Tyr Ala Ser Lys Ile Ile Ser Tyr Ala Gln Gly Phe Met  
 180 185 190  
 Leu Leu Gly Glu Ala Ser Lys Glu Tyr Asn Trp Gly Leu Asp Leu Gly  
 195 200 205  
 Glu Ile Ala Leu Met Trp Arg Gly Gly Cys Ile Ile Gln Ser Ala Phe  
 210 215 220  
 Leu Asp Val Ile His Lys Gly Phe Ala Ala Asn Pro Glu Asn Thr Ser  
 225 230 235 240  
 Leu Ile Phe Gln Glu Tyr Phe Arg Gly Ala Leu Arg His Ala Glu Met  
 245 250 255  
 Gly Trp Arg Arg Thr Val Val Thr Ala Ile Gly Ala Gly Leu Pro Ile  
 260 265 270  
 Pro Cys Leu Ala Ala Ala Ile Thr Phe Tyr Asp Gly Tyr Arg Thr Ala  
 275 280 285  
 Ser Ser Ser Met Ser Leu Ala Gln Gly Leu Arg Asp Tyr Phe Gly Ala  
 290 295 300  
 His Thr Tyr Glu Arg Asn Asp Arg Pro Arg Gly Glu Phe Tyr His Thr  
 305 310 315 320  
 Asp Trp Val His Thr Lys Thr Thr Glu Arg Val Lys

325

330

&lt;210&gt;376

&lt;211&gt;204

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;376

Val Ala Leu Gln Thr Asn Ile Gly Leu Ile Gly Leu Ala Val Met Gly  
 1 5 10 15  
 Lys Asn Leu Val Leu Asn Met Ile Asp His Gly Phe Ser Val Ser Val  
 20 25 30  
 Tyr Asn Arg Thr Pro Glu Lys Thr Arg Asp Phe Leu Lys Glu Tyr Pro  
 35 40 45  
 Asn His Arg Glu Leu Val Gly Phe Glu Ser Leu Glu Asp Phe Val Asn  
 50 55 60  
 Ser Leu Glu Arg Pro Arg Lys Ile Met Leu Met Ile Gln Ala Gly Lys  
 65 70 75 80  
 Pro Val Asp Gln Ser Ile His Ala Leu Leu Pro Phe Leu Glu Pro Gly  
 85 90 95  
 Asp Val Ile Ile Asp Gly Gly Asn Ser Tyr Phe Lys Asp Ser Glu Arg  
 100 105 110  
 Arg Cys Lys Glu Leu Gln Glu Lys Gly Ile Leu Phe Leu Gly Val Gly  
 115 120 125  
 Ile Ser Gly Gly Glu Glu Gly Ala Arg His Gly Pro Ser Ile Met Pro  
 130 135 140  
 Gly Gly Asn Pro Glu Ala Trp Pro Leu Val Ala Pro Ile Phe Gln Ser  
 145 150 155 160  
 Ile Ala Ala Lys Val Gln Gly Arg Pro Cys Cys Ser Trp Val Gly Thr  
 165 170 175  
 Gly Gly Ala Gly His Tyr Val Lys Ala Val His Asn Gly Ile Glu Tyr  
 180 185 190  
 Gly Asp Ile Gln Leu Ile Cys Glu Leu Thr Val Ser  
 195 200

&lt;210&gt;377

&lt;211&gt;422

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;377

Leu Ala Ile Leu Asn Tyr Val Arg Ser Leu Met Gln Ser Trp Leu Gln  
 1 5 10 15  
 Ser Leu Gln Glu Arg Asn Ile Leu Glu Asn Phe Thr Ala Gly Leu Glu  
 20 25 30  
 Ser Val Glu Gly Pro Ile Ala Ala Tyr Leu Gly Phe Asp Pro Thr Ala  
 35 40 45  
 Pro Ala Leu His Ile Gly His Trp Ile Gly Ile Cys Phe Leu Lys Arg  
 50 55 60  
 Leu Ala Ala Leu Gly Ile Thr Pro Ile Ala Leu Val Gly Gly Ala Thr  
 65 70 75 80  
 Gly Met Val Gly Asp Pro Ser Gly Lys Gln Ser Glu Arg Ser Leu Leu  
 85 90 95  
 Gln Thr Ser Glu Val Phe Asp Asn Ser Gln Lys Ile Thr Ala Cys Leu  
 100 105 110  
 Gln Arg Tyr Leu Pro Gly Val Thr Leu Val Asn Asn Ala Asp Trp Leu  
 115 120 125  
 Gln Glu Ile Ser Leu Ile Asp Phe Leu Arg Asp Ile Gly Lys His Phe  
 130 135 140  
 Arg Leu Gly Gln Met Leu Val Lys Asp Thr Ile Lys Gln Arg Val His  
 145 150 155 160  
 Ser Asp Glu Gly Ile Ser Tyr Thr Glu Phe Ser Tyr Leu Ile Leu Gln  
 165 170 175  
 Ser Tyr Asp Phe Tyr His Leu Phe Lys Asn Tyr Gly Thr Ile Leu Gln  
 180 185 190  
 Cys Gly Gly Ser Asp Gln Trp Gly Asn Ile Thr Ser Gly Ile Asp Phe  
 195 200 205  
 Ile Arg Arg Lys Gly Leu Gly Gln Ala Tyr Gly Leu Thr Tyr Pro Leu

210 215 220  
 Leu Thr Asn Ala Gln Gly Lys Lys Ile Gly Lys Thr Glu Ser Gly Thr  
 225 230 235 240  
 Val Trp Leu Asp Ser Asp Leu Thr Ser Pro Phe Glu Leu Tyr Gln Tyr  
 245 250 255  
 Leu Leu Arg Leu Pro Asp Asp Thr Ile Pro Lys Ile Ala Arg Thr Leu  
 260 265 270  
 Thr Leu Leu Ser Asn Glu Glu Ile Gln Asp Ile Asp Arg Arg Val Gln  
 275 280 285  
 Thr Asp Pro Val Ala Val Lys Glu Phe Val Ala Gln Asp Ile Leu Ser  
 290 295 300  
 Ala Ile His Gly Asp Leu Gly Leu Glu Glu Ala Leu Ser Val Thr Arg  
 305 310 315 320  
 Ser Met His Pro Gly Asn Leu Ser Ser Leu Ser Glu Lys Asp Phe His  
 325 330 335  
 Glu Leu Phe Ala Gly Gly Met Gly Ala Ser Leu Asp Lys Ser Glu Val  
 340 345 350  
 Leu Gly Lys Arg Trp Leu Asp Leu Phe Leu Val Leu Gly Leu Cys Lys  
 355 360 365  
 Ser Lys Gly Glu Ile Arg Arg Leu Ile Glu Gln Lys Gly Val Tyr Ile  
 370 375 380  
 Asn Asn Val Pro Ile Ala Asn Glu His Ser Val Cys Glu Glu Gln Asp  
 385 390 395 400  
 Ile Cys Tyr Gly His Tyr Val Leu Leu Ala Gln Gly Lys Lys Arg Lys  
 405 410 415  
 Leu Val Leu Tyr Leu Asn  
 420

&lt;210&gt;378

&lt;211&gt;103

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;378

Val Ala Met Ser Thr Ser Pro Ile Gly Val Pro Ser Met Leu Asn Ala  
 1 5 10 15  
 Ala Thr Ser Leu Asn Ala Thr Thr Ser Lys Ala Pro Leu Pro Thr Ser  
 20 25 30  
 Thr Leu Ala Glu Arg Ile Lys Glu Trp Leu Pro Arg Ile Leu Leu Leu  
 35 40 45  
 Ile Val Gly Ala Ile Phe Thr Ile Ala Gly Cys Ile Val Met Ala Leu  
 50 55 60  
 Thr Lys Gln Ile Leu Tyr Gly Leu Leu Cys Val Val Gly Gly Leu Leu  
 65 70 75 80  
 Leu Ala Leu Gly Leu Leu Lys Pro Glu Asn Cys Ile Tyr Arg Asn  
 85 90 95  
 Ala Glu Ser Leu Arg Glu Ala  
 100

&lt;210&gt;379

&lt;211&gt;291

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;379

Leu Asp Lys Lys Lys Phe Val Lys Thr Gln Gln Thr Gln Asn Ile Ile  
 1 5 10 15  
 Glu Val Trp Asn Phe Tyr Trp Glu Thr Gln Glu Ile Glu Tyr Arg Asp  
 20 25 30  
 Ser Leu Ile Glu Phe Tyr Leu Pro Leu Val Lys Ser Val Val His Arg  
 35 40 45  
 Leu Ile Ser Gly Met Pro Ser His Val Lys Thr Glu Asp Leu Tyr Ala  
 50 55 60  
 Ser Gly Val Glu Gly Leu Val Arg Ala Val Glu Arg Tyr Asn Pro Glu  
 65 70 75 80  
 Arg Ser Arg Arg Phe Glu Gly Tyr Ala Val Phe Leu Ile Lys Ala Ala  
 85 90 95  
 Ile Ile Asp Asp Leu Arg Lys Gln Asp Trp Val Pro Arg Ser Val His

100 105 110  
 Gln Lys Ala Asn Lys Leu Ser Gly Ala Met Asp Ser Leu Arg Gln Ser  
 115 120 125  
 Leu Gly Lys Glu Pro Thr Asp Leu Glu Leu Cys Glu Tyr Leu Asn Ile  
 130 135 140  
 Ser Gln Gln Glu Leu Ser Gly Trp Phe Val Ser Ala Arg Pro Ala Leu  
 145 150 155 160  
 Ile Val Ser Leu Asn Glu Glu Trp Pro Ser Gln Ser Asp Glu Gly Ala  
 165 170 175  
 Gly Met Ala Leu Glu Glu Arg Ile Pro Asp Glu Arg Ala Glu Thr Gly  
 180 185 190  
 Tyr Asp Val Val Asp Lys Gln Glu Phe Ser Leu Cys Leu Ala Asn Ala  
 195 200 205  
 Ile Gln Glu Leu Glu Glu Lys Glu Arg Lys Val Met Ala Leu Tyr Tyr  
 210 215 220  
 Tyr Glu Glu Leu Val Leu Lys Glu Ile Gly Lys Val Leu Gly Val Ser  
 225 230 235 240  
 Glu Ser Arg Val Ser Gln Ile His Ser Lys Ala Leu Leu Lys Leu Arg  
 245 250 255  
 Ala Asp Ser Leu His Phe Asp Lys Tyr Ser Ser Gln Val Leu Arg Ala  
 260 265 270  
 Val Leu Glu Leu Gly Glu Ala Leu Leu Arg His Arg Val Ile Arg Lys  
 275 280 285  
 Glu Phe Val  
 290  
 <210>380  
 <211>544  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>380  
 Phe Cys Ile Val Phe Thr Asn Gly Leu Leu Gly Leu Tyr Leu Lys Phe  
 1 5 10 15  
 Lys Gln Phe Ser Glu Val Phe Pro Pro Phe Phe Leu Tyr Leu Cys Leu  
 20 25 30  
 Leu Arg Leu Gly Leu Asn Leu Ala Ser Thr Arg Trp Ile Val Ser Ser  
 35 40 45  
 Gly Thr Ala Ser Ser Leu Ile Val Ser Leu Gly Ser Phe Phe Ser Leu  
 50 55 60  
 Gly Ser Leu Trp Ala Ala Thr Phe Ala Cys Leu Leu Leu Phe Phe Val  
 65 70 75 80  
 Asn Phe Leu Met Val Ser Lys Gly Ser Glu Arg Ile Ala Glu Val Arg  
 85 90 95  
 Ser Arg Phe Phe Leu Glu Ala Leu Pro Ala Lys Gln Met Ala Leu Asp  
 100 105 110  
 Ser Asp Leu Val Ser Gly Arg Ala Ser Tyr Lys Ala Val Lys Lys Gln  
 115 120 125  
 Lys Asn Ala Leu Ile Glu Glu Gly Asp Phe Phe Ser Ala Met Glu Gly  
 130 135 140  
 Val Phe Arg Phe Val Lys Gly Asp Ala Ile Ile Ser Cys Ile Leu Leu  
 145 150 155 160  
 Leu Val Asn Val Val Ser Val Thr Cys Leu Tyr Tyr Thr Ser Gly Tyr  
 165 170 175  
 Ala Leu Glu Gln Met Trp Phe Thr Val Leu Gly Asp Ala Leu Val Ser  
 180 185 190  
 Gln Val Pro Ala Leu Leu Thr Ser Cys Ala Ala Ala Thr Leu Ile Ser  
 195 200 205  
 Lys Ile Asp Lys Glu Glu Ser Leu Leu Asn Tyr Leu Phe Glu Tyr Tyr  
 210 215 220  
 Lys Gln Leu Arg Gln His Phe Arg Val Val Ser Leu Leu Ile Phe Ser  
 225 230 235 240  
 Leu Cys Cys Ile Pro Ser Ser Pro Lys Phe Pro Ile Val Leu Leu Ala  
 245 250 255  
 Ser Leu Leu Trp Leu Ala Tyr Arg Lys Glu Glu Pro Ala Ser Glu Asp  
 260 265 270

Ser Cys Ile Glu Arg Ala Phe Ser Tyr Val Glu Gly Ala Cys Pro Lys  
 275 280 285  
 Glu Gln Glu Ser Gln Phe Tyr Gln Val Tyr Arg Ala Ala Ser Glu Glu  
 290 295 300  
 Val Phe Glu Asp Leu Gly Val Arg Leu Pro Val Leu Thr Ser Leu Arg  
 305 310 315 320  
 Ile Glu Glu Arg Pro Trp Leu Arg Val Phe Gly Gln Asn Val Tyr Leu  
 325 330 335  
 Asp Glu Met Thr Pro Glu Ala Val Leu Pro Phe Leu Arg Asn Ile Ala  
 340 345 350  
 His Glu Ala Leu Asn Ala Glu Val Val Gln Lys Tyr Leu Glu Glu Ser  
 355 360 365  
 Glu Arg Val Phe Gly Ile Ala Val Glu Asp Ile Val Pro Lys Lys Ile  
 370 375 380  
 Ser Leu Ser Ser Leu Val Val Leu Ser Arg Leu Leu Val Arg Glu Arg  
 385 390 395 400  
 Val Ser Leu Lys Leu Xaa Pro Lys Ile Leu Glu Ala Val Ala Val Tyr  
 405 410 415  
 Gln Asn Ser Gly Asp Ser Leu Glu Ile Leu Ala Glu Lys Val Arg Lys  
 420 425 430  
 Ser Leu Gly Tyr Trp Ile Gly Arg Ser Leu Trp Asp Gln Lys Gln Thr  
 435 440 445  
 Leu Glu Val Ile Thr Ile Asp Phe His Val Glu Glu Leu Ile Asn Ser  
 450 455 460  
 Ser Tyr Ser Lys Ser Asn Pro Val Met Gln Glu Asn Val Ile Arg Arg  
 465 470 475 480  
 Val Asp Ser Leu Leu Glu Arg Ser Val Phe Lys Asp Phe Arg Ala Ile  
 485 490 495  
 Val Thr Ser Cys Glu Thr Arg Phe Glu Met Lys Lys Met Leu Asp Pro  
 500 505 510  
 His Phe Pro Asp Leu Leu Val Leu Ser His Asp Glu Leu Pro Lys Glu  
 515 520 525  
 Ile Pro Ile Ser Phe Leu Gly Ile Val Ser Asp Glu Val Leu Val Pro  
 530 535 540

&lt;210&gt;381

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;381

Met Ala Lys Leu Val Ile Thr Ser Asp Asp Glu Gln Gln Glu Phe Glu  
 1 5 10 15  
 Leu Glu Asp Asn Ser Glu Ile Ala Glu Pro Cys Glu Ser Met Gly Ile  
 20 25 30  
 Pro Phe Ala Cys Thr Glu Gly Val Cys Gly Thr Cys Val Ile Glu Val  
 35 40 45  
 Leu Glu Gly Arg Glu Asn Leu Ser Glu Phe Thr Glu Pro Glu Tyr Asp  
 50 55 60  
 Phe Leu Gly Glu Pro Glu Asp Ser Asn Glu Arg Leu Ala Cys Gln Cys  
 65 70 75 80  
 Arg Ile Lys Gly Gly Cys Val Lys Val Thr Phe  
 85 90

&lt;210&gt;382

&lt;211&gt;191

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;382

Phe Lys Gly Thr Gln Val Asn Ser Leu Ile Met Ala Thr Ile Ser Pro  
 1 5 10 15  
 Ile Ser Leu Thr Val Asp His Pro Leu Val Asp Thr Lys Lys Lys Ser  
 20 25 30  
 Cys Ser Asn Phe Asp Lys Ile Gln Ser Arg Ile Leu Leu Ile Thr Ala  
 35 40 45  
 Ile Phe Ala Val Leu Val Thr Ile Gly Thr Leu Leu Ile Gly Leu Leu  
 50 55 60

Leu Asn Ile Pro Val Ile Tyr Phe Leu Thr Gly Ile Ser Phe Ile Ala  
 65 70 75 80  
 Val Val Leu Ser Asn Phe Ile Leu Tyr Lys Arg Ala Thr Thr Leu Leu  
 85 90 95  
 Lys Pro Arg Ala Cys Gly Lys His Lys Glu Ile Lys Pro Lys Arg Val  
 100 105 110  
 Ser Thr Asn Leu Gln Tyr Ser Ser Ile Ser Ile Ala Ile Asn Arg Ser  
 115 120 125  
 Lys Glu Asn Trp Glu His Gln Pro Lys Asp Leu Gln Asn Leu Pro Ala  
 130 135 140  
 Pro Ser Ala Leu Leu Thr Asp Asn Pro Tyr Glu Ile Trp Lys Ala Lys  
 145 150 155 160  
 His Ser Leu Phe Ser Leu Val Ser Leu Leu Pro Gly Gly Asn Pro Lys  
 165 170 175  
 Thr Ser Leu Lys Phe Lys Leu Pro Lys Ile Tyr Glu Arg Leu Cys  
 180 185 190

&lt;210&gt;383

&lt;211&gt;158

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;383

Leu Lys Lys Pro Arg Lys Met Arg Leu Tyr Pro Pro Tyr Val Asp Thr  
 1 5 10 15  
 Thr Pro Ser Pro Lys Ser Leu Leu Asn Glu Ala Ile Gln Glu Thr Arg  
 20 25 30  
 Val Glu Ile Asn Thr Glu Leu Pro Ala Gly Asp Ser Gly Glu Arg Leu  
 35 40 45  
 Tyr Trp Gln Pro Asp Phe Arg Gly Arg Val Phe Leu Pro Gln Ile Pro  
 50 55 60  
 Thr Thr Pro Glu Ala Ile Tyr Gln Tyr Tyr Tyr Ala Leu Tyr Val Thr  
 65 70 75 80  
 Tyr Ile Gln Thr Ala Ile Asn Thr Asn Thr Gln Ile Ile Gln Ile Pro  
 85 90 95  
 Leu Tyr Ser Leu Arg Glu His Leu Tyr Ser Arg Glu Leu Pro Pro Gln  
 100 105 110  
 Ser Arg Met Gln Gln Ser Leu Ala Met Ile Thr Ala Val Lys Tyr Met  
 115 120 125  
 Ala Glu Leu His Pro Glu Tyr Pro Leu Thr Ile Ala Cys Val Glu Arg  
 130 135 140  
 Ser Leu Ala Gln Leu Pro Gln Glu Ser Ile Glu Asp Leu Ser  
 145 150 155

&lt;210&gt;384

&lt;211&gt;155

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;384

Met Gly Tyr Leu Pro Val Ser Ala Thr Asp Val Leu Phe Glu Ser Pro  
 1 5 10 15  
 Ala Ala Pro Leu Ile Asn Ser Ala Asn Thr Gln Asn Gln Lys Leu Ile  
 20 25 30  
 Glu Leu Lys Gly Lys Gln Gln Ala Glu Ser Ser Pro Arg Thr Ile Thr  
 35 40 45  
 Ser Val Ile Leu Glu Val Leu Leu Val Ile Gly Cys Cys Leu Ile Val  
 50 55 60  
 Leu Ser Leu Leu Ala Ile Arg Pro Ala Leu Gln Phe Thr Leu Glu Thr  
 65 70 75 80  
 Gly His Pro Ala Ala Ile Ala Val Leu Ala Val Ser Gly Thr Ile Leu  
 85 90 95  
 Leu Val Ala Val Ile Ile Leu Phe Cys Phe Leu Ala Ala Val Pro Phe  
 100 105 110  
 Ala Ala Lys Lys Thr Tyr Lys Tyr Val Lys Thr Val Asp Tyr Ala  
 115 120 125  
 Ser Trp His Ser His Gln Gln Thr Pro Thr Leu Gly Thr Ile Phe Ser  
 130 135 140



Gly Ile Val Tyr Ala Glu Ser Gln Ala Gln Leu  
 145 150 155

<210>385

<211>253

<212>PRT

<213>Chlamydia pneumoniae

<400>385

Ser Phe Pro Leu Asn Arg Tyr Phe Met Thr Lys Thr Thr Ser Ile Pro  
 1 5 10 15  
 Asp Val His Glu Asn Gln Ser His Leu Ser Val Asp Glu Arg Leu Ile  
 20 25 30  
 Ser Glu Ser Pro Val Leu Thr Lys Lys Glu Val Ile Ala Lys Ile Ile  
 35 40 45  
 Lys Leu Thr Ala Leu Ile Leu Ala Leu Ala Ile Ala Val Gly Thr Ala  
 50 55 60  
 Val Val Ala Gly Val Leu Gly Met Pro Leu Met Ala Ile Ala Thr Gly  
 65 70 75 80  
 Ala Ala Leu Leu Ala Ala Val Val Leu Ser Cys Leu Leu Leu Arg Arg  
 85 90 95  
 Arg Glu Pro Ser Lys Pro Thr Glu Glu Leu Leu Gly Pro Gln Lys His  
 100 105 110  
 Val Pro Lys Asp Ile Ala Ala Gln Val Gln Pro Ser Val Pro Leu Asp  
 115 120 125  
 Tyr Gln Lys Leu Leu Arg Asn Glu Trp Thr Leu Val Asn Thr Leu Ser  
 130 135 140  
 Glu Ile Asn Ile Ser Trp Thr Leu Gln Asp Pro Asn Gln Arg Tyr Tyr  
 145 150 155 160  
 Val Trp Glu His Gln Gly Ala Pro Ile Thr Leu Val Ala Thr Thr Gly  
 165 170 175  
 Asp Ile Ala Lys Pro Arg Leu Lys Thr Ser Gly Arg Val Met Ile Val  
 180 185 190  
 Asn Ala Ala Asn Ser Asn Met Gln Ser Gly Gly Ala Gly Thr Asn Ala  
 195 200 205  
 Ala Leu Ser Ala Ala Thr His Pro Thr Cys Trp Asn Asn Thr Arg Thr  
 210 215 220  
 Ser Gly Gly Lys Ile Asn Thr Gly Lys Gly Leu Ser Val Gly Glu Cys  
 225 230 235 240  
 Arg Ser Ala Pro Trp Ile Asn Arg Asp Trp Thr Asn Lys  
 245 250

<210>386

<211>114

<212>PRT

<213>Chlamydia pneumoniae

<400>386

Thr Leu Ala Lys Asp Tyr Leu Trp Val Asn Ala Ala Gln His Pro Gly  
 1 5 10 15  
 Ser Ile Glu Thr Gly Arg Ile Asn Asp Thr Asn Pro Gly Glu Ala His  
 20 25 30  
 Phe Leu Ala Gln Leu Leu Gly Pro Lys Tyr Glu Gly Glu Leu Lys Ala  
 35 40 45  
 His Pro Glu Lys Leu Ser Asn Val Ile Lys Lys Ala Tyr Leu Asn Cys  
 50 55 60  
 Phe Asp Glu Ala Leu Asn Asn Gln Ala Thr Val Val Gln Val Pro Leu  
 65 70 75 80  
 Ile Ser Ser Ser Ile Tyr Ser Pro Gly Gly Lys Leu Glu Leu Glu Pro  
 85 90 95  
 Val Asn Gln Thr Lys Pro Asn Ser Ser Ala Tyr Lys Leu Tyr His Ile  
 100 105 110  
 Arg Thr

<210>387

<211>406

<212>PRT

<213>Chlamydia pneumoniae

&lt;400&gt;387

```

Asn Ile Met Thr Asp Ser Asn Pro Leu Pro Ser Tyr Thr Asp Ala Ser
 1           5           10           15
Leu Tyr Arg Thr Pro Ala Lys His Ser Tyr Pro Ile Arg Leu Pro Leu
           20           25           30
Asn Arg Thr Asp Arg Ile Glu Lys Ile Leu Lys Ile Val Thr Leu Thr
           35           40           45
Leu Ala Leu Ala Cys Ala Leu Gly Phe Ser Ile Ala Ala Gly Ile Leu
           50           55           60
Ala Met Pro Ile Phe Ser Ala Val Val Val Ile Thr Leu Ala Ile Ala
           65           70           75           80
Ala Val Ser Leu Tyr Ser Leu Leu Lys Lys Pro Lys Leu Tyr Glu Ile
           85           90           95
Leu Pro Gln Ile Glu Pro Glu Ser Glu Gln Ser Ser Leu Ser Pro Ser
           100          105          110
Pro Gln Pro Pro Glu Gln Gln Asp Leu Pro Leu Gln Ile Asp Pro Leu
           115          120          125
Pro Asp Pro Glu Ser Leu Pro Glu Val Ser Leu Ala Asp Leu Thr Thr
           130          135          140
Pro Pro Glu Glu Leu Thr Ala Ile Thr Val Thr Pro Gly Tyr Glu Ala
           145          150          155          160
Leu Leu Glu Gln Asn Trp Asp Leu Leu Pro Ser Leu Ala Ala Val Asp
           165          170          175
Pro Ser Phe Thr Thr Glu Thr Pro Gln Gln Pro Cys Phe Ile Trp Lys
           180          185          190
Leu Lys Asp Ser Lys Leu Ile Phe Ile Ser Thr Ser Gly Asp Ile Ala
           195          200          205
Val Pro Arg Ile Lys Thr Gln Gly Arg Val Met Ile Val Asn Ala Ala
           210          215          220
Asn Glu Asn Ile Ser Arg Glu Gly Gly Gly Thr Asn Lys Ala Leu Ser
           225          230          235          240
Leu Ala Thr Ser Leu Gln Cys Trp Asn Ala Ser Arg Leu Pro Arg Ala
           245          250          255
His Ser Arg Ser Gly Ser Gln Leu Gln Pro Gly Glu Cys Arg Ser Ala
           260          265          270
Lys Trp Glu Asn Ser Asp His Thr Ser Asn Asp His Val Pro Gly Lys
           275          280          285
Ala His Phe Leu Ala Gln Leu Leu Gly Pro Glu Ala Ala Lys Cys Asn
           290          295          300
Asn Asp Pro Lys Gln Ala Phe Glu Val Ser Lys Lys Ala Phe His Asn
           305          310          315          320
Leu Phe Gln Glu Ala Glu Ile Ile Gly Val Asp Val Ile Gln Leu Pro
           325          330          335
Leu Ile Gly Cys Asn Leu Phe Ala Pro Ser Arg Leu Leu Asn Leu Gly
           340          345          350
Lys Thr Arg Ala Glu Trp Ile Glu Ala Ile Lys Leu Ala Leu Ile Thr
           355          360          365
Ser Leu Gln Asp Phe Gly Trp Glu Gln Asp Asn Gln Glu Glu Gln Lys
           370          375          380
Ile Ile Ile Leu Thr Asp Lys Asp Gln Pro Pro Ile Ile Pro Pro Arg
           385          390          395          400
Phe Asp Leu Thr Thr Pro
           405

```

&lt;210&gt;388

&lt;211&gt;386

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;388

```

Lys Arg Ile Phe Phe Lys Leu Phe Val Phe Tyr Leu Lys Ser Phe Met
 1           5           10           15
Ser Thr Thr Glu Pro Asn Leu Thr Asn Val Asn Leu Thr Met Leu Ile
           20           25           30
Ser Ser Glu Ser Met Pro Thr Gln Leu Ala Ser His Lys Leu Lys Gly
           35           40           45

```

Leu Asp Leu Val Ala Phe Ile Leu Ile Ile Gly Ile Ala Val Ser Ser  
 50 55 60  
 Gly Thr Ala Ala Ile Ile Leu Gly Ile Pro Leu Leu Phe Ile Leu Thr  
 65 70 75 80  
 Ala Leu Ala Val Leu Ala Phe Ser Ile Leu Leu Tyr Phe Leu Leu Arg  
 85 90 95  
 Glu Pro Lys Ser Pro Ile Ser Val Thr His Gln Pro Thr Pro Ile Ile  
 100 105 110  
 Lys Asp Thr Asp Leu Pro Pro Val Pro Pro Leu Ala Leu Thr Pro Val  
 115 120 125  
 Pro Thr Glu Ala Val Leu Glu Glu Pro Pro Leu Pro Ser Pro Arg Thr  
 130 135 140  
 His Gln Thr Leu Leu Gln Glu Asn Trp Asp Arg Ile Pro Asp Leu Gln  
 145 150 155 160  
 Ala Asn Thr Asp Met Pro Phe Ile Ala Ala Asp Asn Gln Thr Gly Tyr  
 165 170 175  
 Ala Trp His Leu Lys Asn Ser Asn Leu Thr Leu Ile Ser Thr Leu Gly  
 180 185 190  
 Pro Ile Glu Lys Pro Arg Tyr Lys Thr Gln Gly Ile Val Met Ile Val  
 195 200 205  
 Asn Ala Ala Thr Pro Asn Met Ala Asn Asn Val Lys Gly Thr Ser Leu  
 210 215 220  
 Ala Leu Ala Lys Ala Thr Ser Val Arg Cys Trp Glu Asn Ser Lys Lys  
 225 230 235 240  
 Ser Pro Asp Pro Leu Arg Ser Lys Gln Pro Leu Gln Leu Gly Glu Cys  
 245 250 255  
 Arg Ser Ala Lys Trp Glu Asn Leu Asn Gly Thr Thr Asn Ala Gly Lys  
 260 265 270  
 Ala Gly Leu Pro Gln Phe Leu Gly Gln Leu Leu Gly Pro Lys Ala Ser  
 275 280 285  
 Asp Tyr Asn Tyr Asn Pro Asn Asp Ala Phe Thr Phe Cys Arg Gln Ala  
 290 295 300  
 Tyr Leu Asn Cys Leu Asn Glu Ala Lys Arg Arg Lys Thr Thr Val Val  
 305 310 315 320  
 Gln Leu Pro Leu Leu Ser Ser His Phe Pro Gly Ser Pro Lys Asp Glu  
 325 330 335  
 Glu Thr Thr Ser Leu Arg Leu Gln Trp Ile Asp Gly Val Lys Leu Ala  
 340 345 350  
 Leu Ile Asp Ala Leu Gln Thr Phe Gly Ser Glu Ala Glu Asn Gln Asn  
 355 360 365  
 Gln Pro Trp Val Ile Ile Leu Thr Thr Leu Ala Arg His Pro Leu Ile  
 370 375 380  
 Thr Pro  
 385  
 <210>389  
 <211>621  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>389  
 Asn Ser Glu Ile Phe Glu Ile Phe Met Thr Leu Ile Thr Pro Ala Ile  
 1 5 10 15  
 Asn Ser Ser Arg Arg Lys Thr His Thr Val Arg Ile Gly Asn Leu Tyr  
 20 25 30  
 Ile Gly Ser Asp His Ser Ile Lys Thr Gln Ser Met Thr Thr Thr Leu  
 35 40 45  
 Thr Thr Asp Ile Asp Ser Thr Val Glu Gln Ile Tyr Ala Leu Ala Glu  
 50 55 60  
 His Asn Cys Asp Ile Val Arg Val Thr Val Gln Gly Ile Lys Glu Ala  
 65 70 75 80  
 Gln Ala Cys Glu Lys Ile Lys Glu Arg Leu Ile Ala Leu Gly Leu Asn  
 85 90 95  
 Ile Pro Leu Val Ala Asp Ile His Phe Pro Gln Ala Ala Met Leu  
 100 105 110  
 Val Ala Asp Phe Ala Asp Lys Val Arg Ile Asn Pro Gly Asn Tyr Ile

<210>390

&lt;211&gt;251

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;390

```

Val Asp Ser Met Thr Leu Ser Phe His Thr His Pro Leu Asn Tyr Trp
 1           5           10           15
Thr Phe Glu Glu Phe Asp Gly Leu Pro Ile Arg His Gly Val Phe Ser
          20           25           30
Lys Gln Lys Asp Ala Glu Gly Thr Val Phe Ala Ala Lys Asn Pro Glu
          35           40           45
Ile Ala Ser Ala Leu Gln Ser Pro Lys Tyr Cys Asp Leu His Gln Arg
          50           55           60
His Gly Thr Ser Val Arg Cys Val Thr Pro Thr Ser Pro Thr Tyr Gln
          65           70           75           80
Pro Ala Asp Gly Leu Cys Thr Gln Ser Pro Leu Leu Ser Leu His Ile
          85           90           95
Arg His Ser Asp Cys Gln Ala Ala Ile Phe Tyr Asp Arg Glu His His
          100          105          110
Ala Ile Ala Asn Val His Ser Gly Trp Arg Gly Leu Leu Gly Asn Ile
          115          120          125
Tyr Ala Val Thr Val Gly Thr Met Lys Lys Leu Phe His Thr Lys Pro
          130          135          140
Gln Asp Leu Phe Val Ala Ile Gly Pro Ser Ile Gly Pro Asp Tyr Ala
          145          150          155          160
Ile Tyr Pro Asp Tyr Ala Thr Leu Phe Pro Arg Ser Phe Leu Pro Phe
          165          170          175
Met Asn Pro Lys Asn His Phe Asp Leu Arg Ala Ile Ala Arg Lys Gln
          180          185          190
Leu Thr Asn Leu Gly Ile Ser Lys Asp Arg Ile Phe Ile Ser Asp Leu
          195          200          205
Cys Thr Tyr Thr Glu His Asp Ala Phe Phe Ser Ser Arg Tyr Leu Ala
          210          215          220
His His Pro Asp Pro Asn Leu Thr Gly Gln His Ser Lys Asn Arg Asn
          225          230          235          240
Asn Val Thr Ala Val Leu Leu Leu Pro Arg Asp
          245          250

```

&lt;210&gt;391

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;391

```

Arg Leu Ser Met Lys Leu Gly Ala Ser Thr Asn His Lys Val His Glu
 1           5           10           15
Pro Val Lys Pro Lys Lys Ala Lys Leu Ala Glu Ile Glu Ala Xaa Lys
          20           25           30
Thr Gln Ala Thr Glu Gly Thr Leu Arg Ser Lys Ser Leu Ala Leu Gln
          35           40           45
Ile Ala Arg Ala Val Leu Tyr Ile Leu Phe Ala Ala Leu Met Leu Ala
          50           55           60
Ala Gly Ile Thr Phe Val Thr Phe Glu Ala Leu Gly Phe Pro Leu Ile
          65           70           75           80
Gln Ala Tyr Ser Ile Ala Gly Ile Ile Thr Leu Val Gly Leu Ala Ile
          85           90           95
Gly Leu Val Leu Leu Ile Leu Ser Leu Leu Pro Lys Glu Asp Glu Glu
          100          105          110
Ala Asp Ala Leu Ser Arg Asn Ala Leu Leu Pro Leu Thr Ile Ile Val
          115          120          125
Ile Glu Gln Gln Pro Ile Thr Pro Lys Pro Glu Ile Pro Tyr Ser Tyr
          130          135          140
Leu Thr Lys Leu Ala Leu Leu Thr Ser Leu Phe Leu Thr Leu Arg Arg
          145          150          155          160
Ser Ser Ser Gln Arg Lys Thr His
          165

```

&lt;210&gt;392

&lt;211&gt;205

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;392

Phe Lys Val Val Thr Ala Lys Ala Pro Asn Leu Thr Glu Ile Arg Asp  
 1 5 10 15  
 His Gly Ala Arg Val Pro Ser Leu Phe Leu Leu Ser Pro Glu Thr Ser  
 20 25 30  
 His Trp Lys Gly Asp Lys Glu Val Ser Ala Pro Leu Lys Gln Leu Gln  
 35 40 45  
 Asp Leu Leu Gly Glu Glu Gln Trp Glu Ala Met Lys Thr Lys Met Asn  
 50 55 60  
 Ser Arg Lys Lys Ala Gly Gln Trp Ala Ile Phe Asn Ser Pro Thr Pro  
 65 70 75 80  
 Gly Val Ser Ser Thr Leu Val Leu Ala Trp Thr Pro Trp Gly Tyr Tyr  
 85 90 95  
 Asp Lys Asp Val Gln Asp Ile Leu Glu Arg Lys Asp Pro Met Ser Ser  
 100 105 110  
 Ser Leu Ser Glu Lys Asp Ser Lys Glu Phe Leu Lys Asn Leu Phe Val  
 115 120 125  
 Asp Leu Leu Glu Asn Gly Phe Thr Ser Val His Ile His Ala Glu Glu  
 130 135 140  
 Ala Phe Thr Pro Leu Asp His Thr Gly Lys Pro His Phe Lys Arg Asp  
 145 150 155 160  
 Asn Val Tyr Leu Pro Gly Lys Leu Leu Gly Ala Leu Asn Glu Ala Ala  
 165 170 175  
 Val Gln Ala Asn Val Ser Ala Asp Thr Gln Phe Thr Leu Phe Leu Thr  
 180 185 190  
 Gln Asp Glu Cys Asn Pro Phe His Asp Lys Lys Arg Gly  
 195 200 205

&lt;210&gt;393

&lt;211&gt;147

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;393

Trp Arg Gly Asp Cys Tyr Arg His Tyr Tyr Asp Ile Ser Ile Ala Val  
 1 5 10 15  
 Gly Ile Asp Arg Gly Leu Val Val Pro Val Ile Arg Asp Cys Asp Lys  
 20 25 30  
 Leu Ser Asn Gly Glu Ile Glu Gln Lys Leu Ala Asp Leu Ser Leu Arg  
 35 40 45  
 Ala Arg Glu Gly Leu Leu Ala Ile Ala Glu Leu Glu Gly Gly Gly Phe  
 50 55 60  
 Thr Ile Thr Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile  
 65 70 75 80  
 Ile Asn Pro Pro Gln Val Gly Ile Leu Gly Met His Lys Ile Glu Lys  
 85 90 95  
 Arg Pro Val Val Leu Asp Asn Glu Ile Val Ile Ala Asp Met Met Tyr  
 100 105 110  
 Val Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Lys Glu Ala Val  
 115 120 125  
 Gly Phe Leu Val Lys Val Lys Glu Gly Leu Glu Asn Pro Ala Ser Leu  
 130 135 140  
 Leu Asp Leu  
 145

&lt;210&gt;394

&lt;211&gt;233

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;394

Ile Met Thr Thr Glu Val Arg Ile Pro Asn Ile Ala Glu Ser Ile Ser  
 1 5 10 15  
 Glu Val Thr Val Ala Ser Leu Leu Val Thr Glu Gly Ala Leu Ile Gln  
 20 25 30

Glu Asn Gln Gly Leu Leu Glu Ile Glu Ser Asp Lys Val Asn Gln Leu  
                   35                  40                  45  
 Ile Tyr Ala Pro Val Ser Gly Arg Ile Phe Trp Glu Val Ser Glu Gly  
           50                  55                  60  
 Asp Val Val Pro Val Gly Gly Val Val Gly Lys Ile Glu Pro Ala Gly  
       65                  70                  75                  80  
 Glu Gly Glu Glu Leu Gly Asp Ser Gln Ser Lys Glu Thr Ile Glu Ala  
                   85                  90                  95  
 Glu Ile Ile Cys Phe Pro Gln Ser Gly Val Arg Gln Ser Pro Glu  
                   100                  105                  110  
 Asn Lys Thr Phe Ile Pro Leu Arg Asp Gln Met Asp Gln Gly Ser Gln  
           115                  120                  125  
 Gly Leu Ser Ala Gly Asp Arg Gly Glu Thr Arg Glu Arg Met Thr Ser  
           130                  135                  140  
 Ile Arg Lys Thr Ile Ser Arg Arg Leu Leu Ser Ala Leu His Glu Ser  
       145                  150                  155                  160  
 Ala Met Leu Thr Thr Phe Asn Glu Val Tyr Met Thr Pro Leu Phe His  
                   165                  170                  175  
 Leu Arg Lys Glu Lys Gln Glu Glu Phe Leu Ser Arg Tyr Gly Val Lys  
                   180                  185                  190  
 Leu Gly Phe Met Ser Phe Phe Val Lys Ala Val Leu Glu Ala Leu Lys  
           195                  200                  205  
 Ala Tyr Pro Arg Val Asn Ala Tyr Ile Asp Gly Glu Glu Ile Val Thr  
           210                  215                  220  
 Val Thr Ile Met Thr Phe Leu Leu Leu  
       225                  230  
 <210>395  
 <211>915  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>395  
 Ile Val Phe Ile Glu Phe Asn Tyr Phe Met Asp Ser Glu Phe Val Gly  
       1                  5                  10                  15  
 Gln Val Tyr Ser Ser Asp Met Asp Trp Ile Glu Ser Met Tyr Gln Arg  
           20                  25                  30  
 Phe Met Asn His Glu Thr Leu Asp Pro Ser Trp Lys Tyr Phe Phe Glu  
           35                  40                  45  
 Gly Tyr Gln Leu Gly Gln Ala Ser Pro Ser Glu Ala Ser Thr Lys  
       50                  55                  60  
 Ile Ser Gly Asn Glu Thr Ile Ala Met Leu Gln Glu Gln Lys Ser Gln  
       65                  70                  75                  80  
 Phe Leu Cys Thr Ile Tyr Arg Tyr Tyr Gly Tyr Leu Gln Ser Gln Ile  
                   85                  90                  95  
 Ser Thr Leu Ala Pro Thr Thr Asp Ser Arg Phe Ile Gln Glu Lys Ile  
                   100                  105                  110  
 Ala Lys Ile Asp Leu Asp Glu Gln Val Pro Ser Ala Gly Leu Leu Pro  
           115                  120                  125  
 Lys Ala Gln Val Ser Val Arg Glu Leu Ile Glu Ala Leu Lys Lys Cys  
           130                  135                  140  
 Tyr Cys Gly Ser Leu Thr Leu Glu Thr Leu Thr Cys Thr Pro Glu Leu  
       145                  150                  155                  160  
 Gln Glu Phe Val Trp Asn Leu Met Glu Lys Arg Gln Val Glu Arg Phe  
                   165                  170                  175  
 Ala Glu Gln Leu Leu Arg Ser Tyr Lys Asp Leu Cys Lys Ala Thr Phe  
                   180                  185                  190  
 Phe Glu Glu Phe Leu Gln Ile Lys Phe Thr Gly Gln Lys Arg Phe Ser  
           195                  200                  205  
 Leu Glu Gly Gly Glu Thr Leu Val Pro Met Leu Glu His Leu Val His  
           210                  215                  220  
 Tyr Gly Ser Ala Leu Gly Ile Ser Asn Tyr Val Leu Gly Met Ala His  
       225                  230                  235                  240  
 Arg Gly Arg Leu Asn Val Leu Thr Asn Val Leu Gly Lys Pro Tyr Arg  
                   245                  250                  255  
 Tyr Val Phe Met Glu Phe Glu Asp Asp Pro Ala Ala Arg Gly Leu Glu

600



770 775 780  
 Gly Gly Phe Arg Ala Ile Leu Glu Asp Ala Asp Pro Asn Tyr Asp Ala  
 785 790 795 800  
 Ser Ile Leu Val Leu Cys Ser Gly Lys Ile Tyr Tyr Asp Tyr Ala Glu  
 805 810 815  
 Met Leu Pro Gln Asp Arg Arg Lys Asp Phe Ser Cys Leu Arg Ile Glu  
 820 825 830  
 Ser Leu Tyr Pro Leu Ala Leu Glu Asp Leu Val Ser Leu Ile Asp Lys  
 835 840 845  
 Tyr Ser His Leu Lys His Phe Val Trp Leu Gln Glu Glu Ser Lys Asn  
 850 855 860  
 Met Gly Ala Tyr Asp Tyr Met Phe Met Ala Leu Gln Asp Ile Leu Pro  
 865 870 875 880  
 Glu Lys Leu Leu Tyr Ile Gly Arg Pro Arg Ser Ser Ser Thr Ala Ser  
 885 890 895  
 Gly Ser Ala Lys Ser Val Val Lys Ser Trp Ser Arg Val Trp Lys Pro  
 900 905 910  
 Ser Phe Leu  
 915  
 <210>396  
 <211>394  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>396  
 Met Lys Thr Leu Ser Ala Ile Ala Ile Ala Gly Asp Ala Val Val Ser  
 1 5 10 15  
 Leu Ile Pro Met Leu Met Asn Gly Lys Ala Pro Leu Ala Leu Tyr Ile  
 20 25 30  
 His Ile Pro Phe Cys Thr Lys Lys Cys Arg Tyr Cys Ser Phe Tyr Thr  
 35 40 45  
 Ile Pro Tyr Lys Ser Glu Ser Val Ser Leu Tyr Cys Asn Ala Val Ile  
 50 55 60  
 Gln Glu Gly Leu Arg Lys Leu Ala Pro Ile Gln Glu Thr His Phe Ile  
 65 70 75 80  
 Glu Thr Val Phe Phe Gly Gly Gly Thr Pro Ser Leu Val Ser Pro Leu  
 85 90 95  
 Asp Leu Lys Arg Ile Leu Lys Glu Leu Ala Pro His Ala Arg Glu Ile  
 100 105 110  
 Thr Leu Glu Ala Asn Pro Glu Asn Leu Thr Val Ser Tyr Leu Arg Gln  
 115 120 125  
 Leu Gln Glu Thr Pro Ile Asn Arg Ile Ser Val Gly Val Gln Thr Phe  
 130 135 140  
 Asp Asp Ser Ile Leu Gln Leu Leu Gly Arg Thr His Ser Ser Ser Ala  
 145 150 155 160  
 Ala Ile Thr Ala Leu Gln Glu Cys Gln Asn His Gly Phe Ser Asn Leu  
 165 170 175  
 Ser Ile Asp Leu Ile Tyr Gly Leu Pro Thr Gln Ser Leu Glu Ile Phe  
 180 185 190  
 Leu Ser Asp Leu His Gln Ala Leu Thr Leu Pro Ile Thr His Ile Ser  
 195 200 205  
 Leu Tyr Asn Leu Thr Ile Asp Pro His Thr Ser Phe Tyr Lys His Arg  
 210 215 220  
 Lys Ile Leu Val Pro Thr Ile Ala Gln Glu Glu Ile Leu Ala Glu Met  
 225 230 235 240  
 Ser Leu Leu Ala Glu Asn Leu Leu Leu Ser Gln Gly Phe Gln Arg Tyr  
 245 250 255  
 Glu Leu Ala Ser Tyr Ala Lys Pro Asp Tyr Pro Ala Lys His Asn Leu  
 260 265 270  
 Tyr Tyr Trp Thr Asp Arg Pro Phe Leu Gly Leu Gly Val Ser Ala Ser  
 275 280 285  
 Gln Tyr Leu His Gly Glu Arg Ser Lys Asn Tyr Ser His Ile Ser His  
 290 295 300  
 Tyr Leu Arg Ala Val Arg Lys Asn Leu Pro Thr Gln Glu Thr Ser Glu  
 305 310 315 320

Ile Leu Pro Lys Lys Glu Arg Ile Lys Glu Ala Leu Ala Leu Arg Leu  
 325 330 335  
 Arg Leu Leu Glu Gly Ala Asp Leu Ala Glu Phe Pro Ser Thr Leu Ile  
 340 345 350  
 Ser Met Leu Thr Gln Asp Val Lys Leu Gln Asn Leu Phe Ser Val His  
 355 360 365  
 Gly Gln Cys Leu Ala Leu Asn Arg Gln Gly Arg Leu Phe His Asp Thr  
 370 375 380  
 Ile Ala Glu Glu Ile Met Gly Tyr Ser Phe  
 385 390  
 <210>397  
 <211>600  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>397  
 Ser Leu Pro Asn Lys Phe Arg Ala Leu Met Thr Ala Pro Thr Glu Ser  
 1 5 10 15  
 Arg Ser Ser Pro Pro Thr Leu Leu Glu Glu Thr Glu Pro Leu Ser Pro  
 20 25 30  
 Asn Pro Ile Pro Ala Asp Ile Gln Ile Pro Arg Ile Thr Ile Ser Pro  
 35 40 45  
 Pro Ser Leu Asp Val Ser Thr Val Ala Ser Ser Ala Glu Asp Ile Ser  
 50 55 60  
 Val Phe Ile Ala Gly Gly Pro Arg Ser Ser Ser Ala Ser Val Ala  
 65 70 75 80  
 Ser Asp Val Tyr Glu Leu Val Cys Leu Cys Gly Gly Asp Glu Asp Pro  
 85 90 95  
 Glu Pro Pro Asp Ser Glu Val Arg Thr Leu Tyr Val Asn Gly Ser Trp  
 100 105 110  
 Gln Thr His Gln Glu Ala Val Gln Glu Leu Leu Tyr Ile Ser Glu Val  
 115 120 125  
 Arg Gly Glu Ala Val Arg Leu Leu Tyr Asn Asp Gly Ser Gly Met Ser  
 130 135 140  
 Pro Trp Pro Ile Ser Pro Cys Arg Thr Leu Pro Thr Leu Asp His Pro  
 145 150 155 160  
 Leu Cys Gln Ala Leu Leu Thr Val Trp Glu Gln Phe Phe Ser Ala Pro  
 165 170 175  
 Glu Asn Gln Asn Arg Glu Phe Leu Val Ile Phe Tyr Gly Asp Ala Ser  
 180 185 190  
 Pro Tyr Ile Gln Gln Ala Leu Thr Gln Ser Arg His Ser Pro Arg Ile  
 195 200 205  
 Val Val Val Gly Ile Ser Pro Thr Val Phe Ile Gln Gly Asp Phe Arg  
 210 215 220  
 Val His Asn Tyr Arg Val Ser Gly Asp Phe Phe Ser Ser Leu Asp Cys  
 225 230 235 240  
 Arg Gly Thr Arg Ala Glu Asn Thr Thr Ile Leu Pro Tyr Ser Ser Gly  
 245 250 255  
 Leu Glu Gly Val Phe Leu Pro Ser Ile Arg Cys Pro Ser Phe Thr Trp  
 260 265 270  
 Ala Val Arg Phe Gly Glu Gln Cys Leu Val Ala Asn Arg Gly Glu Asp  
 275 280 285  
 Val Glu Asp Arg Gly Gly Leu Ser Gln Asp Ala Glu Arg Ser Gln Leu  
 290 295 300  
 Pro His Ser Glu Arg Asp Leu Ala Val Val Ile Asp Ser Thr Asp Pro  
 305 310 315 320  
 Ser Ser Met Ser Arg Leu Val Glu Trp Leu Asn Gln Gly Ser Pro Ser  
 325 330 335  
 Ser Asp Met Glu Ile Asn Pro Tyr Pro Gln Arg Cys Pro Asp Val Ala  
 340 345 350  
 Leu Ser Ala Leu Tyr Ala Ile Ser Arg Val Ser Gly Leu Ala Gln Glu  
 355 360 365  
 Trp Ile Leu Ala Ser Val His Glu Gly Leu Asp Leu Gln Ile Cys Tyr  
 370 375 380  
 Ser Leu Ile Leu Met His Thr Thr Phe Ala Val Arg Tyr Phe Phe Leu

385 390 395 400  
 Leu Phe Thr Asn Tyr Pro Gln Ser Arg Glu Arg Phe Arg Thr Ala Arg  
 405 410 415  
 Ile Val Ala Gln Ser Leu Tyr Leu Pro Ser Ile Leu Val Leu Val Phe  
 420 425 430  
 Asp Cys Gly Asn Val Leu Arg Lys Leu Trp Met Pro Gln Glu Ile Leu  
 435 440 445  
 Arg Ala Ile Phe Ile Ser Ala Ser Thr Ile Ser Gly Ser Ile Val Phe  
 450 455 460  
 Val Glu Cys Thr Arg Trp Met Gly Arg Gly Leu Arg His Arg Val Gln  
 465 470 475 480  
 Gln Phe Val Gln Gln Arg Val Ile Gly Ser Gly Leu Pro Val Gly Thr  
 485 490 495  
 Val Arg Ala Ser Tyr Arg Asp Arg Ala Gly Phe Ile Ile Gly Phe Leu  
 500 505 510  
 Gln Thr Val His Gly Gly Leu Tyr Leu Pro Val Ser Ile Met Val Leu  
 515 520 525  
 Asn Gln Ile Ala Ile Gln Val Pro Arg Ile Leu Val Arg Pro Asn Asn  
 530 535 540  
 Thr Ala Val Tyr Asp Leu His Asn Lys Ser Ala Glu Glu Asn Trp Ser  
 545 550 555 560  
 Ser Gly Asp Val Leu Ala Val Gly Gln Thr Leu Asn Phe Ile Leu Cys  
 565 570 575  
 Ala Phe Val Leu Phe Val Asn Leu Trp Phe Phe Val Lys Ser Val Leu  
 580 585 590  
 Arg His Ser Arg Arg Arg Arg Arg  
 595 600

&lt;210&gt;398

&lt;211&gt;115

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;398

Arg Val Arg Thr Ser Glu Ser Gly Gly Ser Gly Ser Ser Ser Pro Pro  
 1 5 10 15  
 Gln Arg Gln Thr Asn Ser Tyr Thr Ser Glu Ala Thr Glu Ala Asp Glu  
 20 25 30  
 Glu Leu Leu Gly Pro Pro Ala Met Lys Thr Glu Ile Ser Ser Ala Glu  
 35 40 45  
 Asp Ala Thr Val Asp Thr Ser Arg Glu Gly Gly Asp Ile Val Ile Leu  
 50 55 60  
 Gly Ile Trp Ile Ser Ala Gly Ile Gly Phe Gly Asp Arg Gly Ser Val  
 65 70 75 80  
 Ser Ser Ser Ser Val Gly Gly Glu Asp Arg Asp Ser Val Gly Ala Val  
 85 90 95  
 Ile Asn Ala Leu Asn Leu Phe Gly Lys Asp Tyr Lys Ile Ser Ile Asp  
 100 105 110  
 Asn Thr Gln  
 115

&lt;210&gt;399

&lt;211&gt;239

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;399

Pro Val Thr Leu Tyr Leu Leu Pro Asn Thr Leu Gly Thr Arg Ala Val  
 1 5 10 15  
 Glu Thr Leu Pro Ser Val Ile Gly Glu Leu Val His Arg Leu Asp Gly  
 20 25 30  
 Leu Ile Val Glu Ser Asp Arg Gly Gly Arg Ala Phe Leu Ser Leu Trp  
 35 40 45  
 Lys Ile Pro Glu Val His Lys Phe Pro Leu Ala Ile Leu Ser Lys His  
 50 55 60  
 Ala Arg Leu Pro Lys Ala Trp Asp Phe Tyr Leu Glu Pro Ile Val Lys  
 65 70 75 80  
 His Gly Glu Asn Trp Gly Leu Ile Ser Asp Ala Gly Leu Pro Cys Ile

85 90 95  
 Ala Asp Pro Gly Ala Ser Leu Val Arg Arg Ala Leu Gly Ile  
 100 105 110  
 Pro Val Gln Ala Phe Ser Gly Pro Cys Ser Ile Thr Leu Ala Leu Met  
 115 120 125  
 Leu Ser Gly Leu Pro Ser Gln Ser Phe Thr Phe Leu Gly Tyr Leu Pro  
 130 135 140  
 Gln Ser Pro Lys Glu Arg Val Lys Ser Ile Lys Lys Ala Ala Thr Ser  
 145 150 155 160  
 Lys Glu Val Ser Thr Ser Val Cys Ile Glu Thr Pro Tyr Arg Asn Val  
 165 170 175  
 Tyr Thr Phe Glu Ser Leu Leu Asp Thr Leu Pro Ser Tyr Ala Glu Leu  
 180 185 190  
 Cys Val Ala Ser Asp Leu Ser Gly Pro Ser Glu Leu Val Leu Thr Arg  
 195 200 205  
 Gln Val Gln Ser Trp Arg Thr Thr Glu Asp Leu Gly Ser Val Lys Gln  
 210 215 220  
 Ser Ile Thr Lys Val Pro Thr Ile Phe Leu Phe His Ile Pro Asn  
 225 230 235

&lt;210&gt;400

&lt;211&gt;98

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;400

Gly Val Ser Ile His Thr Glu Val Asp Thr Ser Leu Glu Val Ala Ala  
 1 5 10 15  
 Phe Phe Ile Asp Phe Thr Arg Ser Leu Gly Leu Cys Gly Arg Tyr Pro  
 20 25 30  
 Lys Asn Val Lys Leu Trp Glu Gly Lys Pro Glu Ser Met Ser Ala Asn  
 35 40 45  
 Val Ile Glu Gln Gly Pro Glu Lys Ala Cys Thr Gly Ile Pro Lys Ala  
 50 55 60  
 Arg Ala Arg Arg Thr Lys Leu Ala Pro Gly Ser Ala Ile Gln Gly Arg  
 65 70 75 80  
 Pro Ala Ser Glu Ile Ser Pro Gln Phe Ser Pro Cys Phe Thr Ile Gly  
 85 90 95

Ser Arg

&lt;210&gt;401

&lt;211&gt;321

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;401

Val Gln Asp Thr Thr Phe Leu Thr Leu Pro Met Gln Lys Ser Leu Thr  
 1 5 10 15  
 Ser Phe Asp Asp Phe Ser Gln Ala Tyr Ala Glu Lys Val Pro Ala Ile  
 20 25 30  
 Ala Leu Ile Gly Ser Ala Leu Glu Asp Asp Lys Asp Ala Leu Ile Glu  
 35 40 45  
 Leu Leu Val Ser Glu Ser Phe Lys Glu Leu Gly Gly Gln Gly Leu Met  
 50 55 60  
 Pro Ala Thr Leu Met Ser Trp Thr Glu Thr Phe Ala Leu Phe Gln Glu  
 65 70 75 80  
 His Glu Thr Leu Gly Ile Ile His Ala Glu Lys Phe Pro Leu Ala Thr  
 85 90 95  
 Lys Glu Phe Leu Ser Arg Tyr Ala Arg Asn Pro Gln Pro His Leu Thr  
 100 105 110  
 Ile Leu Ile Phe Thr Thr Lys Gln Glu Cys Phe Arg Glu Leu Ser Lys  
 115 120 125  
 Ala Leu Pro Ser Ala Leu Ser Leu Ser Leu Phe Gly Glu Trp Pro Ala  
 130 135 140  
 Asp Arg Gln Lys Arg Ile Ile Arg Leu Leu Leu Gln Arg Ala Glu Arg  
 145 150 155 160  
 Val Gly Ile Ser Cys Ser Gln Ser Leu Ala Ser Leu Phe Leu Arg Ala

165 170 175  
 Leu Ala Ser Thr Ser Leu Pro Asp Ile Leu Ser Glu Phe Asp Lys Leu  
 180 185 190  
 Leu Cys Ser Val Gly Lys Lys Thr Ser Leu Asp His Ser Asp Ile Lys  
 195 200 205  
 Glu Leu Val Val Lys Lys Glu Lys Ala Ser Leu Trp Lys Phe Arg Asp  
 210 215 220  
 Ser Leu Leu Lys Arg Asp Pro Val Glu Gly His Gln Gln Leu His Phe  
 225 230 235 240  
 Leu Leu Glu Asp Gly Glu Asp Pro Leu Gly Ile Ile Thr Phe Leu Arg  
 245 250 255  
 Thr Gln Cys Leu Tyr Gly Leu Arg Ser Ile Glu Glu Gly Ser Lys Glu  
 260 265 270  
 Asn Lys His Arg Met Phe Val Leu Tyr Gly Lys Glu Arg Leu His Gln  
 275 280 285  
 Ala Leu Asn Ser Leu Phe Tyr Ala Glu Thr Leu Ile Lys Asn Asn Val  
 290 295 300  
 Gln Asp Pro Ile Val Ala Val Glu Thr Leu Val Ile Arg Met Val Asn  
 305 310 315 320  
 Leu

&lt;210&gt;402

&lt;211&gt;182

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;402

Val Ile Thr Cys Leu Ile Arg Gly Ile Lys Met Ile Gly Ala Gln Lys  
 1 5 10 15  
 Lys Gln Ser Gly Lys Lys Thr Ala Ser Arg Ala Val Arg Lys Pro Ala  
 20 25 30  
 Lys Lys Val Ala Ala Lys Arg Thr Val Lys Lys Ala Thr Val Arg Lys  
 35 40 45  
 Thr Ala Val Lys Lys Pro Ala Val Arg Lys Thr Ala Ala Lys Lys Thr  
 50 55 60  
 Val Ala Lys Lys Thr Thr Ala Lys Arg Thr Val Arg Lys Thr Val Ala  
 65 70 75 80  
 Lys Lys Pro Ala Val Lys Lys Val Ala Ala Lys Arg Val Val Lys Lys  
 85 90 95  
 Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Ala Val Arg Lys Thr Val  
 100 105 110  
 Ala Lys Lys Pro Val Ala Arg Lys Thr Thr Val Ala Lys Gly Ser Pro  
 115 120 125  
 Lys Lys Ala Ala Ala Cys Ala Leu Ala Cys His Xaa Asn His Lys His  
 130 135 140  
 Thr Ser Ser Cys Lys Arg Val Cys Ser Ser Thr Ala Thr Arg Lys His  
 145 150 155 160  
 Gly Ser Lys Ser Arg Val Arg Thr Ala Xaa Gly Trp Arg His Gln Leu  
 165 170 175  
 Ile Lys Met Met Ser Arg  
 180

&lt;210&gt;403

&lt;211&gt;197

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;403

Arg Gln Pro Xaa Ala Val Arg Thr Arg Leu Leu Glu Pro Cys Phe Leu  
 1 5 10 15  
 Val Ala Val Glu Gln Thr Arg Leu Gln Leu Asp Val Cys Leu Trp  
 20 25 30  
 Phe Xaa Trp His Ala Lys Ala Gln Ala Ala Ala Phe Leu Gly Glu Pro  
 35 40 45  
 Leu Ala Thr Val Val Phe Leu Ala Thr Gly Phe Leu Ala Thr Val Leu  
 50 55 60  
 Arg Thr Ala Leu Leu Ala Val Val Phe Phe Ala Thr Val Phe Phe Thr

65 70 75 80  
 Thr Arg Leu Ala Ala Thr Phe Leu Thr Ala Gly Phe Leu Ala Thr Val  
 85 90 95  
 Leu Arg Thr Val Leu Leu Ala Val Val Phe Phe Ala Thr Val Phe Leu  
 100 105 110  
 Ala Ala Val Leu Arg Thr Ala Gly Phe Phe Thr Ala Val Leu Arg Thr  
 115 120 125  
 Val Ala Phe Leu Thr Val Arg Leu Ala Ala Thr Phe Leu Ala Gly Phe  
 130 135 140  
 Arg Thr Ala Leu Glu Ala Val Phe Leu Pro Leu Cys Phe Phe Cys Ala  
 145 150 155 160  
 Pro Ile Ile Phe Ile Pro Leu Ile Arg Gln Val Ile Thr Tyr Leu Ile  
 165 170 175  
 Tyr Arg Gln Gly Arg Leu Lys Thr Leu Ile Lys Lys Met Thr Phe Ile  
 180 185 190  
 Leu Lys Lys Leu Lys  
 195

&lt;210&gt;404

&lt;211&gt;192

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;404

Met Ser Arg Gly Ser Phe Leu Leu Thr Glu Asn Ala Ile Asp Gly Ala  
 1 5 10 15  
 Ser Tyr Lys Met Gly Asp Val Tyr Val Gly Met Ser Gly Leu Ser Val  
 20 25 30  
 Glu Ile Cys Ser Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala  
 35 40 45  
 Ile Thr Tyr Ala Leu Lys Tyr Cys Lys Pro Thr Arg Ile Ile Asp Phe  
 50 55 60  
 Ala Thr Leu Thr Gly Ala Met Val Val Ser Leu Gly Glu Glu Val Ala  
 65 70 75 80  
 Gly Phe Phe Ser Asn Asn Asp Val Leu Ala Glu Asp Leu Leu Glu Ala  
 85 90 95  
 Ser Ala Glu Thr Ser Glu Pro Leu Trp Arg Leu Pro Leu Val Lys Lys  
 100 105 110  
 Tyr Asp Lys Thr Leu His Ser Asp Ile Ala Asp Met Lys Asn Leu Gly  
 115 120 125  
 Ser Asn Arg Ala Gly Ala Ile Thr Ala Ala Leu Phe Leu Gln Arg Phe  
 130 135 140  
 Leu Glu Glu Ser Ser Val Ala Trp Ala His Leu Asp Ile Ala Gly Thr  
 145 150 155 160  
 Ala Tyr His Glu Lys Glu Glu Asp Arg Tyr Pro Lys Tyr Ala Ser Gly  
 165 170 175  
 Phe Gly Val Arg Ser Ile Leu Tyr Tyr Leu Glu Asn Ser Leu Ser Lys  
 180 185 190

&lt;210&gt;405

&lt;211&gt;325

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;405

Val Val Leu Phe His Ala Gln Ala Ser Gly Arg Asn Arg Val Lys Ala  
 1 5 10 15  
 Asp Ala Ile Val Leu Pro Phe Trp His Phe Lys Asp Ala Lys Asn Ala  
 20 25 30  
 Ala Ser Phe Glu Ala Glu Phe Glu Pro Ser Tyr Leu Pro Ala Leu Glu  
 35 40 45  
 Asn Phe Gln Gly Lys Thr Gly Glu Ile Glu Leu Leu Tyr Ser Ser Pro  
 50 55 60  
 Lys Ala Lys Glu Lys Arg Ile Val Leu Leu Gly Leu Gly Lys Asn Glu  
 65 70 75 80  
 Glu Leu Thr Ser Asp Val Val Phe Gln Thr Tyr Ala Thr Leu Thr Arg  
 85 90 95  
 Val Leu Arg Lys Ala Lys Cys Ser Thr Val Asn Ile Ile Leu Pro Thr

100 105 110  
 Ile Ser Glu Leu Arg Leu Ser Ala Glu Glu Phe Leu Val Gly Leu Ser  
 115 120 125  
 Ser Gly Ile Leu Ser Leu Asn Tyr Asp Tyr Pro Arg Tyr Asn Lys Val  
 130 135 140  
 Asp Arg Asn Leu Glu Thr Pro Leu Ser Lys Val Thr Val Ile Gly Ile  
 145 150 155 160  
 Val Pro Lys Met Ala Asp Ala Ile Phe Arg Lys Glu Ala Ala Ile Phe  
 165 170 175  
 Glu Gly Val Tyr Leu Thr Arg Asp Leu Val Asn Arg Asn Ala Asp Glu  
 180 185 190  
 Ile Thr Pro Lys Lys Leu Ala Glu Val Ala Leu Asn Leu Gly Lys Glu  
 195 200 205  
 Phe Pro Ser Ile Asp Thr Lys Val Leu Gly Lys Asp Ala Ile Ala Lys  
 210 215 220  
 Glu Lys Met Gly Leu Leu Leu Ala Val Ser Lys Gly Ser Cys Val Asp  
 225 230 235 240  
 Pro His Phe Ile Val Val Arg Tyr Gln Gly Arg Pro Lys Ser Lys Asp  
 245 250 255  
 His Thr Val Leu Ile Gly Lys Gly Val Thr Phe Asp Ser Gly Gly Leu  
 260 265 270  
 Asp Leu Lys Pro Gly Lys Ser Met Leu Thr Met Lys Glu Asp Met Ala  
 275 280 285  
 Gly Gly Ala Thr Val Leu Gly Ile Leu Ser Ala Leu Ala Xaa Leu Glu  
 290 295 300  
 Leu Pro Ile Asn Val Thr Gly Ile Ile Pro Ala Tyr Arg Glu Cys Tyr  
 305 310 315 320  
 Arg Trp Arg Leu Leu  
 325

&lt;210&gt;406

&lt;211&gt;105

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;406

Asp Ala Ser Leu Leu Glu Glu Arg Leu Arg Ser His Cys Cys Trp Arg  
 1 5 10 15  
 Tyr Leu Cys Arg Glu Leu His Glu Gln Arg Trp Phe His Arg Asn Ser  
 20 25 30  
 Ser Leu Val Ile Ser Val Asp Ser Leu Lys Phe Ser Pro Phe Gly Arg  
 35 40 45  
 Asn Glu Gly Ser Arg Ser Pro Ser Leu Glu Asp Asn His Gln Gln Val  
 50 55 60  
 Gly Tyr Glu Ser Val Ser Val Gly Phe Glu Gly Glu Ala Leu Asp Ala  
 65 70 75 80  
 Glu Ala Ile Lys Asp Lys Asp Met Tyr Ala Gly Tyr Gly Gln Glu Gln  
 85 90 95  
 Gln Tyr Val Cys Glu Asp Val Pro Phe  
 100 105

&lt;210&gt;407

&lt;211&gt;89

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;407

Met Met Phe Gly His Phe Ala Gly Tyr Leu Gly Ala Asp Pro Glu Glu  
 1 5 10 15  
 Arg Met Thr Ser Lys Gly Lys Arg Val Ile Thr Leu Arg Leu Gly Val  
 20 25 30  
 Lys Thr Arg Val Gly Met Lys Asp Glu Thr Val Trp Cys Lys Cys Asn  
 35 40 45  
 Ile Trp His Asn Arg Tyr Asp Lys Met Leu Pro Tyr Leu Lys Lys Gly  
 50 55 60  
 Ser Gly Val Ile Val Ala Gly Asp Ile Ser Val Glu Ser Tyr Met Ser  
 65 70 75 80  
 Lys Asp Gly Phe Thr Ala Ile Leu Leu

85

&lt;210&gt;408

&lt;211&gt;179

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;408

Leu Glu Thr Thr Thr Ile Tyr Tyr Lys Glu Ile Pro Ser Cys Pro Arg  
 1 5 10 15  
 Gln Asn Ala Glu Glu Asn Leu Lys Asn Phe Ala Lys Glu Leu Lys Leu  
 20 25 30  
 Pro Asp Val Ala Phe Asp Gln Asn Thr Cys Ile Leu Phe Val Asp  
 35 40 45  
 Gly Glu Phe Ser Leu His Leu Thr Tyr Glu Glu His Ser Asp Arg Leu  
 50 55 60  
 Tyr Val Tyr Ala Pro Leu Leu Asp Gly Leu Pro Asp Asn Thr Gln Arg  
 65 70 75 80  
 Lys Leu Ala Leu Tyr Glu Lys Leu Leu Glu Gly Ser Met Leu Gly Gly  
 85 90 95  
 Gln Met Ala Gly Gly Val Gly Val Ala Thr Lys Glu Gln Leu Ile  
 100 105 110  
 Leu Met His Cys Val Leu Asp Met Lys Tyr Ala Glu Thr Asn Leu Leu  
 115 120 125  
 Lys Ala Phe Ala Gln Leu Phe Ile Glu Thr Val Val Lys Trp Arg Thr  
 130 135 140  
 Val Cys Ala Asp Ile Cys Ala Gly Arg Glu Pro Ser Val Asp Thr Met  
 145 150 155 160  
 Pro Gln Met Pro Gln Gly Gly Gly Gly Met Gln Pro Pro Pro Thr Gly  
 165 170 175  
 Ile Arg Ala

&lt;210&gt;409

&lt;211&gt;666

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;409

Ser Thr Met Glu Lys Val Ser Ser Tyr Pro Ser Val Pro Leu Pro Leu  
 1 5 10 15  
 Gly Ala Ser Lys Ile Ser Pro Asn Arg Tyr Arg Phe Ala Leu Tyr Ala  
 20 25 30  
 Ser Gln Ala Thr Glu Val Ile Leu Ala Leu Thr Asp Glu Asn Ser Glu  
 35 40 45  
 Val Ile Glu Val Pro Leu Tyr Pro Asp Thr His Arg Thr Gly Ala Ile  
 50 55 60  
 Trp His Ile Glu Ile Glu Gly Ile Ser Asp Gln Ser Ser Tyr Ala Phe  
 65 70 75 80  
 Arg Val His Gly Pro Lys Lys His Gly Met Gln Tyr Ser Phe Lys Glu  
 85 90 95  
 Tyr Leu Ala Asp Pro Tyr Ala Lys Asn Ile His Ser Pro Gln Ser Phe  
 100 105 110  
 Gly Ser Arg Lys Lys Gln Gly Asp Tyr Ala Phe Cys Tyr Leu Lys Glu  
 115 120 125  
 Glu Pro Phe Pro Trp Asp Gly Asp Gln Pro Leu His Leu Pro Lys Glu  
 130 135 140  
 Glu Met Ile Ile Tyr Glu Met His Val Arg Ser Phe Thr Gln Ser Ser  
 145 150 155 160  
 Ser Ser Arg Val His Ala Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys  
 165 170 175  
 Ile Asp His Leu His Lys Leu Gly Ile Asn Ala Val Glu Leu Leu Pro  
 180 185 190  
 Ile Phe Glu Phe Asp Glu Thr Ala His Pro Phe Arg Asn Ser Lys Phe  
 195 200 205  
 Pro Tyr Leu Cys Asn Tyr Trp Gly Tyr Ala Pro Leu Asn Phe Phe Ser  
 210 215 220  
 Pro Cys Arg Arg Tyr Ala Tyr Ala Ser Asp Pro Cys Ala Pro Ser Arg



BNSDOCID: <WO\_\_9927105A2\_1\_>

Leu Ile Glu Phe Arg Arg Arg Thr Val Lys Leu Leu Lys Asn Val Leu  
 35 40 45  
 Leu Gly Leu Phe Phe Ser Met Ser Ile Ser Gly Phe Ser Glu Val Lys  
 50 55 60  
 Val Ser Asp Thr Phe Val Lys Gln Asp Thr Val Val Glu Pro Lys Ile  
 65 70 75 80  
 Arg Val Leu Leu Ser Asn Glu Ser Thr Thr Ala Leu Ile Glu Ala Lys  
 85 90 95  
 Gly Pro Tyr Arg Ile Tyr Gly Asp Asn Val Leu Leu Asp Thr Ala Ile  
 100 105 110  
 Gln Gly Gln Arg Cys Val Val His Ala Leu Tyr Glu Gly Ile Arg Trp  
 115 120 125  
 Gly Glu Phe Tyr Pro Gly Leu Gln Cys Leu Lys Ile Glu Pro Val Asp  
 130 135 140  
 Asp Thr Ala Ser Leu Phe Phe Asn Gly Ile Gln Tyr Gln Gly Ser Leu  
 145 150 155 160  
 Tyr Val His Arg Lys Asp Asn His Cys Ile Met Val Ser Asn Glu Val  
 165 170 175  
 Thr Ile Glu Asp Tyr Leu Lys Ser Val Leu Ser Ile Lys Tyr Leu Glu  
 180 185 190  
 Glu Leu Asp Lys Glu Ala Leu Ser Ala Cys Ile Ile Leu Glu Arg Thr  
 195 200 205  
 Ala Leu Tyr Glu Lys Leu Leu Ala Arg Asn Pro Gln Asn Phe Trp His  
 210 215 220  
 Val Lys Ala Glu Glu Glu Gly Tyr Ala Gly Phe Gly Val Thr Lys Gln  
 225 230 235 240  
 Phe Tyr Gly Val Glu Glu Ala Ile Asp Trp Thr Ala Arg Leu Val Val  
 245 250 255  
 Asp Ser Pro Gln Gly Leu Ile Ile Asp Ala Gln Gly Leu Leu Gln Ser  
 260 265 270  
 Asn Val Asp Arg Leu Ala Ile Glu Gly Phe Asn Ala Arg Gln Ile Leu  
 275 280 285  
 Glu Lys Phe Tyr Lys Asp Val Asp Phe Val Val Ile Glu Ser Trp Asn  
 290 295 300  
 Glu Glu Leu Asp Gly Glu Ile Arg  
 305 310

&lt;210&gt;411

&lt;211&gt;337

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;411

Met Thr His Gln Val Ala Val Leu His Gln Asp Lys Lys Phe Asp Val  
 1 5 10 15  
 Ser Leu Arg Pro Lys Gly Leu Glu Glu Phe Tyr Gly Gln His Leu  
 20 25 30  
 Lys Glu Arg Leu Asp Leu Phe Leu Cys Ala Ala Leu Gln Arg Gly Glu  
 35 40 45  
 Val Pro Gly His Cys Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr  
 50 55 60  
 Ser Leu Ala His Ile Val Ala Tyr Thr Val Gly Lys Gly Leu Val Leu  
 65 70 75 80  
 Ala Ser Gly Pro Gln Leu Ile Lys Pro Ser Asp Leu Leu Gly Leu Leu  
 85 90 95  
 Thr Ser Leu Gln Glu Gly Asp Val Phe Phe Ile Asp Glu Ile His Arg  
 100 105 110  
 Met Gly Lys Val Ala Glu Glu Tyr Leu Tyr Ser Ala Met Glu Asp Phe  
 115 120 125  
 Lys Val Asp Ile Thr Ile Asp Ser Gly Pro Gly Ala Arg Ser Val Arg  
 130 135 140  
 Val Asp Leu Ala Pro Phe Thr Leu Val Gly Ala Thr Thr Arg Ser Gly  
 145 150 155 160  
 Met Leu Ser Glu Pro Leu Arg Thr Arg Phe Ala Phe Ser Ala Arg Leu  
 165 170 175  
 Ser Tyr Tyr Ser Asp Gln Asp Leu Lys Glu Ile Leu Val Arg Ser Ser

180 185 190  
 His Leu Leu Gly Ile Glu Ala Asp Ser Ser Ala Leu Leu Glu Ile Ala  
 195 200 205  
 Lys Arg Ser Arg Gly Thr Pro Arg Leu Ala Asn His Leu Leu Arg Trp  
 210 215 220  
 Val Arg Asp Phe Ala Gln Ile Arg Glu Gly Asn Cys Ile Asn Gly Asp  
 225 230 235 240  
 Val Ala Glu Lys Ala Leu Ala Met Leu Leu Ile Asp Asp Trp Gly Leu  
 245 250 255  
 Asn Glu Ile Asp Ile Lys Leu Leu Thr Thr Ile Ile Asp Tyr Tyr Gln  
 260 265 270  
 Gly Gly Pro Val Gly Ile Lys Thr Leu Ser Val Ala Val Gly Glu Asp  
 275 280 285  
 Ile Lys Thr Leu Glu Asp Val Tyr Glu Pro Phe Leu Ile Leu Lys Gly  
 290 295 300  
 Phe Ile Lys Lys Thr Pro Arg Gly Arg Met Val Thr Gln Leu Ala Tyr  
 305 310 315 320  
 Asp His Leu Lys Arg His Ala Lys Asn Leu Leu Ser Leu Gly Glu Gly  
 325 330 335  
 Gln

&lt;210&gt;412

&lt;211&gt;190

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;412

Met Ser Ile Lys Glu Asp Lys Trp Ile Arg Glu Met Ala Leu Asn Ala  
 1 5 10 15  
 Asp Met Ile His Pro Phe Val Asn Gly Gln Val Asn Val Asn Glu Glu  
 20 25 30  
 Thr Gly Glu Lys Leu Ile Ser Tyr Gly Leu Ser Ser Tyr Gly Tyr Asp  
 35 40 45  
 Leu Arg Leu Ser Arg Glu Phe Lys Val Phe Thr Asn Val Tyr Asn Ser  
 50 55 60  
 Val Val Asp Pro Lys Cys Phe Thr Glu Asp Ile Phe Ile Ser Ile Thr  
 65 70 75 80  
 Asp Asp Val Cys Ile Val Pro Pro Asn Ser Phe Ala Leu Ala Arg Ser  
 85 90 95  
 Val Glu Tyr Phe Arg Ile Pro Arg Asn Val Leu Thr Met Cys Ile Gly  
 100 105 110  
 Lys Ser Thr Tyr Ala Arg Cys Gly Ile Ile Val Asn Val Thr Pro Phe  
 115 120 125  
 Glu Pro Glu Trp Glu Gly His Val Thr Ile Glu Ile Ser Asn Thr Thr  
 130 135 140  
 Pro Leu Pro Ala Lys Ile Tyr Ala Asn Glu Gly Ile Ala Gln Val Leu  
 145 150 155 160  
 Phe Phe Glu Ser Ser Thr Thr Cys Glu Val Ser Tyr Ala Asp Arg Lys  
 165 170 175  
 Gly Lys Tyr Gln Lys Gln Gln Gly Ile Thr Val Pro Cys Val  
 180 185 190

&lt;210&gt;413

&lt;211&gt;165

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;413

Lys Phe Leu Thr Leu Arg His Cys Gln Arg Lys Phe Thr Leu Met Lys  
 1 5 10 15  
 Gly Leu Pro Arg Ser Tyr Ser Leu Ser Leu Val Arg Pro Ala Arg Phe  
 20 25 30  
 Leu Met Gln Thr Glu Lys Glu Ser Ile Lys Ser Asn Lys Ala Ser Pro  
 35 40 45  
 Tyr Leu Val Ser Lys Val Ser Val Arg Lys Lys Asn Trp Gly Phe Arg  
 50 55 60  
 Leu Leu Glu Glu Val Met Ile Lys Ser Trp Trp Val Ile Phe Ser Ile

```

      65              70              75              80
Leu Ile Gly Gly Phe Val Tyr Asp Arg Ala Ile Gln Glu Leu Arg Thr
      85              90
Glu Glu Leu Arg Leu Gln Ser Lys Val Ser Ser Leu Cys Gln Asp Ile
      100              105              110
Leu Ser Ala Gln Glu Lys Gln Arg Gln Leu Gln Leu His Leu Gln His
      115              120              125
Trp Gln Asp Ser Ala Ala Ile Glu Ala Ala Leu Ile Gln Arg Leu Gly
      130              135              140
Leu Ile Pro Lys Gly Tyr Lys Lys Leu Cys Val Ser Pro Lys Gln Gln
      145              150              155              160
Ser Glu Asn Lys Asp
      165

<210>414
<211>414
<212>PRT
<213>Chlamydia pneumoniae
<400>414
Lys Glu Thr Met Ile Pro Thr Met Leu Met Phe Phe Ile Ile Cys Phe
  1      5      10
Thr Leu Cys Ser Gly Phe Ile Ser Leu Ser Gln Ile Ala Leu Phe Ser
      20      25      30
Leu Pro Thr Ser Leu Ile Ser His Tyr Lys Arg Ser Lys Ser Lys Lys
      35      40      45
Gln Gln Arg Val Ala Thr Leu Leu Leu His Pro His His Leu Leu Ile
      50      55      60
Thr Leu Ile Phe Cys Asp Ile Gly Leu Asn Ile Ala Ile Gln Asn Cys
      65      70      75      80
Phe Ala Ile Leu Phe Gly Asp Ala Ala Ser Trp Trp Phe Thr Val Gly
      85      90      95
Leu Pro Leu Ala Ile Thr Leu Ile Leu Gly Glu Ile Leu Pro Lys Ala
      100      105      110
Val Ala Leu Pro Phe Asn Thr Gln Ile Ala Ser Ser Val Ala Pro Leu
      115      120      125
Ile Leu Cys Val Thr Lys Ile Phe Lys Pro Leu Leu His Trp Gly Ile
      130      135      140
Val Gly Ile Asn Tyr Val Val Gln Trp Ile Leu Ser Lys Gln Gln Ile
      145      150      155      160
Asp Ile Ile Gln Pro Gln Glu Leu Lys Glu Val Leu Gln Ser Cys Lys
      165      170      175
Asp Phe Gly Val Val Asn Gln Glu Glu Ser Arg Leu Leu Tyr Gly Tyr
      180      185      190
Leu Ser Leu Ser Asp Cys Ser Val Lys Glu Arg Met Gln Pro Arg Gln
      195      200      205
Asp Ile Leu Phe Tyr Asp Ile Gln Thr Pro Leu Glu Asn Leu Tyr Leu
      210      215      220
Leu Phe Ser Lys Gln His Cys Ser Arg Val Pro Ile Cys Asn Asp Asn
      225      230      235      240
Leu Gln Asn Leu Leu Gly Ile Cys Thr Ala Arg Ser Leu Leu Leu His
      245      250      255
Asp Lys Pro Leu Gln Ser Ser Asp Asp Leu Leu Pro Leu Leu Lys Lys
      260      265      270
Pro Tyr Tyr Met Pro Glu Thr Ile Ser Ala Lys Met Ala Leu Cys Gln
      275      280      285
Met Ala Ala Glu Asp Glu Thr Leu Gly Met Ile Ile Asp Glu Tyr Gly
      290      295      300
Ser Ile Glu Gly Leu Ile Thr Gln Glu Asp Leu Phe Glu Ile Val Ala
      305      310      315      320
Gly Glu Ile Val Asp Gln Arg Asp Asn Lys Ile Leu Tyr Thr Thr Ser
      325      330      335
Gly Ala Asp Val Ile Ile Ala Ser Gly Thr Leu Glu Leu Arg Glu Phe
      340      345      350
Ser Glu Ile Phe Asp Ile Asn Leu Pro Thr Asn Asn Asn Ile Ala Thr
      355      360      365

```

Ile Gly Gly Trp Leu Ile Glu Gln Ile Gly Thr Ile Pro Thr Thr Gly  
 370 375 380  
 Met Lys Leu Ser Trp Asn Asn Leu Leu Phe Gln Val Leu Asp Ala Ala  
 385 390 395 400  
 Pro Asn Arg Ile Arg Arg Val Tyr Ile Arg Lys Leu Tyr Asp  
 405 410

&lt;210&gt;415

&lt;211&gt;404

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;415

Met Thr Asn Ser Ala Leu Phe Trp Ile Gly Val Asn Ile Ile Cys Ile  
 1 5 10 15  
 Val Leu Gln Gly Phe Tyr Ser Met Met Glu Met Ala Cys Val Ser Phe  
 20 25 30  
 Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Asp His Lys Lys Ala  
 35 40 45  
 Arg Tyr Ile Asn Phe Leu Ile Arg Arg Pro Tyr Arg Leu Phe Gly Thr  
 50 55 60  
 Val Met Leu Gly Val Asn Ile Ala Leu Gln Val Gly Ser Glu Ser Ser  
 65 70 75 80  
 Arg Asn Cys Tyr Arg Ala Leu Gly Ile Thr Pro Asp Tyr Ala Pro Phe  
 85 90 95  
 Thr Gln Ile Phe Ile Val Val Ile Phe Ala Glu Leu Leu Pro Leu Thr  
 100 105 110  
 Ile Ser Arg Lys Ile Pro Glu Lys Leu Ala Leu Trp Gly Ala Pro Ile  
 115 120 125  
 Leu Tyr Tyr Ser His Tyr Ile Phe Tyr Pro Leu Ile Gln Leu Ile Gly  
 130 135 140  
 Ser Leu Thr Glu Gly Leu Tyr Tyr Leu Leu Asn Ile Arg Lys Glu Lys  
 145 150 155 160  
 Leu Asn Ser Thr Leu Ser Arg Asp Glu Phe Gln Lys Ala Leu Glu Thr  
 165 170 175  
 His His Glu Glu Gln Asp Phe Asn Thr Ile Ala Thr Asn Ile Phe Ser  
 180 185 190  
 Leu Ser Ala Thr Cys Ala Asp Gln Val Cys Gln Pro Leu Glu Gln Val  
 195 200 205  
 Thr Met Leu Pro Ser Ser Ala Asn Val Lys Asp Phe Cys Arg Thr Ile  
 210 215 220  
 Lys Asn Thr Asp Ile Asn Phe Ile Pro Val Tyr His Lys Ala Arg Lys  
 225 230 235 240  
 Asn Val Ile Gly Ile Ala His Pro Lys Asp Phe Val Asn Lys Ala Leu  
 245 250 255  
 Asp Glu Pro Leu Ile Asn Asn Leu His Ser Pro Trp Phe Ile Thr Ala  
 260 265 270  
 Lys Ser Lys Leu Ile Arg Ile Leu Lys Glu Phe Arg Asp Asn Arg Ser  
 275 280 285  
 Ser Val Ala Val Val Leu Asn Ala Ser Gly Glu Pro Ile Gly Ile Leu  
 290 295 300  
 Ser Leu Asn Ala Ile Phe Lys Ile Leu Phe Asn Thr Thr Asn Ile Ala  
 305 310 315 320  
 His Leu Lys Pro Lys Thr Ile Ser Val Ile Glu Arg Thr Phe Pro Gly  
 325 330 335  
 Asn Ser Arg Ile Lys Asp Leu Gln Lys Glu Leu Asp Ile Gln Phe Pro  
 340 345 350  
 Gln Tyr Pro Val Glu Thr Leu Ala Gln Leu Val Leu Gln Leu Leu Asp  
 355 360 365  
 Ser Pro Ala Glu Val Gly Thr Ser Val Ile Ile Asn Asn Leu Leu Leu  
 370 375 380  
 Glu Val Lys Glu Met Ser Leu Ser Gly Ile Lys Thr Val Ser Ile Lys  
 385 390 395 400  
 Asn Leu Leu Ser

&lt;210&gt;416

&lt;211&gt;373

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;416

Tyr Ser Met Ile Tyr Leu Asp Asn Asn Ala Met Thr Pro Pro Glu Arg  
 1 5 10 15  
 Gly Leu Leu Glu Phe Leu Gln Lys Thr Phe Leu Ile Glu Gly Thr Tyr  
 20 25 30  
 Ala Asn Pro Ser Ser Val His Gln Leu Gly Lys Lys Ser Arg Gln Leu  
 35 40 45  
 Val Leu Glu Ala Ser His Trp Met Gln Lys Val Leu Ser Phe Gln Gly  
 50 55 60  
 Arg Val Leu Tyr Thr Ser Gly Ala Thr Glu Ser Leu Asn Leu Ala Ile  
 65 70 75 80  
 Ala Ser Leu Pro Lys Asp Ser His Val Ile Thr Ser Gly Ser Glu His  
 85 90 95  
 Pro Ala Ile Leu Glu Pro Leu Lys His Ser Ser Leu Ser Val Ser Tyr  
 100 105 110  
 Leu Asn Pro Glu Glu Gly Arg Cys Val Leu Thr Ile Glu Gln Ile Glu  
 115 120 125  
 Arg Ala Val Thr Pro Lys Thr Ser Ala Ile Ile Leu Gly Trp Val Asn  
 130 135 140  
 Ser Glu Thr Gly Ala Lys Ala Asp Ile Ala Ala Ile Ala His Phe Ala  
 145 150 155 160  
 Gln Glu Arg Gln Leu Gln Phe Ile Val Asp Ala Thr Ala Asn Val Gly  
 165 170 175  
 Lys Glu Arg Ile Val Leu Pro Ser Gly Val Thr Met Ala Ala Phe Ser  
 180 185 190  
 Gly His Lys Phe His Ala Leu Ser Gly Ile Gly Ala Leu Leu Val Ser  
 195 200 205  
 Pro Gly Val Lys Leu His Pro Gln Leu Trp Gly Gly Gly Gln Gln Gly  
 210 215 220  
 Gly Leu Arg Ala Gly Thr Glu Asn Leu Trp Gly Ile Ala Ser Leu Leu  
 225 230 235 240  
 Tyr Ile Phe Lys Tyr Leu Asp Leu His Gln Glu Arg Ile Ser Gln Glu  
 245 250 255  
 Ile Leu Thr His Arg Asn Gly Phe Glu Lys Ala Ile Lys Ala Arg Ile  
 260 265 270  
 Pro Asp Val His Ile His Cys Ala Asp Gln Pro Arg Ala Asn Asn Val  
 275 280 285  
 Ser Ala Ile Ala Phe Pro Pro Leu Glu Gly Glu Val Leu Gln Ile Ala  
 290 295 300  
 Leu Asp Ile Glu Gly Val Ala Cys Gly Tyr Gly Ser Ala Cys Ser Ser  
 305 310 315 320  
 Gly Ala Thr Ala Pro Phe Lys Ser Leu Val Ser Met Gly Val Asp Glu  
 325 330 335  
 Glu Leu Thr Leu Ala Thr Leu Arg Phe Ser Phe Ser His Leu Leu Leu  
 340 345 350  
 Gln Glu Asp Val Glu Arg Ala Val Gly Ile Ile Glu Lys Val Val Glu  
 355 360 365  
 Arg Leu Lys Asn Ser  
 370

&lt;210&gt;417

&lt;211&gt;248

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;417

Glu His Phe Val Asp Phe Asp Tyr Phe Gly Leu Ser Asp Ile Gly Arg  
 1 5 10 15  
 Val Arg Ala Arg Asn Glu Asp Phe Trp Gln Val Asn Leu Met Ser Gln  
 20 25 30  
 Val Val Ala Ile Ala Asp Gly Val Gly Gly Arg Leu Gly Gly Asp Ile  
 35 40 45  
 Ala Ser Gln Glu Ala Val Thr Ser Leu Met Glu Leu Ile Asp Glu Gln

50 55 60  
 Gln Ser Lys Leu Met Gly Tyr Glu Asp Asp Gln Tyr Lys Glu Thr Leu  
 65 70 75 80  
 Lys Lys Ile Leu Leu Val Asn Gly Val Val Tyr Glu His Gly Gln  
 85 90 95  
 Met Glu Glu His Leu Gln Gly Met Gly Thr Thr Leu Ser Phe Ile Gln  
 100 105 110  
 Phe Arg Lys Asp Arg Ala Trp Leu Phe His Val Gly Asp Ser Arg Ile  
 115 120 125  
 Tyr Arg Ile Arg Glu Gly Glu Leu Arg Arg Leu Thr Glu Asp His Ser  
 130 135 140  
 Leu Glu Asn Gln Leu Lys Asn Arg Tyr Gly Leu Pro Lys Gln Ser Asp  
 145 150 155 160  
 Lys Val Tyr Ser Tyr Arg His Ile Leu Thr Asn Val Leu Gly Ser Arg  
 165 170 175  
 Pro Tyr Val Met Pro Asp Ile Arg Asn Leu Pro Cys Glu Lys Glu Asp  
 180 185 190  
 Leu Tyr Cys Leu Cys Ser Asp Gly Leu Thr Asn Met Val Pro Asp Ile  
 195 200 205  
 Asp Ile Arg Asp Ile Leu Asn Gln Pro Ala Thr Leu Glu Glu Arg Gly  
 210 215 220  
 Asn Ala Leu Ile Ser Leu Ala Asn Thr Arg Gly Gly Asp Asp Asn Ala  
 225 230 235 240  
 Thr Val Val Leu Val Arg Ile Gln  
 245

&lt;210&gt;418

&lt;211&gt;255

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;418

Tyr Lys Leu Met Arg Val Leu Asn Gly Lys Ser Leu Asn Cys Glu Ser  
 1 5 10 15  
 Ile Asp Leu Lys Ser Lys Asn Phe Pro Arg Ala Arg Ile Phe Cys Lys  
 20 25 30  
 Ile Ser Asn Leu Arg Thr Val Thr Met Arg Lys Met Leu Val Leu Leu  
 35 40 45  
 Ala Ser Leu Gly Leu Leu Ser Pro Thr Leu Ser Ser Cys Thr His Leu  
 50 55 60  
 Gly Ser Ser Gly Ser Tyr His Pro Lys Leu Tyr Thr Ser Gly Ser Lys  
 65 70 75 80  
 Thr Lys Gly Val Ile Ala Met Leu Pro Val Phe His Arg Pro Gly Lys  
 85 90 95  
 Ser Leu Glu Pro Leu Pro Trp Asn Leu Gln Gly Glu Phe Thr Glu Glu  
 100 105 110  
 Ile Ser Lys Arg Phe Tyr Ala Ser Glu Lys Val Phe Leu Ile Lys His  
 115 120 125  
 Asn Ala Ser Pro Gln Thr Val Ser Gln Phe Tyr Ala Pro Ile Ala Asn  
 130 135 140  
 Arg Leu Pro Glu Thr Ile Ile Glu Gln Phe Leu Pro Ala Glu Phe Ile  
 145 150 155 160  
 Val Ala Thr Glu Leu Glu Glu Lys Thr Gly Lys Glu Ala Gly Val  
 165 170 175  
 Asp Ser Val Thr Ala Ser Val Arg Val Arg Val Phe Asp Ile Arg His  
 180 185 190  
 His Lys Ile Ala Leu Ile Tyr Gln Glu Ile Ile Glu Cys Ser Gln Pro  
 195 200 205  
 Leu Thr Thr Leu Val Asn Asp Tyr His Arg Tyr Gly Trp Asn Ser Lys  
 210 215 220  
 His Phe Asp Ser Thr Pro Met Gly Leu Met His Ser Arg Leu Phe Arg  
 225 230 235 240  
 Glu Val Val Ala Arg Val Glu Gly Tyr Val Cys Ala Asn Tyr Ser  
 245 250 255

&lt;210&gt;419

&lt;211&gt;231

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;419

Gly Asn Val Gln Val Tyr Ser Ser Leu Val Pro Trp Arg Arg Cys Ser  
 1 5 10 15  
 Ser Phe Gln Lys Leu Leu Tyr Leu Ala Ser Thr Leu Trp Glu Asn Thr  
 20 25 30  
 Phe Lys Xaa Arg Gln Val Leu Phe Gly Gly Ala Leu Leu Val Phe Ser  
 35 40 45  
 Ser Leu Val Ala Leu Ser Val Ser Ser Gln Thr Ala Glu Leu Leu Ser  
 50 55 60  
 Thr Met Thr Gly Ile Ser Leu Ala Phe Ala Phe Leu Phe Tyr Leu Xaa  
 65 70 75 80  
 Phe Leu Pro Lys Asp Ile Thr Arg Ala Ile Leu Phe Ser Gly Glu Arg  
 85 90 95  
 Xaa Val Lys Thr Ser Trp Arg Ala Leu Gly Ser Ala Ile Arg Met Trp  
 100 105 110  
 Ile Ile Ile Ile Pro Val Thr Gln Leu Ile Gly Ile Met Met Ser Lys  
 115 120 125  
 Phe Ile Thr Leu Val Leu Pro Thr Gln Glu Ile His Thr Gln Glu Val  
 130 135 140  
 Thr Gln Glu Val Gln Asn Ser Leu Pro Ile Thr Gly His Tyr Ile Ser  
 145 150 155 160  
 Met Ile Leu Asn Leu Gly Val Leu Thr Pro Phe Gly Glu Glu Val Phe  
 165 170 175  
 Phe Arg Gly Ile Leu Gln Thr Phe Leu Lys Asn Lys Met Thr Arg Ile  
 180 185 190  
 Ala Ala Val Leu Cys Ser Ser Ile Ile Phe Ser Phe Ile His Ile Glu  
 195 200 205  
 His Ser Leu Gly Ser Trp Val Phe Cys Pro Arg Ala Leu Cys Phe Ser  
 210 215 220  
 Leu Ile Cys Arg Val Ser Ile  
 225 230

&lt;210&gt;420

&lt;211&gt;130

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;420

Met Arg Asp His Ala Phe Ser Lys Leu Ile Gly Thr Val Arg Ala Met  
 1 5 10 15  
 Val Val Glu Gly Arg Cys Pro Trp Ser Leu Gln Gln Ser Leu Val Ser  
 20 25 30  
 Met Val Glu His Ile Leu Gly Glu Cys Gln Glu Phe His Glu Ala Val  
 35 40 45  
 Leu Gln Gly Lys Thr Val Gln Glu Val Gly Ser Glu Ala Gly Asp Val  
 50 55 60  
 Leu Thr Leu Val Leu Ile Leu Cys Phe Leu Leu Glu Arg Glu Gly Val  
 65 70 75 80  
 Leu Ala Ser Glu Asp Val Ala Asn Glu Ala Met Glu Lys Leu Arg Arg  
 85 90 95  
 Arg Ala Pro Tyr Ile Phe Ala Glu Asp Tyr Lys Pro Val Ser Ile Glu  
 100 105 110  
 Glu Ala Asp Arg Leu Trp Glu Leu Ala Lys His Arg Glu Lys Asn Glu  
 115 120 125  
 Ser Thr  
 130

&lt;210&gt;421

&lt;211&gt;375

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;421

Asn Phe Lys Arg Phe Cys Met Thr Lys Ile Ala Phe Ser Glu Lys Ala  
 1 5 10 15  
 Lys Asn Phe Pro Val Glu Ala Leu Lys Lys Trp Phe Glu Lys Asn Lys



20 25 30  
 Arg Ser Leu Pro Trp Arg Asp Asn Pro Thr Pro Tyr Ser Val Trp Val  
 35 40 45  
 Ser Glu Val Met Leu Gln Gln Thr Arg Ala Glu Val Val Ile Asp Tyr  
 50 55 60  
 Phe Asn Gln Trp Met Glu Arg Phe Pro Thr Ile Glu Ser Leu Ala Ala  
 65 70 75 80  
 Ala Lys Glu Glu Asp Val Ile Lys Leu Trp Glu Gly Leu Gly Tyr Tyr  
 85 90 95  
 Ser Arg Ala Arg His Leu Leu Glu Gly Ala Arg Met Val Met Glu Glu  
 100 105 110  
 Phe His Gly Lys Ile Pro Asp Asp Ala Ile Ser Leu Ala Gln Ile Arg  
 115 120 125  
 Gly Val Gly Pro Tyr Thr Val His Ala Ile Leu Ala Phe Ala Phe Lys  
 130 135 140  
 Arg Arg Ala Ala Ala Val Asp Gly Asn Val Leu Arg Val Leu Ser Arg  
 145 150 155 160  
 Ile Phe Leu Ile Glu Thr Ser Ile Asp Leu Glu Ser Thr Arg Thr Trp  
 165 170 175  
 Val Ser Arg Ile Ala Gln Ala Leu Leu Pro His Lys Ser Pro Glu Val  
 180 185 190  
 Ile Ala Glu Ala Leu Ile Glu Leu Gly Ala Cys Ile Cys Lys Lys Val  
 195 200 205  
 Pro Gln Cys His Arg Cys Pro Val Arg Gln Ala Cys Gly Ala Trp Arg  
 210 215 220  
 Glu Asn Lys Gln Phe Val Leu Pro Val Arg His Ala Arg Lys Lys Val  
 225 230 235 240  
 Ile Phe Leu His Arg Leu Val Ala Ile Val Leu Tyr Asp Gly Ser Leu  
 245 250 255  
 Val Val Glu Lys Arg Arg Pro Lys Glu Met Met Ala Gly Leu Tyr Glu  
 260 265 270  
 Phe Pro Tyr Ile Glu Val Glu Pro Glu Glu Gly Leu Gln Asp Ile Glu  
 275 280 285  
 Gly Phe Thr Lys Lys Met Glu Leu Ser Leu Glu Ser Pro Leu Glu Phe  
 290 295 300  
 Leu Gly Asn Leu Lys Glu Gln Arg His Ala Phe Thr Asn His Lys Val  
 305 310 315 320  
 His Leu Cys Pro Ile Ile Phe Lys Ala Thr Ser Leu Pro Gln Phe Gly  
 325 330 335  
 Glu Leu His Leu Leu Ser Asp Ile Asp His Leu Ala Phe Ser Ser Gly  
 340 345 350  
 His Lys Lys Ile Lys Asp Ala Leu Leu Ile Tyr Leu Gly Asp Val Arg  
 355 360 365  
 Ser Arg Glu Ser Ile Gly Val  
 370 375  
 <210>422  
 <211>234  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>422  
 Asn Phe Met Gln Leu Ser Asn Asp Lys Arg Ala Ala Leu Gln Tyr Phe  
 1 5 10 15  
 Met Glu Asn Phe Ser Trp Leu Ala Thr Gln Val Ser Arg Leu Ser Ser  
 20 25 30  
 Phe Leu Arg Ser Gln Leu Pro Asn His Ser Lys Gln Glu Ile Leu Ala  
 35 40 45  
 Ser Ile Arg Gln His Arg Cys Arg Val Asn Gly Phe Ile Glu Arg Phe  
 50 55 60  
 Glu Ser Tyr Lys Val Gln Pro Gly Asp Arg Val Ser Leu Ser Leu Ile  
 65 70 75 80  
 Pro Ser Thr Lys Gln Gln Pro Ser Ile Leu Trp Glu Asp Asp Tyr Ser  
 85 90 95  
 Ile Ile Tyr Glu Lys Pro Pro His Leu Thr Thr Glu Gln Met Ala His  
 100 105 110

Met Thr Arg Phe Phe Thr Val His Arg Leu Asp Lys Gly Thr Ser Gly  
           115                  120          125  
 Cys Leu Leu Met Gly Lys Ser Lys Gln Ala Ala Thr Glu Leu Met Lys  
       130                  135          140  
 Leu Phe Lys Gln Arg Lys Ile His Lys Gln Tyr Ile Ala Phe Val Phe  
       145                  150          155          160  
 Gly His Pro Lys Lys Lys Phe Gly Thr Val Lys Ser Tyr Thr Ala Pro  
           165                  170          175  
 Val Tyr Arg Arg Cys Gly Ala Val Ile Phe Gly Ala Ala Gly Pro Ser  
           180                  185          190  
 Gln Gly Glu Pro Ile Lys Ser Ala Tyr Lys Trp Asp Cys Trp Val Ile  
       195                  200          205  
 Leu Leu Ser Glu Met Ser Thr Thr Asp Leu Lys Asn Ser Leu Pro Arg  
       210                  215          220  
 Ser Ser Ala Leu Ser Ser Met Leu Thr Pro  
       225                  230  
 <210>423  
 <211>364  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>423  
 Glu Leu Glu Ala Leu Glu Gln Lys Tyr Gly Lys Ala Val Leu Leu Ile  
       1                  5          10          15  
 Ala Leu Ser Glu Leu Gly Ile Asp Thr Met Ser Leu Leu Ser Gly His  
       20                  25          30  
 Arg Leu Glu Gly Phe Pro Pro Ile Ala Glu Val Met Ala Ala Cys Asp  
       35                  40          45  
 Arg Cys Ser Met Asp Phe Cys Glu Ile Leu Lys Ser Gln Ser Met Asp  
       50                  55          60  
 Leu Trp Ala Asp Ala Ala Ser Cys Val Asp Gly Leu Leu Gln Asp Pro  
       65                  70          75          80  
 Phe Trp Ser Thr Ala Ile Ala Ser Gly Ile Ala Lys Ser Ser Leu Gln  
           85                  90          95  
 Glu Thr Glu Phe Glu Cys Glu Ser Lys Val Met Val Leu Ser Ser Trp  
       100                  105          110  
 Gly Glu Gln Gly Ala Gln Val Cys Ser Pro Phe Asn Leu Glu Arg Ile  
       115                  120          125  
 Cys Met Ser Phe Pro Ser Leu Lys Val Phe Ser Leu Lys Lys Asn Gly  
       130                  135          140  
 Cys Glu Asn Met Gly Ile Gln Leu Ser Ala Ser Cys Met Asn Leu Leu  
       145                  150          155          160  
 Met Ser Ile Phe Phe Val Ala Thr Asn Gly Gly Ser Thr Pro Ile Trp  
           165                  170          175  
 Ile Thr Lys Glu Asn Leu Met Ala Leu Val Ala Leu Val Leu Ser His  
           180                  185          190  
 Tyr Gln Cys Tyr Phe Val Pro Ala Thr Gly Asp Pro Gln Arg Gly Asn  
       195                  200          205  
 Ile Leu Gly Asn Pro Glu Val Asn Ala Ile Leu Ala Arg Gly Met Gly  
       210                  215          220  
 Met Arg Val Asp Leu Glu Arg Lys Arg Gly Gly Glu Ser Ser Ser Ser  
       225                  230          235          240  
 Arg Tyr Leu Glu Leu Ala Ala Arg Cys Phe Glu Asn Ser Leu Thr Lys  
           245                  250          255  
 Thr Ser Leu Leu Ser Asp Ala Asn Asn Val Gln Glu Arg Asp Lys Cys  
           260                  265          270  
 Leu Leu Gln Met Ser Thr Ser Leu Met His Thr Ala Gly Leu Asn Leu  
       275                  280          285  
 Gln Arg Pro Pro Val Pro Thr Pro Ser Gly Val Thr Ala His Pro Gln  
       290                  295          300  
 Pro Gln Pro Asp Pro Val Val Thr Ser Gln Pro Ser Leu Leu Gly Ala  
       305                  310          315          320  
 Arg Glu Arg Ser Pro Val Ser Ser Arg Gly Arg Phe Pro Val Val Leu  
           325                  330          335  
 Pro Leu Ser Val Ile Ser Pro Arg Ser His Pro Gly Arg Val Glu Arg

340 345 350  
 Arg Asp Leu Glu Asp Glu Glu Glu Val Met Phe  
 355 360  
 <210>424  
 <211>283  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>424  
 Asn Ile Gln Thr Ser His Ser Arg Val Leu Leu Lys Lys Phe Ser Lys  
 1 5 10 15  
 Glu Phe Thr Ile Arg Thr Tyr Arg Ser Leu Gly Phe Thr Asp Tyr Leu  
 20 25 30  
 Gly Gly Cys Leu Thr Asn Pro Leu Gly Lys Phe Pro Ser Pro Gln Asn  
 35 40 45  
 Pro Gln Val Val Thr Ile Ala Pro Ser Ser Thr Thr Pro Gln Ala Val  
 50 55 60  
 Ser Ser Ala Val Gln Gly Phe Leu Gln Thr Gly Gly Ala Ala Ser Ser  
 65 70 75 80  
 Thr Ala Thr Thr Thr Ala Ser Gly Ala Ser Ala Leu Gly Leu Ser  
 85 90 95  
 Pro Asp Gln Val Gln Ala Leu Leu Thr Asn Leu Leu Asn Val Gly Gln  
 100 105 110  
 Pro Ser Val Gly Gln Pro Ser Thr Ser Ala Gly Thr Ser Gly Ala Ser  
 115 120 125  
 Ser Ser Ser Ala Ser Met Gln Gln Gln Leu Leu Gln Leu Ile Leu Asp  
 130 135 140  
 Lys Thr Thr Gly Ser Gly Ser Ser Val Ser Ser Glu Gln Leu Gln  
 145 150 155 160  
 Gln Leu Leu Ser Leu Val Ser Gln Met Thr Thr Ser Gln Gly Gly Ser  
 165 170 175  
 Gly Gly Thr Gln Ala Gly Gln Ala Ala Ser Val Leu Leu Asn Leu Leu  
 180 185 190  
 Ser Ala Thr Gly Ser Ala Ala Ala Asn Pro Leu Gly Thr Ala Ala Ser  
 195 200 205  
 Leu Ala Gln Ile Ile Tyr Ala Ala Val Thr Ser Pro Gly Ala Lys Lys  
 210 215 220  
 Thr Ser Glu Phe Cys Tyr Asn Tyr Cys Gly Glu Thr Cys Gln Gly Asn  
 225 230 235 240  
 Cys Gly Cys Pro Thr Cys Gly Cys Pro Asp Gly Gln Cys Gly Cys Gly  
 245 250 255  
 Gly Phe Gly Arg Phe Phe Cys Gly Val Trp Lys Asn Cys Cys Gly Ile  
 260 265 270  
 Gly Glu Gly Ser Gln Glu Pro Ala Ile Pro Leu  
 275 280

&lt;210&gt;425

&lt;211&gt;302

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;425

Gly Gly Phe Met Leu Lys Ile Asp Leu Thr Gly Lys Val Ala Phe Val  
 1 5 10 15  
 Ala Gly Ile Gly Asp Asp Gln Gly Tyr Gly Trp Gly Ile Ala Lys Leu  
 20 25 30  
 Leu Ala Glu Ala Gly Ala Thr Ile Ile Val Gly Thr Trp Val Pro Ile  
 35 40 45  
 Tyr Lys Ile Phe Ser Gln Ser Trp Glu Leu Gly Lys Phe Asn Glu Ser  
 50 55 60  
 Arg Lys Leu Ser Asn Gly Thr Leu Leu Glu Ile Ala Lys Ile Tyr Pro  
 65 70 75 80  
 Met Asp Ala Ser Phe Asp Ser Pro Glu Asp Val Pro Glu Asp Ile Ala  
 85 90 95  
 Glu Asn Lys Arg Tyr Lys Gly Ile Thr Gly Phe Thr Ile Ser Glu Val  
 100 105 110  
 Ala Glu Gln Val Lys Lys Asp Phe Gly His Ile Asp Ile Leu Val His

```

      115      120      125
Ser Leu Ala Asn Ser Pro Glu Ile Ser Lys Ser Leu Leu Glu Thr Ser
      130      135      140
Arg Lys Gly Tyr Leu Ala Leu Ser Ala Ser Ser Tyr Ser Phe Val
145      150      155      160
Ser Leu Leu Ser His Phe Gly Ser Ile Met Asn Arg Gly Gly Ser Thr
      165      170      175
Ile Ser Leu Thr Tyr Leu Ala Ser Met Arg Ala Val Pro Gly Tyr Gly
      180      185      190
Gly Gly Met Ser Ser Ala Lys Ala Ala Leu Glu Ser Asp Thr Lys Thr
      195      200      205
Leu Ala Trp Glu Ala Gly Arg Arg Trp Gly Ile Arg Val Asn Thr Ile
      210      215      220
Ser Ala Gly Pro Leu Ala Ser Arg Ala Gly Lys Ala Ile Gly Phe Ile
225      230      235      240
Glu Arg Met Val Asp Tyr Tyr Gln Glu Trp Ala Pro Ile Pro Glu Ala
      245      250      255
Met Asn Ala Glu Gln Val Gly Ala Val Ala Ala Phe Leu Ala Ser Pro
      260      265      270
Leu Ala Ser Ala Ile Thr Gly Glu Thr Leu Tyr Val Asp His Gly Ala
      275      280      285
Asn Val Met Gly Ile Gly Pro Glu Met Phe Pro Lys Asp Ser
      290      295      300
<210>426
<211>300
<212>PRT
<213>Chlamydia pneumoniae
<400>426
Asn Tyr Gly Asp Ala Met Glu Lys Leu Leu Val Thr Asp Ile Asp Gly
 1      5      10      15
Thr Ile Thr His Gln Ser His His Leu Asp Lys Lys Val Tyr Glu Arg
      20      25      30
Leu Tyr Ala Leu His Gln Ala Gly Trp Lys Leu Phe Phe Leu Thr Gly
      35      40      45
Arg Tyr Tyr Lys Tyr Ala Ala Arg Leu Phe Ser Asp Phe Asp Ala Pro
      50      55      60
Tyr Leu Leu Gly Cys Gln Asn Gly Ala Ser Val Trp Ser Ser Thr Ser
      65      70      75      80
Ser Asn Leu Leu Tyr Ser Lys Ser Leu Pro Ser Asp Leu Leu Cys Ile
      85      90      95
Leu Gln Asp Cys Met Glu Gly Ala Thr Ala Leu Phe Ser Val Glu Ser
      100      105      110
Gly Ala Pro Tyr Gly Asp His Tyr Tyr Arg Phe Ser Pro Thr Pro Ile
      115      120      125
Ala Gln Asp Leu His Glu Tyr Val Asp Pro Arg Tyr Phe Pro Asn Ala
      130      135      140
Lys Glu Arg Glu Ile Leu Phe Glu Thr Arg Ser Leu Lys Asp Asp Tyr
145      150      155      160
Ala Phe Pro Ser Phe Ala Ala Ala Lys Val Phe Gly Leu Arg Asp Glu
      165      170      175
Val Ile Arg Ile Gln Lys Glu Leu Glu Arg Gln Glu Ala Leu Thr Ser
      180      185      190
Val Ala Thr Met Thr Leu Met Arg Trp Pro Phe Asp Phe Arg Tyr Ala
      195      200      205
Ile Leu Phe Leu Thr Asp Lys Ser Val Ser Lys Gly Lys Ala Leu Asp
      210      215      220
Arg Val Val Asn Ile Leu Tyr Asp Gly Lys Lys Pro Phe Val Met Ala
225      230      235      240
Ser Gly Asp Asp Ala Asn Asp Leu Asp Leu Ile Glu Arg Gly Asp Phe
      245      250      255
Lys Ile Val Met Ser Ser Ala Pro Glu Glu Met His Val His Ala Asp
      260      265      270
Phe Leu Ala Pro Pro Ala Asp Lys Asn Gly Ile Leu Ser Ala Trp Glu
      275      280      285

```

Ala Gly Val Arg Tyr Tyr Asp Asp Leu Met Ser Leu  
 290 295 300

<210>427

<211>164

<212>PRT

<213>Chlamydia pneumoniae

<400>427

Ser Arg Val Leu His Met Phe Phe Asn Leu Phe Ser Leu Val Phe Lys  
 1 5 10 15  
 Leu Ser Asp Glu Leu Ala Leu Ala Glu Thr Ile Gln Glu Pro Ile Ser  
 20 25 30  
 Val His Glu Met Phe Pro Gly Ser Met Lys Leu Glu Met Phe Lys Met  
 35 40 45  
 Leu Gly Ser Leu Ile Leu Leu Leu Thr Ile Phe Gly Phe Gly Val Trp  
 50 55 60  
 Ala Phe Lys Lys Phe Val Arg Ser Arg Ser His Gly Phe Gly Gly Ser  
 65 70 75 80  
 Ser Gln Ile Lys Ile Leu Glu Arg Arg Ser Leu Thr Pro Lys Thr Ser  
 85 90 95  
 Ile Tyr Leu Ile Arg Val Val Asn Lys Thr Leu Val Ile Ala Glu Thr  
 100 105 110  
 Pro Glu Lys Ile Thr Leu Leu Thr Glu Phe Pro Pro Asp Thr Asp Ile  
 115 120 125  
 Asn His Leu Leu Gln Glu Asn Asn Lys Gln Ser Ser Ser Ser Ala Thr  
 130 135 140  
 Ser Asp Phe Leu Ser Lys Ala Ile Gln Lys Ile Gln Lys Lys Gln Gln  
 145 150 155 160  
 Thr Asn Gln Asp

<210>428

<211>161

<212>PRT

<213>Chlamydia pneumoniae

<400>428

Met Thr Thr Trp Thr Leu Asn Gln Asn Asn Leu Thr Lys Phe Leu Lys  
 1 5 10 15  
 Ser Ser Asp Glu Glu Pro Phe Leu Glu Arg Glu Ser Gly Leu Thr Tyr  
 20 25 30  
 Ile Asn Ile Gln Ala Asn Gly Asn Glu Leu Pro Leu Phe Phe Val Ile  
 35 40 45  
 Arg Ser Glu Gly Glu Ile Leu Gln Leu Ile Cys Tyr Leu Pro Tyr Gln  
 50 55 60  
 Leu His Glu Ser His Lys Ala Ser Thr Ala Arg Leu Leu His Leu Leu  
 65 70 75 80  
 Asn Arg Asp Ile Asp Ile Pro Gly Phe Gly Met Asp Glu Glu Gln Gly  
 85 90 95  
 Leu Ile Phe Tyr Arg Leu Val Leu Pro Cys Leu Asn Gly Glu Ile His  
 100 105 110  
 Asp Thr Leu Leu Arg Ile Tyr Ile Asp Thr Ile Lys Leu Val Cys Asp  
 115 120 125  
 Ser Phe Ser His Ala Ile Gly Leu Ile Ser Ser Gly Asn Met Asn Leu  
 130 135 140  
 Asp Glu Leu Arg Arg Gln Ala Leu Gln Glu Gln Gln Glu Lys Arg Asn  
 145 150 155 160  
 Glu

<210>429

<211>249

<212>PRT

<213>Chlamydia pneumoniae

<400>429

Asp Val Arg Leu Phe Lys Ser Asn Lys Lys Asn Val Met Ser Ser Gln  
 1 5 10 15  
 Thr Met Asp Val Leu Ile Phe Tyr Asp Thr Glu Thr Thr Gly Thr Gln

```

      20      25      30
Ile Glu Arg Asp Arg Ile Ile Glu Ile Ala Ala Tyr Asn Ser Val Thr
      35      40      45
Asp Glu Ser Phe Leu Thr Tyr Val Asn Pro Glu Ile Pro Ile Pro Asp
      50      55      60
Glu Ala Ser Lys Ile His Gly Ile Thr Thr Asp Ala Val Leu Ser Ala
      65      70      75      80
Pro Lys Phe Pro Glu Ala Tyr Glu Gly Phe Arg Lys Phe Cys Gly Glu
      85      90      95
Asp Ser Ile Leu Val Ala His Asn Asn Asp Gly Phe Asp Phe Pro Leu
      100      105      110
Leu Gly Lys Glu Cys Arg Arg His Ser Leu Glu Pro Leu Thr Asn Arg
      115      120      125
Thr Ile Asp Ser Leu Lys Trp Ala Gln Lys Tyr Arg Pro Asp Leu Pro
      130      135      140
Lys His Asn Leu Gln Tyr Leu Arg Gln Val Tyr Gly Phe Ala Glu Asn
      145      150      155      160
Gln Ala His Arg Ala Leu Asp Asp Val Val Ile Leu His Lys Val Phe
      165      170      175
Thr Ser Leu Ile Gly Asp Leu Pro Pro Gln Gln Val Leu Asp Leu Leu
      180      185      190
Gln Gln Ser Tyr His Pro Lys Val Phe Lys Met Pro Phe Gly Lys Tyr
      195      200      205
Lys Gly Gln Pro Leu Val Asp Ile Pro Lys Ser Tyr Phe Glu Trp Leu
      210      215      220
Glu Asn Gln Gly Ala Leu Asp Lys Pro Glu Asn Lys Asp Ile Lys Ala
      225      230      235      240
Ala Ile Ala Leu Leu His Gln Pro Thr
      245

```

&lt;210&gt;430

&lt;211&gt;259

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;430

```

Met Ile Leu Thr Ala Ala Phe Ser Pro Cys Pro Asn Asp Ile Phe Leu
      1      5      10      15
Phe Arg Ser Phe Leu Lys Asp Pro Gln Phe Arg Pro Leu Leu Asn Gln
      20      25      30
Val Thr Ile Ala Asp Ile Glu Thr Leu Asn Thr Leu Ala Leu Gln Arg
      35      40      45
Arg Leu Ser Leu Met Lys Met Ser Ala Ala Leu Phe Pro Leu Val Ser
      50      55      60
Asp Tyr Tyr Asn Leu Met Asp Val Gly Asn Thr Leu Gly Tyr Asn Ser
      65      70      75      80
Gly Pro Ile Val Leu Ser Leu Asp Pro Glu Cys Ser Leu Asp Thr Leu
      85      90      95
Ala Thr Pro Gly Glu Met Thr Thr Ala His Ala Leu Cys Lys Leu Tyr
      100      105      110
Tyr Pro Lys Ala Lys Leu Ile Pro Met Pro Tyr Asp Lys Ile Leu Ser
      115      120      125
Ala Ile Leu Gln Gly Lys Val Asp Gly Gly Ala Leu Ile His Glu Glu
      130      135      140
Arg Phe Ser Tyr Asp Leu Gln Leu Thr Leu Arg Ala Asp Phe Gly Glu
      145      150      155      160
Leu Trp Arg Arg Lys Thr Ile Phe Pro Leu Pro Leu Gly Cys Leu Ala
      165      170      175
Ile Ala Lys Tyr Val Pro Met Ala Thr Val Asp Ala Leu Thr Ala Ala
      180      185      190
Leu Arg Lys Ser Leu Ile Cys Ser Leu Lys Asp Pro Ile Thr Ala Gly
      195      200      205
Ala Lys Ala Val Glu Tyr Ser Lys Asn Lys Asn Val Thr Val Ile His
      210      215      220
Arg Phe Ile Gly Thr Tyr Ile Asn Lys Glu Thr Phe Gln Leu Ser Lys
      225      230      235      240

```

Thr Gly Lys Lys Ala Leu His Met Leu Trp Lys Ala Asn Glu Cys Cys  
 245 250 255

Gln Tyr Thr

<210>431

<211>168

<212>PRT

<213>Chlamydia pneumoniae

<400>431

Glu Pro Ile Ser Thr Lys Lys Pro Phe Asn Tyr Leu Lys Leu Gly Lys  
 1 5 10 15  
 Lys Leu Tyr Ile Cys Ser Gly Arg Pro Met Asn Ala Val Asn Thr Pro  
 20 25 30  
 Lys Lys Ile Leu Cys Ile Val Ala Asp Tyr Arg Glu Ile Ser Pro Leu  
 35 40 45  
 Ile Glu Gln Leu Asp Phe Thr Gln Ile Asn Glu His Leu Tyr Ser Tyr  
 50 55 60  
 Arg Cys Thr Asp Tyr His Leu Asp Leu Tyr Ile Val His Val Trp Gly  
 65 70 75 80  
 Ser Thr Ala Val Leu Asn Ala Leu Gln Ser Tyr Cys Gln Ala Tyr Thr  
 85 90 95  
 Asp Tyr Asp Leu Trp Ile Asn Pro Gly Phe Val Gly Ala Cys Ser Pro  
 100 105 110  
 Glu Ile Pro Leu Gly Gln Cys Tyr Thr Ile Glu Lys Ile Ala Asn Leu  
 115 120 125  
 Thr Thr Asp Thr Pro Pro Val Leu Ser Glu Asp Pro Pro Tyr Ile Phe  
 130 135 140  
 Asp Ala Leu Pro Asp Ser Leu Pro Lys Ser Ser Leu Val Thr Ser Pro  
 145 150 155 160  
 Val Leu Tyr His Tyr Gly Phe Gln  
 165

<210>432

<211>659

<212>PRT

<213>Chlamydia pneumoniae

<400>432

Met Lys Leu Leu Leu Lys Ala Val Leu Arg His Lys Asn His Leu Val  
 1 5 10 15  
 Ile Leu Gly Cys Ser Leu Leu Ala Ile Leu Gly Leu Thr Phe Ser Ser  
 20 25 30  
 Gln Met Glu Ile Phe Ser Leu Gly Met Ile Ala Lys Thr Gly Pro Asp  
 35 40 45  
 Ala Phe Leu Leu Phe Gly Arg Lys Glu Ser Gly Lys Leu Val Lys Val  
 50 55 60  
 Ser Glu Leu Ser Gln Lys Asp Ile Leu Glu Asn Trp Gln Ala Ile Ser  
 65 70 75 80  
 Lys Asp Ser Glu Thr Leu Thr Val Ser Asp Ala Thr Thr Tyr Ile Ala  
 85 90 95  
 Glu His Gly Lys Ser Thr Ala Ser Leu Thr Ser Lys Leu Ser Lys Phe  
 100 105 110  
 Val Arg Asn Tyr Ile Asp Val Ser Arg Phe Arg Gly Leu Ala Ile Phe  
 115 120 125  
 Leu Ile Cys Val Ala Ile Phe Lys Ala Val Thr Leu Phe Phe Gln Arg  
 130 135 140  
 Phe Leu Gly Gln Val Val Ala Ile Arg Val Ser Arg Asp Leu Arg Gln  
 145 150 155 160  
 Asp Tyr Phe Lys Ala Leu Gln Gln Leu Pro Met Thr Phe Phe His Asp  
 165 170 175  
 His Asp Ile Gly Asn Leu Ser Asn Arg Val Met Thr Asp Ser Ala Ser  
 180 185 190  
 Ile Ala Leu Ala Val Asn Ser Leu Met Ile Asn Tyr Ile Gln Ala Pro  
 195 200 205  
 Ile Thr Phe Ile Leu Thr Leu Gly Val Cys Leu Ser Ile Ser Trp Lys  
 210 215 220

Phe Ser Ile Leu Ile Cys Val Ala Phe Pro Ile Phe Ile Leu Pro Ile  
 225 230 235 240  
 Val Val Ile Ala Arg Lys Ile Lys Asn Leu Ala Lys Arg Ile Gln Lys  
 245 250 255  
 Ser Gln Asp Ser Phe Ser Ser Val Leu Tyr Asp Phe Leu Ala Gly Val  
 260 265 270  
 Met Thr Val Lys Val Phe Arg Thr Glu Lys Phe Ala Phe Thr Lys Tyr  
 275 280 285  
 Cys Glu His Asn Asn Lys Ile Ser Ala Leu Glu Glu Lys Ser Ala Ala  
 290 295 300  
 Tyr Gly Leu Leu Pro Arg Pro Leu Leu His Thr Ile Ala Ser Leu Phe  
 305 310 315 320  
 Phe Ala Phe Val Val Val Ile Gly Ile Tyr Lys Phe Ala Ile Pro Pro  
 325 330 335  
 Glu Glu Leu Ile Val Phe Cys Gly Leu Leu Tyr Leu Ile Tyr Asp Pro  
 340 345 350  
 Ile Lys Lys Phe Gly Asp Glu Xaa Thr Ser Ile Met Arg Gly Cys Ala  
 355 360 365  
 Ala Ala Glu Arg Phe Tyr Glu Val Leu Asn His Pro Asp Leu His Ser  
 370 375 380  
 Gln Lys Glu Arg Glu Ile Glu Phe Leu Gly Leu Ser Asn Thr Ile Thr  
 385 390 395 400  
 Phe Glu Asn Val Ser Phe Gly Tyr Gln Glu Asp Lys His Ile Leu Lys  
 405 410 415  
 Asn Leu Ser Phe Thr Leu His Lys Gly Glu Ala Leu Gly Ile Val Gly  
 420 425 430  
 Pro Thr Gly Ser Gly Lys Thr Thr Leu Val Lys Leu Leu Pro Arg Leu  
 435 440 445  
 Tyr Glu Val Ser Gln Gly Lys Ile Leu Ile Asp Ser Leu Pro Ile Thr  
 450 455 460  
 Glu Tyr Asn Lys Gly Ser Leu Arg Asn His Ile Ala Cys Val Leu Gln  
 465 470 475 480  
 Asn Pro Phe Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys Gly  
 485 490 495  
 Lys Asp Met Glu Glu Glu Ala Val Leu Glu Ala Leu Lys Arg Ala Tyr  
 500 505 510  
 Ala Asp Glu Phe Ile Leu Lys Leu Pro Lys Gly Val His Ser Val Leu  
 515 520 525  
 Glu Glu Ser Gly Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu Ala  
 530 535 540  
 Ile Ala Arg Ala Leu Leu Lys Asn Ala Ser Ile Leu Ile Leu Asp Glu  
 545 550 555 560  
 Ala Thr Ser Ala Leu Asp Ala Ile Ser Glu Asn Tyr Ile Lys Asn Ile  
 565 570 575  
 Ile Gly Glu Leu Lys Gly Gln Cys Thr Gln Ile Ile Ile Ala His Lys  
 580 585 590  
 Leu Thr Thr Leu Glu His Val Asp Arg Val Leu Tyr Ile Glu Asn Gly  
 595 600 605  
 Gln Lys Ile Ala Glu Gly Thr Lys Glu Glu Leu Leu Gln Thr Cys Pro  
 610 615 620  
 Glu Phe Leu Lys Met Trp Glu Leu Ser Gly Thr Lys Glu Tyr Asn Arg  
 625 630 635 640  
 Val Phe Val Pro Asp His Lys Leu Val Ala Asn Pro Thr Asp Met Ala  
 645 650 655  
 Ile Thr Thr

&lt;210&gt;433

&lt;211&gt;344

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;433

Leu Cys Leu Arg Ile Val Cys Ile Lys Met Ile Leu Phe Ile Arg Gly  
 1 5 10 15  
 Glu His Ile Leu Met Glu Leu Leu Pro His Glu Lys Gln Val Val Glu



20 25 30  
 Tyr Glu Lys Ala Ile Ala Glu Phe Lys Glu Lys Asn Lys Lys Asn Ser  
 35 40 45  
 Leu Leu Ser Ser Ser Glu Ile Gln Lys Leu Glu Lys Arg Leu Asp Lys  
 50 55 60  
 Leu Lys Glu Lys Ile Tyr Ser Asp Leu Thr Pro Trp Glu Arg Val Gln  
 65 70 75 80  
 Ile Cys Arg His Pro Ser Arg Pro Arg Thr Val Asn Tyr Ile Glu Gly  
 85 90 95  
 Met Cys Glu Glu Phe Val Glu Leu Cys Gly Asp Arg Thr Phe Arg Asp  
 100 105 110  
 Asp Pro Ala Val Val Gly Gly Phe Val Lys Ile Gln Gly Gln Arg Phe  
 115 120 125  
 Val Leu Ile Gly Gln Glu Lys Gly Cys Asp Thr Ala Ser Arg Leu His  
 130 135 140  
 Arg Asn Phe Gly Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg  
 145 150 155 160  
 Leu Gly Lys Leu Ala Glu Lys Phe Gly Leu Pro Val Val Phe Leu Val  
 165 170 175  
 Asp Thr Pro Gly Ala Tyr Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln  
 180 185 190  
 Gly Trp Ala Ile Ala Lys Asn Leu Phe Glu Leu Ser Arg Leu Ala Thr  
 195 200 205  
 Pro Val Ile Ile Val Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu  
 210 215 220  
 Gly Met Ala Val Gly Asp Ser Val Ala Met Leu Glu His Ser Tyr Tyr  
 225 230 235 240  
 Ser Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro  
 245 250 255  
 Lys Lys Asn Ser Glu Ala Ala Ser Met Leu Lys Met His Gly Glu Asn  
 260 265 270  
 Leu Lys Gln Phe Gly Ile Ile Asp Thr Val Ile Lys Glu Pro Ile Gly  
 275 280 285  
 Gly Ala His His Asp Pro Ala Leu Val Tyr Ser Asn Val Arg Glu Phe  
 290 295 300  
 Ile Ile Gln Glu Trp Leu Arg Leu Lys Asp Leu Ala Ile Glu Glu Leu  
 305 310 315 320  
 Leu Glu Lys Arg Tyr Glu Lys Phe Arg Ser Ile Gly Leu Tyr Glu Thr  
 325 330 335  
 Thr Ser Glu Ser Gly Pro Glu Ala  
 340

&lt;210&gt;434

&lt;211&gt;434

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;434

Ser Gln Thr Gly Phe Leu Pro Gly Leu Thr Leu Ile Phe Val Ile Ile  
 1 5 10 15  
 Ile Val Trp Cys Asn Ala Phe Leu Ile Lys Leu Cys Val Ile Met Gly  
 20 25 30  
 Leu Gln Ser Arg Leu Gln His Cys Ile Glu Val Ser Gln Asn Ser Asn  
 35 40 45  
 Phe Asp Ser Gln Val Lys Gln Phe Ile Tyr Ala Cys Gln Asp Lys Thr  
 50 55 60  
 Leu Arg Gln Ser Val Leu Lys Ile Phe Arg Tyr His Pro Leu Leu Lys  
 65 70 75 80  
 Ile His Asp Ile Ala Arg Ala Val Tyr Leu Leu Met Ala Leu Glu Glu  
 85 90 95  
 Gly Glu Asp Leu Gly Leu Ser Phe Leu Asn Val Gln Gln Tyr Pro Ser  
 100 105 110  
 Gly Ala Val Glu Leu Phe Ser Cys Gly Gly Phe Pro Trp Lys Gly Leu  
 115 120 125  
 Pro Tyr Pro Ala Glu His Ala Glu Phe Gly Leu Leu Leu Gln Ile  
 130 135 140

Ala Glu Phe Tyr Glu Glu Ser Gln Ala Tyr Val Ser Lys Met Ser His  
 145 150 155 160  
 Phe Gln Gln Ala Leu Phe Asp His Gln Gly Ser Val Phe Pro Ser Leu  
 165 170 175  
 Trp Ser Gln Glu Asn Ser Arg Leu Leu Lys Glu Lys Thr Thr Leu Ser  
 180 185 190  
 Gln Ser Phe Leu Phe Gln Leu Gly Met Gln Ile His Pro Glu Tyr Ser  
 195 200 205  
 Leu Glu Asp Pro Ala Leu Gly Phe Trp Met Gln Arg Thr Arg Ser Ser  
 210 215 220  
 Ser Ala Phe Val Ala Ala Ser Gly Cys Gln Ser Ser Leu Gly Ala Tyr  
 225 230 235 240  
 Ser Ser Gly Asp Val Gly Val Ile Ala Tyr Gly Pro Cys Ser Gly Asp  
 245 250 255  
 Ile Ser Asp Cys Tyr Tyr Phe Gly Cys Cys Gly Ile Ala Lys Glu Phe  
 260 265 270  
 Val Cys Gln Xaa Ser His Gln Thr Thr Glu Ile Ser Phe Leu Thr Ser  
 275 280 285  
 Thr Gly Lys Pro His Pro Arg Asn Thr Gly Phe Ser Tyr Leu Arg Asp  
 290 295 300  
 Ser Tyr Val His Leu Pro Ile Arg Cys Lys Ile Thr Ile Ser Asp Lys  
 305 310 315 320  
 Gln Tyr Arg Val His Ala Ala Leu Ala Glu Ala Thr Ser Ala Met Thr  
 325 330 335  
 Phe Ser Ile Phe Cys Lys Gly Lys Asn Cys Gln Val Val Asp Gly Pro  
 340 345 350  
 Arg Leu Arg Ser Cys Ser Leu Asp Ser Tyr Lys Gly Pro Gly Asn Asp  
 355 360 365  
 Ile Met Ile Leu Gly Glu Asn Asp Ala Ile Asn Ile Val Ser Ala Ser  
 370 375 380  
 Pro Tyr Met Glu Ile Phe Ala Leu Gln Gly Lys Glu Lys Phe Trp Asn  
 385 390 395 400  
 Ala Asp Phe Leu Ile Asn Ile Pro Tyr Lys Glu Glu Gly Val Met Leu  
 405 410 415  
 Ile Phe Glu Lys Lys Val Thr Ser Glu Lys Gly Arg Phe Phe Thr Lys  
 420 425 430  
 Met Asn

&lt;210&gt;435

&lt;211&gt;85

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;435

Arg Arg Met Pro Asp Ser Leu His Lys Thr Leu Arg Ser Val Thr Gly  
 1 5 10 15  
 Val Gly Gln Ile Pro His Val Leu Gln Asp Lys Val Ile Leu Ser Lys  
 20 25 30  
 Glu Ile Pro His Lys Lys Thr Val Leu Gln His Leu Lys Gly Thr Ala  
 35 40 45  
 Val His Leu Lys Ser Leu Ser Leu Asn Pro Arg Leu Leu Leu Arg Pro  
 50 55 60  
 Ser Lys Asp Arg Arg Pro Glu Gln Tyr His Glu Phe Leu Val Lys Asp  
 65 70 75 80  
 Gly Ser Gly Lys Ser  
 85

&lt;210&gt;436

&lt;211&gt;105

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;436

Glu Ala Leu Ser Asn Met Ala Thr Met Thr Lys Lys Lys Leu Ile Ser  
 1 5 10 15  
 Thr Ile Ser Gln Asp His Lys Ile His Pro Asn His Val Arg Thr Val  
 20 25 30

Ile Gln Asn Phe Leu Asp Lys Met Thr Asp Ala Leu Val Lys Gly Asp  
 35 40 45  
 Arg Leu Glu Phe Arg Asp Phe Gly Val Leu Gln Val Val Glu Arg Lys  
 50 55 60  
 Pro Lys Val Gly Arg Asn Pro Arg Asn Ala Ala Val Pro Ile His Ile  
 65 70 75 80  
 Pro Ala Arg Arg Ala Val Lys Phe Thr Pro Gly Lys Arg Met Lys Arg  
 85 90 95  
 Leu Ile Glu Thr Pro Asn Lys His Ser  
 100 105

&lt;210&gt;437

&lt;211&gt;264

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;437

Met Lys Leu Thr Lys Tyr Leu Asn Thr Lys Gln Leu Arg Ser Met Ile  
 1 5 10 15  
 Ser Arg Leu Phe Val Arg Tyr Ser Leu Pro Met Ser Lys Gln Leu Ser  
 20 25 30  
 Phe Phe Ala Leu Cys Val Leu Gly Ser His Pro Ile Phe Ala Gln Thr  
 35 40 45  
 Pro Asn Pro Pro Gln Arg Val Arg Arg Ser Glu Val Ile Phe Ile Asp  
 50 55 60  
 Pro Gly His Gly Gly Lys Asp Gln Gly Thr Ala Ser Lys Glu Leu His  
 65 70 75 80  
 Tyr Glu Glu Lys Ser Leu Thr Leu Ser Leu Ala Leu Thr Val Gln Ser  
 85 90 95  
 Tyr Leu Lys Arg Met Gly Tyr Lys Pro Gln Leu Thr Arg Ser Ser Asp  
 100 105 110  
 Val Tyr Val Asp Leu Gly Lys Arg Val Ala Leu Ser Asn Arg Gly Gln  
 115 120 125  
 Gly Asp Val Phe Ile Ser Ile His Cys Asn His Ser Ser Asn Ala Ala  
 130 135 140  
 Ala Phe Gly Thr Glu Val Tyr Phe Tyr Asn Gly Lys Val Gly Ser Pro  
 145 150 155 160  
 Thr Arg Asn Arg Met Ser Glu Val Leu Gly Lys Asn Ile Leu Ala Ala  
 165 170 175  
 Met Glu Lys Asn Gly Ile Leu Lys Ser Arg Gly Leu Lys Thr Ala Asn  
 180 185 190  
 Phe Val Val Ile Arg Asp Thr Ser Met Pro Ala Val Leu Val Glu Thr  
 195 200 205  
 Gly Phe Leu Ser Asn Ser Arg Glu Arg Ala Ala Leu Gln Asp Ala Arg  
 210 215 220  
 Tyr Arg Met His Val Ala Lys Gly Ile Ala Glu Gly Val His Asn Phe  
 225 230 235 240  
 Leu Ser Gly Pro Ser Phe Gln Lys Pro Lys Gln Asn Ile Ala Lys Ile  
 245 250 255  
 Arg Lys Pro Gln Ile Gln Ala Asn  
 260

&lt;210&gt;438

&lt;211&gt;483

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;438

Met Asp Leu Lys Glu Leu Leu His Gly Val Gln Ala Lys Ile Tyr Gly  
 1 5 10 15  
 Lys Val Arg Pro Leu Glu Val Arg Asn Leu Thr Arg Asp Ser Arg Cys  
 20 25 30  
 Val Ser Val Gly Asp Ile Phe Ile Ala His Lys Gly Gln Arg Tyr Asp  
 35 40 45  
 Gly Asn Asp Phe Ala Val Asp Ala Leu Ala Asn Gly Ala Ile Ala Ile  
 50 55 60  
 Ala Ser Ser Leu Tyr Asn Pro Phe Leu Ser Val Val Gln Ile Ile Thr  
 65 70 75 80

Arg Asp Pro Phe Arg Arg Gly Thr Phe Phe Ala Asn Thr Thr Val Arg

629

565 570 575  
 Val Met Leu Val Ser Ile Asp Asp Pro Glu Tyr Gly Leu Arg Ala Asp  
 580 585 590  
 Gly Thr Lys Asn Tyr Met Gly Gly Arg Cys Ala Ala Pro Ile Phe Ser  
 595 600 605  
 Arg Val Ala Asp Arg Thr Leu Leu Tyr Leu Gly Ile Leu Pro Asp Lys  
 610 615 620  
 Lys Leu Arg Asn Cys Asp Glu Glu Ala Ala Ala Leu Lys Arg Leu Tyr  
 625 630 635 640  
 Glu Glu Trp Asn Arg Ser Pro Lys Gln Gly Gly Thr Arg  
 645 650

&lt;210&gt;440

&lt;211&gt;300

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;440

Glu Ile Leu Met Ser Glu Arg Ala His Ile Pro Val Leu Val Glu Glu  
 1 5 10 15  
 Cys Leu Ala Leu Phe Ala Gln Arg Pro Pro Gln Thr Phe Arg Asp Val  
 20 25 30  
 Thr Leu Gly Ala Gly Gly His Ala Tyr Ala Phe Leu Glu Ala Tyr Pro  
 35 40 45  
 Ser Leu Thr Cys Tyr Asp Gly Ser Asp Arg Asp Leu Gln Ala Leu Ala  
 50 55 60  
 Ile Ala Glu Lys Arg Leu Glu Thr Phe Gln Asp Arg Val Ser Phe Ser  
 65 70 75 80  
 His Ala Ser Phe Glu Asp Leu Ala Asn Gln Pro Thr Pro Arg Leu Tyr  
 85 90 95  
 Asp Gly Val Leu Ala Asp Leu Gly Val Ser Ser Met Gln Leu Asp Thr  
 100 105 110  
 Leu Ser Arg Gly Phe Ser Phe Gln Gly Glu Lys Glu Glu Leu Asp Met  
 115 120 125  
 Arg Met Asp Gln Thr Gln Glu Leu Ser Ala Ser Asp Val Leu Asn Ser  
 130 135 140  
 Leu Lys Glu Glu Glu Leu Gly Arg Ile Phe Arg Glu Tyr Gly Glu Glu  
 145 150 155 160  
 Pro Gln Trp Lys Ser Ala Ala Lys Ala Val Val His Phe Arg Lys His  
 165 170 175  
 Lys Lys Ile Leu Ser Ile Gln Asp Val Lys Glu Ala Leu Leu Gly Val  
 180 185 190  
 Phe Pro His Tyr Arg Phe His Arg Lys Ile His Pro Leu Thr Leu Ile  
 195 200 205  
 Phe Gln Ala Leu Arg Val Tyr Val Asn Gly Glu Asp Arg Gln Leu Lys  
 210 215 220  
 Ser Leu Leu Thr Ser Ala Ile Ser Trp Leu Ala Pro Gln Gly Arg Leu  
 225 230 235 240  
 Val Ile Ile Ser Phe Cys Ser Ser Glu Asp Arg Pro Val Lys Trp Phe  
 245 250 255  
 Phe Lys Glu Ala Glu Ala Ser Gly Leu Gly Lys Val Ile Thr Lys Lys  
 260 265 270  
 Val Ile Gln Pro Thr Tyr Gln Glu Val Arg Arg Asn Pro Arg Ser Arg  
 275 280 285  
 Ser Ala Lys Leu Arg Cys Phe Glu Lys Ala Ser Gln  
 290 295 300

&lt;210&gt;441

&lt;211&gt;184

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;441

Gly Leu Ala Met Val Glu Ile Phe Asn Tyr Ser Thr Ser Ile Tyr Glu  
 1 5 10 15  
 Gln His Ala Ser Asn Asn Arg Ile Val Ser Asp Phe Arg Lys Glu Ile  
 20 25 30  
 Gln Met Glu Gly Ile Ser Ile Arg Asp Val Ala Lys His Ala Gln Ile

```

          35          40          45
Leu Asp Met Asn Pro Lys Pro Ser Ala Leu Thr Ser Leu Leu Gln Thr
  50          55          60
Asn Gln Lys Ser His Trp Ala Cys Phe Ser Pro Pro Asn Asn Phe Tyr
  65          70          75          80
Lys Gln Arg Phe Ser Thr Pro Tyr Leu Ala Pro Ser Leu Gly Ser Pro
          85          90          95
Asp Gln Gln Asp Glu Asp Ile Glu Lys Ile Ser Ser Phe Leu Lys Val
          100          105          110
Leu Thr Arg Gly Lys Phe Ser Tyr Arg Ser Gln Ile Thr Pro Phe Leu
          115          120          125
Ser Tyr Lys Asp Lys Glu Glu Glu Glu Asp Glu Asp Pro Glu Glu Asp
          130          135          140
Asp Asp Asp Pro Arg Val Gln Gln Gly Lys Val Leu Leu Lys Ala Leu
          145          150          155          160
Asp Leu Gly Val Lys Ser Thr Asn Val Met Ile Asp Tyr Val Ile Ser
          165          170          175
Arg Ile Phe Gln Phe Val Gln Gly
          180

```

&lt;210&gt;442

&lt;211&gt;143

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;442

```

Cys Met Leu Asp Asn Glu Trp Lys Ala Ile Leu Gly Trp Gly Asp Asp
  1          5          10          15
Glu Leu Glu Glu Leu Arg Ile Ser Gly Tyr Ser Phe Leu Arg Gln Gly
          20          25          30
His Tyr Ser Lys Ala Ile Leu Phe Phe Glu Ala Leu Val Ile Leu Asp
          35          40          45
Pro Leu Ser Ile Tyr Asp His Gln Thr Leu Gly Gly Leu Tyr Leu Gln
          50          55          60
Ile Gly Glu Asn Ser Gln Ala Leu Ala Val Leu Asp Gln Ala Leu Arg
          65          70          75          80
Met Gln Gly Asp His Leu Pro Thr Leu Leu Asn Lys Thr Lys Ala Leu
          85          90          95
Phe Cys Leu Gly Arg Ile Glu Glu Ala Thr Ala Ile Ala Thr Tyr Leu
          100          105          110
Ser Ser Cys Pro Ile Pro Ala Ile Ala Asn Asp Ala Glu Ala Leu Leu
          115          120          125
Met Ser Tyr Ser Lys Ala Thr Lys Lys Asn Ala Ala Leu Val Arg
          130          135          140

```

&lt;210&gt;443

&lt;211&gt;467

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;443

```

Met Gly Trp Val Asp Cys Ile Trp Glu Ser Phe Ile Asn Lys Glu Ser
  1          5          10          15
Gly Met Leu Thr Cys Asn Glu Cys Thr Thr Trp Glu Gln Phe Leu Asn
          20          25          30
Tyr Val Lys Thr Arg Cys Ser Lys Thr Ala Phe Glu Asn Trp Ile Ser
          35          40          45
Pro Ile Gln Val Leu Glu Glu Thr Gln Glu Lys Ile Arg Leu Glu Val
          50          55          60
Pro Asn Ile Phe Val Gln Asn Tyr Leu Leu Asp Asn Tyr Lys Arg Asp
          65          70          75          80
Leu Cys Ser Phe Val Pro Leu Asp Val His Gly Glu Pro Ala Leu Glu
          85          90          95
Phe Val Val Ala Glu His Lys Lys Pro Ser Ala Pro Val Ala Ser Gln
          100          105          110
Lys Glu Ser Asn Glu Gly Ile Ser Glu Val Phe Glu Glu Thr Lys Asp
          115          120          125
Phe Glu Leu Lys Leu Asn Leu Ser Tyr Arg Phe Asp Asn Phe Ile Glu

```

130 135 140  
 Gly Pro Ser Asn Gln Phe Val Lys Ser Ala Ala Val Gly Ile Ala Gly  
 145 150 155 160  
 Lys Pro Gly Arg Ser Tyr Asn Pro Leu Phe Ile His Gly Gly Val Gly  
 165 170 175  
 Leu Gly Lys Thr His Leu Leu His Ala Val Gly His Tyr Val Arg Glu  
 180 185 190  
 His His Lys Asn Leu Arg Ile His Cys Ile Thr Thr Glu Ala Phe Ile  
 195 200 205  
 Asn Asp Leu Val Tyr His Leu Lys Ser Lys Ser Val Asp Lys Met Lys  
 210 215 220  
 Asn Phe Tyr Arg Ser Leu Asp Leu Leu Leu Val Asp Asp Ile Gln Phe  
 225 230 235 240  
 Leu Gln Asn Arg Gln Asn Phe Glu Glu Glu Phe Cys Asn Thr Phe Glu  
 245 250 255  
 Thr Leu Ile Asn Leu Ser Lys Gln Ile Val Ile Thr Ser Asp Lys Pro  
 260 265 270  
 Pro Ser Gln Leu Lys Leu Ser Glu Arg Ile Ile Ala Arg Met Glu Trp  
 275 280 285  
 Gly Leu Val Ala His Val Gly Ile Pro Asp Leu Glu Thr Arg Val Ala  
 290 295 300  
 Ile Leu Gln His Lys Ala Glu Gln Lys Gly Leu Leu Ile Pro Asn Glu  
 305 310 315 320  
 Met Ala Phe Tyr Ile Ala Asp His Ile Tyr Gly Asn Val Arg Gln Leu  
 325 330 335  
 Glu Gly Ala Ile Asn Lys Leu Thr Ala Tyr Cys Arg Leu Phe Gly Lys  
 340 345 350  
 Ser Leu Thr Glu Thr Thr Val Arg Glu Thr Leu Lys Glu Leu Phe Arg  
 355 360 365  
 Ser Pro Thr Lys Gln Lys Ile Ser Val Glu Thr Ile Leu Lys Ser Val  
 370 375 380  
 Ala Thr Val Phe Gln Val Lys Leu Asn Asp Leu Lys Gly Asn Ser Arg  
 385 390 395 400  
 Ser Lys Asp Leu Val Leu Ala Arg Gln Ile Ala Met Tyr Leu Ala Lys  
 405 410 415  
 Thr Leu Ile Thr Asp Ser Leu Val Ala Ile Gly Ala Ala Phe Gly Lys  
 420 425 430  
 Thr His Ser Thr Val Leu Tyr Ala Cys Lys Thr Ile Glu His Lys Leu  
 435 440 445  
 Gln Asn Asp Glu Thr Leu Lys Arg Gln Val Asn Leu Cys Lys Asn His  
 450 455 460  
 Ile Val Gly  
 465

&lt;210&gt;444

&lt;211&gt;195

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;444

Met Phe Arg Arg Thr Gly Lys Gly Pro Phe Glu Asp Val Gln Thr Leu  
 1 5 10 15  
 Tyr Glu Glu Glu Thr Ser Ser Pro Ser Tyr Ser Pro Tyr Ser Arg  
 20 25 30  
 Ser Glu Arg Pro Glu Thr Pro Pro Ser Leu Phe Asp Asn Pro Lys Ala  
 35 40 45  
 Ser Glu Ala Arg Pro Leu Asn His Asn Leu Thr Glu Glu Ser Ser Leu  
 50 55 60  
 Pro Gln Trp Ser Ser Thr Pro Arg Thr Glu Ser Leu Leu Pro Leu Glu  
 65 70 75 80  
 Glu Pro Glu Thr Thr Leu Gly Glu Gly Val Thr Phe Lys Gly Glu Leu  
 85 90 95  
 Ala Phe Glu Arg Leu Leu Arg Ile Asp Gly Thr Phe Glu Gly Ile Leu  
 100 105 110  
 Val Ser Lys Gly Lys Ile Ile Ile Gly Pro Lys Gly Val Lys Ala  
 115 120 125



Asp Ile Gln Leu Gln Glu Ala Ile Ile Glu Gly Val Val Glu Gly Asn  
 130 135 140  
 Ile Thr Val Ser Gly Lys Val Glu Leu Arg Gly Gly Ala Ile Ile Lys  
 145 150 155 160  
 Gly Asp Ile Gln Ala Asn Thr Leu Cys Val Asp Glu Gly Val Arg Ile  
 165 170 175  
 Leu Gly Tyr Leu Ala Ile Ala Gly Ile Thr Asp His Ser Glu Arg Glu  
 180 185 190  
 Arg Asp Leu  
 195

&lt;210&gt;445

&lt;211&gt;192

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;445

Met Val Leu Phe Ser Leu Leu Phe Pro Lys Leu Cys Tyr Gly Cys Gln  
 1 5 10 15  
 Ala Pro Gly Ala Tyr Phe Cys Ser Asn Cys Leu Glu Lys Leu Leu Val  
 20 25 30  
 Glu Asp Arg Glu Gly Arg Cys Leu His Cys Phe Arg Tyr Leu Gly Ser  
 35 40 45  
 Ser Glu Thr Arg Leu Cys Ser Gln Cys Ser Pro Ser Ser Gln Leu Gln  
 50 55 60  
 Ala Phe Ser Leu Tyr Leu Pro Ser Gln Thr Ala Leu Ser Val Tyr Ala  
 65 70 75 80  
 Arg Ala Cys Glu Gly Lys Arg Pro Ala Leu Gln Phe Phe Ser Lys Ser  
 85 90 95  
 Ile Ala Phe Glu Leu Ala Ser Leu Asp Glu Thr Pro Ser Cys Ile Ala  
 100 105 110  
 Tyr Ile Thr Ser Thr Ile Ser Arg Lys Ile Val Val Glu Val Ala Lys  
 115 120 125  
 Leu Glu Lys Leu Leu Arg Ile Pro Leu Trp Pro Trp Leu Pro Lys Lys  
 130 135 140  
 Arg Gln Ile Glu Lys Leu Pro Lys Gly Glu Gly Ile Cys Phe Leu Ser  
 145 150 155 160  
 Ala Tyr Pro Leu Ser Gln Lys Trp Met Gln Thr Ile Val Gly Gly Ser  
 165 170 175  
 Ala Ser Pro Leu Val Ser Ile Ser Leu Phe Leu Ser Gln Asn Asp Gln  
 180 185 190

&lt;210&gt;446

&lt;211&gt;517

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;446

Val Phe Glu Arg Val Glu Ala Ser Thr Phe Leu Ser Ile Thr Met Leu  
 1 5 10 15  
 Lys Lys Phe Ile Asn Ser Leu Trp Lys Leu Cys Gln Gln Asp Lys Tyr  
 20 25 30  
 Gln Arg Phe Thr Pro Ile Val Asp Ala Ile Asp Thr Phe Cys Tyr Glu  
 35 40 45  
 Pro Ile Glu Thr Pro Ser Lys Pro Pro Phe Ile Arg Asp Ser Val Asp  
 50 55 60  
 Val Lys Arg Trp Met Met Leu Val Val Ile Ala Leu Phe Pro Ala Thr  
 65 70 75 80  
 Phe Val Ala Ile Trp Asn Ser Gly Leu Gln Ser Ile Val Tyr Ser Ser  
 85 90 95  
 Gly Asn Pro Val Leu Met Glu Gln Phe Leu His Ile Ser Gly Phe Gly  
 100 105 110  
 Ser Tyr Leu Ser Phe Val Tyr Lys Glu Ile His Ile Val Pro Ile Leu  
 115 120 125  
 Trp Glu Gly Leu Lys Ile Phe Ile Pro Leu Leu Thr Ile Ser Tyr Val  
 130 135 140  
 Val Gly Gly Thr Cys Glu Val Leu Phe Ala Val Val Arg Gly His Lys  
 145 150 155 160

Ile Ala Glu Gly Leu Leu Val Thr Gly Ile Leu Tyr Pro Leu Thr Leu  
 165 170 175  
 Pro Pro Thr Ile Pro Tyr Trp Met Ala Ala Leu Gly Ile Ala Phe Gly  
 180 185 190  
 Ile Val Val Ser Lys Glu Leu Phe Gly Gly Thr Gly Met Asn Ile Leu  
 195 200 205  
 Asn Pro Ala Leu Ser Gly Arg Ala Phe Leu Phe Phe Thr Phe Pro Ala  
 210 215 220  
 Lys Met Ser Gly Asp Val Trp Val Gly Ser Asn Pro Gly Val Ile Lys  
 225 230 235 240  
 Asp Ser Leu Met Lys Met Asn Ser Ser Thr Gly Lys Val Leu Ile Asp  
 245 250 255  
 Gly Phe Ser Gln Ser Thr Cys Leu Gln Thr Leu Asn Ser Thr Pro Pro  
 260 265 270  
 Ser Val Lys Arg Leu His Val Asp Ala Ile Ala Ala Asn Met Leu His  
 275 280 285  
 Ile Pro His Val Pro Thr Gln Asp Val Ile His Ser Gln Phe Ser Leu  
 290 295 300  
 Trp Thr Glu Thr His Pro Gly Trp Val Leu Asp Asn Leu Thr Leu Thr  
 305 310 315 320  
 Gln Leu Gln Thr Phe Val Thr Ala Pro Val Ala Glu Gly Gly Leu Gly  
 325 330 335  
 Leu Leu Pro Thr Gln Phe Asp Ser Ala Tyr Ala Ile Thr Asp Val Ile  
 340 345 350  
 Tyr Gly Ile Gly Lys Phe Ser Ala Gly Asn Leu Phe Trp Gly Asn Ile  
 355 360 365  
 Ile Gly Ser Leu Gly Glu Thr Ser Thr Phe Ala Cys Leu Leu Gly Ala  
 370 375 380  
 Ile Phe Leu Ile Val Thr Gly Ile Ala Ser Trp Arg Thr Met Ala Ala  
 385 390 395 400  
 Phe Gly Ile Gly Ala Phe Leu Thr Gly Trp Leu Phe Lys Phe Ile Ser  
 405 410 415  
 Val Leu Ile Val Gly Gln Asn Gly Ala Trp Ala Pro Ala Arg Phe Phe  
 420 425 430  
 Ile Pro Ala Tyr Arg Gln Leu Phe Leu Gly Gly Leu Ala Phe Gly Leu  
 435 440 445  
 Val Phe Met Ala Thr Asp Pro Val Ser Ser Pro Thr Met Lys Leu Gly  
 450 455 460  
 Lys Trp Ile Tyr Gly Phe Phe Ile Gly Phe Met Thr Ile Val Ile Arg  
 465 470 475 480  
 Leu Ile Asn Pro Ala Tyr Pro Glu Gly Val Met Leu Ala Ile Leu Leu  
 485 490 495  
 Gly Asn Val Phe Ala Pro Leu Ile Asp Tyr Phe Ala Val Arg Lys Tyr  
 500 505 510  
 Arg Lys Arg Gly Val  
 515  
 <210>447  
 <211>320  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>447  
 Met Ser Lys Gly Ser Ser Lys His Thr Val Arg Ile Asn Gln Thr Trp  
 1 5 10 15  
 Tyr Ile Val Ser Phe Ile Leu Gly Leu Ser Leu Phe Ala Gly Val Leu  
 20 25 30  
 Leu Ser Thr Ile Tyr Tyr Val Leu Ser Pro Ile Gln Glu Gln Ala Ala  
 35 40 45  
 Thr Phe Asp Arg Asn Lys Gln Met Leu Leu Ala Ala His Ile Leu Asp  
 50 55 60  
 Phe Lys Gly Arg Phe Gln Ile Gln Glu Lys Lys Glu Trp Val Pro Ala  
 65 70 75 80  
 Thr Phe Asp Lys Lys Thr Gln Leu Leu Glu Val Ala Thr Lys Lys Val  
 85 90 95  
 Ser Glu Val Ser Tyr Pro Glu Leu Glu Leu Tyr Ala Glu Arg Phe Val

100 105 110  
 Arg Pro Leu Leu Thr Asp Ala Gln Gly Lys Val Phe Ser Phe Glu Glu  
 115 120 125  
 Lys Asn Leu Asn Pro Ile Glu Phe Phe Glu Lys Tyr Gln Glu Ser Pro  
 130 135 140  
 Pro Cys Gln Gln Ser Pro Leu Pro Phe Tyr Val Ile Leu Glu Asn Thr  
 145 150 155 160  
 Ser Arg Thr Glu Asn Met Ser Gly Ala Asp Val Ala Lys Asp Leu Ser  
 165 170 175  
 Thr Val Gln Ala Leu Ile Phe Pro Ile Ser Gly Phe Gly Leu Trp Gly  
 180 185 190  
 Pro Ile His Gly Tyr Leu Gly Val Lys Asn Asp Gly Asp Thr Val Leu  
 195 200 205  
 Gly Thr Ala Trp Tyr Gln Gln Gly Glu Thr Pro Gly Leu Gly Ala Asn  
 210 215 220  
 Ile Thr Asn Pro Glu Trp Gln Glu Gln Phe Tyr Gly Lys Lys Ile Phe  
 225 230 235 240  
 Leu Gln Asp Ser Ser Gly Thr Thr Asn Phe Ala Thr Thr Asp Leu Gly  
 245 250 255  
 Leu Glu Val Val Lys Gly Ser Val Arg Thr Thr Leu Gly Asp Ser Pro  
 260 265 270  
 Lys Ala Leu Ser Ala Ile Asp Gly Ile Ser Gly Ala Thr Leu Thr Cys  
 275 280 285  
 Asn Gly Val Thr Glu Ala Tyr Val Gln Ser Leu Ala Cys Tyr Arg Gln  
 290 295 300  
 Leu Leu Ile Asn Phe Ser Asn Leu Thr His Glu Lys Lys Thr Gly Glu  
 305 310 315 320  
 <210>448  
 <211>223  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>448  
 Met Thr Ser Lys Lys Ser Tyr Lys Ser Tyr Phe Phe Asp Pro Leu Trp  
 1 5 10 15  
 Ser Asn Asn Gln Ile Leu Ile Ala Ile Leu Gly Ile Cys Ser Ala Leu  
 20 25 30  
 Ala Val Thr Thr Thr Val Gln Thr Ala Ile Thr Met Gly Ile Ala Val  
 35 40 45  
 Ser Ile Val Thr Gly Cys Ser Ser Phe Phe Val Ser Leu Leu Arg Lys  
 50 55 60  
 Phe Thr Pro Asp Ser Val Arg Met Ile Thr Gln Leu Ile Ile Ile Ser  
 65 70 75 80  
 Leu Phe Val Ile Val Ile Asp Gln Phe Leu Lys Ala Phe Phe Phe Asp  
 85 90 95  
 Ile Ser Lys Thr Leu Ser Val Phe Val Gly Leu Ile Ile Thr Asn Cys  
 100 105 110  
 Xaa Xaa Met Gly Arg Ser Glu Ser Leu Ala Arg His Val Thr Pro Ile  
 115 120 125  
 Pro Ala Phe Leu Asp Gly Phe Ala Ser Gly Leu Gly Tyr Gly Trp Val  
 130 135 140  
 Leu Leu Val Ile Gly Val Ile Arg Glu Leu Phe Gly Phe Gly Thr Pro  
 145 150 155 160  
 Tyr Gly Val Ser His His Pro Ser Ile Cys Tyr Ala Ser Glu Thr His  
 165 170 175  
 Pro Asp Gly Tyr Gln Asn Leu Ser Leu Met Val Leu Ala Pro Ser Ala  
 180 185 190  
 Phe Phe Leu Leu Gly Ile Met Ile Trp Leu Val Asn Ile Arg Asp Ser  
 195 200 205  
 Lys Glu Lys Xaa Val Val Tyr Val Val Arg Cys Val Tyr Leu Ala  
 210 215 220  
 <210>449  
 <211>256  
 <212>PRT  
 <213>Chlamydia pneumoniae

&lt;400&gt;449

```

Met Trp Leu Gly Ala Tyr Thr Trp Leu Asn Val Phe Gly Ile Leu Leu
 1          5          10          15
Gln Ala Ala Phe Ile Gln Asn Ile Leu Leu Ala Asn Phe Leu Gly Met
          20          25          30
Cys Ser Tyr Leu Ala Cys Ser Thr Arg Val Ser Thr Ala Asn Gly Leu
          35          40          45
Gly Met Ser Val Ala Leu Val Leu Thr Val Thr Gly Ser Ile Asn Trp
          50          55          60
Phe Val His Ala Phe Ile Thr Gly Pro Lys Ala Leu Thr Trp Ile Ser
          65          70          75          80
Pro Ser Leu Ala Ser Val Asn Leu Gly Phe Leu Glu Leu Ile Ile Phe
          85          90          95
Ile Val Val Ile Ala Ala Phe Thr Gln Ile Leu Glu Leu Leu Leu Glu
          100          105          110
Lys Val Ser Arg Asn Leu Tyr Leu Ser Leu Gly Ile Phe Leu Pro Leu
          115          120          125
Ile Ala Val Asn Cys Ala Ile Leu Gly Gly Val Leu Phe Gly Ile Thr
          130          135          140
Arg Ser Tyr Pro Phe Ile Pro Met Met Ile Phe Ser Leu Gly Ala Gly
          145          150          155          160
Cys Gly Trp Trp Leu Ala Ile Val Ile Leu Ala Thr Ile Lys Glu Lys
          165          170          175
Leu Ala Tyr Ser Asp Ile Pro Lys Asn Leu Gln Gly Met Gly Ile Ser
          180          185          190
Phe Ile Thr Thr Gly Leu Ile Ala Met Ala Phe Met Ser Leu Thr Gly
          195          200          205
Ile Asp Ile Ser Lys Pro Ser Ala Lys Ile Gln Arg Ala Pro Leu Glu
          210          215          220
Thr Glu Val Val Glu Asn Thr Thr Asn Pro Leu Lys Glu Ser Ser Ser
          225          230          235          240
Lys His Gln Pro Ser Ile Ser Lys Ala Arg Thr Gln Arg Arg Ser Leu
          245          250          255

```

&lt;210&gt;450

&lt;211&gt;113

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;450

```

Lys Ile Met Thr Thr Leu Pro Lys Tyr Val Pro Arg Ser Arg Gln Asn
 1          5          10          15
Pro Asp Thr Leu Thr Phe Leu Lys Arg Tyr Ser Ser Val Leu Leu His
          20          25          30
Ser Glu Asn Ser Leu Ser Tyr Arg Ile Phe Ala Lys Val Leu Ala Ile
          35          40          45
Leu Leu Thr Ser Leu Ala Val Ala Phe Ala Val Thr Leu Phe Ser Cys
          50          55          60
Glu Gly Ser Gln Leu Arg Leu Cys Ala Leu Tyr Ile Gly Ile Ala Leu
          65          70          75          80
Ala Ile Cys Val Leu Leu Thr Ile Val Val Tyr Cys Ile Ala Ser Lys
          85          90          95
Ile Ala Thr Ala Cys Lys Lys Pro Pro Ser Ile Ser Arg Ile Glu Ile
          100          105          110
Val

```

&lt;210&gt;451

&lt;211&gt;436

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;451

```

Gly Glu Xaa Ala Tyr Thr Lys Ile Ser Lys Asn Lys Glu Phe Ser Leu
 1          5          10          15
Gly Phe Glu Glu Phe Val Asn Ser Tyr Phe Gln Phe Leu Glu Ile Ser
          20          25          30
Glu Ser Glu Phe Phe Asn Met Tyr Arg Asp Ile Leu Leu Cys Lys Arg

```

35 40 45  
 Ala Leu Leu Leu Leu Gln Gly Gly Val Ser Phe Asp Phe Gln Pro Leu  
 50 55 60  
 Thr Thr Phe Phe Val Gln Gly Lys Asp Ser Ile Gln Val Glu Phe Phe  
 65 70 75 80  
 Arg Leu Pro Lys Glu Tyr Ser Phe Lys Thr Lys Gln Glu Leu Lys Ala  
 85 90 95  
 Phe Glu Val Tyr Leu Lys Leu Val Ser Leu Pro Lys Ser Asp Ser Leu  
 100 105 110  
 Asp Val Pro Asn Glu Ile Leu Pro Ile Ala Thr Ile Lys Ala Lys Glu  
 115 120 125  
 Pro Arg Leu Val Gly Arg Arg Phe Ser Ile Asp Tyr Lys Arg Val Ala  
 130 135 140  
 Leu Gln Asp Leu Ala Ala Thr Val Pro Met Val Glu Val Leu His Trp  
 145 150 155 160  
 Gln Gln Asn Ser Glu His Phe Gln Glu Ile Leu Gln Gln Phe Pro Asp  
 165 170 175  
 Val Glu Thr Cys Gln Ser Tyr Lys Asp Phe Gln His Leu Lys Pro Ala  
 180 185 190  
 Leu Arg Asp Lys Ile Ser Leu Phe Thr Arg Lys Glu Ile Leu Arg Ala  
 195 200 205  
 Arg Pro Glu Arg Ile Leu Gln Ser Leu Gln Gln Val Pro Lys Gln Ser  
 210 215 220  
 Gln Glu Val Leu Leu Ser Ala Gly Lys Asn Ser Ala Leu Pro Gly Ile  
 225 230 235 240  
 Ser Asp Gly Gln Gln Leu Ala Lys Val Leu Leu Glu Asn Glu Val Leu  
 245 250 255  
 Asp Leu Tyr Ser Gln Asp Ala Glu Thr Tyr Tyr Thr Ile Ile Val Asn  
 260 265 270  
 Ser Ser Phe Glu Lys Glu Glu Val Leu Pro Tyr Arg Glu Val Leu Lys  
 275 280 285  
 Arg Asp Leu Ala Ser Gln Leu Leu Thr Ser His Gly His Leu Val Asp  
 290 295 300  
 Met Glu Arg Leu Glu Ser Ala Leu Arg Thr Arg Tyr Pro Gly Glu Glu  
 305 310 315 320  
 Gly Ala Ser Leu Trp Gln Arg Arg Leu Trp Lys Val Val Glu Asn His  
 325 330 335  
 Arg Leu Gly Arg His Leu Glu Gly Ser Phe Ser Trp Ser Leu Asp Arg  
 340 345 350  
 Ser Leu Lys Thr Phe Ser Arg Gly Asp Lys Glu Leu Pro Gln Glu Phe  
 355 360 365  
 Asp Arg Ile Phe Ser Met Lys Val Gly Asp Tyr Ser Ser Val Phe Met  
 370 375 380  
 Ser Pro Asn Glu Gly Pro Cys Tyr Tyr Gln Cys Leu Ser His Leu Leu  
 385 390 395 400  
 Tyr Asp Arg Pro Ala Ser Val Asp Lys Leu Phe Leu Ala Lys Ser Gln  
 405 410 415  
 Leu Asp Glu Glu Leu Leu Gly Ser Tyr Met Glu Arg Phe Ile Glu Gln  
 420 425 430  
 Gly Val Val Arg  
 435  
 <210>452  
 <211>84  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>452  
 Ser Gln Ala Leu Phe Arg Arg Glu Lys Val Pro Ser Leu Cys Ala Ser  
 1 5 10 15  
 Thr Asn Val Gly Val Pro Gln Gln Met Phe Ala Leu Pro Pro Asp Glu  
 20 25 30  
 Ala Leu Ser Arg Gly Lys Asp Leu Arg Leu Phe Gly Tyr Gln Thr Ile  
 35 40 45  
 Gln Asp Trp Phe Gly Asp Ala Tyr Leu Ser Ala Ala Val Glu Leu Leu  
 50 55 60

Ile Arg Phe Ile Asp Glu Gln Lys Lys Val Leu Pro Arg Pro Ser Lys  
 65 70 75 80  
 Gln Glu Ser Ser

&lt;210&gt;453

&lt;211&gt;269

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;453

Arg Pro Trp Val Arg Ile Tyr Gln Gln Asp Leu Phe Cys Arg Leu Cys  
 1 5 10 15  
 Arg Asp Pro Ala Trp Phe Phe Ser Leu Leu Ser Phe Thr Leu Arg Phe  
 20 25 30  
 Tyr Cys Leu Gly Arg Gly Trp Thr Leu Leu Ser Phe Phe Tyr Lys His  
 35 40 45  
 Gln Lys Lys Phe Ile Gly Ile Val Ile Ala Val Val Cys Val Ser Gly  
 50 55 60  
 Ile Gly Val Gly Trp Gly Arg Phe Ser Arg Lys Gly Ser Ala Glu Ser  
 65 70 75 80  
 Thr Ser Arg Arg Thr Val Phe Thr Thr Ala Ser Gly Lys Arg Tyr Val  
 85 90 95  
 Glu Lys Asp Phe Met Ala Met Lys Lys Phe Phe Ala His Glu Ala Tyr  
 100 105 110  
 Pro Phe Thr Gly Asn Pro Arg Ala Trp Asn Phe Ile Asn Glu Gly Leu  
 115 120 125  
 Leu Thr Asp Tyr Phe Leu Thr Thr Arg Val Gly Glu Lys Leu Phe Leu  
 130 135 140  
 Lys Val Tyr His Pro Gly Glu Lys Ile Phe Ser Lys Glu Lys Ala Tyr  
 145 150 155 160  
 Gln Pro Tyr Arg Arg Phe Asp Ala Pro Phe Ile Ser Ser Glu Glu Val  
 165 170 175  
 Trp Lys Ser Ser Ala Pro Gln Leu Leu Glu Ile Leu Lys Val Phe Gln  
 180 185 190  
 Gln Ile Glu Asn Pro Ile Ser Lys Glu Gly Phe Leu Ala Arg Ala Lys  
 195 200 205  
 Leu Phe Leu Glu Glu Arg Arg Phe Pro His Tyr Val Leu Arg Gln Met  
 210 215 220  
 Leu Glu Tyr Arg Ser Lys Cys Leu Leu Phe Pro Gln Met Lys Pro Tyr  
 225 230 235 240  
 Leu Ala Gly Lys Thr Cys Gly Tyr Leu Ala Thr Arg Arg Phe Lys Thr  
 245 250 255  
 Gly Leu Gly Met Pro Thr Phe Leu Leu Leu Ser Ser  
 260 265

&lt;210&gt;454

&lt;211&gt;196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;454

Ala Thr Gln Ser Trp Thr Gln Glu Tyr Leu Lys Leu Ile Gln Gly Ala  
 1 5 10 15  
 Arg Ser Ser Val Lys Leu Ala His Met Tyr Phe Ile Pro Lys Asp Glu  
 20 25 30  
 Leu Leu Asn Ala Leu Val Asp Val Ser His Asn His Gly Val His Leu  
 35 40 45  
 Ser Leu Ile Thr Asn Gly Cys His Glu Leu Ser Pro Ala Ile Thr Gly  
 50 55 60  
 Pro Tyr Ala Trp Gly Asn Arg Ile Asn Tyr Phe Ala Leu Leu Tyr Gly  
 65 70 75 80  
 Lys Arg Tyr Pro Leu Trp Lys Lys Trp Phe Cys Glu Lys Leu Lys Pro  
 85 90 95  
 Tyr Glu Arg Val Ser Ile Tyr Glu Phe Ala Ile Trp Glu Thr Gln Leu  
 100 105 110  
 His Lys Lys Cys Met Ile Ile Asp Asp Glu Ile Phe Val Ile Gly Ser  
 115 120 125

Tyr Asn Phe Gly Lys Lys Ser Asp Ala Phe Asp Tyr Glu Ser Ile Val  
 130 135 140  
 Val Ile Glu Ser Pro Glu Val Ala Ala Lys Ala Asn Lys Val Phe Asn  
 145 150 155 160  
 Lys Asp Ile Gly Leu Ser Ile Pro Val Ser His Gly Asp Ile Phe Ser  
 165 170 175  
 Trp Tyr Phe His Ser Val His His Thr Leu Gly His Leu Gln Leu Thr  
 180 185 190  
 Tyr Met Pro Ala  
 195

&lt;210&gt;455

&lt;211&gt;214

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;455

Arg Asp Gly Lys Ile Thr Ser Arg Leu Val Trp Ile Trp Phe Gln Ser  
 1 5 10 15  
 Ser Val Ala Asn Ile Ile Ile Gln Pro Thr Phe Thr Asp Ala Glu Asp  
 20 25 30  
 Gln Lys Leu Leu Lys Ala Leu Lys Glu Arg His Pro Asn Arg Phe Phe  
 35 40 45  
 Tyr Val Phe Thr Gly Cys Pro Pro Ser Thr Ser Ile Leu Ala Pro Asn  
 50 55 60  
 Val Ile Glu Met His Ile Lys Leu Ser Ile Ile Asp Gly Lys Tyr Cys  
 65 70 75 80  
 Ile Leu Gly Gly Thr Asn Phe Glu Glu Phe Met Cys Thr Pro Gly Asp  
 85 90 95  
 Glu Val Pro Glu Lys Val Asp Asn Pro Arg Leu Phe Val Ser Gly Val  
 100 105 110  
 Arg Arg Pro Leu Ala Phe Arg Asp Gln Asp Ile Met Leu Arg Ser Thr  
 115 120 125  
 Ala Phe Gly Leu Gln Leu Arg Glu Glu Tyr His Lys Gln Phe Ala Met  
 130 135 140  
 Trp Asp Tyr Tyr Ala His Met Trp Phe Ile Asp Asn Pro Glu Gln  
 145 150 155 160  
 Phe Ala Gly Ala Cys Pro Pro Leu Thr Leu Glu Gln Ala Glu Glu Thr  
 165 170 175  
 Val Phe Pro Gly Phe Asp Lys His Glu Asp Leu Val Leu Val Asp Ser  
 180 185 190  
 Ser Lys Ile Arg Ile Val Leu Gly Gly Pro His Asp Lys Gln Pro Asn  
 195 200 205  
 Pro Gly Leu Lys Asn Ile  
 210

&lt;210&gt;456

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;456

Gly Val Met Met Ser Arg Leu Arg Phe Arg Leu Ala Ala Leu Gly Ile  
 1 5 10 15  
 Phe Phe Ile Leu Leu Val Pro Asn Ser Val Ser Ala Lys Thr Ile Val  
 20 25 30  
 Ala Ser Asp Lys Glu Lys Val Gly Val Leu Val Tyr Asp Asn Ser Val  
 35 40 45  
 Glu Ala Phe Gln Gln Ile Leu Asp Cys Ile Asp His Ala Asn Phe Tyr  
 50 55 60  
 Val Glu Leu Cys Pro Cys Met Thr Gly Gly Arg Thr Leu Lys Glu Met  
 65 70 75 80  
 Val Arg Ser Pro Arg Gly Ser Tyr Gly Ser Gly Ser Arg Ala Leu  
 85 90 95

&lt;210&gt;457

&lt;211&gt;244

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;457

Phe Tyr Val Cys Tyr Met Lys Val Arg Ile Val Asp Ser Gly Lys Ser  
 1 5 10 15  
 Ser Ala Ala Ser His Met Ala Lys Asp Arg Asp Leu Leu Glu Ser Leu  
 20 25 30  
 Gln Asp Gly Glu Leu Ile Leu His Leu Tyr Glu Trp Glu Asn Pro Cys  
 35 40 45  
 Ser Leu Thr Tyr Gly His Phe Met Arg Pro Glu Lys Phe Leu Leu Ser  
 50 55 60  
 Asn Tyr Ala Asp Leu Gly Leu Asp Ala Ala Val Arg Pro Thr Gly Gly  
 65 70 75 80  
 Gly Phe Val Phe His Lys Gly Asp Tyr Ala Phe Ser Val Leu Met Ser  
 85 90 95  
 Ala Thr His Pro Ser Tyr Ser Ser Ser Val Leu Glu Asn Tyr His Thr  
 100 105 110  
 Val Asn Ser Phe Val Ala Lys Val Leu Glu Lys Val Phe Arg Ile Gln  
 115 120 125  
 Gly Met Leu Ala Pro Glu Asp Glu Asn Ser Ser Ser Arg Asp Ser Gly  
 130 135 140  
 Asn Phe Cys Met Ala Lys Thr Ser Lys Tyr Asp Val Leu Xaa Trp Gly  
 145 150 155 160  
 Gln Glu Asp Arg Gly Ala Ala Gln Arg Lys Val Gln Gln Gly Phe Leu  
 165 170 175  
 His Gln Gly Ser Leu Phe Leu Ser Gly Ser Ser Ser Glu Phe Tyr Gln  
 180 185 190  
 Arg Phe Leu Lys Pro Glu Val Leu Glu Glu Ile Ile Glu Gln Ile Gln  
 195 200 205  
 Ile His Ala Phe Phe Pro Leu Gly Leu Glu Ala Ala Asp Glu Val Leu  
 210 215 220  
 Gln Glu Ala Arg Gln Gln Val Lys Glu Ala Phe Ile Lys Leu Phe Cys  
 225 230 235 240  
 Gly Glu Gly Leu

&lt;210&gt;458

&lt;211&gt;845

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;458

Met Phe Glu Lys Phe Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala  
 1 5 10 15  
 Lys Lys Glu Ala Gln Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His  
 20 25 30  
 Ile Leu Leu Gly Leu Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val  
 35 40 45  
 Leu Arg Asn Leu Gly Ile Asp Phe Asp Thr Ala Arg Gln Glu Val Glu  
 50 55 60  
 Arg Leu Ile Gly Tyr Gly Pro Glu Ile Gln Val Tyr Gly Asp Ala Ala  
 65 70 75 80  
 Leu Thr Gly Arg Val Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala  
 85 90 95  
 Ser Leu Leu Glu His Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly  
 100 105 110  
 Ile Leu His Gln Ser Asp Ser Val Ala Leu Gln Val Leu Glu Asn Leu  
 115 120 125  
 His Ile Asp Pro Arg Glu Val Arg Lys Glu Ile Leu Lys Glu Leu Glu  
 130 135 140  
 Thr Phe Asn Leu Gln Leu Pro Pro Ser Ser Ser Ser Ser Ser Ser  
 145 150 155 160  
 Ser Arg Ser Asn Pro Ser Ser Ser Lys Ser Pro Leu Gly Gln Ser Leu  
 165 170 175  
 Gly Ser Asp Lys Asn Glu Lys Leu Ser Ala Leu Lys Ala Tyr Gly Tyr  
 180 185 190  
 Asp Leu Thr Glu Met Val Arg Glu Ser Lys Leu Asp Pro Val Ile Gly  
 195 200 205



Arg Ser Ser Glu Val Glu Arg Leu Ile Leu Ile Leu Cys Arg Arg Arg  
 210 215 220  
 Lys Asn Asn Pro Val Leu Ile Gly Glu Ala Gly Val Gly Lys Thr Ala  
 225 230 235 240  
 Ile Val Glu Gly Leu Ala Gln Lys Ile Ile Leu Asn Glu Val Pro Asp  
 245 250 255  
 Ala Leu Arg Lys Lys Arg Leu Ile Thr Leu Asp Leu Ala Leu Met Ile  
 260 265 270  
 Ala Gly Thr Lys Tyr Arg Gly Gln Phe Glu Glu Arg Ile Lys Ala Val  
 275 280 285  
 Met Asp Glu Val Arg Lys His Gly Asn Ile Leu Leu Phe Ile Asp Glu  
 290 295 300  
 Leu His Thr Ile Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala  
 305 310 315 320  
 Ser Asn Ile Leu Lys Pro Ala Leu Ala Arg Gly Glu Ile Gln Cys Ile  
 325 330 335  
 Gly Ala Thr Thr Ile Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala  
 340 345 350  
 Ala Leu Glu Arg Arg Phe Gln Lys Ile Val Val His Pro Pro Ser Val  
 355 360 365  
 Asp Glu Thr Ile Glu Ile Leu Arg Gly Leu Lys Lys Lys Tyr Glu Glu  
 370 375 380  
 His His Asn Val Phe Ile Thr Glu Glu Ala Leu Lys Ala Ala Ala Thr  
 385 390 395 400  
 Leu Ser Asp Gln Tyr Val His Gly Arg Phe Leu Pro Asp Lys Ala Ile  
 405 410 415  
 Asp Leu Leu Asp Glu Ala Gly Ala Arg Val Arg Val Asn Thr Met Gly  
 420 425 430  
 Gln Pro Thr Asp Leu Met Lys Leu Glu Ala Glu Ile Glu Asn Thr Lys  
 435 440 445  
 Leu Ala Lys Glu Gln Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala  
 450 455 460  
 Gly Leu Arg Asp Glu Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met  
 465 470 475 480  
 Lys Gln Glu Trp Glu Asn His Lys Glu Glu His Gln Val Pro Val Asp  
 485 490 495  
 Glu Glu Ala Val Ala Gln Val Val Ser Leu Gln Thr Gly Ile Pro Ser  
 500 505 510  
 Ala Arg Leu Thr Glu Ala Glu Ser Glu Lys Leu Leu Lys Leu Glu Asp  
 515 520 525  
 Thr Leu Arg Arg Lys Val Ile Gly Gln Asn Asp Ala Val Thr Ser Ile  
 530 535 540  
 Cys Arg Ala Ile Arg Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg  
 545 550 555 560  
 Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Ser  
 565 570 575  
 Leu Leu Ala Gln Gln Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ala  
 580 585 590  
 Leu Ile Gln Val Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr  
 595 600 605  
 Lys Met Met Gly Ser Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly  
 610 615 620  
 His Leu Thr Glu Gln Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe  
 625 630 635 640  
 Asp Glu Ile Glu Lys Ala His Pro Asp Ile Met Asp Leu Met Leu Gln  
 645 650 655  
 Ile Leu Glu Gln Gly Arg Leu Thr Asp Ser Phe Gly Arg Lys Val Asp  
 660 665 670  
 Phe Arg His Ala Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu  
 675 680 685  
 Ile Arg Lys Ser Gly Glu Ile Gly Phe Gly Leu Lys Ser His Met Asp  
 690 695 700  
 Tyr Lys Val Ile Gln Glu Lys Ile Glu His Ala Met Lys Lys His Leu  
 705 710 715 720

BNSDOCID: <WO\_\_9927105A2\_1\_>

340 345 350  
 Phe Tyr Gln Gly Asp Thr Cys Leu Gly Ser Gly Val Ile Asp Val Pro  
 355 360 365  
 Met Ile Pro Ser Glu Gly  
 370  
 <210>460  
 <211>185  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>460  
 Ile Ile Ser Ser Asn Asn Arg Val Leu Phe Val Ser Ser Thr Leu Asn  
 1 5 10 15  
 Gly Val Phe Pro Ser Ser Leu Pro Glu Glu Ser Ala Asp Leu Phe Ile  
 20 25 30  
 Thr Asn Lys Glu Ile Val Ala Leu Gly Glu Lys Gly Asn Val Phe Leu  
 35 40 45  
 Thr His Ser Ile Pro Met His Ile Ala Ala Ile Thr Ile Leu Val Ile  
 50 55 60  
 Val Ala Leu Ala Gly Ile Ala Ile Ile Cys Leu Gly Cys Tyr Ser Gln  
 65 70 75 80  
 Ser Ile Leu Leu Ile Ala Val Gly Ile Val Leu Thr Ile Leu Thr Leu  
 85 90 95  
 Leu Cys Leu Gln Ala Leu Val Gly Phe Ile Lys Phe Ile Arg Gln Leu  
 100 105 110  
 Pro Gln Gln Leu His Thr Thr Val Gln Phe Ile Arg Glu Lys Ile Arg  
 115 120 125  
 Pro Glu Ser Ser Leu Gln Leu Val Thr Asn Ala Gln Arg Lys Thr Thr  
 130 135 140  
 Gln Asp Thr Leu Lys Leu Tyr Glu Glu Leu Cys Asp Leu Ser Gln Lys  
 145 150 155 160  
 Glu Phe Lys Leu Gln Ser Thr Leu Tyr Gln Lys Arg Phe Glu Leu Ser  
 165 170 175  
 His Lys Asn Glu Lys Thr Asn Gln Asn  
 180 185  
 <210>461  
 <211>220  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>461  
 Leu Ala Thr Ile Arg Gly Asn Asn Met Ala Thr Ser Val Ala Pro Ser  
 1 5 10 15  
 Pro Val Pro Glu Ser Ser Pro Leu Ser His Ala Thr Glu Val Leu Asn  
 20 25 30  
 Leu Pro Asn Ala Tyr Ile Thr Gln Pro His Pro Ile Pro Ala Ala Pro  
 35 40 45  
 Trp Glu Thr Phe Arg Ser Lys Leu Ser Thr Lys His Thr Leu Cys Phe  
 50 55 60  
 Ala Leu Thr Leu Leu Leu Thr Leu Gly Gly Thr Ile Ser Ala Gly Tyr  
 65 70 75 80  
 Ala Gly Tyr Thr Gly Asn Trp Ile Ile Cys Gly Ile Gly Leu Gly Ile  
 85 90 95  
 Ile Val Leu Thr Leu Ile Leu Ala Leu Leu Leu Ala Ile Pro Leu Lys  
 100 105 110  
 Asn Lys Gln Thr Gly Thr Lys Leu Ile Asp Glu Ile Ser Gln Asp Ile  
 115 120 125  
 Ser Ser Ile Gly Ser Gly Phe Val Gln Arg Tyr Gly Leu Met Phe Ser  
 130 135 140  
 Thr Ile Lys Ser Val His Leu Pro Glu Leu Thr Thr Gln Asn Gln Glu  
 145 150 155 160  
 Lys Thr Arg Ile Leu Asn Glu Ile Glu Ala Lys Lys Glu Ser Ile Gln  
 165 170 175  
 Asn Leu Glu Leu Lys Ile Thr Glu Cys Gln Asn Lys Leu Ala Gln Lys  
 180 185 190  
 Gln Pro Lys Arg Lys Ser Ser Gln Lys Ser Phe Met Arg Ser Ile Lys

195 200 205  
 His Leu Ser Lys Asn Pro Val Ile Leu Phe Asp Cys  
 210 215 220  
 <210>462  
 <211>159  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>462  
 Arg Trp Arg Ile Leu Gln Asn Met Phe Lys Leu Leu Phe His Ile Ala  
 1 5 10 15  
 Ala Phe Ala Gly His Val Leu Ser Thr Pro Ile Phe Ile Val Gln Asp  
 20 25 30  
 Ala Cys Gly Ile Asp Glu Glu Ala Cys Lys Asn Pro Pro Pro Arg Pro  
 35 40 45  
 Phe Ser Ala Gln Val Gln Tyr Leu Lys Val Asn Asp Ala Lys Phe Lys  
 50 55 60  
 Lys Leu Pro His Gln Thr Ile Gly Tyr Arg Gln Tyr Asp Gly Thr Phe  
 65 70 75 80  
 Leu Cys Thr Leu Pro Ile Thr Glu His Ser Gly Leu Leu Phe Ser Thr  
 85 90 95  
 Gly Tyr Ile Gly Ala Asp Ile Gln Trp Lys Ser Ser Leu Pro Ile Ser  
 100 105 110  
 Glu Thr Asp Pro Asn Gly Leu Gly Trp Ala Thr Phe Gln Asp Thr Ser  
 115 120 125  
 Phe Tyr Asn Tyr Val Leu Leu Ser Leu Gly Ala Tyr Thr Leu Ser Xaa  
 130 135 140  
 Lys Lys Leu Ala Val Val Tyr His Ser Phe Trp Ala Cys Gly Ser  
 145 150 155

&lt;210&gt;463

&lt;211&gt;186

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;463

Glu Leu Ile His Ser Pro Leu Lys Asn Trp Gln Trp Ser Ile Ile Leu  
 1 5 10 15  
 Ser Gly Leu Val Asp Pro Lys Asn Ile Glu Met Gly Tyr Gly Leu Tyr  
 20 25 30  
 Gln Gly Val Leu Ser Gly Lys Tyr Gln Ala Thr Glu Lys Leu Ser Ala  
 35 40 45  
 Ile Phe Gly Val Ile Asn Glu Thr Gly Leu His Gln Glu Lys Ala Trp  
 50 55 60  
 Pro Leu Val Gly Val Ser Tyr Lys Ala Thr Asp Gln Leu Thr Leu Asn  
 65 70 75 80  
 Cys Ile Tyr Pro Val Asn Phe Ser Ile Asp Tyr Arg Ser Thr Ser Val  
 85 90 95  
 Cys Asn Leu Gly Leu Ala Tyr Arg Leu Thr Arg Phe Arg Lys Lys Leu  
 100 105 110  
 Tyr Lys Asn His Leu Ile Ser Ser Arg Gly Ile Phe Glu Tyr Gln Gly  
 115 120 125  
 Arg Glu Ile Glu Ala Asn Val Lys Leu Thr Pro Trp Pro Gly Ser Phe  
 130 135 140  
 Ile Lys Gly Phe Tyr Gly Trp Ser Ile Gly Asn Asp Ile Ser Ile Ala  
 145 150 155 160  
 Asp Asp His Asn Asn Asn Lys Thr Ser His Thr Phe Lys Thr Ser Ala  
 165 170 175  
 Phe Phe Gly Gly Ser Ala Val Met Asn Phe  
 180 185

&lt;210&gt;464

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;464

Val Asp Ser Met Ser Gln Pro Pro Ile Asn Pro Leu Gly Gln Pro Gln  
 1 5 10 15

Val Pro Ala Ala Ala Ser Pro Ser Gly Gln Pro Ser Val Val Lys Arg  
 20 25 30  
 Leu Lys Thr Ser Ser Thr Gly Leu Phe Lys Arg Phe Ile Thr Val Pro  
 35 40 45  
 Asp Lys Tyr Pro Lys Met Arg Tyr Val Tyr Asp Thr Gly Ile Ile Ala  
 50 55 60  
 Leu Ala Ala Ile Ala Ile Leu Ser Ile Leu Leu Thr Ala Ser Gly Asn  
 65 70 75 80  
 Ser Leu Met Leu Tyr Ala Leu Ala Pro Ala Leu Ala Leu Gly Ala Leu  
 85 90 95  
 Gly Val Thr Leu Leu Ile Ser Asp Ile Leu Asp Ser Pro Lys Pro Arg  
 100 105 110  
 Lys Ser Val Arg Gln Ser Leu Leu Ser Ser Phe Leu Ser Leu Tyr  
 115 120 125

&lt;210&gt;465

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;465

Tyr Ser Gly Gln Ser Glu Ala Lys Lys Ile Gly Glu Ala Ile Thr Ala  
 1 5 10 15  
 Ile Val Val Pro Ile Ile Val Leu Ala Ile Ala Ala Gly Leu Ile Ala  
 20 25 30  
 Gly Ala Phe Val Ala Ser Ser Gly Thr Met Leu Val Phe Ala Asn Pro  
 35 40 45  
 Met Phe Val Met Gly Leu Ile Thr Val Gly Leu Tyr Phe Met Ser Leu  
 50 55 60  
 Asn Lys Leu Thr Leu Asp Tyr Phe Arg Arg Glu His Leu Leu Arg Met  
 65 70 75 80  
 Glu Lys Lys Thr Gln Glu Thr Ala Asp Leu Phe  
 85 90

&lt;210&gt;466

&lt;211&gt;1132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;466

Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe  
 1 5 10 15  
 Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp  
 20 25 30  
 Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu  
 35 40 45  
 Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser  
 50 55 60  
 Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr  
 65 70 75 80  
 Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val  
 85 90 95  
 Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr  
 100 105 110  
 Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser  
 115 120 125  
 Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr  
 130 135 140  
 Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr  
 145 150 155 160  
 Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr  
 165 170 175  
 Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn  
 180 185 190  
 Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr  
 195 200 205  
 Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr  
 210 215 220

Asp	Lys	Gly	Gly	Gly	Ile	Tyr	Ser	Lys	Glu	Lys	Asp	Ser	Thr	Leu	Asp	225	230	235	240
Ala	Asn	Thr	Gly	Val	Val	Thr	Phe	Lys	Ser	Asn	Thr	Ala	Lys	Thr	Gly	245	250	255	
Gly	Ala	Trp	Ser	Ser	Asp	Asp	Asn	Leu	Ala	Leu	Thr	Gly	Asn	Thr	Gln	260	265	270	
Val	Leu	Phe	Gln	Glu	Asn	Lys	Thr	Thr	Gly	Ser	Ala	Ala	Gln	Ala	Asn	275	280	285	
Asn	Pro	Glu	Gly	Cys	Gly	Gly	Ala	Ile	Cys	Cys	Tyr	Leu	Ala	Thr	Ala	290	295	300	
Thr	Asp	Lys	Thr	Gly	Leu	Ala	Ile	Ser	Gln	Asn	Gln	Glu	Met	Ser	Phe	305	310	315	320
Thr	Ser	Asn	Thr	Thr	Thr	Ala	Asn	Gly	Gly	Ala	Ile	Tyr	Ala	Thr	Lys	325	330	335	
Cys	Thr	Leu	Asp	Gly	Asn	Thr	Thr	Leu	Thr	Phe	Asp	Gln	Asn	Thr	Ala	340	345	350	
Thr	Ala	Gly	Cys	Gly	Gly	Ala	Ile	Tyr	Thr	Glu	Thr	Glu	Asp	Phe	Ser	355	360	365	
Leu	Lys	Gly	Ser	Thr	Gly	Thr	Val	Thr	Phe	Ser	Thr	Asn	Thr	Ala	Lys	370	375	380	
Thr	Gly	Gly	Ala	Leu	Tyr	Ser	Lys	Glu	Asn	Ser	Ser	Leu	Thr	Gly	Asn	385	390	395	400
Thr	Asn	Leu	Leu	Phe	Ser	Gly	Asn	Lys	Ala	Thr	Gly	Pro	Ser	Asn	Ser	405	410	415	
Ser	Ala	Asn	Gln	Glu	Gly	Cys	Gly	Gly	Ala	Ile	Leu	Ser	Phe	Leu	Glu	420	425	430	
Ser	Ala	Ser	Val	Ser	Thr	Lys	Lys	Gly	Leu	Trp	Ile	Glu	Asp	Asn	Glu	435	440	445	
Asn	Val	Ser	Leu	Ser	Gly	Asn	Thr	Ala	Thr	Val	Ser	Gly	Gly	Ala	Ile	450	455	460	
Tyr	Ala	Thr	Lys	Cys	Ala	Leu	His	Gly	Asn	Thr	Thr	Leu	Thr	Phe	Asp	465	470	475	480
Gly	Asn	Thr	Ala	Glu	Thr	Ala	Gly	Gly	Ala	Ile	Tyr	Thr	Glu	Thr	Glu	485	490	495	
Asp	Phe	Thr	Leu	Thr	Gly	Ser	Thr	Gly	Thr	Val	Thr	Phe	Ser	Thr	Asn	500	505	510	
Thr	Ala	Lys	Thr	Ala	Gly	Ala	Leu	His	Thr	Lys	Gly	Asn	Thr	Ser	Phe	515	520	525	
Thr	Lys	Asn	Lys	Ala	Leu	Val	Phe	Ser	Gly	Asn	Ser	Ala	Thr	Ala	Thr	530	535	540	
Ala	Thr	Thr	Thr	Thr	Asp	Gln	Glu	Gly	Cys	Gly	Gly	Ala	Ile	Leu	Cys	545	550	555	560
Asn	Ile	Ser	Glu	Ser	Asp	Ile	Ala	Thr	Lys	Ser	Leu	Thr	Leu	Thr	Glu	565	570	575	
Asn	Glu	Ser	Leu	Ser	Phe	Ile	Asn	Asn	Thr	Ala	Lys	Arg	Ser	Gly	Gly	580	585	590	
Gly	Ile	Tyr	Ala	Pro	Lys	Cys	Val	Ile	Ser	Gly	Ser	Glu	Ser	Ile	Asn	595	600	605	
Phe	Asp	Gly	Asn	Thr	Ala	Glu	Thr	Ser	Gly	Gly	Ala	Ile	Tyr	Ser	Lys	610	615	620	
Asn	Leu	Ser	Ile	Thr	Ala	Asn	Gly	Pro	Val	Ser	Phe	Thr	Asn	Asn	Ser	625	630	635	640
Gly	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ile	Ala	Asp	Ser	Gly	Glu	Leu	Ser	645	650	655	
Leu	Glu	Ala	Ile	Asp	Gly	Asp	Ile	Thr	Phe	Ser	Gly	Asn	Arg	Ala	Thr	660	665	670	
Glu	Gly	Thr	Ser	Thr	Pro	Asn	Ser	Ile	His	Leu	Gly	Ala	Gly	Ala	Lys	675	680	685	
Ile	Thr	Lys	Leu	Ala	Ala	Ala	Pro	Gly	His	Thr	Ile	Tyr	Phe	Tyr	Asp	690	695	700	
Pro	Ile	Thr	Met	Glu	Ala	Pro	Ala	Ser	Gly	Gly	Thr	Ile	Glu	Glu	Leu	705	710	715	720
Val	Ile	Asn	Pro	Val	Val	Lys	Ala	Ile	Val	Pro	Pro	Pro	Gln	Pro	Lys	725	730	735	

Asn Gly Pro Ile Ala Ser Val Pro Val Val Pro Val Ala Pro Ala Asn  
 740 745 750  
 Pro Asn Thr Gly Thr Ile Val Phe Ser Ser Gly Lys Leu Pro Ser Gln  
 755 760 765  
 Asp Ala Ser Ile Pro Ala Asn Thr Thr Thr Ile Leu Asn Gln Lys Ile  
 770 775 780  
 Asn Leu Ala Gly Gly Asn Val Val Leu Lys Glu Gly Ala Thr Leu Gln  
 785 790 795 800  
 Val Tyr Ser Phe Thr Gln Gln Pro Asp Ser Thr Val Phe Met Asp Ala  
 805 810 815  
 Gly Thr Thr Leu Glu Thr Thr Thr Thr Asn Asn Thr Asp Gly Ser Ile  
 820 825 830  
 Asp Leu Lys Asn Leu Ser Val Asn Leu Asp Ala Leu Asp Gly Lys Arg  
 835 840 845  
 Met Ile Thr Ile Ala Val Asn Ser Thr Ser Gly Gly Leu Lys Ile Ser  
 850 855 860  
 Gly Asp Leu Lys Phe His Asn Asn Glu Gly Ser Phe Tyr Asp Asn Pro  
 865 870 875 880  
 Gly Leu Lys Ala Asn Leu Asn Leu Pro Phe Leu Asp Leu Ser Ser Thr  
 885 890 895  
 Ser Gly Thr Val Asn Leu Asp Asp Phe Asn Pro Ile Pro Ser Ser Met  
 900 905 910  
 Ala Ala Pro Asp Tyr Gly Tyr Gln Gly Ser Trp Thr Leu Val Pro Lys  
 915 920 925  
 Val Gly Ala Gly Gly Lys Val Thr Leu Val Ala Glu Trp Gln Ala Leu  
 930 935 940  
 Gly Tyr Thr Pro Lys Pro Glu Leu Arg Ala Thr Leu Val Pro Asn Ser  
 945 950 955 960  
 Leu Trp Asn Ala Tyr Val Asn Ile His Ser Ile Gln Gln Glu Ile Ala  
 965 970 975  
 Thr Ala Met Ser Asp Ala Pro Ser His Pro Gly Ile Trp Ile Gly Gly  
 980 985 990  
 Ile Gly Asn Ala Phe His Gln Asp Lys Gln Lys Glu Asn Ala Gly Phe  
 995 1000 1005  
 Arg Leu Ile Ser Arg Gly Tyr Ile Val Gly Gly Ser Met Thr Thr Pro  
 1010 1015 1020  
 Gln Glu Tyr Thr Phe Ala Val Ala Phe Ser Gln Leu Phe Gly Lys Ser  
 1025 1030 1035 1040  
 Lys Asp Tyr Val Val Ser Asp Ile Lys Ser Gln Val Tyr Ala Gly Ser  
 1045 1050 1055  
 Leu Cys Ala Gln Ser Ser Tyr Val Ile Pro Leu His Ser Ser Leu Arg  
 1060 1065 1070  
 Arg His Val Leu Ser Lys Val Leu Pro Glu Leu Pro Gly Glu Thr Pro  
 1075 1080 1085  
 Leu Val Leu His Gly Gln Val Ser Tyr Gly Arg Asn His His Asn Met  
 1090 1095 1100  
 Thr Thr Lys Leu Ala Asn Asn Thr Gln Gly Lys Ser Asp Trp Asp Ser  
 1105 1110 1115 1120  
 His Ser Ser Leu Leu Lys Ser Val Val Leu Phe Leu  
 1125 1130

&lt;210&gt;467

&lt;211&gt;154

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;467

Phe Ala Val Glu Val Gly Gly Ser Leu Pro Val Asp Leu Asn Tyr Arg  
 1 5 10 15  
 Tyr Leu Thr Ser Tyr Ser Pro Tyr Val Lys Leu Gln Val Val Ser Val  
 20 25 30  
 Asn Gln Lys Gly Phe Gln Glu Val Ala Ala Asp Pro Arg Ile Phe Asp  
 35 40 45  
 Ala Ser His Leu Val Asn Val Ser Ile Pro Met Gly Leu Thr Phe Lys  
 50 55 60  
 His Glu Ser Ala Lys Pro Pro Ser Ala Leu Leu Leu Thr Leu Gly Tyr

```

      65              70              75              80
Ala Val Asp Ala Tyr Arg Asp His Pro His Cys Leu Thr Ser Leu Thr
      85              90
Asn Gly Thr Ser Trp Ser Thr Phe Ala Thr Asn Leu Ser Arg Gln Ala
      100              105              110
Phe Phe Ala Glu Ala Ser Gly His Leu Lys Leu Leu His Gly Leu Asp
      115              120              125
Cys Phe Ala Ser Gly Ser Cys Glu Leu Arg Ser Ser Ser Arg Ser Tyr
      130              135              140
Asn Ala Asn Cys Gly Thr Arg Tyr Ser Phe
145              150
<210>468
<211>671
<212>PRT
<213>Chlamydia pneumoniae
<400>468
Met Lys Ser Ser Val Ser Trp Leu Phe Phe Ser Ser Ile Pro Leu Phe
  1              5              10              15
Ser Ser Leu Ser Ile Val Ala Ala Glu Val Thr Leu Asp Ser Ser Asn
      20              25              30
Asn Ser Tyr Asp Gly Ser Asn Gly Thr Thr Phe Thr Val Phe Ser Thr
      35              40              45
Thr Asp Ala Ala Ala Gly Thr Thr Tyr Ser Leu Leu Ser Asp Val Ser
      50              55              60
Phe Gln Asn Ala Gly Ala Leu Gly Ile Pro Leu Ala Ser Gly Cys Phe
      65              70              75              80
Leu Glu Ala Gly Gly Asp Leu Thr Phe Gln Gly Asn Gln His Ala Leu
      85              90              95
Lys Phe Ala Phe Ile Asn Ala Gly Ser Ser Ala Gly Thr Val Ala Ser
      100              105              110
Thr Ser Ala Ala Asp Lys Asn Leu Leu Phe Asn Asp Phe Ser Arg Leu
      115              120              125
Ser Ile Ile Ser Cys Pro Ser Leu Leu Leu Ser Pro Thr Gly Gln Cys
      130              135              140
Ala Leu Lys Ser Val Gly Asn Leu Ser Leu Thr Gly Asn Ser Gln Ile
145              150              155              160
Ile Phe Thr Gln Asn Phe Ser Ser Asp Asn Gly Gly Val Ile Asn Thr
      165              170              175
Lys Asn Phe Leu Leu Ser Gly Thr Ser Gln Phe Ala Ser Phe Ser Arg
      180              185              190
Asn Gln Ala Phe Thr Gly Lys Gln Gly Gly Val Val Tyr Ala Thr Gly
      195              200              205
Thr Ile Thr Ile Glu Asn Ser Pro Gly Ile Val Ser Phe Ser Gln Asn
      210              215              220
Leu Ala Lys Gly Ser Gly Gly Ala Leu Tyr Ser Thr Asp Asn Cys Ser
225              230              235              240
Ile Thr Asp Asn Phe Gln Val Ile Phe Asp Gly Asn Ser Ala Trp Glu
      245              250              255
Ala Ala Gln Ala Gln Gly Gly Ala Ile Cys Cys Thr Thr Thr Asp Lys
      260              265              270
Thr Val Thr Leu Thr Gly Asn Lys Asn Leu Ser Phe Thr Asn Asn Thr
      275              280              285
Ala Leu Thr Tyr Gly Gly Ala Ile Ser Gly Leu Lys Val Ser Ile Ser
      290              295              300
Ala Gly Gly Pro Thr Leu Phe Gln Ser Asn Ile Ser Gly Ser Ser Ala
305              310              315              320
Gly Gln Gly Gly Gly Gly Ala Ile Asn Ile Ala Ser Ala Gly Glu Leu
      325              330              335
Ala Leu Ser Ala Thr Ser Gly Asp Ile Thr Phe Asn Asn Asn Gln Val
      340              345              350
Thr Asn Gly Ser Thr Ser Thr Arg Asn Ala Ile Asn Ile Ile Asp Thr
      355              360              365
Ala Lys Val Thr Ser Ile Arg Ala Ala Thr Gly Gln Ser Ile Tyr Phe
370              375              380

```



Tyr Asp Pro Ile Thr Asn Pro Gly Thr Ala Ala Ser Thr Asp Thr Leu  
 385 390 395 400  
 Asn Leu Asn Leu Ala Asp Ala Asn Ser Glu Ile Glu Tyr Gly Gly Ala  
 405 410 415  
 Ile Val Phe Ser Gly Glu Lys Leu Ser Pro Thr Glu Lys Ala Ile Ala  
 420 425 430  
 Ala Asn Val Thr Ser Thr Ile Arg Gln Pro Ala Val Leu Ala Arg Gly  
 435 440 445  
 Asp Leu Val Leu Arg Asp Gly Val Thr Val Thr Phe Lys Asp Leu Thr  
 450 455 460  
 Gln Ser Pro Gly Ser Arg Ile Leu Met Asp Gly Gly Thr Thr Leu Ser  
 465 470 475 480  
 Ala Lys Glu Ala Asn Leu Ser Leu Asn Gly Leu Ala Val Asn Leu Ser  
 485 490 495  
 Ser Leu Asp Gly Thr Asn Lys Ala Ala Leu Lys Thr Glu Ala Ala Asp  
 500 505 510  
 Lys Asn Ile Ser Leu Ser Gly Thr Ile Ala Leu Ile Asp Thr Glu Gly  
 515 520 525  
 Ser Phe Tyr Glu Asn His Asn Leu Lys Ser Ala Ser Thr Tyr Pro Leu  
 530 535 540  
 Leu Glu Leu Thr Thr Ala Gly Ala Asn Gly Thr Ile Thr Leu Gly Ala  
 545 550 555 560  
 Leu Ser Thr Leu Thr Leu Gln Glu Pro Glu Thr His Tyr Gly Tyr Gln  
 565 570 575  
 Gly Asn Trp Gln Leu Ser Trp Ala Asn Ala Thr Ser Ser Lys Ile Gly  
 580 585 590  
 Ser Ile Asn Trp Thr Arg Thr Gly Tyr Ile Pro Ser Pro Glu Arg Lys  
 595 600 605  
 Ser Asn Leu Pro Leu Asn Ser Leu Trp Gly Asn Phe Ile Asp Ile Arg  
 610 615 620  
 Ser Ile Asn Gln Leu Ile Glu Thr Lys Ser Ser Gly Glu Pro Phe Glu  
 625 630 635 640  
 Arg Glu Tyr Gly Phe Gln Glu Leu Arg Ile Ser Ser Ile Glu Ile Leu  
 645 650 655  
 Cys Pro Pro Ala Met Val Ser Ala Ile Ser Ala Gly Val Met His  
 660 665 670

&lt;210&gt;469

&lt;211&gt;294

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;469

Val Trp Leu Ser Gly Ile Ala Asn Phe Phe Tyr Arg Asp Ser Met Pro  
 1 5 10 15  
 Thr Arg His Gly Phe Arg His Ile Ser Gly Gly Tyr Ala Leu Gly Ile  
 20 25 30  
 Thr Ala Thr Thr Pro Ala Glu Asp Gln Leu Thr Phe Ala Phe Cys Gln  
 35 40 45  
 Leu Phe Ala Arg Asp Arg Asn His Ile Thr Gly Lys Asn His Gly Asp  
 50 55 60  
 Thr Tyr Gly Ala Ser Leu Tyr Phe His His Thr Glu Gly Leu Phe Asp  
 65 70 75 80  
 Ile Ala Asn Phe Leu Trp Gly Lys Ala Thr Arg Ala Pro Trp Val Leu  
 85 90 95  
 Ser Glu Ile Ser Gln Ile Ile Pro Leu Ser Phe Asp Ala Lys Phe Ser  
 100 105 110  
 Tyr Leu His Thr Asp Asn His Met Lys Thr Tyr Tyr Thr Asp Asn Ser  
 115 120 125  
 Ile Ile Lys Gly Ser Trp Arg Asn Asp Ala Phe Cys Ala Asp Leu Gly  
 130 135 140  
 Ala Ser Leu Pro Phe Val Ile Ser Val Pro Tyr Leu Leu Lys Glu Val  
 145 150 155 160  
 Glu Pro Phe Val Lys Val Gln Tyr Ile Tyr Ala His Gln Gln Asp Phe  
 165 170 175  
 Tyr Glu Arg Tyr Ala Glu Gly Arg Ala Phe Asn Lys Ser Glu Leu Ile

```

      180      185      190
Asn Val Glu Ile Pro Ile Gly Val Thr Phe Glu Arg Asp Ser Lys Ser
      195      200      205
Glu Lys Gly Thr Tyr Asp Leu Thr Leu Met Tyr Ile Leu Asp Ala Tyr
      210      215      220
Arg Arg Asn Pro Lys Cys Gln Thr Ser Leu Ile Ala Ser Asp Ala Asn
      225      230      235      240
Trp Met Ala Tyr Gly Thr Asn Leu Ala Arg Gln Gly Phe Ser Val Arg
      245      250      255
Ala Ala Asn His Phe Gln Val Asn Pro His Met Glu Ile Phe Gly Gln
      260      265      270
Phe Ala Phe Glu Val Arg Ser Ser Ser Arg Asn Tyr Asn Thr Asn Leu
      275      280      285
Gly Ser Lys Phe Cys Phe
      290
<210>470
<211>930
<212>PRT
<213>Chlamydia pneumoniae
<400>470
Met Lys Ile Pro Leu His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr
  1      5      10      15
Pro Ile Leu Leu Ser Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser
      20      25      30
Pro Thr Asp Ser Phe Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys
      35      40      45
Ser Thr Ala Asp Ala Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val
      50      55      60
Tyr Ile Asn Asp Ala Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe
      65      70      75      80
Thr Glu Thr Thr Gly Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe
      85      90      95
Ser Phe Asn Thr Val Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser
      100      105      110
Thr Thr Ala Asp Lys Ala Leu Thr Phe Thr Gly Phe Ser Asn Leu Ser
      115      120      125
Phe Ile Ala Ala Pro Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu
      130      135      140
Ser Ser Ala Gly Ala Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe
      145      150      155      160
Ser Gln Asn Val Ser Asn Glu Ala Asn Asn Gly Gly Ala Ile Thr
      165      170      175
Ala Lys Thr Leu Ser Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr
      180      185      190
Ser Asn Ser Ala Lys Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala
      195      200      205
Ala Ser Ile Ser Gly Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys
      210      215      220
Gly Glu Thr Gly Gly Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile
      225      230      235      240
Thr Gln Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala
      245      250      255
Ala Gly Lys Gly Gly Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro
      260      265      270
Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser
      275      280      285
Ser Val Thr Gln Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser
      290      295      300
Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala
      305      310      315      320
Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser
      325      330      335
Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr
      340      345      350

```

Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser  
 355 360 365  
 Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr  
 370 375 380  
 Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu  
 385 390 395 400  
 Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr  
 405 410 415  
 Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala  
 420 425 430  
 Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly  
 435 440 445  
 Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr  
 450 455 460  
 Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys  
 465 470 475 480  
 Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser  
 485 490 495  
 Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn  
 500 505 510  
 Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly  
 515 520 525  
 Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu  
 530 535 540  
 Val Val Phe Thr Ala Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala  
 545 550 555 560  
 Leu Leu Thr Ser Pro Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln  
 565 570 575  
 Gly His Trp Glu Ala Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly  
 580 585 590  
 Thr Met Thr Trp Val Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg  
 595 600 605  
 Ala Ser Val Val Pro Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg  
 610 615 620  
 Thr Leu Gln Gln Ile Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln  
 625 630 635 640  
 Arg Gly Leu Trp Ala Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys  
 645 650 655  
 Ser Gly Thr Asn Gln Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val  
 660 665 670  
 Gly Gly Ser Ala Glu Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe  
 675 680 685  
 Cys Gln Leu Phe Gly Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr  
 690 695 700  
 Ser His Asn Tyr Leu Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu  
 705 710 715 720  
 Gly Gly Leu Pro Met Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys  
 725 730 735  
 Asp Ile Pro Leu Ile Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys  
 740 745 750  
 Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser  
 755 760 765  
 Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu  
 770 775 780  
 Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu  
 785 790 795 800  
 Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly  
 805 810 815  
 Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile  
 820 825 830  
 Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn  
 835 840 845  
 Phe Glu Ile Ser Leu Ala Tyr Ile Gly Asp Val Tyr Arg Lys Asn Pro  
 850 855 860

Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu  
 865 870 875 880  
 Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His  
 885 890 895  
 Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu  
 900 905 910  
 Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr  
 915 920 925  
 Ser Phe  
 930

&lt;210&gt;471

&lt;211&gt;138

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;471

Ile Ala Pro Pro Asn Phe Phe Ala Leu Leu Leu Val Lys Val Ile Glu  
 1 5 10 15  
 Glu Val Phe Pro Glu Ile Glu Arg Val Phe Ala Val Ile Ala Pro Pro  
 20 25 30  
 Leu Leu Leu Ala Ser Leu Glu Thr Phe Trp Leu Lys Arg Ile Val Pro  
 35 40 45  
 Leu Ser Val Arg Phe Lys Ala Pro Ala Glu Leu Lys Val Leu Phe Pro  
 50 55 60  
 Glu Ala Thr Val Val Pro Gly Ala Ala Met Lys Glu Arg Leu Glu Asn  
 65 70 75 80  
 Pro Val Asn Val Arg Ala Leu Ser Ala Val Val Leu Ala Ala Pro  
 85 90 95  
 Ala Phe Glu Pro Ala Ser Thr Val Leu Asn Glu Asn Glu Tyr Pro Phe  
 100 105 110  
 Pro Val Asn Val Arg Ser Pro Val Val Ser Val Lys Gln Gln Pro Val  
 115 120 125  
 Asn Ala Val Pro Phe Pro Ala Ser Phe Ile  
 130 135

&lt;210&gt;472

&lt;211&gt;927

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;472

Met Lys Ser Ser Leu His Trp Phe Leu Ile Ser Ser Ser Leu Ala Leu  
 1 5 10 15  
 Pro Leu Ser Leu Asn Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn  
 20 25 30  
 Leu Gly Pro Thr Asn Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro  
 35 40 45  
 Ala Gln Thr Thr Asn Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp  
 50 55 60  
 Val Ser Ile Thr Asn Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys  
 65 70 75 80  
 Phe Lys Glu Thr Thr Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln  
 85 90 95  
 Phe Leu Leu Gln Asn Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn  
 100 105 110  
 Thr Ala Ala Asn Lys Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser  
 115 120 125  
 Leu Ile Gln Thr Thr Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser  
 130 135 140  
 Thr Gly Ala Cys Ser Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln  
 145 150 155 160  
 Asn Phe Ser Asn Asp Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser  
 165 170 175  
 Leu Ser Leu Asn Pro Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln  
 180 185 190  
 Lys Gly Gly Ala Leu Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr  
 195 200 205

Leu Asn Ser Ala Ser Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly  
 210 215 220  
 Ala Ile Tyr Thr Glu Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile  
 225 230 235 240  
 Ser Phe Ile Asn Asn Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala  
 245 250 255  
 Ile Tyr Cys Ser Ser Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser  
 260 265 270  
 Asp Asn Gly Glu Leu Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly  
 275 280 285  
 Gly Ala Ile Tyr Thr Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr  
 290 295 300  
 Leu Phe Lys Asn Asn Ser Ala Ile Asp Thr Ala Ala Pro Leu Gly Gly  
 305 310 315 320  
 Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly  
 325 330 335  
 Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser  
 340 345 350  
 Ser Gln Thr Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala  
 355 360 365  
 Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr  
 370 375 380  
 Asp Pro Ile Thr Thr Ser Ile Thr Ala Ala Leu Ser Asp Ala Leu Asn  
 385 390 395 400  
 Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile  
 405 410 415  
 Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp  
 420 425 430  
 Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln  
 435 440 445  
 Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln  
 450 455 460  
 Ser Pro Gly Ser Thr Leu Met Asp Ala Gly Thr Thr Leu Glu Thr  
 465 470 475 480  
 Ala Asp Gly Ser Leu Ser Ile Ile Cys Ser Gln Cys Arg Phe Leu Lys  
 485 490 495  
 Arg Asp Gln Glu Xaa Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr Val  
 500 505 510  
 Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val Tyr  
 515 520 525  
 Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr Leu  
 530 535 540  
 Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala Asp  
 545 550 555 560  
 Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp Ala  
 565 570 575  
 Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr Leu  
 580 585 590  
 Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly Thr  
 595 600 605  
 Leu Val Ala Asn Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile  
 610 615 620  
 Gln Gln Leu Val Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg Gly  
 625 630 635 640  
 Ile Trp Cys Glu Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr Lys  
 645 650 655  
 Ile Asn Lys Gly Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly Ala  
 660 665 670  
 Thr Thr Thr Leu Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys Gln  
 675 680 685  
 Leu Phe Gly Lys Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala Ser  
 690 695 700  
 Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser Ser  
 705 710 715 720

Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro Val  
 725 730 735  
 Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met Lys  
 740 745 750  
 Thr Tyr Tyr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn Asp  
 755 760 765  
 Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu Ser  
 770 775 780  
 His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu Ala  
 785 790 800  
 Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu Val  
 805 810 815  
 Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile Gly  
 820 825 830  
 Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu Ala  
 835 840 845  
 Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys Thr  
 850 855 860  
 Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr Asn  
 865 870 875 880  
 Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala Phe  
 885 890 895  
 Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg Gly  
 900 905 910  
 Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe  
 915 920 925  
 <210>473  
 <211>393  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>473  
 Phe Ile Gln Pro Ser Arg Arg Glu Ile His Glu Trp Lys Cys Ile Leu  
 1 5 10 15  
 Leu Gly Ser Ser Leu Arg Met Glu Met Met Ser Pro Phe Gln Gln Pro  
 20 25 30  
 Glu Gln Cys His Phe Asp Val Val Gly Ser Phe Leu Arg Pro Glu Ser  
 35 40 45  
 Leu Thr Arg Ala Arg Ser Asp Phe Glu Glu Gly Arg Ile Val Tyr Glu  
 50 55 60  
 Gln Met Arg Val Val Glu Asp Ala Ala Ile Arg Asn Leu Ile Lys Lys  
 65 70 75 80  
 Gln Thr Glu Ala Gly Leu Ile Phe Phe Thr Asp Gly Glu Phe Arg Arg  
 85 90 95  
 Tyr Ser Trp Asp Phe Asp Phe Met Trp Gly Phe His Gly Val Asp Arg  
 100 105 110  
 Arg Arg Asp Ser Asn Asp Pro Glu Ile Gly Val Tyr Leu Lys Asp Lys  
 115 120 125  
 Ile Ser Val Ser Lys His Pro Phe Ile Glu His Phe Glu Phe Val Lys  
 130 135 140  
 Thr Phe Glu Lys Gly Asn Ala Lys Ala Lys Gln Thr Ile Pro Ser Pro  
 145 150 155 160  
 Ser Gln Phe Phe His Glu Met Ile Phe Ala Pro Asn Leu Lys Asn Thr  
 165 170 175  
 Arg Lys Phe Tyr Pro Thr Asn Gln Glu Leu Ile Asp Asp Ile Val Phe  
 180 185 190  
 Tyr Tyr Arg Gln Val Ile Gln Asp Leu Tyr Ala Ala Gly Cys Arg Asn  
 195 200 205  
 Leu Gln Leu Asp Asp Cys Ala Trp Cys Arg Leu Leu Asp Ile Arg Ala  
 210 215 220  
 Pro Ser Trp Tyr Gly Val Asp Ser His Asp Arg Leu Gln Glu Ile Leu  
 225 230 235 240  
 Glu Gln Phe Leu Trp Ile His Asn Leu Val Met Lys Asp Arg Pro Glu  
 245 250 255  
 Asp Leu Phe Val Ser Leu His Val Cys Arg Gly Asp Tyr Gln Ala Glu

260 265 270  
 Phe Phe Ser Arg Arg Ala Tyr Asp Ser Ile Glu Glu Pro Leu Phe Ala  
 275 280 285  
 Lys Thr Asp Val Asp Ser Tyr His Tyr Tyr Trp Ala Leu Asp Asp Lys  
 290 295 300  
 Tyr Ser Gly Gly Ala Glu Pro Leu Ala Tyr Val Ser Gly Glu Lys His  
 305 310 315 320  
 Val Cys Leu Gly Leu Ile Ser Ser Asn His Ser Cys Ile Glu Asp Arg  
 325 330 335  
 Asp Ala Val Val Ser Arg Ile Tyr Glu Ala Ala Ser Tyr Ile Pro Leu  
 340 345 350  
 Glu Arg Leu Ser Leu Ser Pro Gln Cys Gly Phe Ala Ser Cys Glu Gly  
 355 360 365  
 Asp His Arg Met Thr Glu Glu Glu Gln Trp Lys Lys Ile Ala Phe Val  
 370 375 380  
 Lys Glu Ile Ala Lys Glu Ile Trp Gly  
 385 390  
 <210>474  
 <211>643  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>474  
 Leu Met Ala Glu Pro Phe Met Leu Arg Ser Leu His Trp Leu Pro Gly  
 1 5 10 15  
 Gly Gly Gly Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr  
 20 25 30  
 Ala Gly Asn Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser  
 35 40 45  
 Leu Ser Ala Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val  
 50 55 60  
 Ala Thr Thr Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser  
 65 70 75 80  
 Thr Ala Lys Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe  
 85 90 95  
 Phe Tyr Asp Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr  
 100 105 110  
 Leu Asn Leu Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly  
 115 120 125  
 Ser Ile Val Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val  
 130 135 140  
 Ala Asp Asn Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala  
 145 150 155 160  
 Gly Asn Leu Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe  
 165 170 175  
 Thr Gln Thr Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu  
 180 185 190  
 Lys Ala Ser Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val  
 195 200 205  
 Asp Ser Leu Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala  
 210 215 220  
 Ser Lys Asn Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln  
 225 230 235 240  
 Gly Asn Ala Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser  
 245 250 255  
 Phe Val Gln Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro  
 260 265 270  
 Ala Val Pro Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr  
 275 280 285  
 Trp Gly Met Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys  
 290 295 300  
 Thr Ala Thr Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu  
 305 310 315 320  
 Arg Gln Gly Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp  
 325 330 335

Ile Gln Ala Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys  
 340 345 350  
 Ser Asp Arg Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys  
 355 360 365  
 Asp Lys Lys Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr  
 370 375 380  
 Ala Ile Gly Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe  
 385 390 395 400  
 Ala Phe Cys Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys  
 405 410 415  
 Asn His Thr Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr  
 420 425 430  
 Glu Cys Ser Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser  
 435 440 445  
 Trp Ser His Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His  
 450 455 460  
 Val Ser Asn Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys  
 465 470 475 480  
 Gly Ser Trp Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser  
 485 490 495  
 His Ser Tyr Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr  
 500 505 510  
 Ile Lys Leu Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys  
 515 520 525  
 Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn Leu Ser  
 530 535 540  
 Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn Asp Phe  
 545 550 555 560  
 Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg Asn Asp  
 565 570 575  
 Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr  
 580 585 590  
 Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser  
 595 600 605  
 His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe  
 610 615 620  
 Glu Val Arg Gly Ser Ser Arg Ile Tyr Asn Val Asp Leu Gly Gly Lys  
 625 630 635 640  
 Phe Gln Phe

&lt;210&gt;475

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;475

Lys Lys Met Leu Cys Pro Asp Ile Ala Arg Lys Phe Val Ile Phe Ala  
 1 5 10 15  
 Val Asp Pro Met Ser Ile Glu Phe Leu Phe Val Val Cys Gly Val Val  
 20 25 30  
 Ala Thr Met Ala Phe Pro Leu Lys Val Met Ser Pro Ala Ser Ala Glu  
 35 40 45  
 Arg Leu His Ser Pro Ala Ala Ser Ile Glu Met Ala Pro Pro Leu Pro  
 50 55 60  
 Ala Val Val Pro Trp Thr Ile Leu Leu Glu Lys Glu Ile Pro Pro Pro  
 65 70 75 80  
 Pro Pro Gly Ser Gln Cys Lys Leu Leu Ser Ile Asn Gly Ser Ala Ile  
 85 90 95  
 Ser Tyr Ser Leu Val Ser  
 100

&lt;210&gt;476

&lt;211&gt;174

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;476



Ser Gln Pro Pro Gln Glu Lys Val Gln Leu Asn Val Glu Gly Ile Leu  
 1 5 10 15  
 His Leu Ile Thr Met Glu Leu Phe Tyr Leu Asn Lys Ile Thr Val Arg  
 20 25 30  
 Lys Met Ala Asp Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn Ser Thr  
 35 40 45  
 Gly Ser Ile Ser Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly Lys Lys  
 50 55 60  
 Gly Gly Ala Ile Cys Ala Thr Gly Thr Val Asp Ile Thr Asn Asn Thr  
 65 70 75 80  
 Ala Pro Thr Leu Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly Gly Ala  
 85 90 95  
 Ile Asn Ser Thr Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser Leu Val  
 100 105 110  
 Phe Ser Glu Asn Ser Val Thr Ala Thr Ala Gly Asn Gly Gly Ala Leu  
 115 120 125  
 Ser Gly Asp Ala Asp Val Thr Ile Ser Gly Asn Gln Ser Val Thr Phe  
 130 135 140  
 Ser Gly Asn Gln Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala Lys Lys  
 145 150 155 160  
 Leu Thr Leu Ala Ser Gly Gly Gly Gly Gly Tyr Leu Leu Phe  
 165 170

&lt;210&gt;477

&lt;211&gt;118

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;477

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys  
 1 5 10 15  
 Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly  
 20 25 30  
 Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro  
 35 40 45  
 Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr  
 50 55 60  
 Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser  
 65 70 75 80  
 Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser  
 85 90 95  
 Phe Leu Asn Xaa Lys Ser Ser Ala Glu Gly Ala Xaa Phe Leu Leu Gln  
 100 105 110  
 Leu Ile Lys Ile Cys Arg  
 115

&lt;210&gt;478

&lt;211&gt;949

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;478

Leu Ile Tyr Leu Phe Cys Phe Tyr Ile Asp Ala Asn Ser Ser Leu Lys  
 1 5 10 15  
 Asn Lys Ser Ile Thr Met Lys Thr Ser Ile Pro Trp Val Leu Val Ser  
 20 25 30  
 Ser Val Leu Ala Phe Ser Cys His Leu Gln Ser Leu Ala Asn Glu Glu  
 35 40 45  
 Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly Asn Ile Asp Ser Gly Thr  
 50 55 60  
 Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr Ser Leu Thr Gly Asp Val  
 65 70 75 80  
 Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro Leu Ser Asp Ser Cys Phe  
 85 90 95  
 Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu Gly Asn Gly His Ser Leu  
 100 105 110  
 Thr Phe Gly Phe Ile Asp Ala Gly Thr His Ala Gly Ala Ala Ser  
 115 120 125

Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser Gly Phe Ser Leu Leu Ser  
 130 135 140  
 Phe Asp Ser Ser Pro Ser Thr Thr Val Thr Thr Gly Gln Gly Thr Leu  
 145 150 155 160  
 Ser Ser Ala Gly Gly Val Asn Leu Glu Asn Ile Arg Lys Leu Val Val  
 165 170 175  
 Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly Ala Ile Lys Gly Ala Ser  
 180 185 190  
 Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala Leu Phe Ser Asn Asn Ser  
 195 200 205  
 Ser Ser Thr Lys Gly Gly Ala Ile Ala Thr Thr Ala Gly Ala Arg Ile  
 210 215 220  
 Ala Asn Asn Thr Gly Xaa Val Arg Phe Leu Ser Asn Ile Ala Ser Thr  
 225 230 235 240  
 Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr Ser Ile Leu Ser Asn Asn  
 245 250 255  
 Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala Lys Thr Thr Gly Gly Ala  
 260 265 270  
 Ile Cys Asn Thr Lys Ala Ser Gly Ser Pro Glu Leu Ile Ile Ser Asn  
 275 280 285  
 Asn Lys Thr Leu Ile Phe Ala Ser Asn Val Ala Glu Thr Ser Gly Gly  
 290 295 300  
 Ala Ile His Ala Lys Lys Leu Ala Leu Ser Ser Gly Gly Phe Thr Glu  
 305 310 315 320  
 Phe Leu Arg Asn Asn Val Ser Ser Ala Thr Pro Lys Gly Gly Ala Ile  
 325 330 335  
 Ser Ile Asp Ala Ser Gly Glu Leu Ser Leu Ser Ala Glu Thr Gly Asn  
 340 345 350  
 Ile Thr Phe Val Arg Asn Thr Leu Thr Thr Thr Gly Ser Thr Asp Thr  
 355 360 365  
 Pro Lys Arg Asn Ala Ile Asn Ile Gly Ser Asn Gly Lys Phe Thr Glu  
 370 375 380  
 Leu Arg Ala Ala Lys Asn His Thr Ile Phe Phe Tyr Asp Pro Ile Thr  
 385 390 395 400  
 Ser Glu Gly Thr Ser Ser Asp Val Leu Lys Ile Asn Asn Gly Ser Ala  
 405 410 415  
 Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile Leu Phe Ser Gly Glu Thr  
 420 425 430  
 Leu Thr Ala Asp Glu Leu Lys Val Ala Asp Asn Leu Lys Ser Ser Phe  
 435 440 445  
 Thr Gln Pro Val Ser Leu Ser Gly Gly Lys Leu Leu Leu Gln Lys Gly  
 450 455 460  
 Val Thr Leu Glu Ser Thr Ser Phe Ser Gln Glu Ala Gly Ser Leu Leu  
 465 470 475 480  
 Gly Met Asp Ser Gly Thr Thr Leu Ser Thr Thr Ala Gly Ser Ile Thr  
 485 490 495  
 Ile Thr Asn Leu Gly Ile Asn Val Asp Ser Leu Gly Leu Lys Gln Pro  
 500 505 510  
 Val Ser Leu Thr Ala Lys Gly Ala Ser Asn Lys Val Ile Val Ser Gly  
 515 520 525  
 Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn Ile Tyr Glu Ser His Met  
 530 535 540  
 Phe Ser His Asp Gln Leu Phe Ser Leu Leu Lys Ile Thr Val Asp Ala  
 545 550 555 560  
 Asp Val Asp Thr Asn Val Asp Ile Ser Ser Leu Ile Pro Val Pro Ala  
 565 570 575  
 Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln Gly Gln Trp Asn Val Asn  
 580 585 590  
 Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys Glu Ala Thr Ala Thr Trp  
 595 600 605  
 Thr Lys Thr Gly Phe Val Pro Ser Pro Glu Arg Lys Ser Ala Leu Val  
 610 615 620  
 Cys Asn Thr Leu Trp Gly Val Phe Thr Asp Ile Arg Ser Leu Gln Gln  
 625 630 635 640

Leu Val Glu Ile Gly Ala Thr Gly Met Glu His Lys Gln Gly Phe Trp  
 645 650 655  
 Val Ser Ser Met Thr Asn Phe Leu His Lys Thr Gly Asp Glu Asn Arg  
 660 665 670  
 Lys Gly Phe Arg His Thr Ser Gly Gly Tyr Val Ile Gly Gly Ser Ala  
 675 680 685  
 His Thr Pro Lys Asp Asp Leu Phe Thr Phe Ala Phe Cys His Leu Phe  
 690 695 700  
 Ala Arg Asp Lys Asp Cys Phe Ile Ala His Asn Asn Ser Arg Thr Tyr  
 705 710 715 720  
 Gly Gly Thr Leu Phe Phe Lys His Ser His Thr Leu Gln Pro Gln Asn  
 725 730 735  
 Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser Glu Ser Ala Ile Glu Lys  
 740 745 750  
 Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp Val Gln Val Ser Phe Ser  
 755 760 765  
 His Ser Asp Asn Arg Met Glu Thr His Tyr Thr Ser Leu Pro Glu Ser  
 770 775 780  
 Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala Gly Gly Ile Gly Leu Asp  
 785 790 795 800  
 Leu Pro Phe Val Leu Ser Asn Pro His Pro Leu Phe Lys Thr Phe Ile  
 805 810 815  
 Pro Gln Met Lys Val Glu Met Val Tyr Val Ser Gln Asn Ser Phe Phe  
 820 825 830  
 Glu Ser Ser Ser Asp Gly Arg Gly Phe Ser Ile Gly Arg Leu Leu Asn  
 835 840 845  
 Leu Ser Ile Pro Val Gly Ala Lys Phe Val Gln Gly Asp Ile Gly Asp  
 850 855 860  
 Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe Val Ser Asp Val Tyr Arg  
 865 870 875 880  
 Asn Asn Pro Gln Ser Thr Ala Thr Leu Val Met Ser Pro Asp Ser Trp  
 885 890 895  
 Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln Ala Phe Leu Leu Arg Gly  
 900 905 910  
 Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys Glu Leu Phe Gly His Tyr  
 915 920 925  
 Ala Met Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp Val Gly  
 930 935 940  
 Thr Lys Leu Arg Phe  
 945  
 <210>479  
 <211>519  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>479  
 Phe Asn Glu Glu Thr Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser  
 1 5 10 15  
 Ala Leu Phe Leu Ala Leu Pro Ala Ala Gln Val Val Tyr Leu His  
 20 25 30  
 Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro  
 35 40 45  
 Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp  
 50 55 60  
 Val Arg Ile Ser Asn Val Lys His Asp Gln Glu Asp Ala Gly Val Phe  
 65 70 75 80  
 Ile Asn Arg Ser Gly Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe  
 85 90 95  
 Thr Phe His Asn Leu Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn  
 100 105 110  
 Arg Val Gly Asp Thr Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala  
 115 120 125  
 Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser  
 130 135 140  
 Leu Gly Ser Val Met Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly

145 150 155 160  
 Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu  
 165 170 175  
 Gly Ser Lys Ala Ser Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr  
 180 185 190  
 Leu Val Phe Arg Asp Asn Val Ser Gln Gly Tyr Gly Gly Ala Ile Ser  
 195 200 205  
 Thr His Asn Leu Thr Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn  
 210 215 220  
 Asn His Ala Tyr His Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile  
 225 230 235 240  
 Ala Pro Gly Gly Ser Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile  
 245 250 255  
 Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser  
 260 265 270  
 Ile His Leu Gln Ser Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser  
 275 280 285  
 Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His  
 290 295 300  
 Lys Ile Thr Asp Leu Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr  
 305 310 315 320  
 Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val  
 325 330 335  
 Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala  
 340 345 350  
 Gly Gly Thr Leu Ser Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser  
 355 360 365  
 Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr  
 370 375 380  
 Leu Leu Cys Ser Gly Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile  
 385 390 395 400  
 Glu Asp Thr Asp Asn Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys  
 405 410 415  
 Asp Ala Leu Val Ser Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr  
 420 425 430  
 Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro  
 435 440 445  
 Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu  
 450 455 460  
 Thr Thr Leu Glu Arg Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg  
 465 470 475 480  
 Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys  
 485 490 495  
 Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn  
 500 505 510  
 Pro Glu Ile Thr Ser Thr Pro  
 515

&lt;210&gt;480

&lt;211&gt;522

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;480

Asn Cys Val Leu Leu Tyr Leu Phe Phe Tyr Ser Leu Ser Leu Ile Cys  
 1 5 10 15  
 Arg Ile Ile Trp Phe His Leu Tyr Val Gln Met Lys Thr Ser Ile Arg  
 20 25 30  
 Lys Phe Leu Ile Ser Thr Thr Leu Ala Pro Cys Phe Ala Ser Thr Ala  
 35 40 45  
 Phe Thr Val Glu Val Ile Met Pro Ser Glu Asn Phe Asp Gly Ser Ser  
 50 55 60  
 Gly Lys Ile Phe Pro Tyr Thr Thr Leu Ser Asp Pro Arg Gly Thr Leu  
 65 70 75 80  
 Cys Ile Phe Ser Gly Asp Leu Tyr Ile Ala Asn Leu Asp Asn Ala Ile  
 85 90 95

Ser Arg Thr Ser Ser Ser Cys Phe Ser Asn Arg Ala Gly Ala Leu Gln  
 100 105 110  
 Ile Leu Gly Lys Gly Gly Val Phe Ser Phe Leu Asn Ile Arg Ser Ser  
 115 120 125  
 Ala Asp Gly Ala Ala Ile Ser Ser Val Ile Thr Gln Asn Pro Glu Leu  
 130 135 140  
 Cys Pro Leu Ser Phe Ser Gly Phe Ser Gln Met Ile Phe Asp Asn Cys  
 145 150 155 160  
 Glu Ser Leu Thr Ser Asp Thr Ser Ala Ser Asn Val Ile Pro His Ala  
 165 170 175  
 Ser Ala Ile Tyr Ala Thr Thr Pro Met Leu Phe Thr Asn Asn Asp Ser  
 180 185 190  
 Ile Leu Phe Gln Tyr Asn Arg Ser Ala Gly Phe Gly Ala Ala Ile Arg  
 195 200 205  
 Gly Thr Ser Ile Thr Ile Glu Asn Thr Lys Lys Ser Leu Leu Phe Asn  
 210 215 220  
 Gly Asn Gly Ser Ile Ser Asn Gly Gly Ala Leu Thr Gly Ser Ala Ala  
 225 230 235 240  
 Ile Asn Leu Ile Asn Asn Ser Ala Pro Val Ile Phe Ser Thr Asn Ala  
 245 250 255  
 Thr Gly Ile Tyr Gly Gly Ala Ile Tyr Leu Thr Gly Gly Ser Met Leu  
 260 265 270  
 Thr Ser Gly Asn Leu Ser Gly Val Leu Phe Val Asn Asn Ser Ser Arg  
 275 280 285  
 Ser Gly Gly Ala Ile Tyr Ala Asn Gly Asn Val Thr Phe Ser Asn Asn  
 290 295 300  
 Ser Asp Leu Thr Phe Gln Asn Asn Thr Ala Ser Pro Gln Asn Ser Leu  
 305 310 315 320  
 Pro Ala Pro Thr Pro Pro Pro Thr Pro Pro Ala Val Thr Pro Leu Leu  
 325 330 335  
 Gly Tyr Gly Gly Ala Ile Phe Cys Thr Pro Pro Ala Thr Pro Pro Pro  
 340 345 350  
 Thr Gly Val Ser Leu Thr Ile Ser Gly Glu Asn Ser Val Thr Phe Leu  
 355 360 365  
 Glu Asn Ile Ala Ser Glu Gln Gly Gly Ala Leu Tyr Gly Lys Lys Ile  
 370 375 380  
 Ser Ile Asp Ser Asn Lys Ser Thr Ile Phe Leu Gly Asn Thr Ala Gly  
 385 390 395 400  
 Lys Gly Gly Ala Ile Ala Ile Pro Glu Ser Gly Glu Leu Ser Leu Ser  
 405 410 415  
 Ala Asn Gln Gly Asp Ile Leu Phe Asn Lys Asn Leu Ser Ile Thr Ser  
 420 425 430  
 Gly Thr Pro Thr Arg Asn Ser Ile His Phe Gly Lys Asp Ala Lys Phe  
 435 440 445  
 Ala Thr Leu Gly Leu Arg Lys Ala Ile Pro Tyr Thr Ser Met Ile Arg  
 450 455 460  
 Leu His Leu Met Ile Tyr Leu Cys Ile Arg Ser Arg Tyr Cys Gly Arg  
 465 470 475 480  
 Gln Ser Gln Ser Gln Cys Arg Trp Cys Val Phe Arg Asp Tyr Cys Leu  
 485 490 495  
 Phe Arg Arg Asn Pro His Cys Tyr Arg Ser Ser Asn Pro Cys Lys Cys  
 500 505 510  
 Tyr Ile Tyr Ile Lys Pro Lys Ala Arg Thr  
 515 520  
 <210>481  
 <211>85  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>481  
 Arg Ala Pro Pro Cys Ser Glu Ala Met Phe Ser Arg Asn Val Thr Leu  
 1 5 10 15  
 Phe Ser Pro Asp Ile Val Arg Leu Thr Pro Val Gly Gly Gly Val Ala  
 20 25 30  
 Gly Gly Val Gln Lys Met Ala Pro Pro Tyr Pro Asn Lys Gly Val Thr

35 40 45  
 Ala Gly Gly Val Gly Gly Gly Val Gly Ala Gly Lys Glu Phe Cys Gly  
 50 55 60  
 Asp Ala Val Leu Phe Trp Lys Val Arg Ser Leu Leu Leu Glu Asn Val  
 65 70 75 80  
 Thr Phe Pro Leu Ala  
 85  
 <210>482  
 <211>530  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>482  
 Phe Ile Ser Ala Ser Ala Ala Ala Thr Val Val Val Asn Pro Lys Ala  
 1 5 10 15  
 Ser Ala Asp Gly Ala Tyr Ser Gly Thr Ile Val Phe Ser Gly Glu Thr  
 20 25 30  
 Leu Thr Ala Thr Glu Ala Ala Thr Pro Ala Asn Ala Thr Ser Thr Leu  
 35 40 45  
 Asn Gln Lys Leu Glu Leu Glu Gly Gly Thr Leu Ala Leu Arg Asn Gly  
 50 55 60  
 Ala Thr Leu Asn Val His Asn Phe Thr Gln Asp Glu Lys Ser Val Val  
 65 70 75 80  
 Ile Met Asp Ala Gly Thr Thr Leu Ala Thr Thr Asn Gly Ala Asn Asn  
 85 90 95  
 Thr Asp Gly Ala Ile Thr Leu Asn Lys Leu Val Ile Asn Leu Asp Ser  
 100 105 110  
 Leu Asp Gly Thr Lys Ala Ala Val Asn Val Gln Ser Thr Asn Gly  
 115 120 125  
 Ala Leu Thr Ile Ser Gly Thr Leu Gly Leu Val Lys Asn Ser Gln Asp  
 130 135 140  
 Cys Cys Asp Asn His Gly Met Phe Asn Lys Asp Leu Gln Gln Val Pro  
 145 150 155 160  
 Ile Leu Glu Leu Lys Ala Thr Ser Asn Thr Val Thr Thr Thr Asp Phe  
 165 170 175  
 Ser Leu Gly Thr Asn Gly Tyr Gln Gln Ser Pro Tyr Gly Tyr Gln Gly  
 180 185 190  
 Thr Trp Glu Phe Thr Ile Asp Thr Thr Thr His Thr Val Thr Gly Asn  
 195 200 205  
 Trp Lys Lys Thr Gly Tyr Leu Pro His Pro Glu Arg Leu Ala Pro Leu  
 210 215 220  
 Ile Pro Asn Ser Leu Trp Ala Asn Val Ile Asp Leu Arg Ala Val Ser  
 225 230 235 240  
 Gln Ala Ser Ala Ala Asp Gly Glu Asp Val Pro Gly Lys Gln Leu Ser  
 245 250 255  
 Ile Thr Gly Ile Thr Asn Phe Phe His Ala Asn His Thr Gly Asp Ala  
 260 265 270  
 Arg Ser Tyr Arg His Met Gly Gly Gly Tyr Leu Ile Asn Thr Tyr Thr  
 275 280 285  
 Arg Ile Thr Pro Asp Ala Ala Leu Ser Leu Gly Phe Gly Gln Leu Phe  
 290 295 300  
 Thr Lys Ser Lys Asp Tyr Leu Val Gly His Gly His Ser Asn Val Tyr  
 305 310 315 320  
 Phe Ala Thr Val Tyr Ser Asn Ile Thr Lys Ser Leu Phe Gly Ser Ser  
 325 330 335  
 Arg Phe Phe Ser Gly Gly Thr Ser Arg Val Thr Tyr Ser Arg Ser Asn  
 340 345 350  
 Glu Lys Val Lys Thr Ser Tyr Thr Lys Leu Pro Lys Gly Arg Cys Ser  
 355 360 365  
 Trp Ser Asn Asn Cys Trp Leu Gly Glu Leu Glu Gly Asn Leu Pro Ile  
 370 375 380  
 Thr Leu Ser Ser Arg Ile Leu Asn Leu Lys Gln Ile Ile Pro Phe Val  
 385 390 395 400  
 Lys Ala Glu Val Ala Tyr Ala Thr His Gly Gly Ile Gln Glu Asn Thr  
 405 410 415

Pro Glu Gly Arg Ile Phe Gly His Gly His Leu Leu Asn Val Ala Val  
 420 425 430  
 Pro Val Gly Val Arg Phe Gly Lys Asn Ser His Asn Arg Pro Asp Phe  
 435 440 445  
 Tyr Thr Ile Ile Val Ala Tyr Ala Pro Asp Val Tyr Arg His Asn Pro  
 450 455 460  
 Asp Cys Asp Thr Thr Leu Pro Ile Asn Gly Ala Thr Trp Thr Ser Ile  
 465 470 475 480  
 Gly Asn Asn Leu Thr Arg Ser Thr Leu Leu Val Gln Ala Ser Ser His  
 485 490 495  
 Thr Ser Val Asn Asp Val Leu Glu Ile Phe Gly His Cys Gly Cys Asp  
 500 505 510  
 Ile Arg Arg Thr Ser Arg Gln Tyr Thr Leu Asp Ile Gly Ser Lys Leu  
 515 520 525  
 Arg Phe  
 530  
 <210>483  
 <211>280  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>483  
 Gly Met Pro Leu Ser Phe Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys  
 1 5 10 15  
 Leu Cys Ser Ala Ser Cys Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn  
 20 25 30  
 Phe Val Pro Ile Thr Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser  
 35 40 45  
 Asp Phe Val Cys Ser Asn Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe  
 50 55 60  
 Ile Asn Ser Ser Ser Asn Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu  
 65 70 75 80  
 Thr Phe Thr Ser Cys Gln Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu  
 85 90 95  
 Ser Ala Ala Glu Thr Leu Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe  
 100 105 110  
 Thr Gly Asn Gln Ser Thr Gly Leu Gly Gly Leu Ile Tyr Gly Lys Asp  
 115 120 125  
 Ile Val Phe Gln Ser Ile Lys Asp Leu Ile Phe Thr Thr Asn Arg Val  
 130 135 140  
 Ala Tyr Ser Pro Ala Ser Val Thr Thr Ser Ala Thr Pro Ala Ile Thr  
 145 150 155 160  
 Thr Val Thr Thr Gly Ala Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr  
 165 170 175  
 Val Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn  
 180 185 190  
 Phe Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile  
 195 200 205  
 Asn Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly  
 210 215 220  
 Gly Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser  
 225 230 235 240  
 Gly Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly  
 245 250 255  
 Val Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ser  
 260 265 270  
 Ala Ser Leu Arg Glu Leu Ser Asn  
 275 280  
 <210>484  
 <211>82  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>484  
 Ile Thr Pro Pro Pro Asp Glu Val Lys Leu Trp Glu Lys Leu Met Val  
 1 5 10 15

Ala Val Leu Leu Met Asn Leu Thr Thr Ala Val Gly Glu Leu Leu Ile  
 20 25 30  
 Ala Glu Pro Lys Leu Ala Arg Phe Pro Lys Asn Leu Ile Asp Trp Asp  
 35 40 45  
 Met Phe Ser Thr Val Ser Glu Ser Val Gly Trp Arg Ala Glu Ala Pro  
 50 55 60  
 Val Val Thr Val Val Ile Ala Gly Val Ala Asp Val Val Thr Asp Ala  
 65 70 75 80  
 Gly Glu

&lt;210&gt;485

&lt;211&gt;492

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;485

Lys Gln Phe Trp Met His His Leu His Arg Gln Leu Leu Cys Glu Gln  
 1 5 10 15  
 Leu Lys Arg Arg His Pro Phe Ile Arg Asn Leu Cys Phe Arg Lys Trp  
 20 25 30  
 Arg Ser Ile Cys Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln  
 35 40 45  
 Gly Lys Cys Thr Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala  
 50 55 60  
 Ile Tyr Ala Glu Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu  
 65 70 75 80  
 Leu Asp Ser Asn Thr Ala Ala Arg Asn Gly Glu Ala Ile Cys Ala Lys  
 85 90 95  
 Val Leu Asn Ile Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg  
 100 105 110  
 Ala Glu Lys Gly Gly Ala Ile Phe Ile Gly Pro Ser Val Gly Asp Pro  
 115 120 125  
 Ala Lys Gln Thr Ser Thr Leu Thr Ile Leu Ala Ser Glu Gly Asn Ile  
 130 135 140  
 Ala Phe Gln Gly Asn Met Leu Asn Thr Lys Pro Gly Ile Arg Asn Ala  
 145 150 155 160  
 Ile Thr Val Glu Ala Gly Gly Glu Ile Val Ser Leu Ser Ala Gln Gly  
 165 170 175  
 Gly Ser Arg Leu Val Phe Tyr Asp Pro Ile Thr His Ser Leu Pro Thr  
 180 185 190  
 Thr Ser Pro Ser Asn Lys Asp Ile Thr Ile Asn Ala Asn Gly Ala Ser  
 195 200 205  
 Gly Ser Val Val Phe Thr Ser Lys Gly Leu Ser Ser Thr Glu Leu Leu  
 210 215 220  
 Leu Pro Ala Asn Thr Thr Thr Ile Leu Leu Gly Thr Val Lys Ile Ala  
 225 230 235 240  
 Ser Gly Glu Leu Lys Ile Thr Asp Asn Ala Val Val Asn Val Leu Gly  
 245 250 255  
 Phe Ala Thr Gln Gly Ser Gly Gln Leu Thr Leu Gly Ser Gly Gly Thr  
 260 265 270  
 Leu Gly Leu Ala Thr Pro Thr Gly Ala Pro Ala Ala Val Asp Phe Thr  
 275 280 285  
 Ile Gly Lys Leu Ala Phe Asp Pro Phe Ser Phe Leu Lys Arg Asp Phe  
 290 295 300  
 Val Ser Ala Ser Val Asn Ala Gly Thr Lys Asn Val Thr Leu Thr Gly  
 305 310 315 320  
 Ala Leu Val Leu Asp Glu His Asp Val Thr Asp Leu Tyr Asp Met Val  
 325 330 335  
 Ser Leu Gln Ser Pro Val Ala Ile Pro Ile Ala Val Phe Lys Gly Ala  
 340 345 350  
 Thr Val Thr Lys Thr Gly Phe Pro Asp Gly Glu Ile Ala Thr Pro Ser  
 355 360 365  
 His Tyr Gly Tyr Gln Gly Lys Trp Ser Tyr Thr Trp Ser Arg Pro Leu  
 370 375 380  
 Leu Ile Pro Ala Pro Asp Gly Gly Phe Pro Gly Gly Pro Ser Pro Ser



Asn	Arg	Gln	Arg	Leu	His	Ala	Pro	Leu	Ser	Gln	Gly	Ser	His	Cys	His
1				5					10					15	
Ser	Tyr	Leu	Ala	Asp	Leu	Thr	His	Glu	Glu	Leu	Lys	Ile	Leu	Leu	Phe
			20					25					30		
Ser	Ala	Phe	Val	Asp	Ala	Lys	Asn	Ile	Ser	Lys	Lys	Glu	Leu	Arg	Glu
		35					40					45			
Val	Ser	Leu	Asn	Phe	Ala	Asn	Asp	Thr	Ser	Val	Glu	Ser	Trp	Leu	Arg

```

      50      55      60
Phe Leu Leu Leu Val Ser Tyr Asp Glu Lys Glu Lys Asp Val Val Val
65      70      75      80
Val Cys Asn His Ser Glu Pro Asn Ile Leu Gly Leu Pro Pro Glu Ala
      85      90      95
Val Ser Gln Leu Ile Glu Glu Leu Ser Asp Glu Gly Tyr Ser Tyr Leu
      100      105      110
Asn Val Val Arg Cys Asp Leu Ser Gly Glu Thr Thr Val Gln Gln Arg
      115      120      125
Leu Leu Leu Asn Ala Asp Glu Gly Arg Ser Met Thr Val Val Ile Ser
      130      135      140
Glu Leu Pro Glu Gly His Pro Asp Ile Arg Asn Leu Gln Leu Ala Ser
145      150      155      160
Glu Arg Ile Phe Val Ser Arg Glu Lys Glu Ala Ala Asp Ala Tyr Ala
      165      170      175
Ser Gly Cys Lys Val Val Ala Phe Asp Asp Glu His Leu Pro Trp Val
      180      185      190
Ser Ser His Ile Ala Tyr Ala Glu Ile Arg Glu Lys Gln Glu Gln
      195      200      205
Thr Met Gln Gly Ser Leu Thr Glu Glu Gln Leu Gly Ala Leu Leu Cys
      210      215      220
Asn Thr Val Ser Thr Glu Lys Asn Leu Ala Phe Ala Leu Asp Ala Val
225      230      235      240
Ile Lys Gln Ser Val Trp Arg Phe Arg Asn Pro Asp Leu Phe Ala Tyr
      245      250      255
Glu Arg Glu Ala Leu Glu Ala Ser Val Thr Asp Ala Leu Val Ser Tyr
      260      265      270
Val Ser Asn Leu Asp Met Ile Pro Tyr Thr Ser Ser Gln Gly Ile Val
      275      280      285
Ile Glu Asp Ser Ser Ile Val Arg Thr Ser Gln Glu His Thr Leu Ile
      290      295      300
Val Asn Cys Ala Ala Phe Asp Lys Leu Ala Ser Gln Ile Glu Phe Leu
305      310      315      320
Cys Pro Ser Asp Val Leu Pro Ile Ser Gly Lys Asp Pro Leu Ile Ser
      325      330      335
Asp Asp Glu Asp Glu Glu Leu Asn Pro Lys Val Ser Ser Ala Ala Asp
      340      345      350
Ser Lys Asp Lys Thr
      355

```

&lt;210&gt;488

&lt;211&gt;347

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;488

```

Ile Pro Cys Thr Phe Glu Ser Lys Arg Lys Phe Leu Met Thr His Cys
1      5      10      15
Leu His Gly Trp Phe Ser Val Val Arg His His Phe Val Gln Ala Phe
      20      25      30
Asn Phe Ser Arg Pro Leu Tyr Ser Arg Ile Thr His Phe Ala Leu Gly
      35      40      45
Val Ile Lys Ala Ile Pro Ile Val Gly His Leu Val Met Gly Val Asp
      50      55      60
Trp Leu Ile Ser His Cys Phe Glu Arg Gly Val Ser His Pro Gly Phe
65      70      75      80
Pro Ser Asp Ile Ala Pro Ile Leu Lys Val Glu Lys Ile Ala Gly Arg
      85      90      95
Asp His Ile Ser Arg Ile Glu Asn Gln Leu Lys Ser Leu Arg Lys Thr
      100      105      110
Ile Glu Val Glu Asp Leu Asp Lys Val His Gly Gln Tyr Gln Glu Asn
      115      120      125
Pro Tyr Ala Asp Met Ala Ser Ser Glu Val Leu Lys Leu Asp Lys Gly
      130      135      140
Val His Val Ser Glu Leu Gly Lys Ala Phe Ser Arg Val Arg Asn Arg
145      150      155      160

```

Ile Thr Arg Ser Tyr Ser Tyr Ala Pro Thr Pro Gln Leu Asp Ser Ile  
 165 170 175  
 Ala Ile Val Gly Ile Asp Leu Val Ser Pro Glu Glu Gln Glu Asn Leu  
 180 185 190  
 Val Arg Leu Ala Asn Glu Val Ile Gln Leu Tyr Pro Lys Ser Lys Thr  
 195 200 205  
 Thr Leu Tyr Leu Leu Ile Asp Phe Asn Xaa Glu Trp Val Gly Asp Ile  
 210 215 220  
 Ser Ser Asp Lys Glu Lys Gln Leu Arg Ser Leu Gly Leu His Ser Glu  
 225 230 235 240  
 Val Gln Cys Leu Ser Val Leu Glu Pro Gln Gly Ala Glu Gly Glu Asp  
 245 250 255  
 Thr Lys His Phe Asp Leu Met Val Gly Cys Tyr Gly Lys Asp Ser Tyr  
 260 265 270  
 Leu Arg Glu Gly Lys Ile Leu Gln Gln Ala Leu Gly Thr Ser Leu Gly  
 275 280 285  
 Thr Val Pro Trp Val Asn Val Met His Thr Leu Pro Ser Arg Tyr Arg  
 290 295 300  
 Ser Arg Leu Ser Leu Pro Ile Asn Thr Glu Lys Asp Lys Thr Glu Leu  
 305 310 315 320  
 Tyr Lys Glu Ile Ser Arg Thr His His Gln Leu His Thr Leu Gly Met  
 325 330 335  
 Gly Leu Gly Ala Gln Asp Phe Arg Asp Cys Ser  
 340 345

&lt;210&gt;489

&lt;211&gt;636

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;489

Val Phe Leu Pro Ser Arg Val Met Ala Ser Cys Leu Ser Ala Trp Phe  
 1 5 10 15  
 Ser Ile Val Arg Glu His Phe Tyr Arg Ala Phe Asp Phe Ser Leu Pro  
 20 25 30  
 Phe Cys Ala Arg Ile Thr Glu Phe Val Leu Gly Val Ile Lys Gly Ile  
 35 40 45  
 Pro Val Val Gly His Ile Ile Val Gly Ile Glu Trp Leu Val Ser Arg  
 50 55 60  
 Tyr Leu Glu Ser Phe Val Thr Lys Pro Thr Phe Val Ser Asp Val Val  
 65 70 75 80  
 Ser Leu Leu Lys Thr Glu Lys Val Ala Gly Arg Asp His Ile Ala Arg  
 85 90 95  
 Val Val Glu Thr Leu Lys Arg Gln Arg Val Ala Val Ala Pro Glu Asp  
 100 105 110  
 Glu Asp Lys Val His Gly Lys Ile Pro Val His Pro Phe Gly Gly Ile  
 115 120 125  
 Gln Pro Val Glu Val Leu Thr Leu Tyr Pro Glu Val Gln Asp Ala Thr  
 130 135 140  
 Leu Gly Leu Ala Phe Ser Lys Ile Arg Asn Arg Val Arg Gln Ala Tyr  
 145 150 155 160  
 Leu Gln Ala Pro Arg Pro Lys Leu Gln Lys Ile Tyr Ile Ile Gly Asn  
 165 170 175  
 Asp Met Asn Pro Phe Glu Val Asp Asp Phe Leu His Leu Ala Arg Leu  
 180 185 190  
 Cys Asn Glu Thr Gln Arg Leu Tyr Pro Asp Ala Thr Ile Ser Leu Tyr  
 195 200 205  
 Leu Thr Ala Ser Gly Gly Arg Asn Ala Met Asp Lys Lys Asn Arg Lys  
 210 215 220  
 Leu Leu Ser Asp Cys Glu Leu Asn Pro Lys Ile Ala Cys Leu Asp Phe  
 225 230 235 240  
 Asn Gln Gly Asp Val Val Lys Gln Ala Thr Cys Asp Cys Trp Met Val  
 245 250 255  
 Tyr His Gly Glu Asn Asp Gln Gly Thr Leu Asn Gln Ile Gln Glu Glu  
 260 265 270  
 Leu Glu Lys Ser Gly Glu Glu Thr Pro Trp Ile His Val Gly Gln Lys

275 280 285  
 Pro Leu Ser Gln Ser Leu Trp Asp Phe Ser Pro Phe Ser Ser Leu Glu  
 290 295 300  
 Met Lys Gly Asp Lys Glu Lys Ala Leu Glu Tyr Ser Glu Leu Glu Lys  
 305 310 315 320  
 Glu Gln Leu Tyr Ser Arg Leu Val Tyr Val Gly Glu Arg Ser Ser Val  
 325 330 335  
 Leu Ser Leu Gly Phe Gly Asp Ser Arg Ser Gly Ile Leu Met Asp Pro  
 340 345 350  
 Lys Arg Val His Ala Pro Leu Ser Glu Gly His Tyr Cys His Ser Tyr  
 355 360 365  
 Leu Ala Asp Leu Glu Asn Pro Gly Leu Gln Lys Thr Ile Leu Ala Ala  
 370 375 380  
 Phe Leu Asn Pro Lys Glu Leu Ser Ser Thr Ile Leu Gln Pro Ile Ser  
 385 390 395 400  
 Leu Asn Leu Ile Leu Asn Ser Lys Thr Tyr Leu Arg Gln His Phe Gly  
 405 410 415  
 Phe Phe Glu Arg Met Ser Arg Ser Asp Arg Asn Val Val Val Val  
 420 425 430  
 Cys Asp Ser Trp Trp Gly Thr Asp Trp Lys Glu Glu Pro Ser Phe Gln  
 435 440 445  
 His Phe Ile Met Glu Leu Glu Cys Arg Gly Tyr Ser His Phe Asn Ile  
 450 455 460  
 Phe Ala Phe Arg Ser Asn Ser Met Cys Val Glu Glu Arg Arg Ile Leu  
 465 470 475 480  
 Asn Glu Ser Ser Gln Glu Lys Ala Phe Thr Met Ile Phe Cys Glu Asp  
 485 490 495  
 Ser Val Ser Gln Gly Asp Ile Arg Cys Leu His Leu Ala Ser Glu Gly  
 500 505 510  
 Met Leu Cys Gly Lys Glu Cys Tyr Ala Val Asp Val Tyr Thr Ser Gly  
 515 520 525  
 Cys Ala Asn Phe Met Met Glu Glu Val Leu Thr Leu Glu Arg Glu Ser  
 530 535 540  
 Asn Leu Trp Asn Arg Lys His Gly Leu Trp Lys Arg Glu Val Arg Lys  
 545 550 555 560  
 Gln Lys Gln Glu Ala Ala Leu Asp Gln Asp Glu Ser Glu Ile Tyr Val  
 565 570 575  
 Cys Asn Gln Leu Thr Ala Gln Gln Asn Phe Ala Cys Ser Leu Asp Ala  
 580 585 590  
 Ala Ile Arg Gln Ser Ile Trp Arg Ser Arg Met Pro Glu Leu Leu Ser  
 595 600 605  
 Ile Glu Arg Arg Ala Leu Gly Glu Gln Leu Phe Thr Thr Val His His  
 610 615 620  
 Tyr Leu Thr Thr Gln Lys Lys Ile Leu Arg Gly Ile  
 625 630 635

&lt;210&gt;490

&lt;211&gt;703

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;490

Tyr Phe Leu Cys Cys Tyr Leu Lys Leu Phe Val Ser Asn Phe Ile Phe  
 1 5 10 15  
 Phe Val Xaa Met Pro Ile Pro Tyr Ile Ser Ser Trp Ile Ser Thr Val  
 20 25 30  
 Arg Gln His Phe Val Lys Ala Phe Asp Phe Ser Arg Pro Phe Cys Ser  
 35 40 45  
 Arg Val Thr Asn Phe Ala Leu Gly Val Ile Lys Ala Ile Pro Ile Val  
 50 55 60  
 Gly His Ile Val Met Gly Met Glu Trp Leu Val Ser Ser Cys Val Ala  
 65 70 75 80  
 Gly Ile Ile Thr Arg Ser Ser Phe Thr Ser Asp Val Val Gln Ile Val  
 85 90 95  
 Lys Thr Glu Lys Ala Leu Gly Arg Asp His Ile Ser Arg Val Ala Glu  
 100 105 110

Ile Leu Gln Arg Glu Arg Gly Thr Ile Thr Pro Glu Asn Gln Asp Lys  
 115 120 125  
 Val His Gly Lys Phe Pro Val Cys Pro Phe Gly Arg Leu Lys Ser Glu  
 130 135 140  
 Glu Thr Leu Lys Leu Lys Pro Gly Glu Arg Gly Gly Thr Leu Asp Thr  
 145 150 155 160  
 Val Phe Ser Pro Ile Arg Thr Arg Val Thr Arg Ala Tyr Leu Gln Ala  
 165 170 175  
 Pro Arg Pro Glu Ile Arg Thr Ile Ser Ile Val Gly Ser Lys Leu Lys  
 180 185 190  
 Thr Pro Gln Asp Phe Ser Gln Phe Val Ser Leu Ala Asn Glu Thr Gln  
 195 200 205  
 Arg Leu His Pro Glu Ala Leu Val Cys Leu Tyr Leu Thr Gly Leu Asn  
 210 215 220  
 Arg Glu Ser Gln Met Cys Asp Thr Thr Thr Ala Glu Lys Lys Gln Tyr  
 225 230 235 240  
 Leu His Asn Ser Gly Leu Asp Ser Arg Ile Gln Cys Lys Asp Ser Lys  
 245 250 255  
 Glu Asp Asp Ala Gly Ser Pro Glu Asn Pro Glu Leu Trp Ile Gly Tyr  
 260 265 270  
 Tyr Ser Arg Glu Gln Gln His Asn Ile Asp Gly Gln Tyr Ile Gln Gln  
 275 280 285  
 Cys Leu Gly Lys Ser Ala Asp Pro Ile Pro Trp Ile His Val Thr Glu  
 290 295 300  
 Asp Thr Lys Asp Phe Tyr Tyr Pro Pro Asn Phe Thr Ser Tyr Ser His  
 305 310 315 320  
 Thr Arg Gln Ser Thr Asp Pro Thr Ser Pro Pro Arg Leu Pro Glu Ser  
 325 330 335  
 Glu Gly Asp Lys Asp Ser Leu Tyr Gly Gln Leu Ser Arg Ser Tyr His  
 340 345 350  
 His Glu Tyr Met Leu Gly Leu Gly Leu Lys Pro Glu Asp Ala Gly Leu  
 355 360 365  
 Leu Met Asp Pro Asp Arg Ile Tyr Ala Pro Leu Ser Gln Gly His Tyr  
 370 375 380  
 Cys His Ser Tyr Leu Ala Asp Ile Glu Asn Glu Asp Leu Arg Thr Leu  
 385 390 395 400  
 Val Leu Ser Pro Phe Leu Asp Pro Gly Asn Leu Ser Ser Glu Asp Leu  
 405 410 415  
 Arg Pro Val Ala Phe Asn Ile Ala Arg Leu Pro Leu Glu Leu Asp Ser  
 420 425 430  
 Leu Phe Phe Arg Leu Val Ala Gly Gln Gln Glu Gly Arg Asn Ile Val  
 435 440 445  
 Thr Leu Ala His Gly Thr Pro Arg Pro Glu Asp Leu Asp Pro Asp Ser  
 450 455 460  
 Met Asn Ile Leu Thr Arg Arg Leu Gln Met Ser Gly Tyr Ser Tyr Leu  
 465 470 475 480  
 Asn Ile Phe Ser Tyr Lys Ser Arg Lys Met Ile Val Lys Glu Arg Gln  
 485 490 495  
 Phe Phe Gly Asp Arg Ser Glu Gly Lys Ser Phe Thr Leu Ile Leu Phe  
 500 505 510  
 Glu Asp Pro Ile Ser Ala Ala Asp Phe Arg Cys Leu Gln Leu Ala Ala  
 515 520 525  
 Glu Gly Met Val Ala Lys Asp Leu Pro Ser Val Ala Asp Ile Cys Ala  
 530 535 540  
 Ser Gly Cys Ser Cys Ile Gln Phe Ser Glu Met Gln Ser Pro Gln Ala  
 545 550 555 560  
 Ile Glu Tyr Arg Gln Trp Glu Ala Arg Val Glu Asp Glu Ala Gly Glu  
 565 570 575  
 Glu Ala Arg Glu Pro Val Ile Tyr Ser Gln Asp Gln Leu Ser Ser Met  
 580 585 590  
 Leu Thr Thr Gln Gln Asn Phe Val Phe Ser Leu Asp Ala Val Val Lys  
 595 600 605  
 Gln Ala Ile Trp Arg Phe Arg Ser Lys Gly Leu Leu Thr Met Glu Arg  
 610 615 620

Lys Ala Leu Gly Glu Glu Phe Leu Thr Ala Ile Phe Ser Tyr Leu Gly  
 625 630 635 640  
 Ser Gln Glu Arg Asn Glu Asn Met Gly Lys Arg Thr Thr Glu Glu His  
 645 650 655  
 Glu Val Val Ile Ser Phe Glu Glu Leu Asp Arg Met Val Gln Val Leu  
 660 665 670  
 Pro Ala Glu Val Pro Ala Asp Ser Gly Asn Asp Pro Thr His Pro Val  
 675 680 685  
 Pro Asn Pro Asp Ser Asn Pro Asp Ser Ser Gln Asn Glu Gly Ser  
 690 695 700

&lt;210&gt;491

&lt;211&gt;148

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;491

Ser Thr Lys Ile Gln Met His Pro Gly Leu Arg Asn Trp Arg Thr Ser  
 1 5 10 15  
 Thr Asn Lys Leu Arg Glu Glu Gly Ser Val Ser Phe Arg Glu Tyr Phe  
 20 25 30  
 Arg Ala Tyr Met Cys Asp Lys Ile Val Ala Gln Lys Asn Phe Leu Phe  
 35 40 45  
 Thr Leu Asp Ala Val Ile Lys Gln Ala Gly Trp Arg Ser Gln Glu Lys  
 50 55 60  
 Leu Asn Leu Phe Tyr Val Glu Ser Gln Ala Leu Gly Arg Glu Ile Lys  
 65 70 75 80  
 Val Ser Leu Glu Glu Tyr Ile Gln Ser Met Val Gly Ile Leu Gly Ser  
 85 90 95  
 Gln Arg Thr Lys Lys Ser Phe Lys Phe Ser Val Asp Phe Thr Pro Leu  
 100 105 110  
 Glu Gln Ala Leu Gln Glu Arg Cys Ser Ser Asp Asp Asp Glu Asp Ala  
 115 120 125  
 Thr Ala Ala Ser Thr Ala Thr Gly Ala Thr Ala Ser Pro Thr Asp Met  
 130 135 140  
 His Glu Asp Glu  
 145

&lt;210&gt;492

&lt;211&gt;283

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;492

Val Ile Gln His Leu Leu Asn Phe Ala Leu Glu Glu Thr Pro Ser Ile  
 1 5 10 15  
 Ser Val Gln Tyr Gln Glu Gln Glu Lys Leu Ser Pro Cys Asp His Ser  
 20 25 30  
 Pro Glu Ile Gly Lys Lys Lys Arg Trp Asn Lys Leu Glu Ser Phe Ser  
 35 40 45  
 Thr Tyr Cys Ser Leu Phe Met Ser Val Lys Asp His Tyr Lys Leu Asn  
 50 55 60  
 Leu Gly Ile Gln Asn Ser Leu Ser Gly Trp Leu Leu Asp Pro Tyr Arg  
 65 70 75 80  
 Val Cys Ala Pro Leu Ser Ser Pro Tyr Ser Cys Pro Ser Tyr Leu Leu  
 85 90 95  
 Asp Leu Gln Asn Lys Glu Leu Arg Arg Ser Leu Leu Ser Thr Phe Leu  
 100 105 110  
 Asp Pro Lys Asn Leu Thr Ser Glu Thr Phe Arg Ser Val Ser Ile Asn  
 115 120 125  
 Phe Gly Asn Ser Ser Phe Gly Gln Arg Trp Ser Glu Phe Leu Ser Arg  
 130 135 140  
 Val Leu His Asp Glu Lys Glu Lys His Val Ala Val Val Cys Asn Asp  
 145 150 155 160  
 Ala Lys Leu Leu Glu Glu Gly Leu Ser Pro Glu Ala Leu Ser Leu Leu  
 165 170 175  
 Glu Glu Asp Leu Arg Glu Ser Gly Tyr Ser Tyr Leu Asn Ile Leu Ser  
 180 185 190

Val Ser Pro Glu Gly Val Ser Lys Val Gln Glu Arg Gln Ile Leu Arg  
 195 200 205  
 Arg Asp Leu Gln Gly Arg Ser Phe Thr Val Met Ile Thr Asp Leu Pro  
 210 215 220  
 Leu Gly Ser Glu Asp Ile Arg Ser Leu Gln Leu Ala Ser Asp Arg Ile  
 225 230 235 240  
 Leu Val Ser Ser Ser Leu Asp Ala Ala Asp Ala Cys Ala Ser Gly Cys  
 245 250 255  
 Lys Val Leu Val Tyr Glu Asn Pro Asn Ala Ser Trp Ala Gln Glu Leu  
 260 265 270  
 Glu Asn Phe Tyr Lys Gln Val Glu Arg Arg Arg  
 275 280

&lt;210&gt;493

&lt;211&gt;169

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;493

Leu Glu Ser Pro His Phe Pro Arg Arg Ser Arg Gln Ser Thr Arg Glu  
 1 5 10 15  
 Asn Pro Arg Arg Ser Leu Arg Arg Tyr His Thr His Arg Asn Cys Pro  
 20 25 30  
 Thr Phe Ser Leu Ile Glu Glu Leu Ser Thr Val Asp Glu Ala Leu Gln  
 35 40 45  
 Gly Val Arg Ser Arg Leu Thr Tyr Ala Tyr Arg Ser Val Glu Lys Pro  
 50 55 60  
 Met Ile Gln Asp Leu Ala Leu Val Gly Phe Gly Leu Arg Asp Ser Ala  
 65 70 75 80  
 Asp Leu Ile Asn Phe Val Arg Leu Ala Asn Gly Val Gln Asn His Tyr  
 85 90 95  
 Pro His Thr Lys Val Lys Leu Tyr Leu Ala Lys Asn Leu Ala Asp Val  
 100 105 110  
 Trp Asp Cys Glu Ile Ser Glu Glu Glu Lys Gly Gln Leu Arg Ala Leu  
 115 120 125  
 Gly Leu Asp Pro Lys Ile Glu Ser Ile Ser Leu Thr Ser Ala Gly Leu  
 130 135 140  
 Pro Ser Val Pro Glu Val Ala Thr Val Asp Phe Met Ile Thr Cys Tyr  
 145 150 155 160  
 Gly Lys Asp Gln Glu Val Gln Asp Pro  
 165

&lt;210&gt;494

&lt;211&gt;135

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;494

Ile Ser Thr Val Ala Cys Pro Ser Ile Ser Ser Trp Phe Thr Val Val  
 1 5 10 15  
 Arg Gln His Phe Val Asn Ala Phe Asp Phe Thr His Pro Val Cys Ser  
 20 25 30  
 Arg Ile Thr Asn Phe Ala Leu Gly Ile Ile Lys Ala Ile Pro Val Leu  
 35 40 45  
 Gly His Ile Val Met Gly Ile Glu Trp Leu Ile Ser Trp Ile Pro Arg  
 50 55 60  
 His Thr Val Arg His Gly Met Phe Thr Ser Asp Val Ser Ser Ala Ile  
 65 70 75 80  
 Lys Val Glu Gln Thr Arg Gly His Asn Cys Leu Ala Pro Leu Glu Ala  
 85 90 95  
 Tyr Leu Ser Ser Leu Arg Val Pro Ile Ser Gln Glu Asp Leu Gly Lys  
 100 105 110  
 Val His Gly Arg Thr Pro Glu Asp Pro Phe Val Asp Ile Thr Pro Thr  
 115 120 125  
 Glu Ile Val Gln Pro Ser Pro  
 130 135

&lt;210&gt;495

&lt;211&gt;156

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;495

```

Phe Leu Ser Ala Leu Asp Ala Ala Asp Ala Cys Ala Ser Glu Cys Lys
 1           5           10           15
Ile Leu Glu Tyr Glu Asp Pro Glu Gln Glu Trp Ala Gln Gln Tyr Ala
          20           25           30
Ser Phe Tyr Arg Asn Ile Asp Arg Ala Gly Asp Leu Gln Arg Gln Gly
          35           40           45
Ile Pro Gly Glu Pro Leu Gly Val Ser Ala Ser Thr Arg Val Val Leu
          50           55           60
Glu Lys Asp Ile Val Phe Asn Leu Asn Ala Val Ile Gln Gln Ala Met
          65           70           75           80
Trp Lys Phe Lys Lys Arg Asp Leu Phe Ala Val Glu Ser Gln Ala Leu
          85           90           95
Gly Asp Asp Met Arg Arg Ala Leu Glu Gly Tyr Ile Gly Ser Ser Leu
          100          105          110
Leu Val Glu Gly Thr Ile Gln Pro Gln Val Ala Cys Asn Val Asn Val
          115          120          125
Ser Phe Ala Thr Leu Asp Glu Ala Val Cys Ala Ala Cys Asp Ser Ala
          130          135          140
Gln Asp Ala Pro Ser Glu Glu Asn Asn Thr Asp Asp
          145          150          155

```

&lt;210&gt;496

&lt;211&gt;542

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;496

```

Leu Ile Phe Tyr Leu Phe Leu Asn Leu Tyr Ile Ala Cys Val Arg Phe
 1           5           10           15
His Phe Gln Cys Trp Phe Asp Pro Met Ala Cys Tyr Ile Ser Ile Trp
          20           25           30
Ile Ser Thr Val Lys Gln His Phe Ile Arg Ala Phe Asp Phe Thr Arg
          35           40           45
Pro Leu Gly Ser Arg Ile Thr Asn Phe Ala Leu Gly Val Ile Lys Ala
          50           55           60
Ile Pro Ile Leu Gly Cys Val Val Ile Gly Val Ser Trp Leu Val Ser
          65           70           75           80
Thr Cys Ser Ala Arg Arg Phe Gly Lys Pro Ala Phe Thr Ser Asp Val
          85           90           95
Ala Ser Ile Val Lys Ile Glu Lys Thr Arg Gly Tyr Asn Pro Leu Ala
          100          105          110
Trp Val Glu Gln Tyr Leu Arg Gln Leu Arg Val Arg Leu Pro Glu Gly
          115          120          125
Asp Leu Gly Lys Ile His Gly Lys Val Ser Arg Asp Tyr Val Cys Asp
          130          135          140
Arg Thr Pro Gln Glu Asn Leu Asn Met Val Pro His Gln Tyr Leu Gly
          145          150          155          160
Glu Leu Gly Arg Ala Phe Tyr Gly Ile Arg Asn Arg Val Thr Lys Ala
          165          170          175
Tyr Gln Arg Val Thr Pro Leu Glu Val Pro Cys Leu Thr Leu Val Gly
          180          185          190
Phe Asp Ile Leu Asp Pro Glu Asp Gln Val Asn Phe Val Arg Leu Ala
          195          200          205
Asn Gly Ile Gln Thr Gln Tyr Pro Gln Thr Gln Ile Lys Leu Tyr Leu
          210          215          220
Ile Ser Ile Gln Lys Ile Trp Asn Gln Cys Asp Gly Thr Ile Ser Gln
          225          230          235          240
Glu Lys Glu Gln Gln Leu Arg Ser Leu Gly Leu Asp Ala Lys Ile Lys
          245          250          255
Cys Val Ser Ala Pro Ala Leu Leu Leu Gln Lys Tyr Leu Gln Ser Glu
          260          265          270
Asn Leu Pro Ser Cys Asp Leu Leu Ile Asn Tyr Tyr Gly Lys Gln Gln
          275          280          285

```



Ser Val Arg Asp Val Asp Ser Ile Lys Ser Leu Leu Asn Leu Ser Ser  
 290 295 300  
 Glu His Ile Pro Ala Ile Ser Val Thr Tyr Arg Pro Asp Asp Pro Phe  
 305 310 315 320  
 Tyr Ser Tyr Tyr Phe Phe Pro Gly Ser Gln Gly Gly Thr Ala Pro Asp  
 325 330 335  
 Gln Arg Ile Pro Trp Ser Glu Gln Glu His Leu Gln Thr Tyr Thr Thr  
 340 345 350  
 Leu Ser Asn Pro Arg Cys Asp Arg Tyr Ala Val His Leu Gly Met Glu  
 355 360 365  
 Asp Phe Ala Ser Gly Val Phe Leu Asp Pro Leu Arg Val Ser Ala Pro  
 370 375 380  
 Leu Ser Gly Glu Tyr Ser Cys Pro Ser Tyr Leu Leu Asp Leu Lys Ser  
 385 390 395 400  
 Glu Glu Leu Arg Cys Phe Leu Leu Ser Ala Phe Ile Asp Pro Asn Asn  
 405 410 415  
 Ser Gly Gln Gly Asn Pro Arg Pro Met Ser Ile Asn Phe Gly Asn Ser  
 420 425 430  
 Pro Leu Gly Gln Arg Trp Ser Glu Phe Leu Ser Arg Val Leu His Asp  
 435 440 445  
 Glu Thr Glu Lys His Val Ala Val Val Cys Asn Asn Pro Gln Leu Ile  
 450 455 460  
 Lys Lys Ser Phe Pro Ser His Ser Leu Ser Leu Leu Glu Asn Glu Leu  
 465 470 475 480  
 Glu Glu Ser Gly Tyr Ser Tyr Leu Asn Ile Val Ser Val Ser Gln Glu  
 485 490 495  
 Arg Thr Cys Val Lys Glu Arg Arg Ile Leu Ser Ser Asp Pro Ser Gly  
 500 505 510  
 Arg Ser Phe Thr Val Ile Leu Thr Asp Leu Pro Glu Gly Ser Ser Asp  
 515 520 525  
 Ile Arg Asn Leu Gln Leu Ala Ser Asp Arg Ile Leu Val Ser  
 530 535 540  
 <210>497  
 <211>430  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>497  
 Leu Ser Ser Pro Tyr Glu Lys Thr Glu Gln Leu Leu Gly Thr Pro Asn  
 1 5 10 15  
 Cys Arg Thr Pro Arg Val Asn Ile Ser Thr Val Gly Ile Pro Ile Asp  
 20 25 30  
 Glu Thr Ser Asn Ala Phe Val Asp Ser Met Met Lys Gln Gly Val Gly  
 35 40 45  
 Gln Asp Ala Lys Glu Leu Tyr Thr Phe Leu Ser Arg Gly Asn Glu His  
 50 55 60  
 Tyr Gln Pro Cys Leu Trp Phe Ser Leu Glu Glu Glu Leu Gly Phe Leu  
 65 70 75 80  
 Phe Asp Glu Lys Met Leu Cys Ala Pro Leu Ser Glu Asp His Tyr Cys  
 85 90 95  
 His Ser Tyr Leu Val Asp Leu Val Asp Gln His Leu Lys Asp Leu Ile  
 100 105 110  
 Leu Ser Met Phe Leu Asp Pro Gln Asn Ile Ser Ala Gly Glu Leu Leu  
 115 120 125  
 Lys Val Ser Ile Asn Val Gly Asp Ser Phe Ser Pro Leu Gln Gln Lys  
 130 135 140  
 Asp Phe Leu Ser Met Val Leu Arg Asp Glu Thr Gly Lys Asn Val Val  
 145 150 155 160  
 Val Val Phe Lys Gly Val Leu Ser Leu Pro Ala Thr Gln Val Cys Lys  
 165 170 175  
 Leu Val Glu Glu Leu Asn Ser Lys Asp Tyr Ser Tyr Leu Asn Ile Phe  
 180 185 190  
 Ser Cys His Gly Asp Ser Ser Pro Gln Leu Leu Phe Arg Lys Glu Leu  
 195 200 205  
 Glu Gly Thr Ser Gly Arg Tyr Phe Thr Val Ile Cys Ala Leu Tyr Leu

210	215	220
Gly Asp Thr Asp Met Arg Ser Leu Gln Leu Ala Ser Glu Arg Ile Met		
225	230	235
Val Ser Arg Glu Phe Asp Leu Val Asp Ala Tyr Ala Ala Arg Cys Lys		240
	245	250
Leu Leu Lys Ile Asp His Thr Asn Trp Arg Pro Gly Thr Phe Ser Arg		255
	260	265
His Ala Asp Phe Ala Asp Ala Val Asp Val Ser Ala Gly Phe Asn Ser		270
	275	280
Arg Glu Phe Lys Leu Ile Thr Gln Ala Asn Gln Gly Ile Leu Glu Ser		285
	290	295
Gly Glu Leu Pro Leu Pro Ser Lys Thr Phe Trp Glu Gly Phe Leu Ala		300
305	310	315
Phe Cys Asp Arg Val Thr Val Thr Arg His Phe Ile Pro Met Leu Asp		320
	325	330
Ala Ala Ile Lys Gln Ala Val Trp Thr His Lys His Pro Ser Leu Ile		335
	340	345
Asp Lys Glu Cys Glu Ala Leu Asp Leu Lys Thr Gln Cys Leu Pro Ser		350
	355	360
Ile Val Ser Tyr Leu Glu Tyr Val Thr Asn Ser His Glu Lys Thr Ser		365
	370	375
Lys Gly Pro Phe Ile Gln Lys Glu Ile Ile Ala Asp Cys Ser Pro Leu		380
385	390	395
Lys Glu Ala Leu Phe Pro Gly Ser Asp Glu Asp Val Pro Ser Thr Ser		400
	405	410
Glu Asp Pro Ser Asp Asp His Pro Ser Asp Leu Glu Asp Ser		415
	420	425
		430

&lt;210&gt;498

&lt;211&gt;186

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;498

Ser Leu Glu Thr Arg Gly Arg Phe Ala Glu Ile Cys Leu Gln Leu Leu		
1	5	10
Phe Phe Asp Ile Gln Ser Leu Lys Phe Leu Gln Leu Phe Ser Glu Gly		15
	20	25
Thr Ala Leu Asn Leu Phe Arg Ile Phe Ala Pro Leu Arg Asn Arg Val		30
	35	40
Thr Thr Glu Tyr Ser Arg Ala Arg Gln Pro Asp Leu His Arg Ile Ala		45
	50	55
Ile Val Tyr Ile Gly Val Leu Asp Ser Glu Ser Ser Lys Ile Leu Glu		60
65	70	75
Arg Leu Ile Ser Tyr Met Ser Cys Ile Tyr Ser Glu Ser Gln Met Tyr		80
	85	90
Leu Arg Phe Phe Met Gly Lys Asn Val Asn Gln Ser Ala Val Leu Ser		95
	100	105
Lys Leu His Val Glu Asn Leu His Ile Arg Cys Gly Phe Phe Ser Glu		110
	115	120
Asp Ala Val Pro Glu Ser Glu Pro Phe Asp Leu Ser Ile Tyr Val His		125
	130	135
Thr Asp Arg Ser Cys Pro Leu Pro Thr Lys Lys Arg Ser Ser Ser Trp		140
145	150	155
Glu Leu Gln Thr Val Glu Leu Pro Glu Ser Ile Tyr Pro Gln Ser Glu		160
	165	170
Phe Leu Leu Met Arg Pro Arg Met Leu Ser		175
	180	185

&lt;210&gt;499

&lt;211&gt;136

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;499

Leu Leu Glu Asn Asn Arg Phe Phe Leu Phe Phe Lys Val Lys Tyr Phe		
1	5	10
Leu Lys Asp Ser Phe Leu Met Ser Tyr Tyr Phe Ser Leu Trp Tyr Leu		15

20 25 30  
 Lys Val Gln Gln His Phe Gln Ala Ala Phe Asp Phe Thr Arg Ser Leu  
 35 40 45  
 Cys Ser Arg Ile Ser Asn Phe Ala Leu Gly Val Ile Ala Leu Leu Pro  
 50 55 60  
 Ile Ile Gly Gln Leu Tyr Val Gly Leu Asp Trp Leu Leu Ser Arg Ile  
 65 70 75 80  
 Lys Lys Pro Glu Phe Pro Ser Asp Val Asp Gln Ile Val Arg Val Glu  
 85 90 95  
 His Val Val Gly His Asp His Arg Ser Arg Val Glu Asp Ile Leu Lys  
 100 105 110  
 Arg Gln Arg Leu Ser Leu Glu Pro Arg Asp Glu Gly Lys Val Arg Gly  
 115 120 125  
 Asp Leu Pro Ser Ala Pro Phe Phe  
 130 135  
 <210>500  
 <211>940  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>500  
 Thr Ser Met Arg Phe Phe Cys Phe Gly Met Leu Leu Pro Phe Thr Phe  
 1 5 10 15  
 Val Leu Ala Asn Glu Gly Leu Gln Leu Pro Leu Glu Thr Tyr Ile Thr  
 20 25 30  
 Leu Ser Pro Glu Tyr Gln Ala Ala Pro Gln Val Gly Phe Thr His Asn  
 35 40 45  
 Gln Asn Gln Asp Leu Ala Ile Val Gly Asn His Asn Asp Phe Ile Leu  
 50 55 60  
 Asp Tyr Lys Tyr Tyr Arg Ser Asn Gly Gly Ala Leu Thr Cys Lys Asn  
 65 70 75 80  
 Leu Leu Ile Ser Glu Asn Ile Gly Asn Val Phe Phe Glu Lys Asn Val  
 85 90 95  
 Cys Pro Asn Ser Gly Gly Ala Ile Tyr Ala Ala Gln Asn Cys Thr Ile  
 100 105 110  
 Ser Lys Asn Gln Asn Tyr Ala Phe Thr Thr Asn Leu Val Ser Asp Asn  
 115 120 125  
 Pro Thr Ala Thr Ala Gly Ser Leu Leu Gly Gly Ala Leu Phe Ala Ile  
 130 135 140  
 Asn Cys Ser Ile Thr Asn Asn Leu Gly Gln Gly Thr Phe Val Asp Asn  
 145 150 155 160  
 Leu Ala Leu Asn Lys Gly Gly Ala Leu Tyr Thr Glu Thr Asn Leu Ser  
 165 170 175  
 Ile Lys Asp Asn Lys Gly Pro Ile Ile Ile Lys Gln Asn Arg Ala Leu  
 180 185 190  
 Asn Ser Asp Ser Leu Gly Gly Gly Ile Tyr Ser Gly Asn Ser Leu Asn  
 195 200 205  
 Ile Glu Gly Asn Ser Gly Ala Ile Gln Ile Thr Ser Asn Ser Ser Gly  
 210 215 220  
 Ser Gly Gly Gly Ile Phe Ser Thr Gln Thr Leu Thr Ile Ser Ser Asn  
 225 230 235 240  
 Lys Lys Leu Ile Glu Ile Ser Glu Asn Ser Ala Phe Ala Asn Asn Tyr  
 245 250 255  
 Gly Ser Asn Phe Asn Pro Gly Gly Gly Gly Leu Thr Thr Thr Phe Cys  
 260 265 270  
 Thr Ile Leu Asn Asn Arg Glu Gly Val Leu Phe Asn Asn Asn Gln Ser  
 275 280 285  
 Gln Ser Asn Gly Gly Ala Ile His Ala Lys Ser Ile Ile Ile Lys Glu  
 290 295 300  
 Asn Gly Pro Val Tyr Phe Leu Asn Asn Thr Ala Thr Arg Gly Gly Ala  
 305 310 315 320  
 Leu Leu Asn Leu Ser Ala Gly Ser Gly Asn Gly Ser Phe Ile Leu Ser  
 325 330 335  
 Ala Asp Asn Gly Asp Ile Ile Phe Asn Asn Asn Thr Ala Ser Lys His  
 340 345 350

Ala	Leu	Asn	Pro	Pro	Tyr	Arg	Asn	Ala	Ile	His	Ser	Thr	Pro	Asn	Met
		355					360					365			
Asn	Leu	Gln	Ile	Gly	Ala	Arg	Pro	Gly	Tyr	Arg	Val	Leu	Phe	Tyr	Asp
	370					375					380				
Pro	Ile	Glu	His	Glu	Leu	Pro	Ser	Ser	Phe	Pro	Ile	Leu	Phe	Asn	Phe
385					390					395					400
Glu	Thr	Gly	His	Thr	Gly	Thr	Val	Leu	Phe	Ser	Gly	Glu	His	Val	His
			405						410					415	
Gln	Asn	Phe	Thr	Asp	Glu	Met	Asn	Phe	Ser	Tyr	Leu	Arg	Asn	Thr	
			420					425				430			
Ser	Glu	Leu	Arg	Gln	Gly	Val	Leu	Ala	Val	Glu	Asp	Gly	Ala	Gly	Leu
	435					440						445			
Ala	Cys	Tyr	Lys	Phe	Phe	Gln	Arg	Gly	Gly	Thr	Leu	Leu	Leu	Gly	Gln
	450					455					460				
Gly	Ala	Val	Ile	Thr	Thr	Ala	Gly	Thr	Ile	Pro	Thr	Pro	Ser	Ser	Thr
465					470					475					480
Pro	Thr	Thr	Val	Gly	Ser	Thr	Ile	Thr	Leu	Asn	His	Ile	Ala	Ile	Asp
				485					490					495	
Leu	Pro	Ser	Ile	Leu	Ser	Phe	Gln	Ala	Gln	Ala	Pro	Lys	Ile	Trp	Ile
			500					505					510		
Tyr	Pro	Thr	Lys	Thr	Gly	Ser	Thr	Tyr	Thr	Glu	Asp	Ser	Asn	Pro	Thr
	515						520					525			
Ile	Thr	Ile	Ser	Gly	Thr	Leu	Thr	Leu	Arg	Asn	Ser	Asn	Asn	Glu	Asp
	530					535					540				
Pro	Tyr	Asp	Ser	Leu	Asp	Leu	Ser	His	Ser	Leu	Glu	Lys	Val	Pro	Leu
545					550					555					560
Leu	Tyr	Ile	Val	Asp	Val	Ala	Ala	Gln	Lys	Ile	Asn	Ser	Ser	Gln	Leu
			565					570						575	
Asp	Leu	Ser	Thr	Leu	Asn	Ser	Gly	Glu	His	Tyr	Gly	Tyr	Gln	Gly	Ile
			580					585					590		
Trp	Ser	Thr	Tyr	Trp	Val	Glu	Thr	Thr	Thr	Ile	Thr	Asn	Pro	Thr	Ser
	595					600						605			
Leu	Leu	Gly	Ala	Asn	Thr	Lys	His	Lys	Leu	Leu	Tyr	Ala	Asn	Trp	Ser
	610					615					620				
Pro	Leu	Gly	Tyr	Arg	Pro	His	Pro	Glu	Arg	Arg	Gly	Glu	Phe	Ile	Thr
625					630					635					640
Asn	Ala	Leu	Trp	Gln	Ser	Ala	Tyr	Thr	Ala	Leu	Ala	Gly	Leu	His	Ser
				645					650					655	
Leu	Ser	Ser	Trp	Asp	Glu	Glu	Lys	Gly	His	Ala	Ala	Ser	Leu	Gln	Gly
			660					665					670		
Ile	Gly	Leu	Val	His	Gln	Lys	Asp	Lys	Asn	Gly	Phe	Lys	Gly	Phe	
	675					680					685				
Arg	Ser	His	Met	Thr	Gly	Tyr	Ser	Ala	Thr	Thr	Glu	Ala	Thr	Ser	Ser
	690					695					700				
Gln	Ser	Pro	Asn	Phe	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Ser	Lys	Ala
705					710					715					720
Lys	Glu	His	Glu	Ser	Gln	Asn	Ser	Thr	Ser	Ser	His	His	Tyr	Phe	Ser
				725					730					735	
Gly	Met	Cys	Ile	Glu	Asn	Thr	Leu	Phe	Lys	Glu	Trp	Ile	Arg	Leu	Ser
			740					745					750		
Val	Ser	Leu	Ala	Tyr	Met	Phe	Thr	Ser	Glu	His	Thr	His	Thr	Met	Tyr
			755				760					765			
Gln	Gly	Leu	Leu	Glu	Gly	Asn	Ser	Gln	Gly	Ser	Phe	His	Asn	His	Thr
	770					775					780				
Leu	Ala	Gly	Ala	Leu	Ser	Cys	Val	Phe	Leu	Pro	Gln	Pro	His	Gly	Glu
785					790					795					800
Ser	Leu	Gln	Ile	Tyr	Pro	Phe	Ile	Thr	Ala	Leu	Ala	Ile	Arg	Gly	Asn
				805					810					815	
Leu	Ala	Ala	Phe	Gln	Glu	Ser	Gly	Asp	His	Ala	Arg	Glu	Phe	Ser	Leu
			820					825					830		
His	Arg	Pro	Leu	Thr	Asp	Val	Ser	Leu	Pro	Val	Gly	Ile	Arg	Ala	Ser
	835						840					845			
Trp	Lys	Asn	His	His	Arg	Val	Pro	Leu	Val	Trp	Leu	Thr	Glu	Ile	Ser
	850					855					860				

Tyr Arg Ser Thr Leu Tyr Arg Gln Asp Pro Glu Leu His Ser Lys Leu  
 865 870 875 880  
 Leu Ile Ser Gln Gly Thr Trp Thr Thr Gln Ala Thr Pro Val Thr Tyr  
 885 890 895  
 Asn Ala Leu Gly Ile Lys Val Lys Asn Thr Met Gln Val Phe Pro Lys  
 900 905 910  
 Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp Ile Ser Ser Ser Thr Leu  
 915 920 925  
 Ser His Tyr Leu Asn Val Ala Ser Arg Met Arg Phe  
 930 935 940  
 <210>501  
 <211>969  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>501  
 Asn Glu Ile Leu Thr Ile Ser Asp Gln Asn Arg Lys Ile Lys Glu Pro  
 1 5 10 15  
 Leu Val Ser Lys Thr Pro Pro Lys Phe Leu Phe Tyr Leu Gly Asn Phe  
 20 25 30  
 Thr Ala Cys Met Phe Gly Met Thr Pro Ala Val Tyr Ser Leu Gln Thr  
 35 40 45  
 Asp Ser Leu Glu Lys Phe Ala Leu Glu Arg Asp Glu Glu Phe Arg Thr  
 50 55 60  
 Ser Phe Pro Leu Leu Asp Ser Leu Ser Thr Leu Thr Gly Phe Ser Pro  
 65 70 75 80  
 Ile Thr Thr Phe Val Gly Asn Arg His Asn Ser Ser Gln Asp Ile Val  
 85 90 95  
 Leu Ser Asn Tyr Lys Ser Ile Asp Asn Ile Leu Leu Leu Trp Thr Ser  
 100 105 110  
 Ala Gly Gly Ala Val Ser Cys Asn Asn Phe Leu Leu Ser Asn Val Glu  
 115 120 125  
 Asp His Ala Phe Phe Ser Lys Asn Leu Ala Ile Gly Thr Gly Gly Ala  
 130 135 140  
 Ile Ala Cys Gln Gly Ala Cys Thr Ile Thr Lys Asn Arg Gly Pro Leu  
 145 150 155 160  
 Ile Phe Phe Ser Asn Arg Gly Leu Asn Asn Ala Ser Thr Gly Gly Glu  
 165 170 175  
 Thr Arg Gly Gly Ala Ile Ala Cys Asn Gly Asp Phe Thr Ile Ser Gln  
 180 185 190  
 Asn Gln Gly Thr Phe Tyr Phe Val Asn Asn Ser Val Asn Asn Trp Gly  
 195 200 205  
 Gly Ala Leu Ser Thr Asn Gly His Cys Arg Ile Gln Ser Asn Arg Ala  
 210 215 220  
 Pro Leu Leu Phe Phe Asn Asn Thr Ala Pro Ser Gly Gly Gly Ala Leu  
 225 230 235 240  
 Arg Ser Glu Asn Thr Thr Ile Ser Asp Asn Thr Arg Pro Ile Tyr Phe  
 245 250 255  
 Lys Asn Asn Cys Gly Asn Asn Gly Gly Ala Ile Gln Thr Ser Val Thr  
 260 265 270  
 Val Ala Ile Lys Asn Asn Ser Gly Ser Val Ile Phe Asn Asn Asn Thr  
 275 280 285  
 Ala Leu Ser Gly Ser Ile Asn Ser Gly Asn Gly Ser Gly Gly Ala Ile  
 290 295 300  
 Tyr Thr Thr Asn Leu Ser Ile Asp Asp Asn Pro Gly Thr Ile Leu Phe  
 305 310 315 320  
 Asn Asn Asn Tyr Cys Ile Arg Asp Gly Gly Ala Ile Cys Thr Gln Phe  
 325 330 335  
 Leu Thr Ile Lys Asn Ser Gly His Val Tyr Phe Thr Asn Asn Gln Gly  
 340 345 350  
 Asn Trp Gly Gly Ala Leu Met Leu Leu Gln Asp Ser Thr Cys Leu Leu  
 355 360 365  
 Phe Ala Glu Gln Gly Asn Ile Ala Phe Gln Asn Asn Glu Val Phe Leu  
 370 375 380  
 Thr Thr Phe Gly Arg Tyr Asn Ala Ile His Cys Thr Pro Asn Ser Asn

385		390		395		400									
Leu	Gln	Leu	Gly	Ala	Asn	Lys	Gly	Tyr	Thr	Thr	Ala	Phe	Phe	Asp	Pro
		405							410					415	
Ile	Glu	His	Gln	His	Pro	Thr	Thr	Asn	Pro	Leu	Ile	Phe	Asn	Pro	Asn
		420						425					430		
Ala	Asn	His	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Ala	Tyr	Ile	Pro	Glu
		435					440					445			
Ala	Ser	Asp	Tyr	Glu	Asn	Asn	Phe	Ile	Ser	Ser	Ser	Lys	Asn	Thr	Ser
		450				455					460				
Glu	Leu	Arg	Asn	Gly	Val	Leu	Ser	Ile	Glu	Asp	Arg	Ala	Gly	Trp	Gln
465					470					475				480	
Phe	Tyr	Lys	Phe	Thr	Gln	Lys	Gly	Gly	Ile	Leu	Lys	Leu	Gly	His	Ala
			485						490					495	
Ala	Ser	Ile	Ala	Thr	Thr	Ala	Asn	Ser	Glu	Thr	Pro	Ser	Thr	Ser	Val
			500						505				510		
Gly	Ser	Gln	Val	Ile	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile
		515					520					525			
Leu	Ala	Lys	Gly	Lys	Ala	Pro	Thr	Leu	Trp	Ile	Arg	Pro	Leu	Gln	Ser
		530				535					540				
Ser	Ala	Pro	Phe	Thr	Glu	Asp	Asn	Asn	Pro	Thr	Ile	Thr	Leu	Ser	Gly
545					550					555				560	
Pro	Leu	Thr	Leu	Leu	Asn	Glu	Glu	Asn	Arg	Asp	Pro	Tyr	Asp	Ser	Ile
				565					570					575	
Asp	Leu	Ser	Glu	Pro	Leu	Gln	Asn	Ile	His	Leu	Leu	Ser	Leu	Ser	Asp
			580					585					590		
Val	Thr	Ala	Arg	His	Ile	Asn	Thr	Asp	Asn	Phe	His	Pro	Glu	Ser	Leu
		595					600					605			
Asn	Ala	Thr	Glu	His	Tyr	Gly	Tyr	Gln	Gly	Ile	Trp	Ser	Pro	Tyr	Trp
		610				615					620				
Val	Glu	Thr	Ile	Thr	Thr	Thr	Asn	Asn	Ala	Ser	Ile	Glu	Thr	Ala	Asn
625					630					635				640	
Thr	Leu	Tyr	Arg	Ala	Leu	Tyr	Ala	Asn	Trp	Thr	Pro	Leu	Gly	Tyr	Lys
			645						650					655	
Val	Asn	Pro	Glu	Tyr	Gln	Gly	Asp	Leu	Ala	Thr	Thr	Pro	Leu	Trp	Gln
			660					665					670		
Ser	Phe	His	Thr	Met	Phe	Ser	Leu	Leu	Arg	Ser	Tyr	Asn	Arg	Thr	Gly
		675					680					685			
Asp	Ser	Asp	Ile	Glu	Arg	Pro	Phe	Leu	Glu	Ile	Gln	Gly	Ile	Ala	Asp
		690				695					700				
Gly	Leu	Phe	Val	His	Gln	Asn	Ser	Ile	Pro	Gly	Ala	Pro	Gly	Phe	Arg
705					710					715				720	
Ile	Gln	Ser	Thr	Gly	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Thr	Ser	Leu
			725						730					735	
His	Gln	Lys	Ile	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Thr	Arg	Thr	Lys
			740					745					750		
Glu	Ile	Gly	Ser	Ser	Asn	Asn	Val	Ser	Ala	His	Asn	Thr	Val	Ser	Ser
		755				760						765			
Leu	Tyr	Val	Glu	Leu	Pro	Trp	Phe	Gln	Glu	Ala	Phe	Ala	Thr	Ser	Thr
		770				775						780			
Val	Leu	Ala	Tyr	Gly	Tyr	Gly	Asp	His	His	Leu	His	Ser	Leu	His	Pro
785					790					795				800	
Ser	His	Gln	Glu	Gln	Ala	Glu	Gly	Thr	Cys	Tyr	Ser	His	Thr	Leu	Ala
				805					810					815	
Ala	Ala	Ile	Gly	Cys	Ser	Phe	Pro	Trp	Gln	Gln	Lys	Ser	Tyr	Leu	His
			820					825					830		
Leu	Ser	Pro	Phe	Val	Gln	Ala	Ile	Ala	Ile	Arg	Ser	His	Gln	Thr	Ala
		835					840					845			
Phe	Glu	Ile	Gly	Asp	Asn	Pro	Arg	Lys	Phe	Val	Ser	Gln	Lys	Pro	
		850			855					860					
Phe	Tyr	Asn	Leu	Thr	Leu	Pro	Leu	Gly	Ile	Gln	Gly	Lys	Trp	Gln	Ser
865					870					875				880	
Lys	Phe	His	Val	Pro	Thr	Glu	Trp	Thr	Leu	Glu	Leu	Ser	Tyr	Glu	Pro
				885					890					895	
Val	Leu	Tyr	Gln	Gln	Asn	Pro	Gln	Ile	Gly	Val	Thr	Leu	Leu	Ala	Ser

900 905 910  
 Gly Gly Ser Trp Asp Ile Leu Gly His Asn Tyr Val Arg Asn Ala Leu  
 915 920 925  
 Gly Tyr Lys Val His Asn Gln Thr Ala Leu Phe Arg Ser Leu Asp Leu  
 930 935 940  
 Phe Leu Asp Tyr Gln Gly Ser Val Ser Ser Ser Thr Ser Thr His His  
 945 950 955 960  
 Leu Gln Ala Gly Ser Thr Leu Lys Phe  
 965

&lt;210&gt;502

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;502

Arg Cys Pro Val Ala Leu Asp Ala Ala Val Ser Ile Gly Gly Glu Gly  
 1 5 10 15  
 Ser Ser Pro Val Val Asp Gly Ile Val Asp Lys Val Glu Ser Pro Leu  
 20 25 30  
 Ile Leu Arg Asn Arg Glu Val Ser Ile Thr Gly Asn Arg Thr Pro Thr  
 35 40 45  
 Ser Phe Ser Ser Cys Thr Arg Ile Val Lys Thr Ser Ile Ala Glu Lys  
 50 55 60  
 Asn Lys Gly Ser Ser Ile Leu Arg Asp Cys Ala Gly Ser Leu Ala Ser  
 65 70 75 80  
 Asn Arg Ala Ser Ser Pro Asn Arg Glu Ile Phe Thr Glu Glu Gly Met  
 85 90 95  
 Val Phe Asn Ile  
 100

&lt;210&gt;503

&lt;211&gt;275

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;503

Ile Tyr Lys Leu Leu Asp Asn Lys Leu Met Ile Phe Tyr Asp Lys Leu  
 1 5 10 15  
 Tyr Phe His Ile Lys Val Trp Met Phe Met Arg Pro Ile Cys Leu Ser  
 20 25 30  
 Ile Leu Ser Thr Ala Leu Cys Cys Ser Leu Ser Gly Asn Glu Val Pro  
 35 40 45  
 Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His  
 50 55 60  
 Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser  
 65 70 75 80  
 Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly His Asp Ile Thr  
 85 90 95  
 Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr  
 100 105 110  
 Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys Lys Asn Leu Phe  
 115 120 125  
 Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His  
 130 135 140  
 Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys Trp Ile Ser Lys  
 145 150 155 160  
 Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr  
 165 170 175  
 Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile  
 180 185 190  
 Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn  
 195 200 205  
 Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser Ile Thr Asp Asn  
 210 215 220  
 Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser  
 225 230 235 240  
 Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile Glu Arg Asn Tyr

245 250 255  
 Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr  
 260 265 270  
 Phe Leu Pro  
 275  
 <210>504  
 <211>354  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>504  
 Cys Phe Arg Thr Arg Gly Gly Ile Phe Ser Ala Leu Gly Val Ile Ile  
 1 5 10 15  
 Ser Ser Asn Lys Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser  
 20 25 30  
 Ile Asn Thr Ala Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met  
 35 40 45  
 Cys Thr Ser Leu Val Ile Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn  
 50 55 60  
 Asn Lys Thr Ala Ala Leu Ser Gly Gly Ala Ile His Thr Arg Ser Phe  
 65 70 75 80  
 Ile Phe Gln Asn Asn Gly Pro Thr Ala Phe Ile Asn Asn Ser Ala Thr  
 85 90 95  
 Ser Gly Gly Ala Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln  
 100 105 110  
 Asn Phe Phe Leu Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn  
 115 120 125  
 Thr Ile Thr Ser Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr  
 130 135 140  
 Ala Ala Pro Gly Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys  
 145 150 155 160  
 Ile Leu Phe Tyr Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro  
 165 170 175  
 Ile Val Phe Asn Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser  
 180 185 190  
 Gly Ile Asn Val Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser  
 195 200 205  
 Lys Phe Ser Asn Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu  
 210 215 220  
 Asp Arg Ala Ala Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile  
 225 230 235 240  
 Leu Arg Leu Gly Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser  
 245 250 255  
 Ser Ile Asn Phe Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln  
 260 265 270  
 Ser Glu Ala Ser Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly  
 275 280 285  
 Ser Thr Tyr Ser Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro  
 290 295 300  
 Leu Thr Phe Leu Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp  
 305 310 315 320  
 Leu Ser Glu Pro Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys  
 325 330 335  
 Asp Cys Lys Lys Asn Arg Tyr Phe Glu Ser His Cys Arg Ser His Glu  
 340 345 350  
 Leu Arg

&lt;210&gt;505

&lt;211&gt;392

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;505

Ile Ser Leu Asn Leu Glu Arg Ile Ser Pro Leu Leu Tyr Leu Leu Asp  
 1 5 10 15  
 Val Thr Ala Lys Lys Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met



20 25 30  
 Asn Leu Asp Glu His Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp  
 35 40 45  
 Met Glu Thr Thr Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn  
 50 55 60  
 Thr Asn His Arg Gln Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg  
 65 70 75 80  
 Pro Asn Pro Glu Arg His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln  
 85 90 95  
 Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn  
 100 105 110  
 Leu Lys Glu His Asp Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu  
 115 120 125  
 Ile Asn Gln His Asn Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr  
 130 135 140  
 Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser  
 145 150 155 160  
 Phe Ser Leu Gly Phe Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln  
 165 170 175  
 Ser Pro Ser Thr Thr Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe  
 180 185 190  
 Asp Ser Leu Leu Phe Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly  
 195 200 205  
 Tyr Ser Tyr Gly Asp His His Met Leu Cys His Tyr Thr Glu Ile Leu  
 210 215 220  
 Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser  
 225 230 235 240  
 Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu  
 245 250 255  
 Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe  
 260 265 270  
 Gln Glu Thr Gly Asp His Ile Arg Lys Phe His Pro Lys His Pro Leu  
 275 280 285  
 Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser  
 290 295 300  
 His His Ile Pro Met Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr  
 305 310 315 320  
 Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn  
 325 330 335  
 Gly Thr Trp Thr Thr Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala  
 340 345 350  
 Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser  
 355 360 365  
 Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu  
 370 375 380  
 Lys Ala Glu Ser His Cys Thr Phe  
 385 390  
 <210>506  
 <211>822  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>506  
 Thr Val Gln Asn Asn Arg Ser Leu Ser Lys Ser Ser Phe Phe Val Gly  
 1 5 10 15  
 Ala Leu Ile Leu Gly Lys Thr Thr Ile Leu Leu Asn Ala Thr Pro Leu  
 20 25 30  
 Ser Asp Tyr Phe Asp Asn Gln Ala Asn Gln Leu Thr Thr Leu Phe Pro  
 35 40 45  
 Leu Ile Asp Thr Leu Thr Asn Met Thr Pro Tyr Ser His Arg Ala Thr  
 50 55 60  
 Leu Phe Gly Val Arg Asp Asp Thr Asn Gln Asp Ile Val Leu Asp His  
 65 70 75 80  
 Gln Asn Ser Ile Glu Ser Trp Phe Glu Asn Phe Ser Gln Asp Gly Gly  
 85 90 95

Ala	Leu	Ser	Cys	Lys	Ser	Leu	Ala	Ile	Thr	Asn	Thr	Lys	Asn	Gln	Ile
			100					105					110		
Leu	Phe	Leu	Asn	Ser	Phe	Ala	Ile	Lys	Arg	Ala	Gly	Ala	Met	Tyr	Val
		115					120					125			
Asn	Gly	Asn	Phe	Asp	Leu	Ser	Glu	Asn	His	Gly	Ser	Ile	Ile	Phe	Ser
	130					135					140				
Gly	Asn	Leu	Ser	Phe	Pro	Asn	Ala	Ser	Asn	Phe	Ala	Asp	Thr	Cys	Thr
145					150					155					160
Gly	Gly	Ala	Val	Leu	Cys	Ser	Lys	Asn	Val	Thr	Ile	Ser	Lys	Asn	Gln
			165						170					175	
Arg	Thr	Ala	Tyr	Phe	Ile	Asn	Asn	Lys	Ala	Lys	Ser	Ser	Gly	Gly	Ala
		180						185					190		
Ile	Gln	Ala	Ala	Ile	Ile	Asn	Ile	Lys	Asp	Asn	Thr	Gly	Pro	Cys	Leu
	195						200					205			
Phe	Phe	Asn	Asn	Ala	Ala	Gly	Xaa	Thr	Ala	Gly	Gly	Ala	Leu	Phe	Ala
	210					215					220				
Asn	Ala	Cys	Arg	Ile	Glu	Asn	Asn	Ser	Gln	Pro	Ile	Tyr	Phe	Leu	Asn
225					230					235					240
Asn	Gln	Ser	Gly	Leu	Gly	Gly	Ala	Ile	Arg	Val	His	Gln	Glu	Cys	Ile
			245						250					255	
Leu	Thr	Lys	Asn	Thr	Gly	Ser	Val	Ile	Phe	Asn	Asn	Asn	Phe	Ala	Met
		260					265						270		
Glu	Ala	Asp	Ile	Ser	Ala	Asn	His	Ser	Ser	Gly	Gly	Ala	Ile	Tyr	Cys
	275						280					285			
Ile	Ser	Cys	Ser	Ile	Lys	Asp	Asn	Pro	Gly	Ile	Ala	Ala	Phe	Asp	Asn
	290					295				300					
Asn	Thr	Ala	Ala	Arg	Asp	Gly	Gly	Ala	Ile	Cys	Thr	Gln	Ser	Leu	Thr
305					310					315					320
Ile	Gln	Asp	Ser	Gly	Pro	Val	Tyr	Phe	Thr	Asn	Asn	Gln	Gly	Thr	Trp
			325						330					335	
Gly	Gly	Ala	Ile	Met	Leu	Arg	Gln	Asp	Gly	Ala	Cys	Thr	Leu	Phe	Ala
		340						345					350		
Asp	Gln	Gly	Asp	Ile	Ile	Phe	Tyr	Asn	Asn	Arg	His	Phe	Lys	Asp	Thr
	355						360					365			
Phe	Ser	Asn	His	Val	Ser	Val	Asn	Cys	Thr	Arg	Asn	Val	Ser	Leu	Thr
	370					375					380				
Val	Gly	Ala	Ser	Gln	Gly	His	Ser	Ala	Thr	Phe	Tyr	Asp	Pro	Ile	Leu
385					390					395					400
Gln	Arg	Tyr	Thr	Ile	Gln	Asn	Ser	Ile	Gln	Lys	Phe	Asn	Pro	Asn	Pro
			405						410					415	
Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Ala	Tyr	Ile	Pro	Asp	Thr
		420						425					430		
Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser	His	Phe	Arg	Asn	His	Ile	Gly
	435					440						445			
Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu	Asp	Arg	Ala	Glu	Trp	Lys	Val
	450					455					460				
Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr	Leu	Arg	Leu	Gly	Ser	Arg	Ala
465					470					475					480
Val	Phe	Ser	Thr	Thr	Asp	Glu	Glu	Gln	Ser	Ser	Ser	Ser	Val	Gly	Ser
			485						490					495	
Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile	Leu	Gly
		500						505					510		
Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile	Arg	Pro	Thr	Gly	Ser	Ser	Ala
	515						520					525			
Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile	Ile	Asn	Leu	Ser	Gly	Pro	Leu
	530					535					540				
Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	Pro	Tyr	Asp	Thr	Ala	Asp	Leu
545					550					555					560
Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	Leu	Tyr	Leu	Leu	Asp	Val	Thr
			565						570					575	
Ala	Lys	His	Ile	Asn	Thr	Asp	Asn	Phe	Tyr	Pro	Glu	Gly	Leu	Asn	Thr
			580					585					590		
Thr	Gln	His	Tyr	Gly	Tyr	Gln	Gly	Val	Trp	Ser	Pro	Tyr	Trp	Ile	Glu
		595					600					605			

Thr Ile Thr Thr Ser Asp Thr Ser Ser Glu Asp Thr Val Asn Thr Leu  
 610 615 620  
 His Arg Gln Leu Tyr Gly Asp Trp Thr Pro Thr Gly Tyr Lys Val Asn  
 625 630 635 640  
 Pro Glu Asn Lys Gly Asp Ile Ala Leu Ser Ala Phe Trp Gln Ser Phe  
 645 650 655  
 His Asn Leu Phe Ala Thr Leu Arg Tyr Gln Thr Gln Gln Gly Gln Ile  
 660 665 670  
 Ala Pro Thr Ala Ser Gly Glu Ala Thr Arg Leu Phe Val His Gln Asn  
 675 680 685  
 Ser Asn Asn Asp Ala Lys Gly Phe His Met Glu Ala Thr Gly Tyr Ser  
 690 695 700  
 Leu Gly Thr Thr Ser Asn Thr Ala Ser Asn His Ser Phe Gly Val Asn  
 705 710 715 720  
 Phe Ser Gln Leu Phe Ser Asn Leu Tyr Glu Ser His Ser Asp Asn Ser  
 725 730 735  
 Val Ala Ser His Thr Thr Thr Val Ala Leu Gln Ile Asn Asn Pro Trp  
 740 745 750  
 Leu Gln Glu Arg Phe Ser Thr Ser Ala Ser Leu Ala Tyr Ser Tyr Ser  
 755 760 765  
 Asn His His Ile Lys Ala Ser Gly Tyr Ser Gly Lys Ile Gln Thr Glu  
 770 775 780  
 Gly Lys Cys Tyr Ser Thr Thr Leu Arg Gly Gly Ser Leu Leu Leu Ser  
 785 790 795 800  
 Ile Ser Thr Met Ala Ile Thr Thr Ser Pro Leu His Ser Phe Tyr Pro  
 805 810 815  
 Ser Asn Cys Arg Ser Phe  
 820

&lt;210&gt;507

&lt;211&gt;155

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;507

Gly Ala Ala Leu Ser Cys Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro  
 1 5 10 15  
 Leu His Phe Thr Pro Phe Ile Gln Ala Ile Ala Val Arg Ser Asn Gln  
 20 25 30  
 Thr Ala Phe Gln Glu Ser Gly Asp Lys Ala Arg Lys Phe Ser Val His  
 35 40 45  
 Lys Pro Leu Tyr Asn Leu Thr Val Pro Leu Gly Ile Gln Ser Ala Trp  
 50 55 60  
 Glu Ser Lys Phe Arg Leu Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr  
 65 70 75 80  
 Gln Pro Val Leu Tyr Gln Gln Asn Pro Glu Val Asn Val Ser Leu Glu  
 85 90 95  
 Ser Ser Gly Ser Ser Trp Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn  
 100 105 110  
 Ala Ile Ala Phe Lys Gly Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu  
 115 120 125  
 Ser Val Phe Leu Asp Tyr Gln Gly Ser Val Ser Ser Ser Thr Thr Thr  
 130 135 140  
 His Tyr Leu His Ala Gly Thr Thr Phe Lys Phe  
 145 150 155

&lt;210&gt;508

&lt;211&gt;778

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;508

Glu Val Phe Met Ala Ser Gly Ile Gly Gly Ser Ser Gly Leu Gly Lys  
 1 5 10 15  
 Ile Pro Pro Lys Asp Asn Gly Asp Arg Ser Arg Ser Pro Ser Pro Lys  
 20 25 30  
 Gly Glu Leu Gly Ser His Glu Ile Ser Leu Pro Pro Gln Glu His Gly  
 35 40 45

Glu	Glu	Gly	Ala	Ser	Gly	Ser	Ser	His	Ile	His	Ser	Ser	Ser	Ser	Phe
50						55					60				
Leu	Pro	Glu	Asp	Gln	Glu	Ser	Gln	Ser	Ser	Ser	Ser	Ala	Ala	Ser	Ser
65					70					75					80
Pro	Gly	Phe	Phe	Ser	Arg	Val	Arg	Ser	Gly	Val	Asp	Arg	Ala	Leu	Lys
				85					90					95	
Ser	Phe	Gly	Asn	Phe	Phe	Ser	Ala	Glu	Ser	Thr	Ser	Gln	Ala	Arg	Glu
			100					105					110		
Thr	Arg	Gln	Ala	Phe	Val	Arg	Leu	Ser	Lys	Thr	Ile	Thr	Ala	Asp	Glu
		115					120					125			
Arg	Arg	Asp	Val	Asp	Ser	Ser	Ser	Ala	Ala	Ala	Thr	Glu	Ala	Arg	Val
	130					135					140				
Ala	Glu	Asp	Ala	Ser	Val	Ser	Gly	Glu	Asn	Pro	Ser	Gln	Gly	Val	Pro
145					150					155					160
Glu	Thr	Ser	Ser	Gly	Pro	Glu	Pro	Gln	Arg	Leu	Phe	Ser	Leu	Pro	Ser
				165					170					175	
Val	Lys	Lys	Gln	Ser	Gly	Leu	Gly	Arg	Leu	Val	Gln	Thr	Val	Arg	Asp
			180					185					190		
Arg	Ile	Val	Leu	Pro	Ser	Gly	Ala	Pro	Pro	Thr	Asp	Ser	Glu	Pro	Leu
	195						200					205			
Ser	Leu	Tyr	Glu	Leu	Asn	Leu	Arg	Leu	Ser	Ser	Leu	Arg	Gln	Glu	Leu
	210					215					220				
Ser	Asp	Ile	Gln	Ser	Asn	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Lys	Ala	Glu
225					230					235					240
Ala	Thr	Val	Thr	Ile	Gln	Gln	Leu	Ile	Gln	Ile	Thr	Glu	Phe	Gln	Cys
				245					250					255	
Gly	Tyr	Met	Glu	Ala	Thr	Gln	Ser	Ser	Val	Ser	Leu	Ala	Glu	Ala	Arg
			260					265					270		
Phe	Lys	Gly	Val	Glu	Thr	Ser	Asp	Glu	Ile	Asn	Ser	Leu	Cys	Ser	Glu
		275					280					285			
Leu	Thr	Asp	Pro	Glu	Leu	Gln	Glu	Leu	Met	Ser	Asp	Gly	Asp	Ser	Leu
	290					295					300				
Gln	Asn	Leu	Leu	Asp	Glu	Thr	Ala	Asp	Asp	Leu	Glu	Ala	Ala	Leu	Ser
305					310					315					320
His	Ala	Arg	Leu	Ser	Phe	Ser	Leu	Asp	Asp	Asn	Pro	Thr	Pro	Ile	Asp
				325					330					335	
Asn	Asn	Pro	Thr	Leu	Ile	Ser	Gln	Glu	Glu	Pro	Ile	Tyr	Glu	Glu	Ile
			340					345					350		
Gly	Gly	Ala	Ala	Asp	Pro	Gln	Arg	Thr	Arg	Glu	Asn	Trp	Ser	Thr	Arg
		355					360					365			
Leu	Trp	Asn	Gln	Ile	Arg	Glu	Ala	Leu	Val	Ser	Leu	Leu	Gly	Met	Ile
	370					375					380				
Leu	Ser	Ile	Leu	Gly	Ser	Ile	Leu	His	Arg	Leu	Arg	Ile	Ala	Arg	His
385					390					395					400
Ala	Ala	Ala	Glu	Ala	Val	Gly	Arg	Cys	Cys	Thr	Cys	Arg	Gly	Glu	Glu
				405					410					415	
Cys	Thr	Ser	Ser	Glu	Glu	Asp	Ser	Met	Ser	Val	Gly	Ser	Pro	Ser	Glu
			420					425					430		
Ile	Asp	Glu	Thr	Glu	Arg	Thr	Gly	Ser	Pro	His	Asp	Val	Pro	Arg	Arg
		435					440					445			
Asn	Gly	Ser	Pro	Arg	Glu	Asp	Ser	Pro	Leu	Met	Asn	Ala	Leu	Val	Gly
	450					455					460				
Trp	Ala	His	Lys	His	Gly	Ala	Lys	Thr	Lys	Glu	Ser	Ser	Glu	Ser	Ser
465					470					475					480
Thr	Pro	Glu	Ile	Ser	Ile	Ser	Ala	Pro	Ile	Val	Arg	Gly	Trp	Ser	Gln
				485					490					495	
Asp	Ser	Ser	Val	Ser	Phe	Ile	Val	Met	Glu	Asp	Asp	His	Ile	Phe	Tyr
			500					505					510		
Asp	Val	Pro	Arg	Arg	Lys	Asp	Gly	Ile	Tyr	Asp	Val	Pro	Ser	Ser	Pro
		515					520					525			
Arg	Trp	Ser	Pro	Ala	Arg	Glu	Leu	Glu	Glu	Asp	Val	Phe	Gly	Asp	Tyr
	530					535					540				
Glu	Val	Pro	Ile	Thr	Ser	Ala	Glu	Pro	Ser	Lys	Asp	Lys	Asn	Ile	Tyr
545					550					555					560

Met Thr Pro Arg Leu Ala Thr Pro Ala Ile Tyr Asp Leu Pro Ser Arg  
565 570 575  
Pro Gly Ser Ser Gly Ser Ser Arg Ser Pro Ser Ser Asp Arg Val Arg  
580 585 590  
Ser Ser Ser Pro Asn Arg Arg Gly Val Pro Leu Pro Pro Val Pro Ser  
595 600 605  
Pro Ala Met Ser Glu Glu Gly Ser Ile Tyr Glu Asp Met Ser Gly Ala  
610 615 620  
Ser Gly Ala Gly Glu Ser Asp Tyr Glu Asp Met Ser Arg Ser Pro Ser  
625 630 635 640  
Pro Arg Gly Asp Leu Asp Glu Pro Ile Tyr Ala Asn Thr Pro Glu Asp  
645 650 655  
Asn Pro Phe Thr Gln Arg Asn Ile Asp Arg Ile Leu Gln Glu Arg Ser  
660 665 670  
Gly Gly Ala Ser Ala Ser Pro Val Glu Pro Ile Tyr Asp Glu Ile Pro  
675 680 685  
Trp Ile His Gly Arg Pro Pro Ala Thr Leu Pro Arg Pro Glu Asn Thr  
690 695 700  
Leu Thr Asn Val Ser Leu Arg Val Ser Pro Gly Phe Gly Pro Glu Val  
705 710 715 720  
Arg Ala Ala Leu Leu Ser Glu Ser Val Ser Ala Val Met Val Glu Ala  
725 730 735  
Glu Ser Ile Val Pro Pro Thr Glu Pro Gly Asp Gly Glu Ser Glu Tyr  
740 745 750  
Leu Glu Pro Leu Gly Gly Leu Val Ala Thr Thr Lys Ile Leu Leu Gln  
755 760 765  
Lys Gly Trp Pro Arg Gly Glu Ser Asn Ala  
770 775

&lt;210&gt;509

&lt;211&gt;511

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;509

Gly Ser Ile Met Ala Val Gly Gly Val Gly Gly Ser Arg Ser Pro Ser  
1 5 10 15  
Pro Ile Pro Pro Asn Arg Arg Asn Ser Glu Asp Gly Lys Val Ser Pro  
20 25 30  
Lys Asp Asn Leu Gly Glu His Thr Val Ser Ser Ser Asp Ser Ser Leu  
35 40 45  
Ala Ser Gln Gly Pro Thr Ile Glu Glu Arg Lys Ala Gln Leu Gly Gly  
50 55 60  
Thr Asp Lys Ile Pro Leu Pro Ser Val Lys Glu Pro Gly Asp Ser Pro  
65 70 75 80  
Thr Ser Gly Arg Ser Gly Val Leu Gln Arg Ile Trp Lys Gly Val Lys  
85 90 95  
Gly Val Phe Lys Lys Thr Pro Gln Ala Arg Pro Glu Val Ser Ser Pro  
100 105 110  
Arg Leu Pro Ser His Val Gln His Gly Gln Arg Leu Pro Gly Leu Glu  
115 120 125  
Gly Phe Arg Asp Arg Ile Gln Lys Arg Ser Glu Asn Pro Glu Ala Asp  
130 135 140  
Leu Gly Lys Met Lys Arg Ser Tyr Ser Asp Gly Asp Leu Asp Arg Val  
145 150 155 160  
Gly His Asp Ser Asn Glu Asp Ser Thr Glu Asp Ser Arg Ser Glu Gly  
165 170 175  
Gly Glu Pro Ser Lys Ser Ser Ser Phe Leu Ser Gly Val Arg Gly  
180 185 190  
Ala Val Ser Lys Val His Gly Ala Leu Gly Asp Ile Lys Gly Lys Phe  
195 200 205  
Gln Arg Ser Ala Ser Glu Asp Asp Leu Thr Thr Gln Gly Glu Asp Ser  
210 215 220  
Ala Gly Asp Thr Val Lys Glu Arg Arg Ser Glu Glu Ala Glu Ala Ser  
225 230 235 240  
Ser Lys Ser Ser Ser Phe Leu Ser Gly Val Arg Gly Ala Thr Ser Thr

245 250 255  
 Val Gln Gly Ala Leu Gly Asp Ala Lys Glu Lys Val Ser Ala Phe Gly  
 260 265 270  
 Glu Gln Ala Ala Gly Ala Ile Arg Ser Ala Pro Gly Asn Ile Arg Thr  
 275 280 285  
 Arg Phe Gln Arg Ser Ser Ser Glu Gly Asp Leu Ser Asn Val Asn Lys  
 290 295 300  
 Ala Ala Lys His Leu Arg Lys Ala Leu Glu Asn Leu Glu Lys Val Ala  
 305 310 315 320  
 Pro Glu Gln Val Ser Pro Glu Val Ala Ser Arg Val Gln Ser Leu Leu  
 325 330 335  
 Ala Arg Met Glu Gln Leu Thr His Gln Glu Pro Pro Thr Val Glu Asp  
 340 345 350  
 Leu Ile Thr Phe Val Glu Ser Asn Val Gly Ser Asp Ser Val Glu Tyr  
 355 360 365  
 Ala Ser Ile Val Pro Gln Asp Gly Ser Gln Ala Pro Ala Glu Thr Ala  
 370 375 380  
 Glu Ala Pro Glu Thr Gly Gly Val Glu Gly Ser Ala Ala Gln Gly Ala  
 385 390 395 400  
 Trp Lys Ala Leu Arg Asp Phe Val Val Ser Ile Phe Gln Ala Val Ala  
 405 410 415  
 Ser Phe Phe Arg Ala Ile Ala Ser Arg Leu Ser Ser Ala Arg Arg Glu  
 420 425 430  
 Ser Ala Val Asp Asp Leu Ala Ser Glu Ser Asn Thr Gln Trp Phe Val  
 435 440 445  
 Glu Gln Glu Gly Val Ser Asn Pro Ser Ala Ala Pro Ser Leu Ser Phe  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Arg Ala Ala Glu Met Ser Asn Arg Asn Ala  
 465 470 475 480  
 Gln Ser Leu Glu Lys Leu Glu Ser Gly Asn Val Thr Asp Pro Val Ile  
 485 490 495  
 Gln Gln Gly Leu Gly Leu Ala Arg Ser Phe Ala Pro Glu Gly Gln  
 500 505 510

&lt;210&gt;510

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;510

Met Thr Gly Ser Val Thr Leu Pro Asp Ser Asn Phe Ser Arg Leu Trp  
 1 5 10 15  
 Ala Phe Leu Leu Ile Ser Ala Ala Leu Arg Ala Ile Ser Ser Ala  
 20 25 30  
 Lys Asp Lys Leu Gly Ala Ala Asp Gly Phe Glu Thr Pro Ser Cys Ser  
 35 40 45  
 Thr Asn His Cys Val Leu Leu Ser Asp Ala Arg Ser Ser Thr Ala Asp  
 50 55 60  
 Ser Arg Arg Ala Glu Leu Asn Leu Glu Ala Ile Ala Leu Lys Lys Leu  
 65 70 75 80  
 Ala Thr Ala Trp Asn Met Leu Thr Thr Lys Ser Arg Asn Ala Phe His  
 85 90 95  
 Ala Pro Cys Ala Ala Asp Pro Ser Thr Pro Pro Val Ser Gly Ala Ser  
 100 105 110  
 Ala Val Ser Ala Gly Ala Cys Asp Pro Ser  
 115 120

&lt;210&gt;511

&lt;211&gt;598

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;511

Leu Lys Ile Ile Ile Ser Ile Ser Phe Met Ser Thr Ser Pro Ile Ser  
 1 5 10 15  
 Asn Asp Pro Arg Tyr Leu Ser Leu Ser Asn Ala Thr Glu Lys Thr Ser  
 20 25 30  
 Leu Leu Ala Asn Ser Arg Ser Leu Ser Pro Val Pro Asn Ser Leu Val

35				40				45							
Pro	Ser	Asn	Pro	Glu	Asp	Thr	Gly	Leu	Arg	Lys	Ser	Ile	Phe	Thr	His
50						55					60				
Ser	Val	Thr	Leu	Phe	Ala	Gly	Leu	Val	Val	Leu	Leu	Val	Ala	Val	Ser
65					70					75					80
Val	Val	Val	Val	Ala	Leu	Thr	Val	Leu	Ala	Pro	Gly	Val	Pro	Gln	Ala
				85					90					95	
Ile	Leu	Leu	Gly	Ile	Ala	Ile	Ser	Gly	Val	Gly	Ile	Gly	Gly	Phe	Ser
			100					105					110		
Ile	Met	Lys	Ser	Leu	Val	Tyr	Met	Val	Arg	Asp	Tyr	Met	Ser	Pro	Arg
		115					120					125			
Met	Gln	Glu	Ser	Ser	Arg	Ile	Lys	Ser	Ala	Leu	Ala	Val	Gly	Thr	Gly
	130					135					140				
Phe	Thr	Val	Met	Gly	Leu	Val	Met	Lys	Val	Gly	Ala	Asn	Phe	Val	Pro
145					150					155					160
Gly	Gly	Tyr	Gly	Gly	Leu	Val	Gly	Ser	Leu	Gly	Ser	Ser	Ala	Tyr	Ser
				165					170					175	
Arg	Gly	Ser	Gln	Thr	Thr	Leu	Ala	Ser	Phe	Ser	His	Tyr	Ile	Tyr	Thr
			180					185					190		
Lys	Phe	Phe	Arg	Ser	Glu	Lys	Val	Ala	Lys	Gly	Glu	Lys	Leu	Thr	Glu
		195					200					205			
Ala	Glu	Thr	Ile	Lys	Glu	Ala	Lys	Lys	Leu	His	Tyr	Ile	Thr	Leu	Ser
	210					215					220				
Ile	Ala	Thr	Ile	Gly	Val	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Leu	Ala
225					230					235					240
Ile	Ala	Gly	Thr	Val	Leu	Leu	Gly	Gly	Ala	Pro	Ala	Thr	Ile	Ala	Ile
				245					250					255	
Ile	Leu	Ala	Pro	Pro	Leu	Ile	Ser	Ile	Gly	Leu	Thr	Thr	Val	Leu	Gln
			260				265						270		
Thr	Ile	Leu	His	Ser	Ser	Ile	Gly	Lys	Trp	Arg	Ala	Phe	Leu	Leu	Thr
		275					280					285			
Gln	Glu	Lys	Lys	Asp	Leu	Phe	Val	Asp	Thr	Ser	Leu	Lys	Asp	Ile	Arg
	290				295						300				
Leu	Glu	Lys	Leu	Pro	Pro	Ser	Glu	Val	Glu	Glu	Ser	Glu	Thr	Ser	Gln
305					310					315					320
Ser	Val	Ile	Glu	Val	Pro	Asp	Ser	Glu	Gly	Ile	Ala	Glu	Thr	Arg	Ile
				325					330					335	
Ser	Ala	Glu	Glu	Ile	Asp	Thr	Arg	Leu	Ser	Leu	Thr	Thr	Arg	Gln	Lys
			340					345					350		
Val	Ile	Phe	Ala	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Ala	Ser	Ile	Ala	Ala
		355					360					365			
Phe	Ile	Val	Thr	Gly	Phe	Gly	Gly	Leu	Thr	Val	Met	Gln	Val	Leu	Leu
	370					375					380				
Val	Ala	Ser	Val	Gly	Ser	Ala	Val	Ala	Ser	Val	Thr	Leu	Pro	Met	Val
385					390					395					400
Ser	Ser	Gly	Phe	Ser	Tyr	Val	Ala	Tyr	Gln	Leu	Lys	Ala	Arg	Leu	Asn
				405					410					415	
Ile	Ser	Lys	Leu	Arg	Trp	Lys	Glu	Ala	Lys	Asn	Lys	Lys	Arg	Val	Arg
			420					425					430		
Gln	Phe	Leu	Ile	Glu	Ser	Gly	Val	Ile	Ala	Ser	Asp	Arg	Glu	Phe	Asn
		435					440					445			
Gln	Met	Trp	Lys	Thr	Val	Tyr	Lys	Lys	Gln	Ile	Gln	Lys	Thr	Asp	Ala
	450					455					460				
Ala	Ile	Arg	Glu	Glu	Val	Arg	Asn	Phe	Glu	Lys	Gly	Gly	Glu	Val	Asn
465					470					475					480
Ser	Ala	Leu	Val	Gly	Gly	Ile	Leu	Leu	Gly	Val	Gly	Thr	Gly	Ile	Met
				485					490					495	
Leu	Leu	Ala	Leu	Val	Pro	Ala	Phe	Ala	Pro	Ile	Val	Pro	Gly	Ile	Leu
		500					505						510		
Ala	Leu	Gly	Gly	Ser	Thr	Leu	Gly	Ile	Ala	Gly	Ser	Ile	Leu	Met	Arg
		515					520					525			
Lys	Phe	Val	Asn	Trp	Leu	Tyr	Asp	Glu	Leu	Val	Lys	Leu	Tyr	Glu	Arg
	530					535					540				
Arg	Arg	Asn	Arg	Arg	Glu	Leu	Leu	Tyr	Gly	Pro	Glu	Ser	Lys	Met	Arg





```
<210>514
<211>340
<212>PRT
<213>Chlamydia pneumoniae
<400>514
```

Gly Arg Gly Arg Arg Ala Asp Trp Gly Asp Cys Met Ile Asp Ile Met  
 1 5 10 15  
 Gln His Phe Lys Pro Tyr Thr Met Val Pro Gly Gln Lys Leu Pro Ile  
 20 25 30  
 Pro Gly Ser Leu Leu Tyr Ala Gln Val Phe Pro Thr Leu Trp Arg Leu  
 35 40 45  
 Phe Ser Ser Lys His Glu Ile Leu Asn Glu Gln Thr Leu Gln Val Gln  
 50 55 60  
 Gly Pro Leu Lys Arg Phe Ala Val Phe Gln Asp Leu His Arg Gly Gly  
 65 70 75 80  
 Leu Ala Val Thr Ser Glu Arg Tyr Lys Tyr Tyr Leu Leu Pro Ser Gly  
 85 90 95  
 Glu Cys Thr Gln Ser Ile Lys Gly Lys Leu Pro Ser Ala Ala Gln Ala  
 100 105 110  
 Gly Pro Leu Leu Ser Leu Gly Val His Lys His Ala Asp Trp Gln Lys  
 115 120 125  
 Val Arg Cys Arg Arg Asp Leu Lys Glu Ile Leu Pro Leu Trp Phe Arg  
 130 135 140  
 Phe Ala Ala Met Ala Pro Lys Gly Ser Tyr Arg Asp Leu Glu Thr Thr  
 145 150 155 160  
 Ala Ile Gly Ser Leu Val Lys Thr Ala His Gln Arg Val Leu His Arg  
 165 170 175  
 Glu Thr Thr Glu Ile Ala Pro Ala Leu Leu Ser Ile Ala Leu Ala Gly  
 180 185 190  
 Phe Ser Glu Cys Phe Leu Pro Arg Ser Tyr Asp Glu Glu Phe Gln Gly  
 195 200 205  
 Ile Leu Pro Gln Asp Gly Asp Pro Glu Gly Gly Val Pro Phe Glu Leu  
 210 215 220  
 Leu Ser Tyr Ser Phe Gly Met Ile Gln Asp Ile Phe Leu Arg His Gln  
 225 230 235 240  
 Gly Gln Leu Val Glu Ile Leu Pro Ala Leu Pro Pro Glu Phe Pro Cys  
 245 250 255  
 Gly Arg Leu Ile His Val Ala Leu Pro Asn Leu Gly Thr Leu Ser Ile  
 260 265 270  
 Val Trp Thr Lys Lys Thr Ile Arg Gln Val Glu Leu His Ala Glu Tyr  
 275 280 285  
 Ser Gly Glu Val Phe Leu Lys Phe Cys Ser Ser Leu Cys Ser Ala Arg  
 290 295 300  
 Leu Arg Glu Trp Ser Glu Arg Arg Leu Ser Gly Ser Lys Arg Leu Ser  
 305 310 315 320  
 Leu Gly Glu Thr Leu Glu Ile Lys Ala Gly Thr Thr Tyr Leu Trp Asp  
 325 330 335  
 Cys Phe His Lys  
 340

&lt;210&gt;515

&lt;211&gt;423

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;515

Arg Tyr Met Thr Val Ala Glu Val Lys Gly Thr Phe Lys Leu Val Cys  
 1 5 10 15  
 Leu Gly Cys Arg Val Asn Gln Tyr Glu Val Gln Ala Tyr Arg Asp Gln  
 20 25 30  
 Leu Thr Ile Leu Gly Tyr Gln Glu Val Leu Asp Ser Glu Ile Pro Ala  
 35 40 45  
 Asp Leu Cys Ile Ile Asn Thr Cys Ala Val Thr Ala Ser Ala Glu Ser  
 50 55 60  
 Ser Gly Arg His Ala Val Arg Gln Leu Cys Arg Gln Asn Pro Thr Ala  
 65 70 75 80  
 His Ile Val Val Thr Gly Cys Leu Gly Glu Ser Asp Lys Glu Phe Phe  
 85 90 95  
 Ala Ser Leu Asp Arg Gln Cys Thr Leu Val Ser Asn Lys Glu Lys Ser  
 100 105 110  
 Arg Leu Ile Glu Lys Ile Phe Ser Tyr Asp Thr Thr Phe Pro Glu Phe

115 120 125  
 Lys Ile His Ser Phe Glu Gly Lys Ser Arg Ala Phe Ile Lys Val Gln  
 130 135 140  
 Asp Gly Cys Asn Ser Phe Cys Ser Tyr Cys Ile Ile Pro Tyr Leu Arg  
 145 150 155 160  
 Gly Arg Ser Val Ser Arg Pro Ala Glu Lys Ile Leu Ala Glu Ile Ala  
 165 170 175  
 Gly Val Val Asp Gln Gly Tyr Arg Glu Val Val Ile Ala Gly Ile Asn  
 180 185 190  
 Val Gly Asp Tyr Cys Asp Gly Glu Arg Ser Leu Ala Ser Leu Ile Glu  
 195 200 205  
 Gln Val Asp Gln Ile Pro Gly Ile Glu Arg Ile Arg Ile Ser Ser Ile  
 210 215 220  
 Asp Pro Asp Asp Ile Thr Glu Asp Leu His Arg Ala Ile Thr Ser Ser  
 225 230 235 240  
 Arg His Thr Cys Pro Ser Ser His Leu Val Leu Gln Ser Gly Ser Asn  
 245 250 255  
 Ser Ile Leu Lys Arg Met Asn Arg Lys Tyr Ser Arg Gly Asp Phe Leu  
 260 265 270  
 Asp Cys Val Glu Lys Phe Arg Ala Ser Asp Pro Arg Tyr Ala Phe Thr  
 275 280 285  
 Thr Asp Val Ile Val Gly Phe Pro Gly Glu Ser Asp Gln Asp Phe Glu  
 290 295 300  
 Asp Thr Leu Arg Ile Ile Glu Asp Val Gly Phe Ile Lys Val His Ser  
 305 310 315 320  
 Phe Pro Phe Ser Ala Arg Arg Arg Thr Lys Ala Tyr Thr Phe Asp Asn  
 325 330 335  
 Gln Ile Pro Asn Gln Val Ile Tyr Glu Arg Lys Lys Tyr Leu Ala Glu  
 340 345 350  
 Val Ala Lys Arg Val Gly Gln Lys Glu Met Met Lys Arg Leu Gly Glu  
 355 360 365  
 Thr Thr Glu Val Leu Val Glu Lys Val Thr Gly Gln Val Ala Thr Gly  
 370 375 380  
 His Ser Pro Tyr Phe Glu Lys Val Ser Phe Pro Val Val Gly Thr Val  
 385 390 395 400  
 Ala Ile Asn Thr Leu Val Ser Val Arg Leu Asp Arg Val Glu Glu Glu  
 405 410 415  
 Gly Leu Ile Gly Glu Ile Val  
 420

&lt;210&gt;516

&lt;211&gt;472

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;516

Leu Asp Thr Ile Asp Thr Pro Gly Glu Gln Gly Ser Gln Ser Phe Gly  
 1 5 10 15  
 Asn Ser Leu Gly Ala Arg Phe Asp Leu Pro Arg Lys Glu Gln Asp Pro  
 20 25 30  
 Ser Gln Ala Leu Ala Val Ala Ser Tyr Gln Asn Lys Thr Asp Ser Gln  
 35 40 45  
 Val Val Glu Glu His Leu Asp Glu Leu Ile Ser Leu Ala Asp Ser Cys  
 50 55 60  
 Gly Ile Ser Val Leu Glu Thr Arg Ser Trp Ile Leu Lys Thr Pro Ser  
 65 70 75 80  
 Ala Ser Thr Tyr Ile Asn Val Gly Lys Leu Glu Glu Ile Glu Glu Ile  
 85 90 95  
 Leu Lys Glu Phe Pro Ser Ile Gly Thr Leu Ile Ile Asp Glu Glu Ile  
 100 105 110  
 Thr Pro Ser Gln Gln Arg Asn Leu Glu Lys Arg Leu Gly Leu Val Val  
 115 120 125  
 Leu Asp Arg Thr Glu Leu Ile Leu Glu Ile Phe Ser Ser Arg Ala Leu  
 130 135 140  
 Thr Ala Glu Ala Asn Ile Gln Val Gln Leu Ala Gln Ala Arg Tyr Leu  
 145 150 155 160

Leu Pro Arg Leu Lys Arg Leu Trp Gly His Leu Ser Arg Gln Lys Ser  
 165 170 175  
 Gly Gly Gly Ser Gly Gly Phe Val Lys Gly Glu Gly Glu Lys Gln Ile  
 180 185 190  
 Glu Leu Asp Arg Arg Met Val Arg Glu Arg Ile His Lys Leu Ser Ala  
 195 200 205  
 Gln Leu Lys Ala Val Ile Lys Gln Arg Ala Glu Arg Arg Lys Val Lys  
 210 215 220  
 Ser Arg Arg Gly Ile Pro Thr Phe Ala Leu Ile Gly Tyr Thr Asn Ser  
 225 230 235 240  
 Gly Lys Ser Thr Leu Leu Asn Leu Leu Thr Ala Ala Asp Thr Tyr Val  
 245 250 255  
 Glu Asp Lys Leu Phe Ala Thr Leu Asp Pro Lys Thr Arg Lys Cys Val  
 260 265 270  
 Leu Pro Gly Gly Arg His Val Leu Leu Thr Asp Thr Val Gly Phe Ile  
 275 280 285  
 Arg Lys Leu Pro His Thr Leu Val Ala Ala Phe Lys Ser Thr Leu Glu  
 290 295 300  
 Ala Ala Phe His Glu Asp Val Leu Leu His Val Val Asp Ala Ser His  
 305 310 315 320  
 Pro Leu Ala Leu Glu His Val Gln Thr Thr Tyr Asp Leu Phe Gln Glu  
 325 330 335  
 Leu Lys Ile Glu Lys Pro Arg Ile Ile Thr Val Leu Asn Lys Val Asp  
 340 345 350  
 Arg Leu Pro Gln Gly Ser Ile Pro Met Lys Leu Arg Leu Leu Ser Pro  
 355 360 365  
 Leu Pro Val Leu Ile Ser Ala Lys Thr Gly Glu Gly Ile Gln Asn Leu  
 370 375 380  
 Leu Ser Leu Met Thr Glu Ile Ile Gln Glu Lys Ser Leu His Val Thr  
 385 390 395 400  
 Leu Asn Phe Pro Tyr Thr Glu Tyr Gly Lys Phe Thr Glu Leu Cys Asp  
 405 410 415  
 Ala Gly Val Val Ala Ser Ser Arg Tyr Gln Glu Asp Phe Leu Val Val  
 420 425 430  
 Glu Ala Tyr Leu Pro Lys Glu Leu Gln Lys Lys Phe Arg Pro Phe Ile  
 435 440 445  
 Ser Tyr Val Phe Pro Glu Asp Cys Gly Asp Asp Glu Gly Arg Gly Pro  
 450 455 460  
 Val Leu Glu Ser Ser Phe Gly Asp  
 465 470  
 <210>517  
 <211>273  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>517  
 Ala Ile Gly Met Val Arg Asp Ile Gln Ser Glu Ser Ile Gly Lys Leu  
 1 5 10 15  
 Val Phe Leu Gly Thr Gly Asn Pro Glu Gly Ile Pro Val Pro Phe Cys  
 20 25 30  
 Ser Cys Arg Val Cys Gln Asn Thr Gly Ile His Arg Leu Arg Ser Ser  
 35 40 45  
 Val Leu Ile Gln Tyr Gln Asn Lys Thr Leu Val Ile Asp Ala Gly Pro  
 50 55 60  
 Asp Phe Arg Thr Gln Met Leu Val Ala Gly Val Ser Glu Leu Asp Gly  
 65 70 75 80  
 Val Phe Leu Thr His Pro His Tyr Asp His Ile Gly Gly Ile Asp Asp  
 85 90 95  
 Leu Arg Ala Trp Tyr Ile Val Thr Gln Arg Ser Leu Pro Leu Val Leu  
 100 105 110  
 Ser Ala Ser Thr Tyr Arg Phe Leu Asn Lys Ala Lys Glu Tyr Leu Phe  
 115 120 125  
 Ala Thr Pro Asn Val Glu Ser Ser Leu Pro Ala Val Leu Glu Phe Thr  
 130 135 140  
 Ile Leu Asn Glu Asp Cys Gly Gln Glu Glu Phe Gln Gly Ile Pro Tyr

145 150 155 160  
 Thr Tyr Val Ser Tyr Tyr Gln Lys Ser Cys His Val Thr Gly Phe Arg  
 165 170 175  
 Phe Gly Asn Leu Ala Tyr Leu Thr Asp Leu Cys Ser Tyr Asp Ala Lys  
 180 185 190  
 Ile Phe Ser Tyr Leu Asp Asn Val Glu Thr Leu Ile Leu Ser Ala Gly  
 195 200 205  
 Pro Ser Glu Thr Pro Ile Pro Phe Gln Gly His Lys Ser Ser His Leu  
 210 215 220  
 Thr Val Glu Glu Ala Lys Ala Phe Ala Asn His Ala Gly Ile Lys Asn  
 225 230 235 240  
 Leu Ile Ile Thr His Ile Ser His Cys Leu Glu Ala Glu Arg Asp Gln  
 245 250 255  
 His Pro Glu Val Thr Phe Ala Tyr Asp Gly Met Glu Val Leu Trp Thr  
 260 265 270  
 Leu

&lt;210&gt;518

&lt;211&gt;242

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;518

Ser Asp Xaa Xaa Ile Ser Trp Gly Ile Ser Gly Arg Leu Gly Glu Phe  
 1 5 10 15  
 Val Ser Lys Lys Glu Gln Asp Cys Met Leu Gly Ser Leu Pro Cys Tyr  
 20 25 30  
 Pro Gly Ala Gly Asn Ile Glu Glu Tyr Lys Asn Arg Tyr Phe Tyr Cys  
 35 40 45  
 Gln Leu Cys Ala Glu Val Val Ser Pro Tyr Val Val Pro Val Ile Val  
 50 55 60  
 Val Asp Val Gln Gly Ala Pro Pro Thr Gly Ile Leu Gln Val Leu Arg  
 65 70 75 80  
 Cys Lys Gln His Lys Phe Gln Gly Leu Pro Val His Gly Pro Ile Thr  
 85 90 95  
 Ser Leu Trp Ala Leu Glu Pro Val Gly Lys Gly Ala Pro Gln Leu Glu  
 100 105 110  
 Ser Ala Met Tyr Glu Leu Cys Ser Gln Val Arg Asn Phe Asp Ile Cys  
 115 120 125  
 Ser Ile Val Ser Trp Val Phe Gly Gly Leu Cys Ile Phe Ala Gly Leu  
 130 135 140  
 Ile Val Gly Val Met Val Glu Ala Pro Leu Ile Ala Gly Leu Ser Ala  
 145 150 155 160  
 Trp Val Ile Pro Cys Ile Ile Gly Gly Val Gly Ala Ile Leu Cys Leu  
 165 170 175  
 Phe Ala Ile Leu Met Ala Tyr Leu Gly Arg Gly Arg Val Arg Glu Trp  
 180 185 190  
 Leu Asn Leu Ser His Glu Tyr Ile Thr Gln Cys His Cys Arg Gln Ile  
 195 200 205  
 Gln Ala His Ser Gln Asn Tyr Ser Val Ile Thr Glu Tyr Pro Ala Thr  
 210 215 220  
 Cys Ala Leu Ser Gln Pro Ile Thr Lys Leu Pro Asn Gly Ser Arg Arg  
 225 230 235 240  
 Asp Asn

&lt;210&gt;519

&lt;211&gt;545

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;519

Ser Cys Leu Arg Ile Glu Gly Ile Leu Met Ala Thr Ser Val Pro Val  
 1 5 10 15  
 Thr Ser Ser Thr Ser Val Gly Glu Ala Asn Ser Ser Asn Glu Arg Phe  
 20 25 30  
 Thr Glu Arg Thr Ser Arg Met Tyr Tyr Ala Ala Leu Val Leu Gly Ala



545

&lt;210&gt;520

&lt;211&gt;237

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;520

```

Met Ile Lys Gln Ile Gly Arg Phe Phe Arg Ala Phe Ile Phe Ile Met
 1           5           10           15
Pro Leu Ser Leu Thr Ser Cys Glu Ser Lys Ile Asp Arg Asn Arg Ile
           20           25           30
Trp Ile Val Gly Thr Asn Ala Thr Tyr Pro Pro Phe Glu Tyr Val Asp
           35           40           45
Ala Gln Gly Glu Val Val Gly Phe Asp Ile Asp Leu Ala Lys Ala Ile
           50           55           60
Ser Glu Lys Leu Gly Lys Gln Leu Glu Val Arg Glu Phe Ala Phe Asp
           65           70           75           80
Ala Leu Ile Leu Asn Leu Lys Lys His Arg Ile Asp Ala Ile Leu Ala
           85           90           95
Gly Met Ser Ile Thr Pro Ser Arg Gln Lys Glu Ile Ala Leu Leu Pro
           100          105          110
Tyr Tyr Gly Asp Glu Val Gln Glu Leu Met Val Val Ser Lys Arg Ser
           115          120          125
Leu Glu Thr Pro Val Leu Pro Leu Thr Gln His Ser Ser Val Ala Val
           130          135          140
Gln Thr Gly Thr Phe Gln Glu His Tyr Leu Leu Ser Gln Pro Gly Ile
           145          150          155          160
Cys Val Arg Ser Phe Asp Ser Thr Leu Glu Val Ile Met Glu Val Arg
           165          170          175
Tyr Gly Lys Ser Pro Val Ala Val Leu Glu Pro Ser Val Gly Arg Val
           180          185          190
Val Leu Lys Asp Phe Pro Asn Leu Val Ala Thr Arg Leu Glu Leu Pro
           195          200          205
Pro Glu Cys Trp Val Leu Gly Cys Gly Leu Gly Val Leu Lys Ile Val
           210          215          220
Leu Lys Lys Tyr Lys Arg Phe Asn Lys Arg Leu Gln Ile
           225          230          235

```

&lt;210&gt;521

&lt;211&gt;369

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;521

```

Lys Leu Pro Asn Asn Arg Leu Arg Met Val Lys Thr Lys Asn Pro Met
 1           5           10           15
Phe Pro Ser Arg Ala Arg Arg Pro Gln Arg Thr His Pro Arg Leu Pro
           20           25           30
Pro Lys Leu Leu His Gln Arg Ala Gln Lys Ser Leu Lys Gln Pro Ala
           35           40           45
Asp Lys Lys Pro Thr Pro Pro Glu Ala Pro Pro Pro Val Arg
           50           55           60
Val Ala Thr Pro Met Pro Leu Arg Pro Ser Ser Gln Gly Tyr Trp Gln
           65           70           75           80
Cys Leu Asn Arg Met Val Ser Met Val Leu Arg Arg Ala Pro Leu Pro
           85           90           95
Leu Pro Ala Met Gln Val Asp Pro Ile Leu Gly Asp Phe Asn Pro His
           100          105          110
Phe Val Ala Ser Tyr Pro Asn Arg Ile Asn Asn Glu Pro Met Tyr Phe
           115          120          125
Gln Ile Lys Gln Phe Lys Lys Ile Ala Gln Asn Pro Asp Leu Pro Gln
           130          135          140
Gln His Arg Arg Leu Ala Gln Leu Ser Leu Glu Gln Ala Leu Tyr Leu
           145          150          155          160
Asn Asp Asn Tyr Tyr Leu Val Asn Val Pro Gly Asp Gly Asn Cys Phe
           165          170          175
Tyr Arg Ala Tyr Ala Val Gly Trp Leu Ser Ala Leu Tyr Glu Glu Ser

```

```
<210>522
<211>637
<212>PRT
<213>Chlamydia pneumoniae
<400>522
```

696



Leu Tyr Thr Gln Ala Val Gln Leu Leu Phe Phe Ile Leu Gln His Pro  
 275 280 285  
 Gln Val Asn Asn Arg Pro Glu Thr Lys Asp Ala Val Lys Glu Leu Lys  
 290 295 300  
 Met Leu Leu Leu Pro Phe Leu Gln Tyr Ala Phe Lys Lys Val Glu Asn  
 305 310 315 320  
 Glu Lys Lys Leu Gln Lys Leu Leu Arg Ser Ile Leu Gly Ser Leu Val  
 325 330 335  
 Leu Lys Pro Pro Ala Arg Tyr Pro Ser Thr Pro Ser Asn Lys Asp Lys  
 340 345 350  
 Glu Thr Phe Cys Lys Phe Trp Ser Arg His Pro Glu Val Met Val Leu  
 355 360 365  
 Asp Pro Ile Leu Glu Lys Asn Cys Met Gln Phe Leu Arg Ala Thr Phe  
 370 375 380  
 Pro Asn Tyr Gln Leu Glu Thr Glu Ala Ile Leu Leu Glu Lys Glu Ile  
 385 390 395 400  
 Glu Ser Thr Phe Arg Asn Gly Trp Asn Val Phe Leu Thr Arg Leu Asn  
 405 410 415  
 Leu Phe Gly Ser Lys Leu Gly Ser Pro Ser Ser Pro Thr Ala Leu Ser  
 420 425 430  
 Asp Gln Phe Ser Lys Ser Phe Leu Ile Phe Cys Phe Leu Asn Asn Tyr  
 435 440 445  
 Pro Lys Leu Leu Gln Lys Lys Thr Pro Leu Ala Ala Arg Leu Asp Ala  
 450 455 460  
 Phe Gln Arg Glu Ala Ser His Arg Phe Thr Gln Val Lys Asp Lys Leu  
 465 470 475 480  
 Leu Leu Ser Leu Lys Tyr Gly Phe Pro Leu Ala Thr Ala Thr Ile Asn  
 485 490 495  
 Gln Tyr Ser Arg Ala Arg Asp Gln Leu Ile Cys Asn Leu Leu Lys Asn  
 500 505 510  
 Thr Val Thr Ala Ser Asp Gly Phe Cys Arg Ser Gly Phe Arg Gln Ser  
 515 520 525  
 Leu Ile Gly Tyr Leu His Ser Leu Ser Ser Asn Glu Leu Gly Asp Ile  
 530 535 540  
 Leu Asp Asp Val Lys Glu Gln Ala Glu Ala Asn Asp Val Ala Ala Met  
 545 550 555 560  
 Thr Thr Val Pro Leu Gln Pro Phe Ala Val Cys Leu Ile Met Ser Asp  
 565 570 575  
 Arg Asp Thr Val Ser Glu Glu Asn Ile Glu Asn Phe Val Ala Met His  
 580 585 590  
 Gly Phe Leu Asn Thr Ile Ser Pro Glu Arg Asp Ala Arg Ile Phe Leu  
 595 600 605  
 Ile Arg Phe Pro Asn His Tyr Gly Cys Leu Leu Pro Arg Asn Pro Arg  
 610 615 620  
 Thr Glu Asp Gln Asn Ser Lys Pro Asp Ser Ser Asn Pro  
 625 630 635

&lt;210&gt;523

&lt;211&gt;298

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;523

Arg Ser Glu Leu Lys Thr Gly Gln Leu Lys Ser Leu Val Leu His Glu  
 1 5 10 15  
 Val Leu Ile Leu Thr Phe Thr Tyr Pro Leu Pro Arg Thr Leu Lys Gln  
 20 25 30  
 His Pro Asp Glu Val His Thr Val Pro Ile Ser Pro Asn Leu Ser Phe  
 35 40 45  
 Gly Glu Gly Ser Pro Ile Leu Ile Ala Gly Pro Cys Thr Leu Glu Ser  
 50 55 60  
 Tyr Glu His Thr Val Ser Ser Ala Leu Thr Val Lys Glu Ala Gly Ala  
 65 70 75 80  
 Gln Val Phe Arg Gly Ser Ile Arg Lys Pro Arg Thr Ser Pro Phe Ser  
 85 90 95  
 Phe Gln Gly Trp Glu Lys Glu Cys Val Leu Trp His Lys Glu Ala Gln

100 105 110  
 Ser Ile His Gly Leu Pro Thr Glu Thr Glu Val Leu Asp Val Arg Asp  
 115 120 125  
 Val Glu Ile Thr Ala Glu His Val Asp Ile Leu Arg Ile Gly Ala Lys  
 130 135 140  
 Asn Met His Asn Thr Pro Leu Leu Gln Glu Val Ser Lys Ser His Arg  
 145 150 155 160  
 Pro Ile Ile Leu Lys Arg Ser Pro Ala Ala Thr Leu Glu Glu Trp Leu  
 165 170 175  
 Cys Ala Ala Glu Tyr Ile Leu Ala Ser Ser Pro Ser Cys Pro Gly Val  
 180 185 190  
 Ile Leu Cys Glu Arg Gly Ile Arg Thr Phe Glu His Ser Thr Arg Tyr  
 195 200 205  
 Thr Leu Asp Leu Asn Thr Val Ala Leu Leu Lys Glu Ile Ser Ser Leu  
 210 215 220  
 Pro Val Ile Val Asp Pro Ser His Ala Ala Gly Lys Arg Ser Leu Val  
 225 230 235 240  
 Leu Pro Leu Ala Ser Ala Gly Leu Ser Val Gly Ala Asp Gly Leu Met  
 245 250 255  
 Ile Glu Val His Ala His Pro Glu Lys Ala Leu Cys Asp Ala Lys Gln  
 260 265 270  
 Gln Ile Thr Pro Glu Glu Leu His Leu Phe Ala Lys Lys His Phe Cys  
 275 280 285  
 Pro Ser Glu Ser Arg Ala His Ala Ile Ser  
 290 295  
 <210>524  
 <211>465  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>524  
 Ala Gln His Arg Ser Leu Leu Lys Gly Asn Ile Xaa His Leu Gly Cys  
 1 5 10 15  
 Gly Val Leu Tyr Phe Met Asn Phe Ser Leu Phe Leu Phe Phe Leu Ile  
 20 25 30  
 Ala Ile Gln Gly Ile Cys Leu Tyr Val Gly Arg Arg Gly Ser Lys Lys  
 35 40 45  
 Val Glu Asp Arg Glu Ser Tyr Phe Leu Ala Gly Arg Ser Leu Lys Ile  
 50 55 60  
 Phe Pro Leu Met Met Thr Phe Ile Ala Thr Gln Ile Gly Gly Gly Val  
 65 70 75 80  
 Leu Leu Gly Ala Ala Glu Glu Ala Phe Cys Tyr Gly Tyr Gly Gly Ile  
 85 90 95  
 Leu Tyr Pro Leu Gly Val Ala Leu Gly Leu Ile Phe Leu Gly Met Gly  
 100 105 110  
 Pro Gly Lys Arg Leu Ala Glu Gly Ser Leu Thr Thr Val Val Ser Ile  
 115 120 125  
 Phe Glu Val Phe Tyr Gly Ser Lys Lys Leu Arg Lys Ile Ala Phe Leu  
 130 135 140  
 Leu Ser Ala Gly Ser Leu Phe Phe Ile Leu Val Ala Gln Val Ile Ala  
 145 150 155 160  
 Leu Asp Arg Leu Phe Ser Ser Phe Pro Phe Gly Lys Tyr Val Thr Val  
 165 170 175  
 Ala Phe Trp Ile Val Leu Ala Ser Tyr Thr Ser Thr Gly Gly Phe Arg  
 180 185 190  
 Gly Val Val Arg Thr Asp Val Ile Gln Ala Gly Phe Leu Leu Ile Ala  
 195 200 205  
 Val Leu Val Cys Gly Val Ser Val Trp Leu Ser Val Pro Lys Ser Leu  
 210 215 220  
 Ser Val Leu Asp Pro Phe Gln Ser Leu Pro Cys Ala Lys Phe Ser Asn  
 225 230 235 240  
 Trp Ile Phe Met Pro Met Leu Phe Met Leu Val Glu Gln Asp Met Val  
 245 250 255  
 Gln Arg Cys Val Ala Ala Ser Ser Pro Lys Arg Leu Gln Trp Ala Ala  
 260 265 270

Val Gly Ala Gly Leu Val Leu Leu Leu Phe Asn Phe Ile Pro Leu Phe  
 275 280 285  
 Leu Gly Ser Leu Gly Ala Lys Ala Gly Leu Lys Ala Gly Cys Pro Leu  
 290 295 300  
 Ile Asp Thr Ile Ala Tyr Phe Cys Asn Pro Ser Leu Ala Ala Val Met  
 305 310 315 320  
 Ala Ala Ala Ile Gly Val Ala Ile Leu Ser Thr Ala Asp Ser Leu Met  
 325 330 335  
 Asn Ala Val Ser Gln Leu Ile Ala Glu Tyr Pro Thr Leu Lys Ala  
 340 345 350  
 Pro Tyr Tyr Arg Tyr Leu Val Leu Gly Leu Ala Val Ala Ala Pro Leu  
 355 360 365  
 Val Ala Ile Gly Phe Thr Asn Ile Val Asp Val Leu Ile Leu Ser Tyr  
 370 375 380  
 Ser Leu Ser Val Cys Cys Leu Ser Val Pro Val Gly Phe Tyr Leu Leu  
 385 390 395 400  
 Ala Pro Lys Gly Arg Arg Val Ser Gly Ala Ala Ala Trp Ala Gly Val  
 405 410 415  
 Leu Val Gly Ala Leu Gly Tyr Gly Trp Val Gln Ile Val Ser Leu Gly  
 420 425 430  
 Met Phe Gly Glu Leu Leu Ala Trp Val Gly Ser Leu Val Ala Phe Ser  
 435 440 445  
 Phe Val Gly Phe Ile Glu Ile Thr Trp Lys Asn Lys Val Lys Thr Gln  
 450 455 460  
 Thr  
 465  
 <210>525  
 <211>237  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>525  
 Gly Leu Arg Ser Pro Gln Pro Leu Val Cys Glu Ala Ala Ser Ala Ala  
 1 5 10 15  
 Leu Cys Ser Leu Gly Ile His Gly Val Pro Leu Ala Lys Glu His Leu  
 20 25 30  
 Glu Ser Leu Ser Ser Arg Lys Ala Ala Ala Asn Leu Ser Ile Leu Leu  
 35 40 45  
 Leu Val Ser Arg Glu Asp Ile Glu Arg Ala Gly Asp Val Ile Ala Arg  
 50 55 60  
 Tyr Leu Ser Asn Pro Glu Met Cys Trp Ala Ile Glu Tyr Phe Leu Trp  
 65 70 75 80  
 Asp Ala Gln Trp Asn Leu Arg Gly Asp Thr Phe Pro Leu Tyr Ser Asp  
 85 90 95  
 Met Ile Lys Arg Glu Ile Gly Arg Lys Leu Ile Arg Leu Leu Ala Val  
 100 105 110  
 Ala Arg Tyr Ser Gln Ala Lys Ala Val Thr Ala Thr Phe Leu Ser Gly  
 115 120 125  
 Gln Gln Ala Gln Gly Trp Ser Phe Phe Ser Gly Met Phe Trp Glu Glu  
 130 135 140  
 Gly Asp Val Lys Thr Ser Glu Asp Leu Val Thr Asp Ala Cys Phe Ala  
 145 150 155 160  
 Ala Lys Leu Glu Gly Ala Leu Ala Ser Leu Cys Gln Lys Lys Asp Gln  
 165 170 175  
 Ala Ser Leu Gln Arg Val Ser Gln Leu Tyr Asn Asp Ser Arg Trp Gln  
 180 185 190  
 Asp Lys Leu Ala Ile Leu Glu Ser Val Ala Phe Ser Glu Asn Leu Asp  
 195 200 205  
 Ala Val Pro Phe Leu Leu Asp Cys Cys His His Glu Ala Pro Ser Leu  
 210 215 220  
 Arg Ser Ala Ala Ala Gly Ala Leu Phe Ser Ile Phe Lys  
 225 230 235  
 <210>526  
 <211>356  
 <212>PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;526

Arg Arg Thr Gly Gly Ile Ser Leu Thr Tyr Ser Ser Phe Arg Trp Ala  
 1 5 10 15  
 Ser Phe Arg Cys Tyr Ser Leu Ile Phe Phe Cys Phe Cys Gly Ser Leu  
 20 25 30  
 Phe Gly Ser Glu Ser Leu Arg Tyr Gln Leu Leu Ile Gln Asp Phe Ala  
 35 40 45  
 Lys Val Ser Glu Glu Gly Ile Gly Leu Leu Glu Ser Lys Glu Tyr Ser  
 50 55 60  
 Leu Leu Gln Ala Lys Leu Val Leu Arg Ala Leu Ala Gln Asn Ser Ser  
 65 70 75 80  
 Phe Asp Asp Trp Phe Arg Ser Phe Lys Lys Cys Gln Ile Ser Tyr Pro  
 85 90 95  
 Glu Leu Ala His Asp Arg Asp Val Leu Glu Glu Phe Gly Ile Gln Val  
 100 105 110  
 Leu Arg Glu Gly Ile Glu Asn Pro Ser Val Thr Val Arg Ala Val Ser  
 115 120 125  
 Val Leu Ala Ile Gly Leu Ala Arg Asp Phe Arg Leu Val Pro Leu Leu  
 130 135 140  
 Leu Gln Ser Cys Asn Asp Asp Ser Ala Ile Val Arg Ser Leu Ala Leu  
 145 150 155 160  
 Gln Val Ala Val Asn Tyr Gly Ser Glu Ser Leu Lys Lys Ala Ile Val  
 165 170 175  
 Glu Leu Ala Arg Asn Asp Asp Ser Ile His Val Arg Ile Thr Ala Tyr  
 180 185 190  
 Gln Val Val Ala Leu Leu Gln Ile Glu Glu Leu Leu Pro Phe Leu Arg  
 195 200 205  
 Glu Arg Ala Glu Asn Lys Leu Val Asp Ser Val Glu Arg Arg Glu Ala  
 210 215 220  
 Trp Lys Ala Cys Leu Glu Leu Ser Ser Gln Phe Leu Glu Thr Gly Val  
 225 230 235 240  
 Ala Lys Asp Asp Ile Asp Gln Ala Leu Phe Thr Cys Glu Val Leu Arg  
 245 250 255  
 Asn Gly Met Leu Pro Glu Thr Thr Glu Ile Phe Thr Glu Leu Leu Ser  
 260 265 270  
 Val Glu His Pro Glu Val Gln Glu Ser Leu Leu Leu Ser Ala Leu Ala  
 275 280 285  
 Trp Ser His Gln Leu Gln Asn His Lys Glu Phe Leu Ser Lys Val Arg  
 290 295 300  
 His Val Met Cys Thr Ser Pro Phe Ala Lys Val Arg Phe Gln Ala Ala  
 305 310 315 320  
 Ala Leu Leu His Leu His Gly Asp Pro Leu Gly Arg Asp Ser Leu Val  
 325 330 335  
 Glu Gly Cys Ala Leu Leu Asn Leu Leu Cys Val Arg Gln Leu Arg Arg  
 340 345 350  
 Leu Ser Ala Leu  
 355

&lt;210&gt;527

&lt;211&gt;110

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;527

Met Thr Val Phe Lys Gln Ile Ile Asp Gly Leu Ile Asp Cys Glu Lys  
 1 5 10 15  
 Val Phe Glu Asn Glu Asn Phe Ile Ala Ile Lys Asp Arg Phe Pro Gln  
 20 25 30  
 Ala Pro Val His Leu Leu Ile Ile Pro Lys Lys Pro Ile Pro Arg Phe  
 35 40 45  
 Gln Asp Ile Pro Gly Asp Glu Met Ile Leu Met Ala Glu Ala Gly Lys  
 50 55 60  
 Ile Val Gln Glu Leu Ala Ala Glu Phe Gly Ile Ala Asp Gly Tyr Arg  
 65 70 75 80  
 Val Val Ile Asn Asn Gly Ala Glu Gly Gly Gln Ala Val Phe His Leu

85 90 95  
 His Ile His Leu Leu Gly Gly Arg Pro Leu Gly Ala Ile Ala  
 100 105 110  
 <210>528  
 <211>130  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>528  
 Asn His Leu Ile Pro Trp Asp Ile Leu Lys Ser Trp Tyr Arg Phe Phe  
 1 5 10 15  
 Arg Asn Asp Lys Lys Met Asn Arg Ser Leu Arg Lys Thr Ile Phe Tyr  
 20 25 30  
 Ser Tyr Glu Ile Phe Val Phe Lys Tyr Leu Phe Thr Ile Tyr Gln Ser  
 35 40 45  
 Ile Asp Asn Leu Phe Glu Tyr Cys His Met Ile Pro Arg Ser Cys Asn  
 50 55 60  
 Val Asn Arg Lys Ala Arg Trp Gln Leu Ser Leu Phe Val His Thr Glu  
 65 70 75 80  
 Arg Lys Arg Pro Leu Trp Gln Asn Thr Ala Pro Gly Ile Pro Asp Thr  
 85 90 95  
 Leu Asp Asn Ser Leu Pro Asn Lys Pro Ala Gln Phe Ser Gly Lys Gly  
 100 105 110  
 Thr Arg Thr Ser Ile Arg Arg Ser Lys Phe Gly Gly Ile Pro Arg Lys  
 115 120 125  
 Ile His  
 130  
 <210>529  
 <211>300  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>529  
 Met Glu Asp Trp Leu Arg Arg Ile Val Gly Met Gln Ile Pro Arg Ser  
 1 5 10 15  
 Ile Gly Thr His Asp Gly Ser Phe His Ala Asp Glu Val Thr Ala Cys  
 20 25 30  
 Ala Leu Leu Ile Ile Phe Asp Leu Val Asp Glu Asn Lys Ile Ile Arg  
 35 40 45  
 Ser Arg Asp Pro Val Val Leu Ser Lys Cys Glu Tyr Val Cys Asp Val  
 50 55 60  
 Gly Gly Val Tyr Ser Ile Glu Asn Lys Arg Phe Asp His His Gln Val  
 65 70 75 80  
 Ser Tyr Asp Gly Ser Trp Ser Ser Ala Gly Met Ile Leu His Tyr Leu  
 85 90 95  
 Lys Glu Phe Gly Tyr Met Asp Cys Glu Glu Tyr His Phe Leu Asn Asn  
 100 105 110  
 Thr Leu Val His Gly Val Asp Glu Gln Asp Asn Gly Arg Phe Phe Ser  
 115 120 125  
 Lys Glu Gly Phe Cys Ser Phe Ser Asp Ile Ile Lys Ile Tyr Asn Pro  
 130 135 140  
 Arg Glu Glu Glu Thr Asn Ser Asp Ala Asp Phe Ser Cys Ala Leu  
 145 150 155 160  
 His Phe Thr Ile Asp Phe Leu Cys Arg Leu Arg Lys Lys Phe Gln Tyr  
 165 170 175  
 Asp Arg Val Cys Arg Gly Ile Val Arg Glu Ala Met Glu Thr Glu Asp  
 180 185 190  
 Met Cys Leu Tyr Phe Asp Arg Pro Leu Ala Trp Gln Glu Asn Phe Phe  
 195 200 205  
 Phe Leu Gly Gly Glu Lys His Pro Ala Ala Phe Val Cys Phe Pro Ser  
 210 215 220  
 Cys Asp Gln Trp Ile Leu Arg Gly Ile Pro Pro Asn Leu Asp Arg Arg  
 225 230 235 240  
 Met Glu Val Arg Val Pro Phe Pro Glu Asn Trp Ala Gly Leu Leu Gly  
 245 250 255  
 Lys Glu Leu Ser Lys Val Ser Gly Ile Pro Gly Ala Val Phe Cys His

260 265 270  
 Lys Gly Leu Phe Leu Ser Val Trp Thr Asn Arg Glu Ser Cys Gln Arg  
 275 280 285  
 Ala Leu Arg Leu Thr Leu Gln Asp Arg Gly Ile Ile  
 290 295 300  
 <210>530  
 <211>154  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>530  
 Ile Met Tyr Asn Leu Leu His Ala His His Asp Ala Ala Ser Pro Asp  
 1 5 10 15  
 Gly Arg Leu Val Ser His Leu Lys Lys Leu Ser Pro His Ile Tyr Glu  
 20 25 30  
 Gly Glu Val Leu Ile Glu Asn Ile Pro Ala Tyr Phe Leu Gly Phe His  
 35 40 45  
 Leu Pro Gln Gln Cys Ile Gln Val Asn Leu Lys Ser Ser Leu Ala Gln  
 50 55 60  
 Leu Gly Val Glu Ala Val Leu Asn His Leu Glu Leu Asn Lys Ala Arg  
 65 70 75 80  
 Lys Glu Ala Arg Leu His Val Leu Phe Met Ser Gln Asp Pro Ile Ala  
 85 90 95  
 Thr Ala Asn Val Gly Ala Pro Arg Ser Leu Xaa Val Leu Ser Ala Ser  
 100 105 110  
 Ser Leu Leu Leu Met Ile Ala Asp Ser Tyr Val Arg Leu Val Ile Ser  
 115 120 125  
 Thr Gly Cys Leu Arg Thr Gln Thr Val Gln Asp Leu Arg Ser Tyr Ala  
 130 135 140  
 Leu Gly Lys Asn Leu Ser Thr Ser Ser Leu  
 145 150

&lt;210&gt;531

&lt;211&gt;230

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;531

Glu Pro Gly Ser Phe Val Cys Lys Leu Phe Ala Ala Asp Asp Arg Arg  
 1 5 10 15  
 Leu Val Arg Ser Pro Cys Tyr Leu Asn Arg Met Phe Thr His Thr Asp  
 20 25 30  
 Arg Thr Gly Ser Pro Leu Leu Arg Phe Gly Lys Lys Leu Glu His Phe  
 35 40 45  
 Ile Thr Leu Glu Ile Ile Asn Asp Arg Leu Val Val Phe Leu Pro Ile  
 50 55 60  
 Leu Pro Gly Thr Ile Cys Tyr Glu Glu Thr Ile Tyr Gly Phe Leu Pro  
 65 70 75 80  
 Leu Met Ser Lys Ser Leu Thr Arg Pro His Leu Lys Ile Arg Lys Phe  
 85 90 95  
 Leu Pro Leu Tyr Gln Met Val Thr Asp Arg Pro Pro Val Pro Glu Asp  
 100 105 110  
 His Lys Ile Leu Leu Ile Lys Thr Glu Pro Leu His Ile Arg Thr Val  
 115 120 125  
 Phe Ala Arg Val Val Gln Asp Leu Leu Pro Gln Gly Leu Arg His Thr  
 130 135 140  
 Ala Ala Asp Ile Leu Glu Pro Thr Thr Gln Glu Ser Gly Asp Ile Tyr  
 145 150 155 160  
 Glu Phe Tyr Gly Ser Thr Ser Glu Pro Ile Glu Arg Ile Pro Leu Glu  
 165 170 175  
 Phe Phe Thr Leu Glu Pro Tyr Lys Glu His Ser Phe Phe Phe Tyr Arg  
 180 185 190  
 Asp Met Leu Gln Glu Thr Leu Xaa Ser Pro Gln Glu Val Phe Arg Val  
 195 200 205  
 Phe Glu Ser Ile Pro Glu Gly Glu Asn Gln Ala Ala Met Phe Ile Ser  
 210 215 220  
 Lys Gly Ser Glu Leu Ala

225 230  
 <210>532  
 <211>356  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>532  
 Ala Cys Leu Ser Ser Pro Lys Thr Leu Gly Ser Ser Asn Leu Glu Ser  
 1 5 10 15  
 Pro His Gln Met Lys Asp Met Leu Gly Lys Phe Lys Ser Thr Leu Lys  
 20 25 30  
 Thr Gln Pro Cys Phe Pro Phe Leu Lys Ala Met Glu Thr Asp His Ile  
 35 40 45  
 Thr Ser Gln Gly Val Leu Phe Ser Arg Tyr Phe Pro Ser Ala Ser Leu  
 50 55 60  
 Lys Gly Met Phe Leu Ser Asn Tyr Ser Arg Tyr Tyr Leu Gln His Ile  
 65 70 75 80  
 Tyr Phe Gln Ile Pro Ser Pro Thr Ser Gly Glu Phe Phe Ser Asn Arg  
 85 90 95  
 Asp Arg Ser Phe Leu Leu Asp Leu Tyr Phe Ala Gly Ile Ser Val Phe  
 100 105 110  
 Trp Ala Asp Leu Glu Ser Lys Arg Leu Leu Gln Tyr Ile Lys Arg Arg  
 115 120 125  
 Asn Lys Asp Val Gly Met Phe Val Pro Lys His Gln Ala Glu Gln Phe  
 130 135 140  
 Ala Gln Ser Tyr Phe Ile Gly Ile His Gly Ser Cys Leu Ile Ala Gly  
 145 150 155 160  
 Asp Tyr Asp Glu Phe Leu Arg Glu Leu Leu Thr Gly Met His Thr Leu  
 165 170 175  
 Ser Gln Gln Phe Thr Ile Pro Glu Phe Pro Pro Gln Thr Pro Leu Ala  
 180 185 190  
 Ile Leu Thr Gly Gly Gly Ser Gly Ala Met Glu Leu Ala Asn Arg Val  
 195 200 205  
 Ala Thr Glu Leu Ser Ile Leu Ser Cys Gly Asn Leu Ile Ser Leu Asp  
 210 215 220  
 Thr Thr Asn Ala Tyr Val Glu Ala Lys Met Ser Tyr Ala Ile Pro Asp  
 225 230 235 240  
 Leu Leu Glu Arg Gln Ala Asp Phe His Val Asp Leu Ala Val Phe Val  
 245 250 255  
 Ile Gly Gly Met Gly Thr Asp Phe Glu Leu Leu Leu Glu Leu Ile Ser  
 260 265 270  
 Leu Lys Thr Gly Lys Lys Ala Leu Val Pro Val Phe Leu Ile Gly Pro  
 275 280 285  
 Val Asp Tyr Trp Lys Ser Lys Ile Thr Ala Leu Tyr Asn Ser Asn His  
 290 295 300  
 Ala Val Gly Thr Ile Arg Gly Ser Glu Trp Val His Asn Cys Leu Phe  
 305 310 315 320  
 Cys Leu Ser Ser Ala Lys Ala Gly Ile Ala Ile Phe Arg Arg Tyr Leu  
 325 330 335  
 Asn His Thr Leu Pro Ile Gly Pro Glu His Pro Val Pro Glu Asp Gly  
 340 345 350  
 Phe Val Ile Val  
 355  
 <210>533  
 <211>420  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>533  
 Ile Leu Ser Ser Leu Tyr Thr Val Phe Thr Met Lys Thr Ala Phe His  
 1 5 10 15  
 Ser Cys Tyr Ser Trp Phe Cys Trp Leu Phe Ser Phe Leu Val Leu Phe  
 20 25 30  
 Val Gly Gly Ile Ala Gly Gly Glu Pro Leu Cys Pro Asp Cys Lys Tyr  
 35 40 45  
 Glu Thr Lys Ser Val Leu Arg Ser Asp Gln Leu Pro Asp His Leu Trp

50 55 60  
 Asn Tyr Glu Asn Asp Cys Tyr Leu Thr Gly Tyr Val Gln Ser Leu Leu  
 65 70 75 80  
 Asp Met His Phe Leu Asp Ser Arg Thr Gln Val Val Ile Glu Lys Asn  
 85 90 95  
 Arg Ala Tyr Leu Phe Ser Leu Pro Val Asp Ser Ser Leu Ser Glu Ala  
 100 105 110  
 Ile Thr Asn Phe Val Arg Asp Leu Pro Phe Ile Cys Ala Val Glu Ile  
 115 120 125  
 Cys Glu Arg Pro Tyr Gly Glu Cys Ile Thr Arg Ser Ser Ala Glu Arg  
 130 135 140  
 Pro Leu Leu Pro Lys Glu Lys Thr Leu Gly Met Pro Ile Phe Cys Gly  
 145 150 155 160  
 Lys Glu Gly Val Trp Leu Pro Gln Asn Thr Ile Leu Phe Ser Pro Leu  
 165 170 175  
 Ile Ala Asp Pro Arg Gln Val Thr Asn Ser Ala Gly Ile Arg Phe Asn  
 180 185 190  
 Glu Lys Val Val Gly Asn Arg Val Gly Ala Thr Ile Phe Gly Gly Asp  
 195 200 205  
 Phe Ile Leu Leu Arg Leu Phe Asp Val Ser Arg Phe His Val Asp Cys  
 210 215 220  
 Asp Phe Gly Ile Gln Gly Gly Val Phe Ser Val Phe Asp Leu Asp His  
 225 230 235 240  
 Pro Glu Ser Cys Met Val Asn Ser Asp Phe Phe Val Ala Gly Leu Trp  
 245 250 255  
 Ser Gly Ala Ile Asp Lys Trp Ser Phe Arg Phe Arg Leu Trp His Leu  
 260 265 270  
 Ser Ser His Leu Gly Asp Glu Phe Ile Leu Thr His Pro Asn Phe Pro  
 275 280 285  
 Arg Phe Asn Leu Ser Asp Glu Gly Val Asp Leu Phe Ile Ser Phe Arg  
 290 295 300  
 Tyr Thr Pro Gln Ile Arg Leu Tyr Gly Gly Cys Gly Tyr Ile Val Ser  
 305 310 315 320  
 Arg Asp Leu Thr Phe Pro Glu Arg Pro Phe Tyr Cys Glu Trp Gly Ala  
 325 330 335  
 Glu Leu Arg Pro Phe Gly Leu Arg Glu Gly Asn Leu His Ala Gln Pro  
 340 345 350  
 Ile Phe Ala Met His Phe Arg Cys Trp Glu Glu Gln Lys Phe Gly Leu  
 355 360 365  
 Asp Gln Ser Tyr Ile Leu Gly Met Glu Trp Ala Lys Phe Gln Glu Ile  
 370 375 380  
 Gly Arg Lys Ile Arg Ala Val Leu Glu Tyr His Gln Gly Phe Ser Lys  
 385 390 395 400  
 Glu Gly Gln Phe Ile Arg Glu Pro Cys Asn Tyr Tyr Gly Phe Arg Leu  
 405 410 415  
 Thr Tyr Gly Phe  
 420

&lt;210&gt;534

&lt;211&gt;96

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;534

Ser Lys Thr Glu Gly Ser His Ser Lys Thr Ser Lys Gly Phe Val Gly  
 1 5 10 15  
 Arg Phe Val Gln Trp Ile Arg Thr Phe Thr Gly Arg Gly Ser Lys Lys  
 20 25 30  
 Arg Ser Pro Ser Ser Phe Ser Pro Thr His Pro Tyr Ile Arg Leu Arg  
 35 40 45  
 Thr Tyr Thr Arg Ser Pro Lys Gln Ser Gly Val Glu Arg Lys Gln Glu  
 50 55 60  
 Asp Ala Glu Thr Ser Phe Ile Glu Thr Pro Lys Gly Ile Leu Lys Lys  
 65 70 75 80  
 Pro Gly Asn Lys Asp Pro Lys Gly Lys His Val His Trp Lys Asp Ser  
 85 90 95



&lt;210&gt;535

&lt;211&gt;421

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;535

```

Met Ala Ile Gln Lys Ala Gly Ala Phe Leu Arg Cys Leu Pro Ser Glu
 1           5           10           15
Ser Arg Pro Tyr Leu Glu His Ala Met Arg Arg Asn Pro His Phe Ser
          20          25          30
Leu Leu Lys Pro Gln Tyr Leu Phe Ser Glu Ile Ser Lys Lys Leu Ala
          35          40          45
Gln Phe Arg Lys Glu Asn Pro Glu Ile Ser Val Ile Asp Leu Ser Ile
          50          55          60
Gly Asp Thr Thr Gln Pro Leu Cys Arg Ser Ile Thr Gln Ala Ile Lys
          65          70          75          80
Glu Phe Cys Val Ser Gln Glu Lys Gln Glu Thr Tyr Arg Gly Tyr Gly
          85          90          95
Pro Glu Thr Gly Leu Glu Lys Leu Arg Thr Lys Ile Ala Ser Glu Val
          100         105         110
Tyr Glu Asn Arg Ile Ser Pro Glu Glu Ile Phe Ile Ser Asp Gly Ala
          115         120         125
Lys Pro Asp Ile Phe Arg Leu Phe Ser Phe Phe Gly Ser Glu Lys Thr
          130         135         140
Leu Gly Leu Gln Asp Pro Val Tyr Pro Ala Tyr Arg Asp Ile Ala His
          145         150         155         160
Ile Thr Gly Ile Arg Asp Ile Ile Pro Leu Ala Cys Arg Lys Glu Thr
          165         170         175
Gly Phe Ile Pro Glu Leu Pro Asn Gln Gln Ser Leu Asp Ile Leu Cys
          180         185         190
Leu Cys Tyr Pro Asn Asn Pro Thr Gly Thr Val Leu Thr Phe Gln Gln
          195         200         205
Leu Gln Ala Leu Val Asn Tyr Ala Asn Gln His Gly Thr Val Leu Ile
          210         215         220
Phe Asp Ala Ala Tyr Ser Ala Phe Val Ser Asp Pro Ser Leu Pro Lys
          225         230         235         240
Ser Ile Phe Glu Ile Pro Glu Ala Lys Tyr Cys Ala Ile Glu Ile Asn
          245         250         255
Ser Phe Ser Lys Ser Leu Gly Phe Thr Gly Met Arg Leu Ala Trp Asn
          260         265         270
Val Ile Pro Lys Glu Leu Thr Tyr Asp Asn Asn Glu Pro Met Ile Asn
          275         280         285
Asp Trp Lys Arg Leu Phe Ala Thr Thr Phe Asn Gly Ala Ser Leu Leu
          290         295         300
Met Gln Glu Ala Gly Tyr Tyr Gly Leu Asp Leu Phe Pro Thr Pro Pro
          305         310         315         320
Ala Ile Ser Leu Tyr Leu Thr Asn Ala Gln Lys Leu Lys Lys Ser Leu
          325         330         335
Glu Thr Ala Gly Phe Ser Val His Gly Gly Asp His Ala Pro Tyr Leu
          340         345         350
Trp Val Glu Leu Pro Glu Gly Ile Ser Asp Glu Glu Ala Phe Asp Phe
          355         360         365
Phe Leu His Gln Tyr His Ile Ala Val Thr Pro Gly His Gly Phe Gly
          370         375         380
Ser Cys Gly Gln Gly Phe Val Arg Phe Ser Ala Leu Thr Gln Pro Gln
          385         390         395         400
Asn Ile Ala Leu Ala Cys Asp Arg Leu Cys Thr Ala Ser Leu Lys Glu
          405         410         415
Thr Met Val Leu Ala
          420

```

&lt;210&gt;536

&lt;211&gt;354

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;536

Pro Pro Leu Tyr Arg Phe Thr Lys Arg Asn Asp Gly Ser Cys Met Thr  
 1 5 10 15  
 Ile Leu Arg Lys Leu Ser Gln Tyr Leu Phe Phe Ser Leu Phe Cys  
 20 25 30  
 Ser Phe Ile Tyr Val Ala Thr Cys Gly Ser Gln Pro Asp Ser Val Ser  
 35 40 45  
 Ser Pro Lys Ile Ala Ile Phe Leu Ser Phe Pro His Pro Leu Leu Glu  
 50 55 60  
 Asp Cys Ser Lys Ser Cys Ile Glu Thr Leu Lys Asp Phe Glu Asn Leu  
 65 70 75 80  
 Pro Glu Ile Val Val Leu Asn Ala Glu Asp Ser Ile Val Lys Ala Arg  
 85 90 95  
 Lys Ile Ala Arg Ser Leu His Thr Asp Lys Asn Val Val Ala Ile Val  
 100 105 110  
 Thr Leu Gly Thr Ile Ala Thr Lys Val Met Ser His Ile Glu Thr Gln  
 115 120 125  
 Lys Pro Val Ile Tyr Ala Ala Val Pro Asp Arg Glu Ser Leu Thr Pro  
 130 135 140  
 Pro Lys Asn Thr Met Asn Ile Tyr Gly Val Asn Asp Thr Leu Asp Ile  
 145 150 155 160  
 Asn Gln Tyr Cys Phe Ala Ile Gln Ala Val Ala Thr Asn Ala Gln Ser  
 165 170 175  
 Ile Val Tyr Leu Lys Pro Ser Glu Pro Phe Pro Ser Asp Leu Gln Lys  
 180 185 190  
 Glu Ile Val Lys Lys Leu His Ala Ser Gly Ile Glu Val Ile Glu Ile  
 195 200 205  
 Ser Ile Thr Ser Ser Thr Phe Lys Thr Arg Ile Arg Gln Ala Ile Asp  
 210 215 220  
 Lys Arg Pro Ser Ala Ile Phe Ile Pro Leu Ser Pro Leu Ser His Lys  
 225 230 235 240  
 Glu Gly Thr Ala Phe Leu Gln Glu Ile Leu Lys Glu Lys Ile Pro Ile  
 245 250 255  
 Ile Thr Asp Asp Thr Ser Leu Ile Ser Glu Glu Pro Ala Leu Pro Val  
 260 265 270  
 Ala Trp Ile Thr Lys Asn Gln Glu Asn Lys Ser Gln Lys Ile Val His  
 275 280 285  
 His Leu Leu Tyr Asn Asn His Asp Val Asp Ser Leu Arg Lys Ile Ile  
 290 295 300  
 Ala Gln Arg Leu Ser Pro Thr Thr Thr Phe Asn Glu Asp Ile Ile Lys  
 305 310 315 320  
 Tyr Leu Gly Ile Lys Leu His Lys Thr Glu Arg Asn Gln Phe Leu Ser  
 325 330 335  
 Phe Lys Ser Lys Lys Leu Glu Lys Ser Glu Lys Gly Lys Asn Val Ala  
 340 345 350  
 Val Ser

&lt;210&gt;537

&lt;211&gt;290

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;537

Gln Ala Lys Ser Arg Cys Ser Ile Asp Lys Tyr Ile Pro Val Val Asn  
 1 5 10 15  
 Arg Leu Leu Glu Val Cys Gly Leu Pro Glu Ala Glu Asn Val Glu Asp  
 20 25 30  
 Leu Ile Glu Ser Ser Ser Ala Trp Val Leu Thr Pro Glu Arg Phe  
 35 40 45  
 Ser Gly Glu Leu Val Ser Ile Cys Gln Val Lys Asp Glu His Ala Phe  
 50 55 60  
 Tyr Asn Asp Leu Ser Leu Leu His Met Thr Gln Ala Val Pro Ser Tyr  
 65 70 75 80  
 Ser Ala Thr Tyr Asp Cys Ala Val Val Phe Gly Gly Pro Leu Pro Ala  
 85 90 95  
 Leu Arg Gln Arg Leu Asp Phe Leu Val Arg Glu Trp Gln Arg Gly Val

100 105 110  
 Arg Phe Lys Lys Ile Val Phe Leu Cys Gly Glu Arg Gly Arg Tyr Gln  
 115 120 125  
 Ser Ile Glu Glu Gln Glu His Phe Phe Asp Ser Arg Tyr Asn Pro Phe  
 130 135 140  
 Pro Thr Glu Glu Asn Trp Glu Ser Gly Asn Arg Val Thr Pro Ser Ser  
 145 150 155 160  
 Glu Glu Glu Val Ala Lys Phe Val Trp Met Gln Met Leu Leu Pro Arg  
 165 170 175  
 Ala Trp Arg Asp Ser Thr Ser Gly Val Arg Val Thr Phe Leu Leu Ala  
 180 185 190  
 Lys Pro Glu Glu Asn Arg Val Val Ala Asn Arg Lys Asp Thr Leu Leu  
 195 200 205  
 Leu Phe Arg Ser Tyr Gln Glu Ala Phe Pro Gly Arg Val Leu Phe Val  
 210 215 220  
 Ser Ser Gln Pro Phe Ile Gly Leu Asp Ala Cys Arg Val Gly Gln Phe  
 225 230 235 240  
 Phe Lys Gly Glu Ser Tyr Asp Leu Ala Gly Pro Gly Phe Ala Gln Gly  
 245 250 255  
 Val Leu Lys Tyr His Trp Ala Pro Arg Ile Cys Leu His Thr Leu Ala  
 260 265 270  
 Glu Trp Leu Lys Glu Thr Asn Gly Cys Leu Asn Ile Ser Glu Gly Cys  
 275 280 285  
 Phe Gly  
 290  
 <210>538  
 <211>400  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>538  
 Leu Ser Val Tyr Leu Leu Ile Phe Tyr Phe Cys Asn Cys Ser Thr Met  
 1 5 10 15  
 Ser Ser Val Asn Gln Ser Ser Gly Thr Pro Asn Pro Glu Glu Val Thr  
 20 25 30  
 Ser Pro Glu Ser Thr Glu Glu Asn Lys Asn Val Val Ser Ser Asp Glu  
 35 40 45  
 Ala Gln Ala Thr His Ala Val Ala Leu Pro Ile Val Thr Gln Leu Ser  
 50 55 60  
 Leu Pro Glu Gly Val Gly Thr Ser Ser Glu Glu Thr Ala Ser Asn Pro  
 65 70 75 80  
 Lys Val Asp Glu Ile Val Ala Glu Val Ser Ser Arg Ala Val Ala  
 85 90 95  
 Asp Gln Ile Ser Ser Leu Val Glu Arg Val Gly Glu Leu Leu Asp Asp  
 100 105 110  
 Leu Lys Gly Ala Gln Ser Leu Phe Thr Ser Phe Gln Ser Glu Leu Lys  
 115 120 125  
 Asn Cys Leu Pro Ala Trp Lys Ser Ser Thr Arg Arg Leu Glu Thr Arg  
 130 135 140  
 Gly Ala Gly Asp Asn Ala Asp Ile Ala Arg Leu Glu Leu Phe Arg Ser  
 145 150 155 160  
 Asp Tyr Glu Ala Val Leu Gly His Ala Asn Gln Phe His Gly Lys Ala  
 165 170 175  
 His Leu Ile Leu Ser Lys Leu Thr Asp Val His His Lys Leu Gln Gly  
 180 185 190  
 Leu Ser Arg Glu Asp Leu Ser Leu Ala Phe Asp Asn Asn Asp Arg Val  
 195 200 205  
 Leu Glu His Leu Gly Ser Leu Gly Leu Asp Val Asp Ala Glu Gly Asn  
 210 215 220  
 Trp Ser Leu Ser Cys Glu Arg Gly Ile Pro Arg Leu Val Leu Thr Ala  
 225 230 235 240  
 Asp Ser Met Leu Val Gln Ile Lys Lys Val Asn Leu Pro Thr Val Glu  
 245 250 255  
 Glu Leu Arg Thr Leu Gln Gly Thr Thr Glu Ser Ser Ser Asp Pro Arg  
 260 265 270

Val Glu Glu Ser Leu Ser Cys Cys Glu Arg Leu Leu Asn Glu Leu Arg  
 275 280 285  
 Arg Leu Trp Ala Asn Phe Val Gly Phe Ile Ser Ser Cys Tyr Asp Asn  
 290 295 300  
 Ile Val Phe Val Leu Met Trp Ile Val Arg Arg Ile Asn Leu Leu Pro  
 305 310 315 320  
 Gly Leu Gly Cys Leu Pro Phe His Asn Pro Asp Ala Ser Gln Glu Asp  
 325 330 335  
 Gln Arg Ser Ser Ser Gly Glu Arg Ser Thr Arg Arg Glu Arg Leu Ser  
 340 345 350  
 Arg Arg Ser Asp Leu Ser Glu Glu Met Ile Val Arg Ala Glu Gly  
 355 360 365  
 Glu Ser Ile His Pro Glu Ser Pro His Gly Asp Gly Arg Asn Gln Pro  
 370 375 380  
 Ser Arg Gly Asp Lys Gln Asp Ser Asp Ser Glu Glu Glu Thr Glu Leu  
 385 390 395 400  
 <210>539  
 <211>568  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>539  
 Met Lys Thr Ser Gln Leu Phe Tyr Lys Thr Ser Lys Asn Ala Asn Lys  
 1 5 10 15  
 Ser Ala Ala Val Leu Ser Asn Glu Leu Leu Glu Lys Ala Gly Tyr Leu  
 20 25 30  
 Phe Lys Val Ser Lys Gly Val Tyr Thr Thr Pro Leu Leu Trp Arg  
 35 40 45  
 Val Val Ser Lys Met Met Asn Ile Ile Arg Glu Glu Leu Asn Ala Ile  
 50 55 60  
 Gly Gly Gln Glu Leu Leu Leu Pro Leu Leu His Asn Ala Glu Leu Trp  
 65 70 75 80  
 Gln His Thr Gly Arg Trp Glu Ala Phe Thr Ser Glu Gly Leu Leu Tyr  
 85 90 95  
 Thr Leu Lys Asp Arg Glu Gly Lys Ser His Cys Leu Ala Pro Thr His  
 100 105 110  
 Glu Glu Val Ile Cys Ser Phe Val Ala Gln Trp Leu Ser Ser Lys Arg  
 115 120 125  
 Gln Leu Pro Leu His Leu Tyr Gln Ile Ala Thr Lys Phe Arg Asp Glu  
 130 135 140  
 Ile Arg Pro Arg Phe Gly Leu Ile Arg Ser Arg Glu Leu Leu Met Glu  
 145 150 155 160  
 Asp Ser Tyr Thr Phe Ser Asp Ser Pro Glu Gln Met Asn Glu Gln Tyr  
 165 170 175  
 Glu Lys Leu Arg Ser Ala Tyr Ser Lys Ile Phe Asp Arg Leu Gly Leu  
 180 185 190  
 Ala Tyr Val Ile Val Thr Ala Asp Gly Gly Lys Ile Gly Lys Gly Lys  
 195 200 205  
 Ser Glu Glu Phe Gln Val Leu Cys Ser Leu Gly Glu Asp Thr Ile Cys  
 210 215 220  
 Val Ser Gly Ser Tyr Gly Ala Asn Ile Glu Ala Ala Val Ser Ile Pro  
 225 230 235 240  
 Pro Gln His Ala Tyr Asp Arg Glu Phe Leu Pro Val Glu Glu Val Ala  
 245 250 255  
 Thr Pro Gly Ile Thr Thr Ile Glu Ala Leu Ala Asn Phe Phe Ser Ile  
 260 265 270  
 Pro Leu His Lys Ile Leu Lys Thr Leu Val Val Lys Leu Ser Tyr Ser  
 275 280 285  
 Asn Glu Glu Lys Phe Ile Ala Ile Gly Met Arg Gly Asp Arg Gln Val  
 290 295 300  
 Asn Leu Val Lys Val Ala Ser Lys Leu Asn Ala Asp Asp Ile Ala Leu  
 305 310 315 320  
 Ala Ser Asp Glu Glu Ile Glu Arg Val Leu Gly Thr Glu Lys Gly Phe  
 325 330 335  
 Ile Gly Pro Leu Asn Cys Pro Ile Asp Phe Xaa Ala Asp Glu Thr Thr

340 345 350  
 Ser Pro Met Thr Asn Phe Val Cys Ala Gly Asn Ala Lys Asp Lys His  
 355 360 365  
 Tyr Val Asn Val Asn Trp Asp Arg Asp Leu Leu Pro Pro Gln Tyr Gly  
 370 375 380  
 Asp Phe Leu Leu Ala Glu Glu Gly Asp Thr Cys Pro Glu Asn Pro Gly  
 385 390 395 400  
 His Pro Tyr Arg Ile Tyr Gln Gly Ile Glu Val Ala His Ile Phe Asn  
 405 410 415  
 Leu Gly Thr Arg Tyr Thr Asp Ser Phe Glu Val Asn Phe Gln Asp Glu  
 420 425 430  
 His Gly Gln Thr Gln Gln Cys Trp Met Gly Thr Tyr Gly Ile Gly Val  
 435 440 445  
 Gly Arg Thr Leu Ala Ala Cys Val Glu Gln Leu Ala Asp Asp Arg Gly  
 450 455 460  
 Ile Val Trp Pro Lys Ala Leu Ala Pro Phe Ser Ile Thr Ile Ala Phe  
 465 470 475 480  
 Asn Gly Gly Asp Thr Val Ser Gln Glu Leu Ala Glu Thr Ile Tyr His  
 485 490 495  
 Glu Leu Gln Ser Gln Gly Tyr Glu Pro Leu Leu Asp Asp Arg Asp Glu  
 500 505 510  
 Arg Leu Gly Phe Lys Leu Lys Asp Ser Asp Leu Ile Gly Ile Pro Tyr  
 515 520 525  
 Lys Leu Ile Leu Gly Lys Ser Tyr Gln Ser Ser Gly Ile Phe Glu Ile  
 530 535 540  
 Glu Ser Arg Ser Gly Glu Lys Tyr Thr Val Ser Pro Glu Ala Phe Pro  
 545 550 555 560  
 Thr Trp Cys Gln Asn His Leu Ala  
 565

&lt;210&gt;540

&lt;211&gt;126

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;540

Leu Thr Phe Ser Gly Ser Phe Pro Ile Met Leu Ser Val Thr Ile Val  
 1 5 10 15  
 Leu Val Gly Leu Glu Met Ala Arg Ser Lys Val Ser Lys Arg Asp Ser  
 20 25 30  
 Lys Ile Leu Asp Ile Leu Phe Ala Thr Thr Glu Leu Tyr Leu Lys Thr  
 35 40 45  
 Gly Gln Pro Val Gly Ser Lys Thr Leu Lys Glu Ser Phe Cys Ser Asp  
 50 55 60  
 Leu Ser Thr Ala Thr Ile Arg Asn Tyr Phe Ala Glu Leu Glu Ala Glu  
 65 70 75 80  
 Gly Phe Leu Lys Xaa Asn His Thr Ser Gly Gly Arg Ile Pro Thr Asp  
 85 90 95  
 Leu Ala Leu Arg His Tyr Val Asp His Gln Glu Glu Cys Pro Glu Ala  
 100 105 110  
 Glu Ile Ser Ala Pro Ile Phe Asp Lys Xaa Ser Xaa Leu Pro  
 115 120 125

&lt;210&gt;541

&lt;211&gt;304

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;541

Ile Thr Lys Lys Asn Ala Gln Lys Leu Arg Phe Leu Pro Pro Phe Leu  
 1 5 10 15  
 Ile Xaa Ser Val Xaa Phe Pro Ser Glu Ser Arg Asn Ile Ile Lys Asp  
 20 25 30  
 Leu Gln Lys Ala Thr Glu Leu Leu Gly Glu Ile Leu Asp Leu Pro Thr  
 35 40 45  
 Phe Phe Ser Ser Pro Arg Phe Glu Asn Asp Ser Val Thr Asn Ile Gln  
 50 55 60  
 Ile Thr Gln Val Asp Lys Gln Arg Ala Val Thr Ile Leu Ser Thr Glu

65 70 75 80  
 Phe Gly Gln Ile Phe Thr Asp Thr Leu Trp Leu Pro Glu Ala Cys Asp  
 85 90 95  
 Thr Leu Ser Ile Lys Arg Ile Glu Lys Phe Leu Gln Asn Tyr Ile Arg  
 100 105 110  
 Lys Leu Pro Thr Asn Glu Glu Leu Ser Lys Lys Glu Glu His Leu Ser  
 115 120 125  
 Met Ser Leu Tyr Asn Glu Val Val Val Arg Tyr Leu Thr Arg Tyr Cys  
 130 135 140  
 Asn Phe Ser Glu Glu Asp Leu Tyr Gln Thr Gly Met Ser Lys Leu Leu  
 145 150 155 160  
 Lys Tyr Glu Ala Phe Lys Asp Pro Glu Val Leu Ala Leu Gly Leu Ser  
 165 170 175  
 Leu Phe Glu Asn Arg Arg Gln Met Cys Glu Leu Leu Asn Ile Gly Met  
 180 185 190  
 His Lys Gly Arg Ala Thr Ala Phe Ile Gly Lys Glu Leu Ser Asp Ile  
 195 200 205  
 Leu Gly Thr Ser Asn Pro Gly Cys Ser Val Ile Thr Ile Pro Tyr Tyr  
 210 215 220  
 Met Asn Arg Ser Pro Leu Gly Ala Leu Gly Ile Leu Gly Pro Ile Asn  
 225 230 235 240  
 Leu Pro Tyr Lys Glu Ala Leu Pro Leu Leu Lys Leu Phe Ala Asn Lys  
 245 250 255  
 Ile Asn Glu Thr Leu Thr Gln Ser Phe Tyr Lys Phe Lys Leu Ser Phe  
 260 265 270  
 Arg Arg Pro Leu Thr Ser Asn Cys Lys Leu Ser Asn Glu Pro Ile Leu  
 275 280 285  
 Arg Thr Glu Tyr Ser Ser Ile Lys Leu Leu Pro Ser Lys Glu Thr Leu  
 290 295 300

&lt;210&gt;542

&lt;211&gt;184

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;542

Met Thr Asp Thr Pro Pro Glu Asn Glu Glu Gln His Glu Ser Asn Val  
 1 5 10 15  
 Gln Asn Glu Asn Glu Val Glu His Leu Gln Gln Glu Ile Val Thr Leu  
 20 25 30  
 Lys Thr Glu Leu Lys Glu Lys Asn Asp Lys Tyr Leu Met Ala Leu Ala  
 35 40 45  
 Glu Ser Glu Asn Ser Arg Lys Arg Leu Gln Lys Glu Arg Gln Glu Leu  
 50 55 60  
 Met Gln Tyr Ala Leu Glu Asn Thr Leu Ile Asp Phe Leu Asn Pro Ile  
 65 70 75 80  
 Glu Ser Met Glu Lys Ala Leu Gly Phe Ala Thr Gln Met Ser Asp Asp  
 85 90 95  
 Val Lys Asn Trp Ala Leu Gly Phe Asn Met Ile Leu Asn Gln Phe Lys  
 100 105 110  
 Gln Ile Phe Glu Glu Lys Gly Ile Ile Glu Tyr Ser Ser Ile Gly Gln  
 115 120 125  
 Lys Phe Asn Pro Phe Leu His Glu Ala Val Gln Thr Glu Glu Thr Ser  
 130 135 140  
 Glu Val Pro Glu Gly Thr Ile Leu Glu Glu Phe Ala Lys Gly Tyr Lys  
 145 150 155 160  
 Ile Gly Glu Arg Pro Ile Arg Val Ala Lys Val Lys Val Ala Lys Ala  
 165 170 175  
 Pro Thr Pro Lys Glu Asn Lys Glu  
 180

&lt;210&gt;543

&lt;211&gt;539

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;543

Met Ser Glu His Lys Lys Ser Ser Lys Ile Ile Gly Ile Asp Leu Gly

1 5 10 15  
 Thr Thr Asn Ser Cys Val Ser Val Met Glu Gly Gly Gln Ala Lys Val  
 20 25 30  
 Ile Thr Ser Ser Glu Gly Thr Arg Thr Thr Pro Ser Ile Val Ala Phe  
 35 40 45  
 Lys Gly Asn Glu Lys Leu Val Gly Ile Pro Ala Lys Arg Gln Ala Val  
 50 55 60  
 Thr Asn Pro Glu Lys Thr Leu Gly Ser Thr Lys Arg Phe Ile Gly Arg  
 65 70 75 80  
 Lys Tyr Ser Glu Val Ala Ser Glu Ile Gln Thr Val Pro Tyr Thr Val  
 85 90 95  
 Thr Ser Gly Ser Lys Gly Asp Ala Val Phe Glu Val Asp Gly Lys Gln  
 100 105 110  
 Tyr Thr Pro Glu Glu Ile Gly Ala Gln Ile Leu Met Lys Met Lys Glu  
 115 120 125  
 Thr Ala Glu Ala Tyr Leu Gly Glu Thr Val Thr Glu Ala Val Ile Thr  
 130 135 140  
 Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Ala Ser Thr Lys Asp Ala  
 145 150 155 160  
 Gly Arg Ile Ala Gly Leu Asp Val Lys Arg Ile Ile Pro Glu Pro Thr  
 165 170 175  
 Ala Ala Ala Leu Ala Tyr Gly Ile Asp Lys Val Gly Asp Lys Lys Ile  
 180 185 190  
 Ala Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu  
 195 200 205  
 Ile Gly Asp Gly Val Phe Glu Val Leu Ser Thr Asn Gly Asp Thr Leu  
 210 215 220  
 Leu Gly Gly Asp Asp Phe Asp Glu Val Ile Ile Lys Trp Met Ile Glu  
 225 230 235 240  
 Glu Phe Lys Lys Gln Glu Gly Ile Asp Leu Ser Lys Asp Asn Met Ala  
 245 250 255  
 Leu Gln Arg Leu Lys Asp Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser  
 260 265 270  
 Gly Val Ser Ser Thr Glu Ile Asn Gln Pro Phe Ile Thr Met Asp Ala  
 275 280 285  
 Gln Gly Pro Lys His Leu Ala Leu Thr Leu Thr Arg Ala Gln Phe Glu  
 290 295 300  
 Lys Leu Ala Ala Ser Leu Ile Glu Arg Thr Lys Ser Pro Cys Ile Lys  
 305 310 315 320  
 Ala Leu Ser Asp Ala Lys Leu Ser Ala Lys Asp Ile Asp Asp Val Leu  
 325 330 335  
 Leu Val Gly Gly Met Ser Arg Met Pro Ala Val Gln Glu Thr Val Lys  
 340 345 350  
 Glu Leu Phe Gly Lys Glu Pro Asn Lys Gly Val Asn Pro Asp Glu Val  
 355 360 365  
 Val Ala Ile Gly Ala Ala Ile Gln Gly Gly Val Leu Gly Gly Glu Val  
 370 375 380  
 Lys Asp Val Leu Leu Leu Asp Val Ile Pro Leu Ser Leu Gly Ile Glu  
 385 390 395 400  
 Thr Leu Gly Gly Val Met Thr Thr Leu Val Glu Arg Asn Thr Thr Ile  
 405 410 415  
 Pro Thr Gln Lys Lys Gln Ile Phe Ser Thr Ala Ala Asp Asn Gln Pro  
 420 425 430  
 Ala Val Thr Ile Val Val Leu Gln Gly Glu Arg Pro Met Ala Lys Asp  
 435 440 445  
 Asn Lys Glu Ile Gly Arg Phe Asp Leu Thr Asp Ile Pro Pro Ala Pro  
 450 455 460  
 Arg Gly His Pro Gln Ile Glu Val Ser Phe Asp Ile Asp Ala Asn Gly  
 465 470 475 480  
 Ile Phe His Val Ser Ala Lys Asp Val Ala Ser Gly Lys Glu Gln Lys  
 485 490 495  
 Ile Arg Ile Glu Ala Ser Ser Gly Leu Gln Glu Asp Glu Ile Gln Arg  
 500 505 510  
 Met Val Arg Asp Ala Glu Ile Asn Lys Glu Glu Asp Lys Asn Val Val

515 520 525  
 Lys Leu Gln Met Leu Lys Met Lys Pro Ile Ala  
 530 535  
 <210>544  
 <211>135  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>544  
 Lys Arg Arg Glu Ala Ser Asp Ala Lys Asn Glu Ala Asp Ser Met Ile  
 1 5 10 15  
 Phe Arg Ala Glu Lys Ala Ile Lys Asp Tyr Lys Glu Gln Ile Pro Glu  
 20 25 30  
 Thr Leu Val Lys Glu Ile Glu Glu Arg Ile Glu Asn Val Arg Asn Ala  
 35 40 45  
 Leu Lys Asp Asp Ala Pro Ile Glu Lys Ile Lys Glu Val Thr Glu Asp  
 50 55 60  
 Leu Ser Lys His Met Gln Lys Ile Gly Glu Ser Met Gln Ser Gln Ser  
 65 70 75 80  
 Ala Ser Ala Ala Ala Ser Ser Ala Ala Asn Ala Lys Gly Gly Pro Asn  
 85 90 95  
 Ile Asn Thr Glu Asp Leu Lys Lys His Ser Phe Ser Thr Lys Pro Pro  
 100 105 110  
 Ser Asn Asn Gly Ser Ser Glu Asp His Ile Glu Glu Ala Asp Val Glu  
 115 120 125  
 Ile Ile Asp Asn Asp Asp Lys  
 130 135  
 <210>545  
 <211>234  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>545  
 Ala Thr Gln Phe Thr Ser Glu Thr Thr Gly Phe Leu Val Gln Cys Pro  
 1 5 10 15  
 Lys Leu Thr Gly Gly Ala Gln Leu Leu Lys Lys Pro Lys Arg Lys Pro  
 20 25 30  
 Gly Arg Arg Thr Tyr Gly Lys Ser Leu Lys Ile Phe Ile Pro Gly Thr  
 35 40 45  
 Leu Phe Val His Ala Arg Lys Gly Phe Gly Phe Val Ser Pro Asp Asn  
 50 55 60  
 Pro Glu Glu Tyr Pro Phe Asp Ile Phe Val Pro Ala Arg Asp Leu Arg  
 65 70 75 80  
 Gly Ala Leu Asp Gly Asp His Val Ile Val Ser Val Leu Pro Tyr Pro  
 85 90 95  
 Arg Asp Gly Gln Lys Leu Lys Gly Thr Ile Ser Glu Val Leu Ala Arg  
 100 105 110  
 Gly Lys Thr Thr Leu Val Gly Thr Ile Thr Ser Leu Val Ser Pro Thr  
 115 120 125  
 Ser Ala Leu Ala Tyr Thr Ser Met Ser Gly Ser Gln Ser Leu Ile Pro  
 130 135 140  
 Val Glu Leu Leu Pro Gly Arg Thr Tyr Lys Ile Gly Asp Arg Ile Leu  
 145 150 155 160  
 Leu Ser Thr Pro Pro Trp Val Asp Lys Pro Gln Glu Gly Ala Ser Pro  
 165 170 175  
 Ala Leu Gln Met Leu Glu Phe Ile Gly His Ile Thr Asn Ala Lys Ala  
 180 185 190  
 Asp Phe Gln Ala Ile Gln Ala Glu Tyr Asn Leu Ala Glu Glu Phe Pro  
 195 200 205  
 Pro Glu Val Ile Glu Glu Ala Ser Leu Phe Ser Gln Xaa Xaa Leu Thr  
 210 215 220  
 Gln Val Leu Gln Leu Ser Gln Arg Ser Pro  
 225 230  
 <210>546  
 <211>258  
 <212>PRT



&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;546

```

Pro Lys Phe Ser Asn Ser Arg Lys Asp Leu Arg Asp Leu Leu Cys Phe
 1           5           10           15
Thr Ile Asp Ser Ser Thr Ala Arg Asp Phe Asp Asp Ala Ile Ser Leu
          20          25          30
Thr Tyr Asp His Asn Asn Asn Tyr Ile Leu Gly Val His Ile Ala Asp
          35          40          45
Val Ser His Tyr Val Thr Pro His Ser His Leu Asp Lys Glu Ala Ala
          50          55          60
Lys Arg Cys Asn Ser Thr Tyr Phe Pro Gly Lys Val Ile Pro Met Leu
65          70          75          80
Pro Ser Ala Leu Ser Asp Asn Leu Cys Ser Leu Lys Pro Asn Val Asp
          85          90          95
Arg Leu Ala Val Ser Val Phe Met Thr Phe Thr Lys Ser Gly His Leu
          100         105         110
Ser Asp Tyr Gln Ile Phe Arg Ser Val Ile Arg Ser Lys Tyr Arg Met
          115         120         125
Thr Tyr Asp Glu Val Asp Asn Ile Ile Glu Lys Lys His Ser His Pro
          130         135         140
Leu Ser Lys Ile Leu Asn Glu Met Ala Thr Leu Ser Lys Lys Phe Ser
145          150          155          160
Asp Ile Arg Glu Glu Arg Gly Cys Ile Arg Phe Val Leu Pro Ser Val
          165          170          175
Thr Met Ser Leu Asp Asn Leu Gln Glu Pro Val Ala Leu Ile Glu Asn
          180         185         190
His Gln Thr Phe Ser His Lys Leu Ile Glu Glu Phe Met Leu Lys Ala
          195         200         205
Asn Glu Val Val Ala Tyr His Ile Ser His Gln Gly Val Ser Leu Pro
          210         215         220
Phe Arg Ser His Glu Pro Pro Asn Asp Glu Asn Leu Leu Ala Phe Gln
225          230          235          240
Glu Xaa Ala Lys Asn Met Gly Phe Asp Ile Thr Phe Thr Pro Thr Gln
          245          250          255
Arg Thr

```

&lt;210&gt;547

&lt;211&gt;286

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;547

```

Lys Thr Thr Arg Pro Ser Pro Ile Asn Ser Ser Lys Ser Leu Cys Leu
 1           5           10           15
Lys Gln Thr Lys Trp Ser Pro Ile Ile Ser Pro Ile Lys Ala Phe Leu
          20          25          30
Tyr Leu Phe Val Val Thr Asn Leu Pro Met Met Lys Thr Tyr Ser Pro
          35          40          45
Ser Lys Xaa Xaa Gln Lys Thr Trp Ala Leu Ile Ser Arg Ser Leu Pro
          50          55          60
His Lys Glu Pro Asp Tyr Gln Tyr Leu Leu Gln Thr Thr Ser Ala Gly
65          70          75          80
His Pro Leu Glu Gln Val Leu His Ser Gln Phe Val Arg Ser Met Lys
          85          90          95
Thr Ala Ser Tyr Ser Thr Glu Asn Lys Gly His Tyr Gly Leu Lys Leu
          100         105         110
Asp Tyr Tyr Thr His Phe Thr Ser Pro Ile Arg Arg Tyr Ile Asp Leu
          115         120         125
Ile Val His Arg Leu Leu Phe Asn Pro Leu Ser Ile Asp Gln Thr His
          130         135         140
Leu Glu Ile Ile Val Arg Ala Cys Ser Thr Lys Glu Arg Val Ser Ala
145          150          155          160
Lys Ala Glu Asn Ser Phe Glu Asn Leu Lys Lys Thr Arg Phe Ile Asn
          165          170          175
Lys Phe Leu Gln Glu Gln Pro Lys Thr Thr Tyr His Ala Tyr Ile Ile

```

180 185 190  
 Thr Ala Asn His Glu Gly Leu Ser Phe Val Val Thr Glu Phe Cys His  
 195 200 205  
 Glu Gly Phe Ile Ala Ala Ala Glu Leu Pro Lys Glu Tyr Ser Leu Lys  
 210 215 220  
 Lys Asn Ala Leu Pro Glu Ser Ile Pro Asp Lys Met Lys Pro Gly Ala  
 225 230 235 240  
 Ser Arg Lys Val Thr Ile Asp Ser Val Asn Leu Leu Thr Gln Lys Ile  
 245 250 255  
 Val Trp Ser Ile Ala Thr Thr Thr Glu Asp Lys Pro Lys Lys Ile Lys  
 260 265 270  
 Lys Thr Pro Ser Lys Lys Lys Gly Thr Lys Lys Arg Ala Ser  
 275 280 285

&lt;210&gt;548

&lt;211&gt;201

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;548

Lys Glu Pro Arg Asn Val Leu Gln Glu His Phe Phe Leu Ser Glu Asp  
 1 5 10 15  
 Val Ile Thr Leu Ala Gln Gln Leu Leu Gly His Lys Leu Ile Thr Thr  
 20 25 30  
 His Glu Gly Leu Ile Thr Ser Gly Tyr Ile Val Glu Thr Glu Ala Tyr  
 35 40 45  
 Arg Gly Pro Asp Asp Lys Ala Cys His Ala Tyr Asn Tyr Arg Lys Thr  
 50 55 60  
 Gln Arg Asn Arg Ala Met Tyr Leu Lys Arg Gly Ser Ala Tyr Leu Tyr  
 65 70 75 80  
 Arg Cys Tyr Gly Met His His Leu Leu Asn Val Val Thr Gly Pro Glu  
 85 90 95  
 Asp Ile Pro His Ala Val Leu Ile Arg Ala Ile Leu Pro Asp Gln Gly  
 100 105 110  
 Lys Glu Leu Met Ile Gln Arg Arg Gln Trp Arg Asp Lys Pro Pro His  
 115 120 125  
 Leu Leu Thr Asn Gly Pro Gly Lys Val Cys Gln Ala Leu Gly Ile Ser  
 130 135 140  
 Leu Glu Asn Asn Arg Gln Arg Leu Asn Thr Pro Ala Leu Tyr Ile Ser  
 145 150 155 160  
 Lys Glu Lys Ile Ser Gly Thr Leu Thr Ala Thr Ala Arg Ile Gly Ile  
 165 170 175  
 Asp Tyr Ala Gln Glu Tyr Arg Asp Val Pro Trp Arg Phe Leu Leu Ser  
 180 185 190  
 Pro Glu Asp Ser Gly Lys Val Leu Ser  
 195 200

&lt;210&gt;549

&lt;211&gt;189

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;549

Ala Trp Leu Arg Asn Ser Leu Thr Lys Phe Ser Phe Tyr Thr Lys His  
 1 5 10 15  
 Arg Ala Leu Leu Lys Phe Val Leu Gln Ile Ile Leu Leu Phe Gly Leu  
 20 25 30  
 Phe Phe Ala Thr Val Leu Leu Gly Phe Leu Thr Arg Ile Met Ile Phe  
 35 40 45  
 Lys Ser Leu Leu Ser Ile Tyr Asp Lys Ile Leu His Arg Ile Pro Ile  
 50 55 60  
 Ile Lys Thr Val Tyr Lys Ala Ala Gln Gln Val Met Thr Thr Ile Phe  
 65 70 75 80  
 Gly Ser Lys Ser Gly Ser Phe Lys Gln Val Val Met Val Pro Phe Pro  
 85 90 95  
 Asn Ala Asn Val Gln Cys Ile Gly Leu Val Ala Gly Asp Ala Pro Thr  
 100 105 110  
 Val Cys Cys Thr Gly Glu Lys Glu Asp Asp Pro Leu Val Thr Val Phe

```

      115      120      125
Ile Pro Thr Thr Pro Asn Pro Thr Ser Gly Phe Leu Thr Leu Phe Arg
      130      135      140
Lys Ser Asp Ile Val Phe Leu Asp Met Lys Ile Glu Asp Ala Phe Lys
145      150      155      160
Tyr Ile Ile Ser Cys Gly Val Leu Ser Thr Pro Met Ala Cys Pro Ser
      165      170      175
Ser Pro Leu Pro Asp Glu Leu His Gln Asp Gln Gly Ser
      180      185

<210>550
<211>390
<212>PRT
<213>Chlamydia pneumoniae
<400>550
Gln Leu Asn Met Leu His Ile Leu Leu Ala Ile Phe Cys Ile Leu Leu
 1      5      10      15
Phe Leu Ala Phe Gly Leu Thr Gln Pro Ser Cys His Gly Ser Ser Lys
      20      25      30
Phe Leu Lys Thr Leu Asn Gln Arg Phe Phe Thr Asp Lys Gly Arg Glu
      35      40      45
Tyr Pro Pro Phe Pro Ser Ala Pro Thr Ile Leu Ala Thr Leu Leu Cys
      50      55      60
Ile Leu Tyr Gly Ala Leu Gly Thr Lys Leu Tyr Thr Leu Leu Pro Pro
      65      70      75      80
Lys Thr Ala His Lys Asp Leu Leu Phe Trp Pro Leu Tyr Ser Leu Ser
      85      90      95
Ala Leu Ile Ala Tyr Gly Phe Leu Pro Pro Trp Ile Ser Thr Lys Val
      100      105      110
Pro Lys Glu Thr Thr Ala His Leu Arg Phe Leu Ala Ser Val Phe Gln
      115      120      125
Leu Gly Leu Phe Pro Leu Gln Leu Leu Phe Tyr Arg Arg Arg Pro Asn
      130      135      140
Gln Gln Val Arg Ser Ser Thr Ser Phe Gln Ser Gln Leu Ser Glu Ala
145      150      155      160
Leu Ser Ala Phe Asp Asn Leu Ile Val Arg Glu Val Met Ile Pro Lys
      165      170      175
Val Asp Ile Phe Ala Leu Pro Glu Glu Thr Thr Leu Gln Glu Ala Leu
      180      185      190
Val Leu Val Ser Glu Glu Gly Tyr Ser Arg Val Pro Val Tyr Lys Lys
      195      200      205
Asn Leu Asp Asn Ile Thr Gly Ile Leu Leu Val Lys Asp Leu Leu Leu
      210      215      220
Leu Tyr Thr Ser Ser His Asp Leu Ser Gln Pro Ile Ser Ser Val Ala
225      230      235      240
Lys Pro Pro Phe Tyr Ala Pro Glu Ile Lys Lys Ala Ser Ser Leu Leu
      245      250      255
Gln Glu Phe Arg Gln Lys His Arg His Leu Ala Ile Ile Val Asn Glu
      260      265      270
Tyr Gly Phe Thr Glu Gly Ile Ala Thr Met Glu Asp Ile Ile Glu Glu
      275      280      285
Ile Ile Gly Glu Ile Ala Asp Glu His Asp Val Gln Glu Asn Thr Pro
      290      295      300
Tyr Lys Lys Ile Gly Ser Ser Trp Ile Val Asp Gly Arg Met Asn Ile
305      310      315      320
Ser Asp Ala Glu Glu Tyr Phe Asn Leu Lys Ile Asp His Glu Asn Ser
      325      330      335
Tyr Asp Thr Leu Gly Gly His Val Phe His Lys Val Gly Ala Val Pro
      340      345      350
Gln Lys Gly Met Arg Ile His His Glu Asn Phe Asp Ile Glu Ile Ile
      355      360      365
Thr Cys Thr Glu Arg Asn Val Gly Lys Leu Lys Ile Thr Pro Arg Lys
      370      375      380
Arg Lys Phe Asn Ile Ser
385      390

```

&lt;210&gt;551

&lt;211&gt;116

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;551

```

Met Ser Asp Ile Gln Lys Glu Glu His Gly Ser Thr Thr Ile Phe His
 1           5           10           15
Leu His Gly Lys Leu Asp Gly Ile Ser Ser Pro Glu Val Gln Glu Asn
           20           25           30
Ile Tyr Gln Ser Leu Ala Ala Gly Ser Lys Asn Ile Ile Leu Asp Cys
           35           40           45
Ala His Leu Asp Tyr Met Ser Ser Ala Gly Ile Arg Val Leu Leu Gln
           50           55           60
Ser Tyr His Gln Val Gly Gln His Ser Gly Lys Ile Val Leu Thr Thr
           65           70           75           80
Val Pro Lys Thr Ile Glu Gln Thr Leu Tyr Val Thr Gly Phe Leu Ser
           85           90           95
Tyr Phe Lys Ile Phe Asn Thr Val Asp Glu Ala Ile Gln Thr Leu Asn
           100           105           110
Lys Asp Gly Asp
           115

```

&lt;210&gt;552

&lt;211&gt;212

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;552

```

Ser Leu Pro Leu Thr Met Arg Arg Ser Val Cys Tyr Val Asn Pro Ser
 1           5           10           15
Ile Ala Arg Ala Gly Gln Ile Ser Thr Trp Lys Phe Leu Tyr Ser Leu
           20           25           30
Ala Thr Pro Leu Pro Ala Gly Thr Lys Cys Lys Phe Asp Leu Ala Gly
           35           40           45
Ser Gly Lys Pro Thr Asp Trp Glu Ala Pro Ala Thr Asp Leu Ser Gln
           50           55           60
Thr Arg Asn Val Ile Tyr Ala Glu Met Pro Glu Gly Glu Ile Ile Glu
           65           70           75           80
Ala Thr Ala Ile Pro Val Lys Asp Asn Pro Val Pro Gln Phe Glu Phe
           85           90           95
Thr Leu Pro Tyr Glu Leu Gln Val Gly Glu Thr Leu Thr Ile Val Met
           100           105           110
Gly Ala Ser Pro Asn His Pro Gln Val Asp Asp Ala Gly Asn Gly Ala
           115           120           125
Gln Leu Phe Ala Gln Arg Arg Lys Pro Phe Tyr Leu Tyr Ile Asp Pro
           130           135           140
Thr Gly Glu Gly Asn Tyr Asp Glu Pro Asp Val Phe Ser Met Asp Ile
           145           150           155           160
Arg Gly Asn Val Leu Lys Lys Ile Glu Ile Phe Thr Pro Ser Tyr Val
           165           170           175
Val Lys Asn Lys Arg Phe Asp Ile Thr Val Arg Phe Glu Asp Glu Phe
           180           185           190
Gly Asn Leu Thr Asn Phe Ser Pro Glu Glu Asp Pro Asn Arg Ala Phe
           195           200           205
Leu Arg Ala Ser
           210

```

&lt;210&gt;553

&lt;211&gt;457

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;553

```

Arg Ser Leu Leu Pro Pro Met Ser Leu Lys Thr Asn Ala Ser Ile Ser
 1           5           10           15
Pro Cys Asp Leu Lys Thr Asn Ser Gly Thr Ser Pro Thr Ser Leu Leu
           20           25           30
Lys Lys Thr Arg Ile Glu Leu Ser Tyr Glu His Leu Arg Glu Asn Leu

```

35 40 45  
 Asn Trp Gln Leu Phe Ile Pro Glu Thr Gly Phe Val Ile Leu Pro Asn  
 50 55 60  
 Leu Tyr Phe Asn Glu Pro Gly Ile Tyr Arg Ile Gln Leu Lys Asn Leu  
 65 70 75 80  
 Ser Thr Gln Xaa Ile Phe Ile Ser Ala Pro Ile Lys Cys Phe Ala Asp  
 85 90 95  
 Ser Ala Pro Asn Leu Met Trp Gly Leu Leu His Gly Glu Ser Glu Arg  
 100 105 110  
 Val Asp Ser Glu Glu Asn Ile Glu Thr Cys Met Arg Tyr Phe Arg Asp  
 115 120 125  
 Asp Arg Ala Leu Asn Phe Tyr Ala Ser Ser Ser Phe Glu Asn Gln Glu  
 130 135 140  
 Asn Leu Ser Pro Asp Ile Trp Lys Leu Ile Asn Gln Thr Val Ser Asp  
 145 150 155 160  
 Phe Asn Glu Glu Asp Arg Phe Ile Thr Leu Ser Gly Phe Gln Tyr Ser  
 165 170 175  
 Gly Glu Pro His Leu Glu Gly Val Arg His Ile Leu His Thr Lys Glu  
 180 185 190  
 Thr Lys Ser His Ser Lys His Lys Glu Tyr Lys His Ile Pro Leu Ala  
 195 200 205  
 Lys Leu Tyr Lys Ser Thr Val Asn His Asp Met Ile Ser Ile Pro Ser  
 210 215 220  
 Phe Thr Ala Ser Lys Glu His Gly Phe Asp Phe Glu Asn Phe Tyr Pro  
 225 230 235 240  
 Glu Phe Glu Arg Val Val Glu Ile Tyr Asn Ala Trp Gly Ser Ser Glu  
 245 250 255  
 Thr Thr Ala Ala Leu Asn Asn Pro Phe Pro Ile Gln Gly Lys Asp Ser  
 260 265 270  
 Glu Asp Pro Arg Gly Thr Val Ile Glu Gly Leu Lys Lys Asn Leu Arg  
 275 280 285  
 Phe Gly Phe Val Ala Gly Gly Leu Asp Asp Arg Gly Ile Tyr Lys Asp  
 290 295 300  
 Tyr Phe Asp Ser Pro Gln Val Gln Tyr Ser Pro Gly Leu Thr Ala Ile  
 305 310 315 320  
 Ile Cys Asn Lys Tyr Thr Arg Glu Ser Leu Val Glu Ala Leu Phe Ala  
 325 330 335  
 Arg His Cys Tyr Ala Thr Thr Gly Pro Arg Ile Val Leu Ser Phe Asn  
 340 345 350  
 Ile Thr Ser Ala Pro Met Gly Ser Glu Leu Ser Thr Gly Ser Lys Pro  
 355 360 365  
 Gly Leu Asn Val Asn Arg His Ile Ser Gly His Val Ala Gly Thr Ala  
 370 375 380  
 Leu Leu Lys Thr Val Glu Ile Ile Arg Asn Gly Glu Val Leu His Thr  
 385 390 395 400  
 Phe Phe Pro Asp Ser Asn Asn Leu Asp Tyr Glu Tyr Asp Asp Met Val  
 405 410 415  
 Pro Leu Ser Ser Val Thr Leu Lys Asp Pro Asn Gly Lys Ala Pro Phe  
 420 425 430  
 Val Phe Tyr Tyr Leu Arg Val Thr Gln Ala Asp Asn Ala Met Ala Trp  
 435 440 445  
 Ser Ser Pro Ile Trp Val Asp Leu Asn  
 450 455  
 <210>554  
 <211>409  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>554  
 Leu Ala Gly Pro Ser Leu Lys Gly Val Lys Asn Gln Ile Ala Ala Lys  
 1 5 10 15  
 Lys Lys His Val Thr Lys Gln Ser Thr Val Leu Gln Asn Leu Glu Arg  
 20 25 30  
 Ile Val His Gln Ser Val His Gln Met Thr Thr Cys Leu Pro Gln Pro  
 35 40 45

Pro Lys Thr Ser Pro Pro Tyr Ser Ile Phe Glu Lys Leu Asp Ala Gln  
 50 55 60  
 Glu Arg Leu Ser Ser Glu Asp Ala Leu His Leu Leu Leu Thr Asn  
 65 70 75 80  
 Lys Glu Asp Gln Arg Thr Leu Trp Asn Phe Ala Asp Gln Val Arg Lys  
 85 90 95  
 Gln Arg Val Gly Asp Thr Val Tyr Tyr Ser Ser Thr Leu Tyr Leu Tyr  
 100 105 110  
 Pro Thr Asn Phe Cys Asp Phe Ser Cys Lys Phe Cys Ser Phe Tyr Ala  
 115 120 125  
 Lys Pro Gly Asp Pro Lys Gly Trp Leu Tyr Ser Pro Asp Asp Leu Leu  
 130 135 140  
 Gln Gln Ile Gln Asn Ile Lys Thr Pro Ile Thr Glu Val His Ile Val  
 145 150 155 160  
 Gly Gly Cys Phe Pro Ser Cys Asn Leu Gln Tyr Tyr Ser Asp Leu Phe  
 165 170 175  
 Thr Lys Ile Lys Glu Tyr Asp Pro Gln Ile His Ile Lys Ala Leu Thr  
 180 185 190  
 Ala Ile Glu Tyr Ala Tyr Leu Ser Asp Leu Asp Asn Leu Ser Ile Arg  
 195 200 205  
 Asp Val Leu Leu Thr Leu Lys Asp Ala Gly Leu Asp Ser Ile Pro Gly  
 210 215 220  
 Gly Gly Ala Glu Ile Leu Val Asp Lys Ile Arg Asn Phe Leu Ala Pro  
 225 230 235 240  
 Lys Arg Leu Ser Ser Ser Asp Phe Leu Asn Ile His Lys Met Ala His  
 245 250 255  
 Gln Leu Gly Ile His Ser Asn Ile Thr Met Leu Cys Tyr His Lys Glu  
 260 265 270  
 Gly Pro Glu Asp Leu Val Thr His Met Val Lys Val Arg Asp Leu Gln  
 275 280 285  
 Asp Glu Thr Gln Gly Phe Lys Asn Phe Ile Leu Leu Lys Phe Ala Gln  
 290 295 300  
 Glu Asn Asn Val Leu Gly Lys Arg Leu Arg Lys Ser Gly Gln Gly His  
 305 310 315 320  
 Ala Ile Pro Leu Lys Ser Leu Met Ala Val Ala Arg Ile Phe Leu Asp  
 325 330 335  
 Asn Phe Ser Asn Met Lys Ala Leu Trp Asn Tyr Leu Gly Ile Glu Ala  
 340 345 350  
 Ala Leu Asp Leu Leu Ser Cys Gly Ala Asn Asp Leu Ser Ser Thr His  
 355 360 365  
 Met Gly Glu Lys Val Phe Gln Met Ala Ser Ser Lys Glu Pro Ile Lys  
 370 375 380  
 Met Asp Ala Glu Gly Met Ala Ala Leu Ile Thr Gln Gln Gly Arg Thr  
 385 390 395 400  
 Pro Cys Leu Thr Asn Ser Ser His Val  
 405

&lt;210&gt;555

&lt;211&gt;277

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;555

Gly Asn Gly Gly Pro His His Thr Thr Arg Glu Asn Ala Met Ser Asn  
 1 5 10 15  
 Gln Leu Gln Pro Cys Ile Ser Leu Gly Cys Val Ser Tyr Ile Asn Ser  
 20 25 30  
 Phe Pro Leu Ser Leu Gln Leu Ile Lys Arg Asn Asp Ile Arg Cys Val  
 35 40 45  
 Leu Ala Pro Pro Ala Asp Leu Leu Asn Leu Leu Ile Glu Gly Lys Leu  
 50 55 60  
 Asp Val Ala Leu Thr Ser Ser Leu Gly Ala Ile Ser His Asn Leu Gly  
 65 70 75 80  
 Tyr Val Pro Gly Phe Gly Ile Ala Ala Asn Gln Arg Ile Leu Ser Ala  
 85 90 95  
 Asn Leu Tyr Ala Ala Pro Thr Phe Phe Asn Ser Pro Gln Pro Arg Ile

100 105 110  
 Ala Ala Thr Leu Glu Ser Arg Ser Ser Ile Gly Leu Leu Lys Val Leu  
 115 120 125  
 Cys Arg His Leu Trp Arg Ile Pro Thr Pro His Ile Leu Arg Phe Ile  
 130 135 140  
 Thr Thr Lys Val Leu Arg Gln Thr Pro Glu Asn Tyr Asp Gly Leu Leu  
 145 150 155 160  
 Leu Ile Gly Asp Ala Ala Leu Gln His Pro Val Leu Pro Gly Phe Val  
 165 170 175  
 Thr Tyr Asp Leu Ala Ser Gly Trp Tyr Asp Leu Thr Lys Leu Pro Phe  
 180 185 190  
 Val Phe Ala Leu Leu Leu His Ser Thr Ser Trp Lys Glu His Pro Leu  
 195 200 205  
 Pro Asn Leu Ala Met Glu Glu Ala Leu Gln Gln Phe Glu Ser Ser Pro  
 210 215 220  
 Glu Glu Val Leu Lys Glu Ala His Gln His Thr Gly Leu Pro Pro Ser  
 225 230 235 240  
 Leu Leu Gln Glu Tyr Tyr Ala Leu Cys Gln Tyr Arg Leu Gly Glu Glu  
 245 250 255  
 His Tyr Glu Ser Phe Glu Lys Phe Arg Glu Tyr Tyr Gly Thr Leu Tyr  
 260 265 270  
 Gln Gln Ala Arg Leu  
 275

&lt;210&gt;556

&lt;211&gt;237

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;556

Leu Lys Asn Ser Gly Asn Ile Met Glu Pro Ser Thr Asn Lys Pro Asp  
 1 5 10 15  
 Cys Lys Lys Ile Phe Asp Ser Ile Ala Ser Lys Tyr Asp Arg Thr Asn  
 20 25 30  
 Thr Ile Leu Ser Leu Gly Met His His Phe Trp Asn Arg Ser Leu Ile  
 35 40 45  
 Gln Ile Leu Gly Ser Gly Tyr Ser Leu Leu Asp Leu Cys Ala Gly Thr  
 50 55 60  
 Gly Lys Val Ala Lys Arg Tyr Ile Ala Ala His Pro Gln Ala Ser Val  
 65 70 75 80  
 Thr Leu Val Asp Phe Ser Ser Ala Met Leu Asp Ile Ala Lys Gln His  
 85 90 95  
 Leu Pro Gln Gly Ser Cys Ser Phe Ile His Ser Asp Ile Asn Gln Leu  
 100 105 110  
 Pro Leu Glu Asn His Ser Tyr Pro Leu Ala Ala Met Ala Tyr Gly Leu  
 115 120 125  
 Arg Asn Leu Ser Asp Pro His Lys Ala Leu Gln Glu Ile Ser Arg Val  
 130 135 140  
 Leu Met Pro Ser Gly Lys Leu Gly Ile Leu Glu Leu Thr Pro Pro Lys  
 145 150 155 160  
 Lys Thr His Pro Thr Tyr Ser Ala His Lys Leu Tyr Leu Arg Ala Val  
 165 170 175  
 Val Pro Trp Ile Gly Lys Ser Val Ser Lys Asp Pro Asp Ala Tyr Ser  
 180 185 190  
 Tyr Leu Ser Lys Ser Ile Gln Gln Leu Pro Lys Asp His Asp Leu Glu  
 195 200 205  
 Asp Leu Phe Ser Lys Ser Gly Phe Tyr Ile Ala Lys Lys Lys Leu  
 210 215 220  
 Phe Leu Gly Ala Ala Thr Ile Trp Leu Leu Glu Lys Gln  
 225 230 235

&lt;210&gt;557

&lt;211&gt;550

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;557

Arg Ile Ser Ile Ser Phe Arg Val Ser Trp Phe Val Lys Ile Ile Leu

1	5	10	15
Ala Val Leu Gly Arg	Ala Ile Ala Lys	Tyr Tyr Val Cys	Met Val
20	25	30	
Ala Arg Gly Leu Cys	Asp Phe Pro Thr	Leu Val Pro Asn	Glu Arg Leu
35	40	45	
Pro Ile Gly Pro Phe	Phe Val Pro Gln	His Thr Ser Gly	Ala Lys Gly
50	55	60	
Lys Glu Phe Ala Lys	Arg Asn Phe Ser	Ile Ile Ser Gly	Leu Asp Asp
65	70	75	80
Ile Leu Lys Leu Cys	Ile Leu Gln Arg	Arg Pro Phe Ala	Leu Gln Trp
85	90	95	
Asp Asn Leu Ser Val	Lys Ser Asp Tyr	Glu Glu Ala Gly	Pro Ala Ile
100	105	110	
Gly Ile Arg Ser Leu	Glu Pro Gln Val	Ser Gln Ile Ser	Pro Ala His
115	120	125	
Gly Arg Leu Cys Ser	Thr Leu Val Gln	Trp Ala Pro Ile	Leu Gly Ser
130	135	140	
Glu Glu Arg Leu Val	Trp Leu Glu Glu	Thr Met Lys Arg	Leu Lys Phe
145	150	155	160
Pro Lys Ser Leu Gly	Ser Lys Asp Ala	Val Ile Val Asp	Ser Glu Met
165	170	175	
Val Pro Val Asn Ala	Asn Pro Thr Gln	Glu Ile Pro Ala	Ala Ser Glu
180	185	190	
Thr Val Glu Ser Ser	Pro Val Ala Pro	Gly Asn Thr Thr	Asp Thr Met
195	200	205	
Pro Ala Ala Ser Gly	Thr Thr Asp Thr	Thr Ser Gly Val	Ser Glu Ala
210	215	220	
Ala Ala Ala Glu Ala	Thr Val Asp Ser	Thr Pro Gly Thr	Glu Glu Glu
225	230	235	240
Pro Ser Phe Ser Leu	Arg Tyr Ala Leu	Val Val Gln Asn	Val Pro Tyr
245	250	255	
Pro Glu Pro Pro Lys	Glu Pro Glu Val	Met Phe Thr Asp	Glu Glu Lys
260	265	270	
Ser Leu Ile Leu Glu	Ala Thr Arg Ala	Arg Arg Met Glu	Leu Asp Leu
275	280	285	
Tyr Asn Gly Tyr Leu	Ala Asp Tyr Glu	Leu Ser Lys Asp	Glu Ile Gln
290	295	300	
Lys His Val Pro Asp	Leu Pro Glu Asn	Trp Arg Thr Asn	Trp Arg Trp
305	310	315	320
Ser Glu Arg Leu Tyr	Lys Phe Phe Phe	Lys Thr Lys Lys	Glu Gly Leu
325	330	335	
Glu Glu Ile Phe Leu	Asn Lys Glu Leu	Gly Asn Met Ile	Leu Ala Arg
340	345	350	
Gly Leu Ala Ala Thr	Gln Ser Gln Ala	Arg Ile Lys Val	Phe Asn Ser
355	360	365	
Leu Val Ala Trp Leu	Leu Gln Ser Phe	Asn Val Gly Arg	Ser Cys Thr
370	375	380	
Ala Lys Pro Leu Pro	Thr Ser Lys Leu	Asp Leu Phe Lys	Ser Glu Phe
385	390	395	400
Glu Ser Lys Pro Lys	Asn Asn Ile Leu	Thr Glu Phe Leu	Val Ala Ser
405	410	415	
Asp Glu Glu Ile Leu	Phe Lys Gly Leu	Arg Val Leu Glu	Pro Gly Ile
420	425	430	
Glu Gly Trp Tyr Asp	His Pro Asp Gln	Ala Gly Glu Ile	Arg Ser Val
435	440	445	
Leu Glu Gly Leu Val	Gln Ala Gly Arg	Ile Ser Gly Tyr	Trp Glu Asn
450	455	460	
Gln Pro Phe Gly Arg	Phe Val Leu Arg	Gly Val Gly Glu	Arg Arg Thr
465	470	475	480
Glu Leu Val Glu Leu	Leu Glu Ser Leu	Val Ala Ser Gly	Glu Ile Met
485	490	495	
Gln Phe Phe Glu Ser	Ser Asp Glu Glu	Gly Ala Phe Ile	Ile Asp Asn
500	505	510	
Glu Pro Ser Lys Thr	Ala Met Leu Lys	Gln Arg Phe Lys	Ser Cys Val



515 520 525  
 Arg Thr Lys Leu Val Gly Ser Phe Ala Asp Glu Ser Leu Pro Arg Gly  
 530 535 540  
 Arg Phe Thr Ile Leu Val  
 545 550  
 <210>558  
 <211>325  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>558  
 Phe Met Met Thr Tyr Pro Val Pro Gln Asn Pro Leu Leu Leu Arg Ile  
 1 5 10 15  
 Leu Arg Leu Met Asp Ala Phe Ser Lys Ser Asp Asp Glu Arg Asp Phe  
 20 25 30  
 Tyr Leu Asp Arg Val Glu Gly Phe Ile Leu Tyr Ile Asp Leu Asp Lys  
 35 40 45  
 Asp Gln Glu Asp Leu Asn Lys Ile Tyr Gln Glu Leu Glu Asn Ala  
 50 55 60  
 Glu Arg Tyr Cys Leu Ile Pro Lys Leu Thr Phe Tyr Glu Val Lys Lys  
 65 70 75 80  
 Ile Met Glu Thr Phe Ile Asn Glu Lys Ile Tyr Asp Ile Asp Thr Lys  
 85 90 95  
 Glu Lys Phe Leu Glu Ile Leu Gln Ser Lys Asn Ala Arg Glu Gln Phe  
 100 105 110  
 Leu Glu Phe Ile Tyr Asp His Glu Ala Glu Leu Glu Lys Trp Gln Gln  
 115 120 125  
 Phe Tyr Val Glu Arg Ser Arg Ile Arg Ile Ile Glu Trp Leu Arg Asn  
 130 135 140  
 Asn Lys Phe His Phe Val Phe Glu Glu Asp Leu Asp Phe Thr Lys Asn  
 145 150 155 160  
 Val Leu Glu Gln Leu Lys Ile His Leu Phe Asp Ala Lys Val Gly Lys  
 165 170 175  
 Glu Ile Thr Gln Ala Arg Gln Leu Leu Ser Asn Lys Ala Lys Ile Tyr  
 180 185 190  
 Tyr Ser Asn Glu Ala Leu Asn Pro Arg Pro Lys Arg Gly Arg Pro Pro  
 195 200 205  
 Lys Gln Ser Ala Lys Val Glu Thr Glu Thr Thr Ile Ser Ser Asp Ile  
 210 215 220  
 Tyr Thr Lys Val Pro Gln Ala Ala Arg Arg Phe Leu Phe Leu Pro Glu  
 225 230 235 240  
 Ile Thr Ser Pro Ser Ser Ile Thr Phe Ser Glu Lys Phe Asp Thr Glu  
 245 250 255  
 Glu Glu Phe Leu Ala Asn Leu Arg Gly Ser Thr Arg Val Glu Asp Gln  
 260 265 270  
 Leu Asn Leu Thr Asn Leu Ser Glu Arg Phe Ala Ser Leu Lys Glu Leu  
 275 280 285  
 Ser Ala Lys Leu Gly Tyr Asp Ser Leu Ser Thr Gly Asp Phe Phe Gly  
 290 295 300  
 Asp Asp Asp Glu Lys Val Thr Lys Thr Lys Gly Ser Lys Arg Gly  
 305 310 315 320  
 Arg Lys Lys Ser Ser  
 325  
 <210>559  
 <211>261  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>559  
 Leu Val Tyr Trp Met Ala Phe Tyr Ser Pro Ser Thr Ile Ser Lys Tyr  
 1 5 10 15  
 Phe Ile Tyr Ser Gly Ala Gly Asn Arg Phe Leu Leu Gly Glu Thr Leu  
 20 25 30  
 Pro Glu Val Glu Asp Val Arg Phe Leu Cys Gln Glu Thr Arg Val Asp  
 35 40 45  
 Gly Phe Leu Tyr Leu Lys Pro Ser Ser Cys Ala Asp Ala Gln Leu Ile

50 55 60  
 Ile Phe Asn Ser Asp Gly Ser Arg Pro Thr Met Cys Gly Asn Gly Leu  
 65 70 75 80  
 Arg Cys Ala Ile Ala His Leu Ala Ser Gln Lys Gly Lys Ser Asp Ile  
 85 90 95  
 Ser Val Ser Thr Asp Ser Gly Leu Tyr Ser Gly Tyr Phe Tyr Ser Trp  
 100 105 110  
 Asp Arg Val Leu Val Asp Met Thr Leu Ala Asp Trp Arg Ala Ser Val  
 115 120 125  
 His Arg Leu Glu Ser Arg Pro Asp Pro Leu Pro Lys Glu Ile Val Cys  
 130 135 140  
 Ile His Thr Gly Val Pro His Ala Val Val Ile Leu Pro Glu Ile Ser  
 145 150 155 160  
 Thr Leu Asp Leu Ser Ile Leu Gly Pro Phe Leu Arg Tyr His Gln Thr  
 165 170 175  
 Phe Ser Pro Asp Gly Val Asn Val Asn Phe Val Gln Ile Leu Gly His  
 180 185 190  
 Cys Gln Leu Arg Val Arg Thr Tyr Glu Arg Gly Val Glu Gly Glu Thr  
 195 200 205  
 Ala Ala Cys Gly Thr Gly Ala Leu Ala Ser Ala Leu Val Val Ser Asn  
 210 215 220  
 Ser Tyr Gly Trp Lys Glu Ser Ile Gln Ile His Thr Trp Gly Gly Glu  
 225 230 235 240  
 Leu Met Thr Val Ser Gln Asn Arg Gly Arg Val Tyr Leu Gln Gly Ser  
 245 250 255  
 Val Thr Arg Asp Leu  
 260

&lt;210&gt;560

&lt;211&gt;196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;560

Glu Arg His Tyr Phe Met Ala Asp Gly Glu Val His Lys Leu Arg Asp  
 1 5 10 15  
 Ile Ile Glu Lys Glu Leu Leu Glu Ala Arg Arg Val Phe Phe Ser Glu  
 20 25 30  
 Pro Val Thr Glu Lys Ser Ala Ser Asp Ala Ile Lys Lys Leu Trp Tyr  
 35 40 45  
 Leu Glu Leu Lys Asp Pro Gly Lys Pro Ile Val Phe Val Ile Asn Ser  
 50 55 60  
 Pro Gly Gly Ser Val Asp Ala Gly Phe Ala Val Trp Asp Gln Ile Lys  
 65 70 75 80  
 Met Leu Thr Ser Pro Val Thr Thr Val Val Thr Gly Leu Ala Ala Ser  
 85 90 95  
 Met Gly Ser Val Leu Ser Leu Cys Ala Ala Pro Gly Arg Arg Phe Ala  
 100 105 110  
 Thr Pro His Ser Arg Ile Met Ile His Gln Pro Ser Ile Gly Gly Pro  
 115 120 125  
 Ile Thr Gly Gln Ala Thr Asp Leu Asp Ile His Ala Arg Glu Ile Leu  
 130 135 140  
 Lys Thr Lys Ala Arg Ile Ile Asp Val Tyr Val Glu Ala Thr Asn Gln  
 145 150 155 160  
 Pro Arg Asp Ile Ile Glu Lys Ala Ile Asp Arg Asp Met Trp Met Thr  
 165 170 175  
 Ala Asn Glu Ala Lys Asp Phe Gly Leu Leu Asp Gly Ile Leu Phe Ser  
 180 185 190  
 Phe Asn Asp Leu  
 195

&lt;210&gt;561

&lt;211&gt;519

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;561

Leu Leu Lys Val Phe Glu Lys Phe Lys Lys Phe Ala Ile Val Glu Ile

1	5	10	15
Phe Thr Lys Val Val Ala Val Val Ser Leu Leu His Lys Phe Leu Glu			
20	25	30	
Asn Ala Ser Gly Lys Lys Gly Gln Ser Leu Ala Ser Thr Ala Tyr Leu			
35	40	45	
Ala Ala Leu Asp His Leu Leu Asn Ala Phe Pro Ser Ile Gly Glu Arg			
50	55	60	
Ile Ile Asp Glu Leu Lys Ser Gln Arg Ser His Leu Lys Met Ile Ala			
65	70	75	80
Ser Glu Asn Tyr Ser Ser Leu Ser Val Gln Leu Ala Met Gly Asn Leu			
85	90	95	
Leu Thr Asp Lys Tyr Cys Glu Gly Ser Pro Phe Lys Arg Phe Tyr Ser			
100	105	110	
Cys Cys Glu Asn Val Asp Ala Ile Glu Trp Glu Cys Val Glu Thr Ala			
115	120	125	
Lys Glu Leu Phe Ala Ala Asp Cys Ala Cys Val Gln Pro His Ser Gly			
130	135	140	
Ala Asp Ala Asn Leu Leu Ala Val Met Ala Ile Leu Thr His Lys Val			
145	150	155	160
Gln Gly Pro Ala Val Ser Lys Leu Gly Tyr Lys Thr Val Asn Glu Leu			
165	170	175	
Thr Glu Glu Glu Tyr Thr Leu Leu Lys Ala Glu Met Ser Ser Cys Val			
180	185	190	
Cys Leu Gly Pro Ser Leu Asn Ser Gly Gly His Leu Thr His Gly Asn			
195	200	205	
Val Arg Leu Asn Val Met Ser Lys Leu Met Arg Cys Phe Pro Tyr Asp			
210	215	220	
Val Asn Pro Asp Thr Glu Cys Phe Asp Tyr Ala Glu Ile Ser Arg Leu			
225	230	235	240
Ala Lys Glu Tyr Lys Pro Lys Val Leu Ile Ala Gly Tyr Ser Ser Tyr			
245	250	255	
Ser Arg Arg Leu Asn Phe Ala Val Leu Lys Gln Ile Ala Glu Asp Cys			
260	265	270	
Gly Ser Val Leu Trp Val Asp Met Ala His Phe Ala Gly Leu Val Ala			
275	280	285	
Gly Gly Val Phe Val Asp Glu Glu Asn Pro Ile Pro Tyr Ala Asp Ile			
290	295	300	
Val Thr Thr Thr Thr His Lys Thr Leu Arg Gly Pro Arg Gly Gly Leu			
305	310	315	320
Val Leu Ala Thr Arg Glu Tyr Glu Ser Thr Leu Asn Lys Ala Cys Pro			
325	330	335	
Leu Met Met Gly Gly Pro Leu Pro His Val Ile Ala Ala Lys Thr Val			
340	345	350	
Ala Leu Lys Glu Ala Leu Ser Val Asp Phe Lys Lys Tyr Ala His Gln			
355	360	365	
Val Val Asn Asn Ala Arg Arg Leu Ala Glu Arg Phe Leu Ser His Gly			
370	375	380	
Leu Arg Leu Leu Thr Gly Thr Asp Asn His Met Met Val Ile Asp			
385	390	395	400
Leu Gly Ser Leu Gly Ile Ser Gly Lys Ile Ala Glu Asp Ile Leu Ser			
405	410	415	
Ser Val Gly Ile Ala Val Asn Arg Asn Ser Leu Pro Ser Asp Ala Ile			
420	425	430	
Gly Lys Trp Asp Thr Ser Gly Ile Arg Leu Gly Thr Pro Ala Leu Thr			
435	440	445	
Thr Leu Gly Met Gly Ile Asp Glu Met Glu Glu Val Ala Asp Ile Ile			
450	455	460	
Val Lys Val Leu Arg Asn Ile Arg Leu Ser Cys His Val Glu Gly Ser			
465	470	475	480
Ser Lys Lys Asn Lys Gly Glu Leu Pro Glu Ala Ile Ala Gln Glu Ala			
485	490	495	
Arg Asp Arg Val Arg Asn Leu Leu Leu Arg Phe Pro Leu Tyr Pro Glu			
500	505	510	
Ile Asp Leu Glu Ala Leu Val			

515

&lt;210&gt;562

&lt;211&gt;367

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;562

Lys Val Phe Tyr Lys Lys Asn Val Met Ser Gly Pro Ser Arg Thr Glu  
 1 5 10 15  
 Ser Ser Gln Val Ser Val Leu Ser Tyr Val Pro Arg Asp Lys Glu Ile  
 20 25 30  
 Ala Pro Lys Lys Gln Phe Thr Ile Ala Lys Ile Ser Thr Leu Ala Ile  
 35 40 45  
 Leu Ala Ser Leu Ala Leu Gly Ala Leu Val Ala Gly Ile Ser Leu Thr  
 50 55 60  
 Ile Val Leu Gly Asn Pro Val Phe Leu Ala Leu Leu Ile Thr Thr Ala  
 65 70 75 80  
 Leu Phe Ser Val Val Thr Phe Leu Val Tyr His Gln Met Thr Ser Lys  
 85 90 95  
 Val Ser Ser Asn Trp Gln Lys Val Leu Glu Gln Asn Phe Lys Pro Leu  
 100 105 110  
 Gly Lys Ala Trp Gln Glu Lys Asn Val Asp Cys Xaa Ser Asn Glu Met  
 115 120 125  
 Gln Phe Tyr Asn Asn His Leu Asn Pro Lys Phe Lys Val Ala Ile Gln  
 130 135 140  
 Thr Asp Ala Xaa Gln Pro Phe Gln Pro Thr Phe Leu Thr Gly Leu Arg  
 145 150 155 160  
 Val Ile Glu Lys Asn Gln Ser Thr Gly Ile Ile Phe Asn Pro Val Gly  
 165 170 175  
 Pro Thr Asn Leu Ile Asp Asn Thr Ala Thr Asn Leu Ser Thr Ile Leu  
 180 185 190  
 Tyr Ser Thr Leu Lys Asp Lys Ser Val Trp Asp Thr Cys Lys Gln Arg  
 195 200 205  
 Glu Gly Gly Pro Ala Lys Gly Glu Asp Pro Phe Ser Pro Thr Glu Val  
 210 215 220  
 Arg Val Val Lys Leu Pro Asn Glu Ala Leu Asp Gln Thr Phe Asn Leu  
 225 230 235 240  
 Asn Leu Ser Ser Ala Glu Lys Lys Ser Ile Leu Pro Thr Phe Leu Gly  
 245 250 255  
 His Val Cys Gly Pro Lys Ser Glu Glu Leu Pro Asn Gln Gln Glu Tyr  
 260 265 270  
 Tyr Arg Gln Ala Leu Leu Ala Tyr Glu Asn Cys Leu Lys Ala Ala Ile  
 275 280 285  
 Glu Ser His Ala Ala Ile Val Ala Leu Pro Leu Phe Thr Ser Val Tyr  
 290 295 300  
 Glu Val Pro Pro Glu Glu Ile Leu Pro Lys Glu Gly Thr Phe Tyr Trp  
 305 310 315 320  
 Asp Asn Gln Thr Gln Ala Phe Cys Lys Arg Ala Leu Leu Asp Ala Ile  
 325 330 335  
 Gln Asn Thr Ala Leu Arg Tyr Pro Gln Arg Ser Leu Leu Val Ile Leu  
 340 345 350  
 Gln Asp Pro Phe Asn Thr Ile Glu Ser Gln Ser Arg Ser Glu Glu  
 355 360 365

&lt;210&gt;563

&lt;211&gt;258

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;563

Gly Ile Ile Phe Met His Asp Ala Leu Leu Ser Ile Leu Ala Ile Gln  
 1 5 10 15  
 Glu Leu Asp Ile Lys Met Ile Arg Leu Met Arg Val Lys Lys Glu His  
 20 25 30  
 Gln Lys Glu Leu Ala Lys Val Gln Ser Leu Lys Ser Asp Ile Arg Arg  
 35 40 45  
 Lys Val Gln Glu Lys Glu Leu Glu Met Glu Asn Leu Lys Thr Gln Ile

50 55 60  
 Arg Asp Gly Glu Asn Arg Ile Gln Glu Ile Ser Glu Gln Ile Asn Lys  
 65 70 75 80  
 Leu Glu Asn Gln Gln Ala Ala Val Lys Lys Met Asp Glu Phe Asn Ala  
 85 90 95  
 Leu Thr Gln Glu Met Thr Thr Ala Asn Lys Glu Arg Arg Ser Leu Glu  
 100 105 110  
 His Gln Leu Ser Asp Leu Met Asp Lys Gln Ala Gly Gly Glu Asp Leu  
 115 120 125  
 Ile Val Ser Leu Lys Glu Ser Leu Ala Ser Thr Glu Asn Ser Ser Ser  
 130 135 140  
 Val Ile Glu Lys Glu Ile Phe Glu Ser Ile Lys Lys Ile Asn Glu Glu  
 145 150 155 160  
 Gly Lys Ala Leu Leu Glu Gln Arg Thr Glu Leu Lys His Ala Thr Asn  
 165 170 175  
 Pro Glu Leu Leu Ser Ile Tyr Glu Arg Leu Leu Asn Asn Lys Lys Asp  
 180 185 190  
 Arg Val Val Val Pro Ile Glu Asn Arg Val Cys Ser Gly Cys His Ile  
 195 200 205  
 Val Leu Thr Pro Gln His Glu Asn Leu Val Arg Xaa Lys Asp Arg Leu  
 210 215 220  
 Ile Phe Cys Glu His Cys Ser Arg Ile Leu Tyr Trp Gln Glu Ser Gln  
 225 230 235 240  
 Val Asn Ala Gln Glu Asn Ser Thr Ala Lys Arg Arg Arg Arg Ala  
 245 250 255  
 Ala Val

&lt;210&gt;564

&lt;211&gt;329

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;564

Met Pro Ser Pro Met Ile Ser Thr Asp Val Cys Gln Asp Ile Leu Gly  
 1 5 10 15  
 Lys Gln Lys Glu Ala Val Asp Phe Phe Phe Gln Ala Phe Gln Pro Lys  
 20 25 30  
 Glu Ala Met Gln Leu Ala Glu Lys Ile Leu Gly His Ser Gly Trp Val  
 35 40 45  
 Phe Phe Ser Gly Val Gly Lys Ser Gly Cys Val Ala Arg Lys Leu Val  
 50 55 60  
 Ala Thr Leu Gln Ser Leu Ser Glu Arg Ala Leu Phe Phe Ser Pro Val  
 65 70 75 80  
 Asp Leu Leu His Gly Asp Leu Gly Leu Val Ser Pro Gly Asp Ile Val  
 85 90 95  
 Cys Leu Phe Ser Lys Ser Gly Glu Thr Gln Glu Leu Leu Asp Thr Val  
 100 105 110  
 Pro His Leu Lys Ser Arg Arg Ala Ile Leu Val Ala Ile Thr Ser Met  
 115 120 125  
 Pro Tyr Ser Asn Leu Ala Ala Leu Ser Asp Leu Val Val Ile Leu Pro  
 130 135 140  
 Ser Val Ala Glu Leu Asp Pro Phe Asn Leu Ile Pro Thr Asn Ser Thr  
 145 150 155 160  
 Thr Cys Gln Met Ile Phe Gly Asp Phe Leu Ala Met Leu Leu Phe His  
 165 170 175  
 Ser Arg Gly Val Ser Leu Ser Thr Tyr Gly Lys Asn His Pro Ser Gly  
 180 185 190  
 Gln Val Gly Met Lys Ala Asn Gly Lys Val Lys Asp Phe Met Phe Pro  
 195 200 205  
 Lys Thr Glu Val Pro Phe Cys His Leu Gly Asp Lys Val Ser Phe Ser  
 210 215 220  
 Leu Glu Val Phe Ser Ala Tyr Gly Cys Gly Cys Val Cys Ile Val Asp  
 225 230 235 240  
 Pro Gln Phe Arg Leu Met Gly Ile Phe Thr Asp Gly Asp Leu Arg Arg  
 245 250 255

Ser Leu Ala Ser Tyr Gly Gly Glu Val Leu Ser Leu Ser Leu Glu Lys  
 260 265 270  
 Val Met Thr Ala Asn Pro Arg Cys Ile Thr Glu Asp Ser Asp Ile Ala  
 275 280 285  
 Ile Ala Leu Gln Leu Met Glu Ser Ser Ser Pro Val Ala Val Leu Pro  
 290 295 300  
 Val Leu Asp Asn Glu Glu Asn Arg His Val Thr Gly Leu Leu His Met  
 305 310 315 320  
 His Thr Leu Ala Lys Ala Gly Leu Leu  
 325

&lt;210&gt;565

&lt;211&gt;393

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;565

Met Ile Phe Glu Phe Arg Phe Pro Lys Ile Gly Glu Thr Ser Ser Gly  
 1 5 10 15  
 Gly Ser Ile Val Arg Trp Leu Lys Asn Leu Gly Asp His Val Ala Arg  
 20 25 30  
 Asp Glu Pro Leu Ile Glu Val Ser Thr Asp Lys Ile Ala Thr Glu Leu  
 35 40 45  
 Pro Ser Pro Lys Ala Gly Arg Leu Val Arg Phe Cys Val Asn Glu Gly  
 50 55 60  
 Asp Glu Val Ala Ser Gly Asp Val Leu Gly Leu Ile Glu Leu Glu Glu  
 65 70 75 80  
 Ile Ser Glu Ala Asp Asp Glu Ser Thr Ser Cys Pro Leu Thr Ser Cys  
 85 90 95  
 Glu Thr Lys Ser Glu Ala Gly Ser Ser Ser Ser Ser Val Trp Phe Ser  
 100 105 110  
 Pro Ala Val Leu Ser Leu Ala Gln Arg Glu Gly Ile Gly Leu Asp Asn  
 115 120 125  
 Leu Gln Lys Ile Ala Gly Thr Gly Lys Gly Gly Arg Val Thr Arg Gln  
 130 135 140  
 Asp Leu Glu Ala Tyr Ile Ser Glu Ser Gln Gln Val Ser Ile Pro Glu  
 145 150 155 160  
 Ile Phe Gln Gly Glu Val Asn Arg Ile Pro Met Ser Pro Leu Arg Arg  
 165 170 175  
 Ala Ile Ala Ser Ser Leu Ser Lys Ser Ser Asp Glu Val Pro His Ala  
 180 185 190  
 Ser Leu Val Val Asp Val Asp Val Thr Asp Leu Met Asn Leu Ile Ser  
 195 200 205  
 Gly Glu Arg Gln Arg Phe Leu Asp Thr His Gly Val Lys Leu Thr Ile  
 210 215 220  
 Thr Ser Phe Ile Val Gln Cys Leu Ala Gln Thr Leu Arg Gln Phe Pro  
 225 230 235 240  
 Leu Leu Asn Gly Ser Leu Asp Gly Thr Thr Ile Val Met Lys Lys Ser  
 245 250 255  
 Val Asn Val Gly Val Ala Val Asn Leu Asn Lys Glu Gly Val Val Val  
 260 265 270  
 Pro Val Ile His Asn Cys Gln Asp Arg Gly Leu Val Ser Ile Ala Lys  
 275 280 285  
 Ala Leu Ala Asp Leu Ser Ser Arg Ala Arg Leu Asn Lys Leu Asp Pro  
 290 295 300  
 Ser Glu Val Gln Asp Gly Ser Val Thr Val Thr Asn Phe Gly Met Thr  
 305 310 315 320  
 Gly Ala Leu Ile Gly Met Pro Ile Ile Arg Tyr Pro Glu Val Ala Ile  
 325 330 335  
 Leu Gly Ile Gly Thr Ile Gln Lys Arg Val Val Arg Asp Asp Asp  
 340 345 350  
 Ser Leu Ala Ile Arg Lys Met Val Tyr Val Thr Leu Thr Phe Asp His  
 355 360 365  
 Arg Val Leu Asp Gly Ile Tyr Gly Ser Glu Phe Leu Thr Ser Leu Lys  
 370 375 380  
 Asn Arg Leu Glu Ser Val Thr Met Gly

385 390  
 <210>566  
 <211>90  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>566  
 Ala Lys Leu Ser Thr Ala Gly Glu Asn His Thr Glu Glu Leu Leu Glu  
 1 5 10 15  
 Pro Ala Ser Asp Phe Val Ser Gln Glu Val Arg Gly His Glu Val Leu  
 20 25 30  
 Ser Ser Ser Ala Ser Glu Ile Ser Ser Ser Ile Asn Pro Lys Thr  
 35 40 45  
 Ser Pro Glu Ala Thr Ser Ser Pro Ser Leu Thr Gln Lys Arg Thr Ser  
 50 55 60  
 Arg Pro Ala Leu Gly Glu Gly Asn Ser Val Ala Ile Leu Ser Val Asp  
 65 70 75 80  
 Thr Ser Ile Arg Gly Ser Ser Leu Ala Thr  
 85 90  
 <210>567  
 <211>415  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>567  
 Leu Met Lys Leu Trp Met Lys Ile Phe Ile Gly Leu Phe Val Gly Val  
 1 5 10 15  
 Thr Leu Gly Leu Val Leu Glu Asp Lys Ala Ile Phe Phe Lys Pro Ile  
 20 25 30  
 Gly Asp Ile Phe Leu Asn Leu Leu Ser Met Val Val Tyr Pro Leu Val  
 35 40 45  
 Phe Cys Ser Met Val Leu Gly Ile Ala Ser Ile Ser Asp Met Lys Lys  
 50 55 60  
 Leu Gly Arg Ile Gly Ile Lys Ser Val Gly Leu Tyr Leu Gly Thr Thr  
 65 70 75 80  
 Ala Leu Ala Ile Val Ile Gly Leu Cys Phe Ala Trp Ile Phe Ser Pro  
 85 90 95  
 Gly Asn Gly Cys Asp Phe Ala Gln Ala Gln Ser Met Asp Ser Ala Val  
 100 105 110  
 Thr Val Ile Asp Ser Asn Lys Thr Ala Ala Tyr Phe Leu Ser Ile Ile  
 115 120 125  
 Ala Gln Val Phe Pro Ser Asn Pro Val Arg Ser Phe Ala Glu Gly Asn  
 130 135 140  
 Ile Leu Gln Ile Ile Ile Phe Ala Ile Phe Leu Gly Ile Ala Leu Arg  
 145 150 155 160  
 Leu Ser Gly Glu Arg Gly Arg Pro Val Glu Arg Phe Ile Asp Gly Phe  
 165 170 175  
 Ser Glu Ile Met Leu Arg Met Val Asn Met Ile Met Ser Phe Ala Pro  
 180 185 190  
 Tyr Gly Val Gly Ala Ser Met Ala Trp Ile Ser Gly Asn His Gly Leu  
 195 200 205  
 Gly Val Leu Trp Gln Leu Gly Lys Phe Ile Ile Ala Tyr Tyr Leu Ala  
 210 215 220  
 Cys Leu Phe His Ala Thr Leu Val Phe Gly Gly Leu Val Arg Phe Gly  
 225 230 235 240  
 Cys Lys Met Ser Phe Ser Lys Phe Leu Ser Ser Met Met Asp Ala Ile  
 245 250 255  
 Ser Cys Ala Val Ser Thr Ala Ser Ser Ala Thr Leu Pro Val Thr  
 260 265 270  
 Met Arg Cys Val Ser Lys Asn Leu Gly Val Ser Ala Glu Val Ser Gly  
 275 280 285  
 Phe Val Leu Pro Leu Gly Ala Thr Val Asn Met Asn Gly Thr Ala Ile  
 290 295 300  
 Phe Gln Gly Met Ala Ala Val Phe Ile Ala Gln Ala Tyr Asn Cys Pro  
 305 310 315 320  
 Leu Ser Leu Ser Ser Leu Leu Leu Val Thr Ala Thr Phe Ser

325 330 335  
 Ala Val Gly Ser Ala Gly Val Pro Gly Gly Gly Met Ile Thr Leu Gly  
 340 345 350  
 Ser Val Leu Ala Ser Val Gly Leu Pro Ile Gln Gly Ile Ala Ile Leu  
 355 360 365  
 Ala Gly Ile Asp Arg Leu Arg Asp Ile Val Gly Thr Pro Met Asn Ile  
 370 375 380  
 Leu Gly Asp Ala Val Val Ala Thr Tyr Val Ala Ser Gly Glu Gly Glu  
 385 390 395 400  
 Leu Ser Pro Tyr Glu Ser Ile Lys Gln Glu Ser Val Glu Thr Thr  
 405 410 415  
 <210>568  
 <211>365  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>568  
 Met Lys Lys Arg Phe Pro Ser Thr Leu Phe Leu Phe Tyr Arg Arg Val  
 1 5 10 15  
 Thr Ile Ala Ile Ser Leu Glu Gly Ile Leu Gly Trp Gly Trp Leu Gly  
 20 25 30  
 Ser Leu Leu Ser Lys Val Phe Ala Phe Leu Val Ala Cys Trp Asn Arg  
 35 40 45  
 Phe Ser Trp Ser Thr Pro Tyr Arg Ala Arg Ser Thr Val Ile Ser Val  
 50 55 60  
 Gly Asn Ile Val Val Gly Gly Ala Gly Lys Thr Pro Thr Val Leu Trp  
 65 70 75 80  
 Leu Ala Glu Ala Leu Arg Leu Arg Gly Tyr Ser Cys Gly Val Leu Ser  
 85 90 95  
 Arg Gly Tyr Lys Ser Gln Ser Ser Arg Gln Lys Lys Leu Thr Val Val  
 100 105 110  
 Asp Ser Lys Val His Ser Ala Ser Tyr Val Gly Asp Glu Pro Leu Leu  
 115 120 125  
 Met Ala Glu Lys Leu Pro Glu Gly Ser Val Trp Val His Lys Asp Arg  
 130 135 140  
 Arg Ile Ser Ala Ala Arg Ala Ala Glu Lys Phe Gly Ile Leu Leu Leu  
 145 150 155 160  
 Asp Asp Gly Leu Gln Tyr Arg Lys Leu His Lys Asp Val Glu Ile Ala  
 165 170 175  
 Val Val Asn Gly Gln Asp Pro Leu Gly Gly Arg Ala Phe Phe Pro Lys  
 180 185 190  
 Gly Arg Leu Arg Asp Phe Pro Leu Arg Leu Lys Thr Val Asp Ala Ile  
 195 200 205  
 Ile Val Asn Gly Gly Gly Lys Glu Ala Gly Thr Val Val Lys Arg Val  
 210 215 220  
 Ser Asn Ala Pro Gln Ile Phe Val Lys Pro Thr Ile Ala Ser Val Val  
 225 230 235 240  
 Trp Thr His Asn Gly Glu Arg Ile Pro Lys Glu Ala Leu Arg Glu Leu  
 245 250 255  
 Arg Val Gly Val Phe Cys Gly Leu Gly Phe Pro Gln Gly Phe Leu Asn  
 260 265 270  
 Met Leu Arg Glu Glu Gly Ile His Ile Leu Gly Lys Tyr Leu Leu Pro  
 275 280 285  
 Asp His Ala Ala Ile Thr Lys Lys Glu Leu Asn Tyr Phe Cys Gln Gln  
 290 295 300  
 Met Ala Met Arg Gln Gly Gln Gly Leu Leu Cys Thr Glu Lys Asp Ser  
 305 310 315 320  
 Val Lys Leu Pro Arg Leu Ser Gly Glu Val Ser Leu Leu Pro Ile Ala  
 325 330 335  
 Lys Val Glu Met Arg Leu Ser Val Asn Gln Asp Asp Thr Leu Ser Leu  
 340 345 350  
 Leu Asn Met Ile Glu Gln Ile His Lys Asn Arg Gly Asn  
 355 360 365  
 <210>569  
 <211>287



&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;569

Val Val Leu Trp Gly Lys Phe Leu Trp Arg Arg Cys Gly Ser Leu Ala  
 1 5 10 15  
 Phe Trp Glu Phe Cys Ser Met Asp Cys Ile Gly Lys His Asn Pro Leu  
 20 25 30  
 Val Lys Glu Ala Leu Ala Leu Lys Arg Ser Arg Cys Arg Lys Ser Ser  
 35 40 45  
 Trp Phe Leu Val Glu Gly Ala Arg Glu Ile Gln Lys Ala Leu Arg Thr  
 50 55 60  
 Gly Tyr Leu Cys Gln His Val Phe Cys Ser Thr His Leu Ser Glu Lys  
 65 70 75 80  
 Glu Lys Glu Phe Leu Tyr Glu Leu Lys Arg Asn Ser Thr Lys Ile Leu  
 85 90 95  
 Tyr Cys Leu Asp Ser Thr Leu Ala Gln Leu Ser Phe Lys Glu His His  
 100 105 110  
 Asp Ser Phe Val Ala Val Ile Gln Lys Arg Val Trp Asn Lys Glu Asp  
 115 120 125  
 Phe Leu Ile Gln Arg Lys Asn Ala Gln Pro Phe Tyr Leu Ile Ile Glu  
 130 135 140  
 Gln Val Glu Lys Pro Gly Asn Val Gly Ala Ile Leu Arg Ile Ala Asp  
 145 150 155 160  
 Gly Ala Gly Val Asp Gly Val Ile Leu Cys Asn Pro Ile Val Asp Leu  
 165 170 175  
 Tyr Asn Pro Asn Val Val Arg Ser Ser Leu Gly Ala Val Phe Ser Leu  
 180 185 190  
 Pro Ile Leu Ser Ile Ser Arg Glu Glu Gly Lys Glu Leu Phe Lys Gln  
 195 200 205  
 Glu Gly Trp Thr Val Phe Val Thr Ser Pro Arg Ala Glu Thr Met Tyr  
 210 215 220  
 Phe Ser Lys Asn Tyr Leu Gly Pro Thr Ala Leu Val Phe Gly Ser Glu  
 225 230 235 240  
 Lys Asp Gly Leu Thr Glu Asp Trp Phe Ser Glu Asp Phe Ser Glu Ile  
 245 250 255  
 Ala Leu Pro Met Leu Gly Glu Ser Asp Ser Leu Asn Leu Ala Thr Ser  
 260 265 270  
 Val Ala Ala Val Ala Tyr Glu Val Val Arg Gln Arg Trp Val Asn  
 275 280 285

&lt;210&gt;570

&lt;211&gt;321

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;570

Asp Ser Ser Lys Asp Asp Phe Arg Lys Glu Lys Gly Arg Arg Lys Ser  
 1 5 10 15  
 Gln Tyr Arg Asp Arg Tyr Val Asn Lys Asp Thr Gly Arg His Ser Lys  
 20 25 30  
 Thr Tyr Phe Ser Leu Ile Arg Glu Arg Leu Val Met Asp Tyr Lys Leu  
 35 40 45  
 Leu Asp Ser Gly Asp Gly Asn Lys Leu Glu Cys Phe Gly Pro Val Thr  
 50 55 60  
 Leu Ile Arg Pro Ser Ser Ile Ala Val Trp Pro Lys Ser Arg Pro Glu  
 65 70 75 80  
 Leu Trp Ser Gln Ala Gln Leu Gln Tyr Val Arg Glu Gly Glu Arg Gly  
 85 90 95  
 Ala Trp Lys Asn Phe Lys Arg Leu Pro Glu Glu Trp Glu Val Ala Phe  
 100 105 110  
 Ser Asp Val Arg Cys Leu Leu Lys Arg Thr Pro Phe Gly His Leu Gly  
 115 120 125  
 Val Phe Pro Glu His Met Gly Phe Trp Pro Ala Leu Lys Gln Ala Ile  
 130 135 140  
 Glu Lys His Lys Glu Arg Gln Val Leu Asn Leu Phe Ala Tyr Thr Gly  
 145 150 155 160

Ala Gly Ser Ile Phe Ala Ala Lys Cys Gly Ala Arg Val Thr His Val  
 165 170 175  
 Asp Ala Ser Gln Ala Ala Val Arg Trp Ala Gln Arg Asn Val Glu Lys  
 180 185 190  
 Asn Ala Phe Pro Glu Arg Arg Ile Phe Trp Val Ile Glu Asp Val Ile  
 195 200 205  
 Ser Phe Leu Lys Lys Glu Ile Arg Arg Asn Lys Lys Tyr Gln Val Ile  
 210 215 220  
 Leu Leu Asp Pro Pro Ser Tyr Gly Arg Gly Pro Asp Gly Glu Val Phe  
 225 230 235 240  
 Lys Ile Asp Lys Asp Leu Phe Pro Leu Leu Ser Leu Cys Ser Lys Leu  
 245 250 255  
 Leu Ala Asp Asp Ala Ser Tyr Phe Leu Leu Thr Ser His Thr Pro Gly  
 260 265 270  
 His Thr Pro Glu Phe Leu Arg Ala Ile Ala Arg Arg Arg Cys Gln Pro  
 275 280 285  
 Leu Phe Leu Lys Arg Gly Leu Val Gly Lys Val Phe Val Glu Lys Val  
 290 295 300  
 Trp Glu Pro Cys Leu Leu Gly Val Leu Phe Asn Gly Leu His Arg Glu  
 305 310 315 320  
 Thr

&lt;210&gt;571

&lt;211&gt;200

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;571

Met Phe Ser Gly Ile Ile Gln Glu Leu Gly Glu Val Cys Phe Phe Glu  
 1 5 10 15  
 Ala Gln Gly Asn Gly Leu Ser Leu Gly Ile Lys Ser Thr Pro Leu Phe  
 20 25 30  
 Val Thr Pro Leu Val Thr Gly Asp Ser Val Ala Val Asp Gly Val Cys  
 35 40 45  
 Leu Thr Leu Thr Ser Cys Asn Glu Ser Lys Ile Phe Phe Asp Val Ile  
 50 55 60  
 Pro Glu Thr Leu Ala Cys Thr Thr Leu Gly Glu Lys Arg Cys Ser Asp  
 65 70 75 80  
 Gln Val Asn Leu Glu Ala Ala Leu Lys Met Gly Asp Ser Ile Gly Gly  
 85 90 95  
 His Leu Leu Ser Gly His Val Phe Gly Thr Ala Glu Ile Phe Leu Ile  
 100 105 110  
 Lys Glu Asn Arg Tyr Tyr Phe Arg Gly Ser Lys Glu Leu Ser Gln Tyr  
 115 120 125  
 Leu Phe Glu Lys Gly Phe Ile Ala Ile Asp Gly Val Ser Leu Thr Leu  
 130 135 140  
 Val Ser Val Asp Ser Asp Thr Phe Ser Val Gly Leu Ile Pro Glu Thr  
 145 150 155 160  
 Leu Gln Arg Thr Thr Leu Gly Lys Lys Arg Glu Gly Glu Arg Val Asn  
 165 170 175  
 Ile Glu Ile Asp Met Ser Thr Lys Ile Gln Val Asp Thr Val Lys Arg  
 180 185 190  
 Ile Leu Ala Ser Ser Gly Lys Asp  
 195 200

&lt;210&gt;572

&lt;211&gt;152

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;572

Met Gln Cys Pro Phe Cys Asn His Gly Glu Leu Lys Val Ile Asp Ser  
 1 5 10 15  
 Arg Asn Ala Pro Glu Ala Asn Ala Ile Lys Arg Arg Arg Glu Cys Leu  
 20 25 30  
 Lys Cys Ser Gln Arg Phe Thr Thr Phe Glu Thr Val Glu Leu Thr Leu  
 35 40 45

Gln Val Leu Lys Arg Asp Gly Arg Tyr Glu Asn Phe Gln Glu Ser Lys  
 50 55 60  
 Leu Ile His Gly Leu Asn Ala Ala Ser Ser His Thr Arg Ile Gly Gln  
 65 70 75 80  
 Asp Gln Val His Ala Ile Ala Ser Asn Val Lys Ser Glu Leu Leu Gly  
 85 90 95  
 Lys Gln Asn Arg Glu Ile Ser Thr Lys Glu Ile Gly Glu Leu Val Met  
 100 105 110  
 Lys Tyr Leu Lys Lys Ala Asp Met Ile Ala Tyr Ile Arg Phe Ala Cys  
 115 120 125  
 Val Tyr Arg Arg Phe Lys Asp Val Gly Glu Leu Met Glu Val Leu Leu  
 130 135 140  
 Ser Ala Thr Pro Asp Met Glu Lys  
 145 150

&lt;210&gt;573

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;573

Leu Asn Phe Ile Arg Ser Lys Val Val Pro Leu Ser Asp Asp Glu Ile  
 1 5 10 15  
 Glu Gln Phe Lys Lys Arg Leu Leu Glu Met Lys Ala Lys Leu Ser His  
 20 25 30  
 Thr Leu Glu Gly Asn Ala Gln Glu Val Lys Lys Pro Asn Glu Ala Thr  
 35 40 45  
 Gly Tyr Ser Gln His Gln Ala Asp Gln Gly Thr Asp Thr Phe Asp Arg  
 50 55 60  
 Thr Ile Ser Leu Glu Val Thr Thr Lys Glu Tyr Glu Leu Leu Arg Gln  
 65 70 75 80  
 Ile Asn Arg Ala Leu Glu Lys Ile Asn Glu Ser Ser Tyr Gly Ile Cys  
 85 90 95  
 Asp Val Ser Gly Glu Glu Ile Pro Leu Ala Arg Leu Ile Ala Ile Pro  
 100 105 110  
 Tyr Ala Thr Met Thr Val Lys Ala Gln Glu Gln Phe Glu Lys Gly Leu  
 115 120 125  
 Leu Ser Gly Asn  
 130

&lt;210&gt;574

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;574

Met Ala Thr Arg Phe Arg Ser Thr Leu Leu Val Ile Thr Leu Phe Val  
 1 5 10 15  
 Leu Ile Asp Trp Val Thr Lys Leu Val Val Leu Leu Gln Tyr Lys Asp  
 20 25 30  
 Leu Gln Ile Leu Thr His Pro Thr Leu Tyr Thr His Ser Trp Gly Arg  
 35 40 45  
 Phe Ser Phe Ser Ile Ala Pro Val Phe Asn Glu Gly Ala Ala Phe Gly  
 50 55 60  
 Leu Phe Ser Asn Tyr Lys Tyr Phe Leu Phe Leu Leu Arg Ile Phe Val  
 65 70 75 80  
 Ile Leu Gly Leu Leu Ala Tyr Leu Phe Phe Lys Lys Lys Ser Ile Gln  
 85 90 95  
 Ser Thr Thr Gln Thr Ala Leu Val Leu Leu Cys Ala Gly Ala Ile Gly  
 100 105 110  
 Asn Val Gly Asp Ile Ile Phe Tyr Gly His Ile Val Asp Phe Ile Ser  
 115 120 125  
 Phe Asn Tyr Lys Gln Trp Ala Phe Pro Thr Phe Asn Val Ala Asp Val  
 130 135 140  
 Leu Ile Ser Leu Gly Thr Leu Leu Leu Val Tyr Lys Phe Tyr Phe Pro  
 145 150 155 160  
 Thr Lys Gln Thr Glu Lys Lys Arg  
 165

&lt;210&gt;575

&lt;211&gt;449

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;575

```

Met Asn Arg Leu Leu Ser Leu Leu Ser Val Phe Asp Asp Phe Phe Trp
 1           5           10           15
Ser Tyr Val Ala Phe Ile Leu Ile Ile Val Leu Gly Val Ser Phe Ser
          20           25           30
Trp Lys Ser Arg Phe Phe Gln Phe Thr Lys Phe Ser Gln Phe Cys Lys
          35           40           45
Leu Phe Arg Tyr Tyr Ser Gln Asn Pro Gln Glu Arg Glu Thr Lys Gln
          50           55           60
Gly Val His Pro Leu Lys Val Phe Phe Ala Ser Ala Gly Gly Asn Ile
          65           70           75           80
Gly Ile Gly Asn Val Val Gly Ile Val Thr Ala Ala Cys Ile Gly Gly
          85           90           95
Pro Gly Ala Leu Phe Trp Val Trp Ile Ala Gly Ile Phe Gly Ser Ile
          100          105          110
Val Lys Tyr Ser Glu Val Tyr Leu Gly Ile Lys Phe Arg Lys Leu Asp
          115          120          125
Arg Asp Gly Val Tyr Gln Gly Gly Pro Met Tyr Phe Leu Ile Lys Ala
          130          135          140
Phe Lys Thr Pro Val Val Ser Val Ile Val Ala Ile Leu Leu Cys Ile
          145          150          155          160
Tyr Gly Val Glu Ile Tyr Gln Phe Ser Val Ile Thr Asp Ser Leu Ala
          165          170          175
His Cys Trp Asn Leu Pro Lys Val Tyr Pro Met Leu Gly Leu Leu Phe
          180          185          190
Leu Val Phe Tyr Ala Ile Arg Gly Gly Leu Gln Arg Ile Gly Lys Ile
          195          200          205
Cys Ser Ile Val Leu Pro Phe Phe Met Leu Leu Tyr Cys Ala Leu Ser
          210          215          220
Leu Tyr Ile Leu Val Lys Glu Phe His Thr Leu Pro His Leu Leu Ser
          225          230          235          240
Thr Val Phe Ser Ser Ala Phe Lys Gly Gln Ser Ala Leu Gly Gly Phe
          245          250          255
Ala Gly Cys Thr Val Ala Thr Thr Ile His Gln Gly Ile Ser Arg Ala
          260          265          270
Ala Tyr Ser Gly Asp Ile Gly Ile Gly Phe Asp Ser Ile Ile Gln Ser
          275          280          285
Glu Ser Ser Ala Lys Asp Pro Ser Thr Gln Ala Gln Leu Ser Ile Val
          290          295          300
Gly Ile Ala Ile Asp Asn Leu Ile Cys Thr Leu Ser Leu Leu Met Val
          305          310          315          320
Leu Ala Ser Gly Ser Trp Ser Leu Gly Leu Glu Asn Ala Ser Gln Val
          325          330          335
Val Glu His Thr Leu Ala Ser Tyr Phe Pro Met Val Lys Phe Phe Leu
          340          345          350
Pro Thr Phe Phe Phe Val Thr Gly Tyr Thr Thr Ile Ile Ser Tyr Phe
          355          360          365
Leu Val Gly Lys Lys Cys Ala Lys Phe Leu Tyr Gly Asn Thr Gly Ala
          370          375          380
Lys Ile Tyr Thr Leu Tyr Gly Leu Leu Ile Leu Pro Leu Phe Cys Phe
          385          390          395          400
Leu Ser Gln Asn Thr Ala Leu Leu Ile Met Ser Val Ser Gly Ala Leu
          405          410          415
Leu Leu Cys Phe Asn Leu Leu Gly Val Phe Ile Leu Arg Lys Glu Val
          420          425          430
Ile Phe Pro Ala Arg Ala Ala Ser Leu Thr Glu Thr Ser Leu Ser Thr
          435          440          445
Glu

```

&lt;210&gt;576

&lt;211&gt;232

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;576

Leu Ile Phe Leu Leu Phe Met Asp Asn Tyr Leu Leu Gly Ser Leu Ile  
 1 5 10 15  
 Phe Cys Cys Val Leu Leu Ser Ile Gly Met Cys Thr Ile Phe Val Met  
 20 25 30  
 Thr Ile Cys Phe Leu Arg Gln Leu Asn Lys Ile Leu Lys Asn Ile His  
 35 40 45  
 Arg Val Thr Thr Ile Leu Asn Phe Glu Ala Lys Ile Leu Ala Pro Leu  
 50 55 60  
 Met Leu Gly Lys Lys Leu Leu Cys Gly Trp Leu Lys Lys Arg Lys Asn  
 65 70 75 80  
 Arg Gly Ser Leu Ser Glu Asp Ile Asp Glu Leu Leu Asp Glu Lys Lys  
 85 90 95  
 Gln Arg Ser Trp Lys Lys Asn Leu Asp Gln Gly Ile Lys Trp Cys Ala  
 100 105 110  
 His Trp Ser Ser Phe Gly Lys Cys Phe Val Ile Lys Ile Lys Thr Leu  
 115 120 125  
 Arg Asp Ile Val Met Phe Arg Asn Asn His Lys Pro Lys Lys Thr Lys  
 130 135 140  
 Cys Lys Arg Phe Arg Trp Leu Arg Gly Val Leu Phe Gly Gly Phe Ile  
 145 150 155 160  
 Ala Thr Leu Leu Thr Cys Leu Phe Thr Pro Lys Ser Gly Val Gln Leu  
 165 170 175  
 Arg Lys Lys Ile Leu Lys Val Lys Asn Ser Gly Ala Lys Lys Ser Arg  
 180 185 190  
 Val Phe Phe Lys Asn Ser Lys Gln His Thr Lys Ser Phe Val Lys Gln  
 195 200 205  
 Ala Lys Leu Leu Ala Lys Asn Ile Ser His Glu Leu Gln Asp Phe Lys  
 210 215 220  
 Lys Gly Ile Leu Asp Asp Lys Asp  
 225 230

&lt;210&gt;577

&lt;211&gt;308

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;577

Gly Tyr Asn Leu Leu Gly Leu Arg His Met Lys Gln Met Arg Leu Trp  
 1 5 10 15  
 Gly Phe Leu Phe Leu Ser Ser Phe Cys Gln Val Ser Tyr Leu Arg Ala  
 20 25 30  
 Asn Asp Val Leu Leu Pro Leu Ser Gly Ile His Ser Gly Glu Asp Leu  
 35 40 45  
 Glu Leu Phe Thr Leu Arg Ser Ser Ser Pro Thr Lys Thr Thr Tyr Ser  
 50 55 60  
 Leu Arg Lys Asp Phe Ile Val Cys Asp Phe Ala Gly Asn Ser Ile His  
 65 70 75 80  
 Lys Pro Gly Ala Ala Phe Leu Asn Leu Lys Gly Asp Leu Phe Phe Ile  
 85 90 95  
 Asn Ser Thr Pro Leu Ala Ala Leu Thr Phe Lys Asn Ile His Leu Gly  
 100 105 110  
 Ala Arg Gly Ala Gly Leu Phe Ser Glu Ser Asn Val Thr Phe Lys Gly  
 115 120 125  
 Leu His Ser Leu Val Leu Glu Asn Asn Glu Ser Trp Gly Gly Val Leu  
 130 135 140  
 Thr Thr Ser Gly Asp Leu Ser Phe Ile Asn Asn Thr Ser Val Leu Cys  
 145 150 155 160  
 Gln Asn Asn Ile Ser Tyr Gly Pro Gly Gly Ala Leu Leu Leu Gln Gly  
 165 170 175  
 Arg Lys Ser Lys Ala Leu Phe Phe Arg Asp Asn Arg Gly Thr Ile Leu  
 180 185 190  
 Phe Leu Lys Asn Lys Ala Val Asn Gln Asp Glu Ser His Pro Gly Tyr

195 200 205  
 Gly Gly Ala Val Ser Ser Ile Ser Pro Gly Ser Pro Ile Thr Phe Ala  
 210 215 220  
 Asp Asn Gln Glu Ile Leu Phe Gln Glu Asn Glu Gly Glu Leu Gly Gly  
 225 230 235 240  
 Ala Ile Tyr Asn Asp Gln Gly Ala Ile Thr Phe Glu Asn Asn Phe Gln  
 245 250 255  
 Thr Thr Ser Phe Phe Ser Asn Lys Ala Ser Phe Gly Gly Ala Val Tyr  
 260 265 270  
 Ser Arg Tyr Cys Asn Leu Tyr Ser Gln Trp Gly Asp Thr Leu Phe Thr  
 275 280 285  
 Lys Asn Ala Ala Lys Val Gly Gly His Pro Cys Gly Leu Cys Ser  
 290 295 300  
 Tyr Lys Arg Leu  
 305  
 <210>578  
 <211>660  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>578  
 Ala Asp Ile His Ala Asp Tyr Val His Ile Arg Asp Cys Lys Gly Ser  
 1 5 10 15  
 Ile Val Phe Glu Glu Asn Ser Ala Thr Ala Gly Gly Ala Ile Ala Val  
 20 25 30  
 Asn Ala Val Cys Asp Ile Asn Ala Gln Gly Pro Val Arg Phe Ile Asn  
 35 40 45  
 Asn Ser Ala Leu Gly Leu Asn Gly Gly Ala Ile Tyr Met Gln Ala Thr  
 50 55 60  
 Gly Ser Ile Leu Arg Leu His Ala Asn Gln Gly Asp Ile Glu Phe Cys  
 65 70 75 80  
 Gly Asn Lys Val Arg Ser Gln Phe His Ser His Ile Asn Ser Thr Ser  
 85 90 95  
 Asn Phe Thr Asn Asn Ala Ile Thr Ile Gln Gly Ala Pro Arg Glu Phe  
 100 105 110  
 Ser Leu Ser Ala Asn Glu Gly His Arg Ile Cys Phe Tyr Asp Pro Ile  
 115 120 125  
 Ile Ser Ala Thr Glu Asn Tyr Asn Ser Leu Tyr Ile Asn His Gln Arg  
 130 135 140  
 Leu Leu Glu Ala Gly Gly Ala Val Ile Phe Ser Gly Ala Arg Leu Ser  
 145 150 155 160  
 Pro Glu His Lys Lys Glu Asn Lys Asn Lys Thr Ser Ile Ile Asn Gln  
 165 170 175  
 Pro Val Arg Leu Cys Ser Gly Val Leu Ser Ile Glu Gly Gly Ala Ile  
 180 185 190  
 Leu Ala Val Arg Ser Phe Tyr Gln Glu Gly Gly Leu Leu Ala Leu Gly  
 195 200 205  
 Pro Gly Ser Lys Leu Thr Thr Gln Gly Lys Asn Ser Glu Lys Asp Lys  
 210 215 220  
 Ile Val Ile Thr Asn Leu Gly Phe Asn Leu Glu Asn Leu Asp Ser Ser  
 225 230 235 240  
 Asp Pro Ala Glu Ile Arg Ala Thr Glu Lys Ala Ser Ile Glu Ile Ser  
 245 250 255  
 Gly Val Pro Arg Val Tyr Gly His Thr Glu Ser Phe Tyr Glu Asn His  
 260 265 270  
 Glu Tyr Ala Ser Lys Pro Tyr Thr Thr Ser Ile Ile Leu Ser Ala Lys  
 275 280 285  
 Lys Leu Val Thr Ala Pro Ser Arg Pro Glu Lys Asp Ile Gln Asn Leu  
 290 295 300  
 Ile Ile Ala Glu Ser Glu Tyr Met Gly Tyr Gly Tyr Gln Gly Ser Trp  
 305 310 315 320  
 Glu Phe Ser Trp Ser Pro Asn Asp Thr Lys Glu Lys Lys Thr Ile Ile  
 325 330 335  
 Ala Ser Trp Thr Pro Thr Gly Glu Phe Ser Leu Asp Pro Lys Arg Arg  
 340 345 350

Gly Ser Phe Ile Pro Thr Thr Leu Trp Ser Thr Phe Ser Gly Leu Asn  
 355 360 365  
 Ile Ala Ser Asn Ile Val Asn Asn Asn Tyr Leu Asn Asn Ser Glu Val  
 370 375 380  
 Ile Pro Leu Gln His Leu Cys Val Phe Gly Gly Pro Val Tyr Gln Ile  
 385 390 395 400  
 Met Glu Gln Asn Pro Lys Gln Ser Ser Asn Asn Leu Leu Val Gln His  
 405 410 415  
 Ala Gly His Asn Val Gly Ala Arg Ile Pro Phe Ser Phe Asn Thr Ile  
 420 425 430  
 Leu Ser Ala Ala Leu Thr Gln Leu Phe Ser Ser Ser Ser Gln Gln Asn  
 435 440 445  
 Val Ala Asp Lys Ser His Ala Gln Ile Leu Ile Gly Thr Val Ser Leu  
 450 455 460  
 Asn Lys Ser Trp Gln Ala Leu Ser Leu Arg Ser Ser Phe Ser Tyr Thr  
 465 470 475 480  
 Glu Asp Ser Gln Val Met Lys His Val Phe Pro Tyr Lys Gly Thr Ser  
 485 490 495  
 Arg Gly Ser Trp Arg Asn Tyr Gly Trp Ser Gly Ser Val Gly Met Ser  
 500 505 510  
 Tyr Ala Tyr Pro Lys Gly Ile Arg Tyr Leu Lys Met Thr Pro Phe Val  
 515 520 525  
 Asp Leu Gln Tyr Thr Lys Leu Val Gln Asn Pro Phe Val Glu Thr Gly  
 530 535 540  
 Tyr Asp Pro Arg Tyr Phe Ser Ser Ser Glu Met Thr Asn Leu Ser Leu  
 545 550 555 560  
 Pro Ile Gly Ile Ala Leu Glu Met Arg Phe Ile Gly Ser Arg Ser Ser  
 565 570 575  
 Leu Phe Leu Gln Val Ser Thr Ser Tyr Ile Lys Asp Leu Arg Arg Val  
 580 585 590  
 Asn Pro Gln Ser Ser Ala Ser Leu Val Leu Asn His Tyr Thr Trp Asp  
 595 600 605  
 Ile Gln Gly Val Pro Leu Gly Lys Glu Ala Leu Asn Ile Thr Leu Asn  
 610 615 620  
 Ser Thr Ile Lys Tyr Lys Ile Val Thr Ala Tyr Met Gly Ile Ser Ser  
 625 630 635 640  
 Thr Gln Arg Glu Gly Ser Asn Leu Ser Ala Asn Ala His Ala Gly Leu  
 645 650 655  
 Ser Leu Ser Phe  
 660

&lt;210&gt;579

&lt;211&gt;609

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;579

Phe Ile His Leu Ile Tyr Leu Ser Leu Ile Glu Phe Val Asn Ile Ser  
 1 5 10 15  
 Asp Arg Phe Ser Ser Met Lys Trp Leu Pro Ala Thr Ala Val Phe Ala  
 20 25 30  
 Ala Val Leu Pro Ala Leu Thr Ala Phe Gly Asp Pro Ala Ser Val Glu  
 35 40 45  
 Ile Ser Thr Ser His Thr Gly Ser Gly Asp Pro Thr Ser Asp Ala Ala  
 50 55 60  
 Leu Thr Gly Phe Thr Gln Ser Ser Thr Glu Thr Asp Gly Thr Thr Tyr  
 65 70 75 80  
 Thr Ile Val Gly Asp Ile Thr Phe Ser Thr Phe Thr Asn Ile Pro Val  
 85 90 95  
 Pro Val Val Thr Pro Asp Ala Asn Asp Ser Ser Ser Asn Ser Ser Lys  
 100 105 110  
 Gly Gly Ser Ser Ser Ser Gly Ala Thr Ser Leu Ile Arg Ser Ser Asn  
 115 120 125  
 Leu His Ser Asp Phe Asp Phe Thr Lys Asp Ser Val Leu Asp Leu Tyr  
 130 135 140  
 His Leu Phe Phe Pro Ser Ala Ser Asn Thr Leu Asn Pro Ala Leu Leu

145		150		155		160
Ser Ser Ser Ser	Ser Gly Gly Ser Ser Ser Ser Ser Ser					
	165		170		175	
Ser Gly Ser Ala	Ser Ala Val Val Ala Ala Asp Pro Lys Gly Gly Ala					
	180		185		190	
Ala Phe Tyr Ser	Asn Glu Ala Asn Gly Thr Leu Thr Phe Thr Thr Asp					
	195		200		205	
Ser Gly Asn Pro	Gly Ser Leu Thr Leu Gln Asn Leu Lys Met Thr Gly					
	210		215		220	
Asp Gly Ala Ala	Ile Tyr Ser Lys Gly Pro Leu Val Phe Thr Gly Leu					
	225		230		235	
Lys Asn Leu Thr	Phe Thr Gly Asn Glu Ser Gln Lys Ser Gly Gly Ala					
	245		250		255	
Ala Tyr Thr Glu	Gly Ala Leu Thr Thr Gln Ala Ile Val Glu Ala Val					
	260		265		270	
Thr Phe Thr Gly	Asn Thr Ser Ala Gly Gln Gly Gly Ala Ile Tyr Val					
	275		280		285	
Lys Glu Ala Thr	Leu Phe Asn Ala Leu Asp Ser Leu Lys Phe Glu Lys					
	290		295		300	
Asn Thr Ser Gly	Gln Ala Gly Gly Gly Ile Tyr Thr Glu Ser Thr Leu					
	305		310		315	
Thr Ile Ser Asn	Ile Thr Lys Ser Ile Glu Phe Ile Ser Asn Lys Ala					
	325		330		335	
Ser Val Pro Ala	Pro Ala Pro Glu Pro Thr Ser Pro Ala Pro Ser Ser					
	340		345		350	
Leu Ile Asn Ser	Thr Thr Ile Asp Thr Ser Thr Leu Gln Thr Arg Ala					
	355		360		365	
Ala Ser Ala Thr	Pro Ala Val Ala Pro Val Ala Ala Val Thr Pro Thr					
	370		375		380	
Pro Ile Ser Thr	Gln Glu Thr Ala Gly Asn Gly Gly Ala Ile Tyr Ala					
	385		390		395	
Lys Gln Gly Ile	Ser Ile Ser Thr Phe Lys Asp Leu Thr Phe Lys Ser					
	405		410		415	
Asn Ser Ala Ser	Val Asp Ala Thr Leu Thr Val Asp Ser Ser Thr Ile					
	420		425		430	
Gly Glu Ser Gly	Gly Ala Ile Phe Ala Ala Asp Ser Ile Gln Ile Gln					
	435		440		445	
Gln Cys Thr Gly	Thr Thr Leu Phe Ser Gly Asn Thr Ala Asn Lys Ser					
	450		455		460	
Gly Gly Gly Ile	Tyr Ala Val Gly Gln Val Thr Leu Glu Asp Ile Ala					
	465		470		475	
Asn Leu Lys Met	Thr Asn Asn Thr Cys Lys Gly Glu Gly Gly Ala Ile					
	485		490		495	
Tyr Thr Lys Lys	Ala Leu Thr Ile Asn Asn Gly Ala Ile Leu Thr Thr					
	500		505		510	
Phe Ser Gly Asn	Thr Ser Thr Asp Asn Gly Gly Ala Ile Phe Ala Val					
	515		520		525	
Gly Gly Ile Thr	Leu Ser Asp Leu Val Glu Val Arg Phe Ser Lys Asn					
	530		535		540	
Lys Thr Gly Asn	Tyr Ser Ala Pro Ile Thr Lys Ala Ala Ser Asn Thr					
	545		550		555	
Ala Pro Val Val	Ser Ser Ser Thr Thr Ala Ala Ser Pro Ala Val Pro					
	565		570		575	
Ala Ala Ala Ala	Ala Pro Val Thr Asn Ala Ala Lys Gly Gly Ala Leu					
	580		585		590	
Tyr Ser Thr Glu	Gly Leu Thr Val Ser Gly Ile Thr Ser Xaa Ile Val					
	595		600		605	
Val						

&lt;210&gt;580

&lt;211&gt;1146

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;580



Leu Tyr Leu Glu Ser His Arg Xaa Leu Ser Phe Glu Asn Asn Glu Cys  
 1 5 10 15  
 Gln Asn Gln Gly Gly Gly Ala Tyr Val Thr Lys Thr Phe Gln Cys Ser  
 20 25 30  
 Asp Ser His Arg Leu Gln Phe Thr Ser Asn Lys Ala Ala Asp Glu Gly  
 35 40 45  
 Gly Gly Leu Tyr Cys Gly Asp Asp Val Thr Leu Thr Asn Leu Thr Gly  
 50 55 60  
 Lys Thr Leu Phe Gln Glu Asn Ser Ser Glu Lys His Gly Gly Gly Leu  
 65 70 75 80  
 Ser Leu Ala Ser Gly Lys Ser Leu Thr Met Thr Ser Leu Glu Ser Phe  
 85 90 95  
 Cys Leu Asn Ala Asn Thr Ala Lys Glu Asn Gly Gly Gly Ala Asn Val  
 100 105 110  
 Pro Glu Asn Ile Val Leu Thr Phe Thr Tyr Thr Pro Thr Pro Asn Glu  
 115 120 125  
 Pro Ala Pro Val Gln Gln Pro Val Tyr Gly Glu Ala Leu Val Thr Gly  
 130 135 140  
 Asn Thr Ala Thr Lys Ser Gly Gly Gly Ile Tyr Thr Lys Asn Ala Ala  
 145 150 155 160  
 Phe Ser Asn Leu Ser Ser Val Thr Phe Asp Gln Asn Thr Ser Ser Glu  
 165 170 175  
 Asn Gly Gly Ala Leu Leu Thr Gln Lys Ala Ala Asp Lys Thr Asp Cys  
 180 185 190  
 Ser Phe Thr Tyr Ile Thr Asn Val Asn Ile Thr Asn Asn Thr Ala Thr  
 195 200 205  
 Gly Asn Gly Gly Gly Ile Ala Gly Gly Lys Ala His Phe Asp Arg Ile  
 210 215 220  
 Asp Asn Leu Thr Val Gln Ser Asn Gln Ala Lys Lys Gly Gly Gly Val  
 225 230 235 240  
 Tyr Leu Glu Asp Ala Leu Ile Leu Glu Lys Val Ile Thr Gly Ser Val  
 245 250 255  
 Ser Gln Asn Thr Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp  
 260 265 270  
 Ile Gln Leu Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys  
 275 280 285  
 Val Glu Thr Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile  
 290 295 300  
 Tyr Ser Ser Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly  
 305 310 315 320  
 Ile Thr Gly Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp  
 325 330 335  
 Ile Gln Gly Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln  
 340 345 350  
 Cys Asn Thr Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys  
 355 360 365  
 Thr Ser Thr Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala  
 370 375 380  
 Val Thr Ile Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser  
 385 390 395 400  
 Ala Lys Ser Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser  
 405 410 415  
 Cys Gly Gly Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro  
 420 425 430  
 Glu Ile Thr Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly  
 435 440 445  
 Cys Ile Asp Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala  
 450 455 460  
 Asp Asn Gly Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly  
 465 470 475 480  
 Gly Ala Ile Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr  
 485 490 495  
 Phe Ile Gly Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser  
 500 505 510

Thr	Ala	Leu	Thr	Leu	Ala	Pro	Asn	Ser	Gln	Leu	Ile	Phe	Glu	Asn	Asn		
	515						520					525					
Lys	Val	Thr	Glu	Thr	Thr	Ala	Thr	Thr	Lys	Ala	Ser	Ile	Asn	Asn	Leu		
	530					535					540						
Gly	Ala	Ala	Ile	Tyr	Gly	Asn	Asn	Glu	Thr	Ser	Asp	Val	Thr	Ile	Ser		
545					550					555					560		
Leu	Ser	Ala	Glu	Asn	Gly	Ser	Ile	Phe	Phe	Lys	Asn	Asn	Leu	Cys	Thr		
				565					570					575			
Ala	Thr	Asn	Lys	Tyr	Cys	Ser	Ile	Ala	Gly	Asn	Val	Lys	Phe	Thr	Ala		
		580						585					590				
Ile	Glu	Ala	Ser	Ala	Gly	Lys	Ala	Ile	Ser	Phe	Tyr	Asp	Ala	Val	Asn		
	595					600						605					
Val	Ser	Thr	Lys	Xaa	Thr	Asn	Ala	Gln	Glu	Leu	Lys	Leu	Asn	Glu	Lys		
	610					615					620						
Ala	Thr	Ser	Thr	Gly	Thr	Ile	Leu	Phe	Ser	Gly	Glu	Leu	His	Glu	Asn		
625					630					635					640		
Lys	Ser	Tyr	Ile	Pro	Gln	Lys	Val	Thr	Phe	Ala	His	Gly	Asn	Leu	Ile		
				645					650					655			
Leu	Gly	Lys	Asn	Ala	Glu	Leu	Ser	Val	Val	Ser	Phe	Thr	Gln	Ser	Pro		
		660						665					670				
Gly	Thr	Thr	Ile	Thr	Met	Gly	Pro	Gly	Ser	Val	Leu	Ser	Asn	His	Ser		
	675					680						685					
Lys	Glu	Ala	Gly	Gly	Ile	Ala	Ile	Asn	Asn	Val	Ile	Ile	Asp	Phe	Ser		
	690					695				700							
Glu	Ile	Val	Pro	Thr	Lys	Asp	Asn	Ala	Thr	Val	Ala	Pro	Pro	Thr	Leu		
705					710					715					720		
Lys	Leu	Val	Ser	Arg	Thr	Asn	Ala	Asp	Ser	Lys	Asp	Lys	Ile	Asp	Ile		
				725					730					735			
Thr	Gly	Thr	Val	Thr	Leu	Leu	Asp	Pro	Asn	Gly	Asn	Leu	Tyr	Gln	Asn		
		740						745					750				
Ser	Tyr	Leu	Gly	Glu	Asp	Arg	Asp	Ile	Thr	Leu	Phe	Asn	Ile	Asp	Asn		
	755					760						765					
Ser	Ala	Ser	Gly	Ala	Val	Thr	Ala	Thr	Asn	Val	Thr	Leu	Gln	Gly	Asn		
	770					775					780						
Leu	Gly	Ala	Lys	Lys	Gly	Tyr	Leu	Gly	Thr	Trp	Asn	Leu	Asp	Pro	Asn		
785					790					795					800		
Ser	Ser	Gly	Ser	Lys	Ile	Ile	Leu	Lys	Trp	Thr	Phe	Asp	Lys	Tyr	Leu		
				805					810					815			
Arg	Trp	Pro	Tyr	Ile	Pro	Arg	Asp	Asn	His	Phe	Tyr	Ile	Asn	Ser	Ile		
		820						825					830				
Trp	Gly	Ala	Gln	Asn	Ser	Leu	Val	Thr	Val	Lys	Gln	Gly	Ile	Leu	Gly		
	835					840						845					
Asn	Met	Leu	Asn	Asn	Ala	Arg	Phe	Glu	Asp	Pro	Ala	Phe	Asn	Asn	Phe		
	850					855					860						
Trp	Ala	Ser	Ala	Ile	Gly	Ser	Phe	Leu	Arg	Lys	Glu	Val	Ser	Arg	Asn		
865					870					875					880		
Ser	Asp	Ser	Phe	Thr	Tyr	His	Gly	Arg	Gly	Tyr	Thr	Ala	Ala	Val	Asp		
				885					890					895			
Ala	Lys	Pro	Arg	Gln	Glu	Phe	Ile	Leu	Gly	Ala	Ala	Phe	Ser	Gln	Val		
		900						905					910				
Phe	Gly	His	Ala	Glu	Ser	Glu	Tyr	His	Leu	Asp	Asn	Tyr	Lys	His	Lys		
	915						920					925					
Gly	Ser	Gly	His	Ser	Thr	Gln	Ala	Ser	Leu	Tyr	Ala	Gly	Asn	Ile	Phe		
	930					935					940						
Tyr	Phe	Pro	Ala	Ile	Arg	Ser	Arg	Pro	Ile	Leu	Phe	Gln	Gly	Val	Ala		
945					950					955					960		
Thr	Tyr	Gly	Tyr	Met	Gln	His	Asp	Thr	Thr	Thr	Tyr	Tyr	Pro	Ser	Ile		
				965					970					975			
Glu	Glu	Lys	Asn	Met	Ala	Asn	Trp	Asp	Ser	Ile	Ala	Trp	Leu	Phe	Asp		
		980						985					990				
Leu	Arg	Phe	Ser	Val	Asp	Leu	Lys	Glu	Pro	Gln	Pro	His	Ser	Thr	Ala		
	995						1000					1005					
Arg	Leu	Thr	Phe	Tyr	Thr	Glu	Ala	Glu	Tyr	Thr	Arg	Ile	Arg	Gln	Glu		
	1010						1015					1020					

Lys Phe Thr Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser  
 1025 1030 1035 1040  
 Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu  
 1045 1050 1055  
 Ala Trp Arg Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu  
 1060 1065 1070  
 Pro Val Ile Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser  
 1075 1080 1085  
 Thr Lys Glu Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala  
 1090 1095 1100  
 Ala Arg Ala Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr  
 1105 1110 1115 1120  
 Leu Tyr Gly Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln  
 1125 1130 1135  
 Met Ala Asn Gly Gly Ile Arg Phe Val Phe  
 1140 1145

&lt;210&gt;581

&lt;211&gt;289

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;581

Asn Asn Arg Ser Ser Tyr Gln Thr Ala Phe Val Met His Lys Val Ile  
 1 5 10 15  
 Val Xaa Ile Phe Leu Thr Leu Tyr Ser Leu Lys Ser Tyr Gly Asn Asp  
 20 25 30  
 Val Ile Asp Lys Pro His Val Leu Val Ser Ile Ala Pro Tyr Lys Phe  
 35 40 45  
 Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe Val Tyr Ala Ile Val  
 50 55 60  
 Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu Pro Pro Gln Gln Ile  
 65 70 75 80  
 Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg Ile Gly Glu Ala Phe  
 85 90 95  
 Glu Lys Thr Cys Glu Arg Asn Leu Thr Cys Gln Gln Val Asp Leu Ser  
 100 105 110  
 Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys Cys Asn Gln His Thr  
 115 120 125  
 Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro Lys Asn Leu Lys Val  
 130 135 140  
 Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys Lys Tyr Pro Gln His  
 145 150 155 160  
 Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu Leu Leu Ala Leu Asp  
 165 170 175  
 Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser Lys Ala Lys Gln Arg  
 180 185 190  
 His Ile Leu Val Ser His Gly Ala Phe Gly Tyr Phe Cys Arg Asp Tyr  
 195 200 205  
 Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser His Val Glu Pro Ser  
 210 215 220  
 Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile Glu Gln Tyr Lys Ile  
 225 230 235 240  
 Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg Arg Ser Ser Ala Met  
 245 250 255  
 Leu Ala Asp Arg Phe His Met His Thr Val Asn Leu Asp Pro Tyr Ala  
 260 265 270  
 Glu Asn Ile Leu Val Asn Leu Lys Thr Ile Ala Thr Thr Phe Ser Ser  
 275 280 285  
 Leu

&lt;210&gt;582

&lt;211&gt;352

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;582

Leu Lys Lys Asp Lys Asn Val Ile Met Phe Val Asp Gln Ile Thr Leu  
 1 5 10 15  
 Glu Leu Arg Ala Gly Lys Gly Gly Asn Gly Val Val Ala Trp Arg Lys  
 20 25 30  
 Glu Lys Tyr Leu Pro Lys Gly Gly Pro Tyr Gly Gly Asn Gly Gly Asn  
 35 40 45  
 Gly Gly Ser Val Ile Ile Glu Ala Thr Thr Ser Val Tyr Ser Phe Glu  
 50 55 60  
 Ala Tyr Arg Asn Ile Arg Phe Leu Lys Ala Pro Asp Gly Gln Ser Gly  
 65 70 75 80  
 Ala Thr Asn Asn Arg Thr Gly Arg Ser Gly Lys Asp Leu Ile Val Ser  
 85 90 95  
 Val Pro Thr Gly Thr Leu Leu Arg Asp Ala Glu Thr Gly Glu Ile Leu  
 100 105 110  
 His Asp Phe Thr Val Asp Gly Glu Arg Leu Leu Val Ser Gln Gly Gly  
 115 120 125  
 Lys Gly Gly Lys Gly Asn Thr Phe Phe Lys Thr Ser Val Asn Arg Ala  
 130 135 140  
 Pro Thr Lys Ala Thr Pro Gly Lys Pro Gly Glu Ile Arg Gln Val Glu  
 145 150 155 160  
 Leu Glu Leu Lys Leu Ile Ala Asp Ile Gly Leu Val Gly Phe Pro Asn  
 165 170 175  
 Ala Gly Lys Ser Thr Leu Phe Asn Thr Leu Ala His Thr Glu Val Lys  
 180 185 190  
 Val Gly Ala Tyr Pro Phe Thr Thr Leu Ala Pro Ser Leu Gly Leu Val  
 195 200 205  
 Leu Cys Lys Asp Arg Leu Tyr Gln Lys Pro Trp Ile Ile Ala Asp Ile  
 210 215 220  
 Pro Gly Ile Ile Glu Gly Ala His Gln Asn Lys Gly Leu Gly Leu Asp  
 225 230 235 240  
 Phe Leu Arg His Ile Glu Arg Thr Leu Leu Leu Phe Val Ile Asp  
 245 250 255  
 Val Ser Lys Arg Glu Arg Asn Ser Pro Glu Glu Asp Leu Glu Thr Leu  
 260 265 270  
 Ile His Glu Leu His Ser His Gln Pro Asp Phe Glu Lys Lys Asp Met  
 275 280 285  
 Leu Val Ala Leu Asn Lys Ile Asp Asp Leu Leu Pro Asp Glu Gln Glu  
 290 295 300  
 Glu Cys Leu Gln Ser Phe Gln Lys Arg Phe Pro Ser Tyr Thr Phe Val  
 305 310 315 320  
 Leu Ile Ser Gly Leu Thr Gly Glu Gly Val Asp Gly Leu Tyr Arg Phe  
 325 330 335  
 Phe Thr Gln Asp Ser Leu Tyr Asn Xaa Thr Pro Ser Ala Met Ile Ser  
 340 345 350

&lt;210&gt;583

&lt;211&gt;84

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;583

Met Ala His Lys Lys Gly Gln Gly Ala Ser Arg Asn Gly Arg Asp Ser  
 1 5 10 15  
 Lys Ser Lys Arg Leu Gly Val Lys Val Gly Ala Gly Gln Lys Val Ser  
 20 25 30  
 Thr Gly Ser Ile Leu Val Arg Gln Arg Gly Thr Arg Trp Asn Pro Ala  
 35 40 45  
 Gln Asn Val Gly Arg Gly Arg Asp Asp Thr Leu Phe Ala Leu Val Asp  
 50 55 60  
 Gly Ile Val Val Met Lys Lys Thr Asn Arg Thr Tyr Ile Ser Val Val  
 65 70 75 80  
 Pro Glu Gln Leu

&lt;210&gt;584

&lt;211&gt;107

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;584

Leu Met Glu Pro Tyr Ala Val Ile Gln Thr Gly Ser Lys Gln Tyr Gln  
 1 5 10 15  
 Val Arg Ser Gly Asp Val Ile Asp Val Glu Leu Leu Gly Glu Val Ala  
 20 25 30  
 Ser Asp Lys Glu Val Ile Phe Gln Asp Val Leu Phe Val Phe Asp Gly  
 35 40 45  
 Thr Lys Ala Ser Leu Gly Ser Pro Thr Ile Ala Asn Ala Gln Val Lys  
 50 55 60  
 Ala Glu Tyr Leu Ser His Val Lys Gly Glu Lys Val Val Ala Tyr Lys  
 65 70 75 80  
 Tyr Lys Lys Arg Lys Asn Tyr His Arg Lys His Gly His Arg Gln Lys  
 85 90 95  
 Tyr Leu Arg Val Lys Ile Arg Glu Ile Leu Ile  
 100 105

&lt;210&gt;585

&lt;211&gt;199

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;585

Val Asn Phe Arg Asn Phe Val Val Ser Ser Val Lys Glu Ile Leu Lys  
 1 5 10 15  
 Lys Asn Ile Tyr Gln Val Val Met Asp Arg Asp Asn Glu Val Pro Leu  
 20 25 30  
 Pro Lys Pro Lys Trp Ile Tyr Arg Thr Gly Ile Gly Gln Asp Ser His  
 35 40 45  
 Arg Phe Leu Pro Glu Ser Ser Thr Lys Pro Cys Ile Leu Gly Gly Ile  
 50 55 60  
 Ile Phe Asp His Cys Pro Gly Phe Gln Ala Asn Ser Asp Gly Asp Ile  
 65 70 75 80  
 Ile Phe His Ala Ile Cys Asn Ala Ile Ser Ser Val Thr Asn Lys Ile  
 85 90 95  
 Ile Leu Gly Lys Val Ala Asp Glu Leu Leu Gln Thr Arg Gly Ile Thr  
 100 105 110  
 Asp Ser Gly Ile Tyr Leu Glu Glu Ala Leu Lys Ser Leu Lys Pro Asn  
 115 120 125  
 Gln Lys Ile Ser His Val Ala Ile Thr Ile Glu Gly Ser Arg Pro Lys  
 130 135 140  
 Phe Leu Cys Lys Leu Ser Ala Leu Arg Gln Asn Ile Ala Gln Val Met  
 145 150 155 160  
 Asn Leu Thr Pro Thr Asp Ile Gly Ile Thr Ala Thr Ser Gly Glu Gly  
 165 170 175  
 Leu Ser Asp Phe Gly Cys Gly Asp Gly Val Gln Cys Phe Cys Val Leu  
 180 185 190  
 Thr Val Met Glu Tyr Cys Asp  
 195

&lt;210&gt;586

&lt;211&gt;246

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;586

Ile Pro Ala Lys Leu Asn Ser Phe Phe Pro Asp Lys Asp Pro Lys Ile  
 1 5 10 15  
 Thr Leu Tyr Asp Ala Ile Gln Glu Tyr Arg Pro Gln Ile Pro Ile Glu  
 20 25 30  
 Leu Phe Ala Glu Ser Val Phe Pro Leu Leu Pro Arg Phe Tyr Ser Ile  
 35 40 45  
 Ala Ser Ser Pro Asp Leu His Pro Lys Ser Ile Glu Leu Leu Val Lys  
 50 55 60  
 His Val Ser Tyr Pro Gly Lys Tyr Gln Lys Arg Phe Gly Val Cys Ser  
 65 70 75 80  
 Ser Phe Leu Cys Ser Glu Leu Gln Val Asn Asp Ser Ala Tyr Ile Phe  
 85 90 95

Val Gln Pro Thr Lys His Phe Thr Leu Ser Thr Gln Thr Glu Gly Lys  
 100 105 110  
 Pro Leu Val Met Ile Gly Ala Gly Thr Gly Ile Ala Pro Tyr Lys Ala  
 115 120 125  
 Phe Leu Glu Glu Arg Leu Phe Asn Lys Asp Pro Gly Asn Asn Leu Leu  
 130 135 140  
 Phe Phe Gly Glu Arg Lys Glu Lys Val Asn Phe Tyr Tyr Arg Glu Phe  
 145 150 155 160  
 Trp Asn His Ala Glu Glu Gly Lys Leu Lys Leu Phe Leu Ala Phe  
 165 170 175  
 Ser Arg Glu Arg Asp Gln Lys Val Tyr Val Gln Asp Leu Leu Arg Ile  
 180 185 190  
 Gln Lys Asp Glu Val Arg Lys Ala Tyr Glu Glu Gly Gly Phe Phe Phe  
 195 200 205  
 Val Cys Gly Arg Lys Val Leu Gly Ile Glu Val Lys His Ala Leu Glu  
 210 215 220  
 Glu Ile Leu Gly Lys Asp Thr Leu Ala Ser Leu Arg Lys Glu His Arg  
 225 230 235 240  
 Tyr Val Val Asp Val Tyr  
 245

&lt;210&gt;587

&lt;211&gt;85

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;587

Lys Met Tyr Leu Gln Glu Lys Phe Lys Ala Gln Gln Val Pro Leu Val  
 1 5 10 15  
 Leu Arg Glu Leu Leu Ser Cys Ser Asp Ser Ile Asn Asp Ser Asp Pro  
 20 25 30  
 Ile Tyr Arg Met Val Phe Asp Ser Asn Asp Thr Thr Ile Ser Tyr Lys  
 35 40 45  
 Val Gly Asp Ala Leu Gly Val Leu Pro Glu Asn Ser Lys Glu Val Ser  
 50 55 60  
 Glu His Val Leu Gln Leu Arg Leu Phe Pro Asn Asp Pro Cys Gln  
 65 70 75 80  
 Arg Lys Lys Asn Phe  
 85

&lt;210&gt;588

&lt;211&gt;118

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;588

Lys Lys Phe Lys Lys Arg Leu Leu Arg Ser Lys Gly Cys Met Lys Gln  
 1 5 10 15  
 Gln Lys Gln Lys Ile Arg Ile Arg Leu Lys Gly Phe Asp Gln Gly Gln  
 20 25 30  
 Leu Asp Arg Ser Thr Ala Asp Ile Val Glu Thr Ala Lys Arg Thr Gly  
 35 40 45  
 Ala Arg Val Val Gly Pro Ile Pro Leu Pro Thr Lys Arg Glu Val Tyr  
 50 55 60  
 Thr Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg Glu Gln Phe  
 65 70 75 80  
 Glu Ile Arg Thr His Lys Arg Leu Val Asp Ile Leu Asp Pro Thr Gly  
 85 90 95  
 Lys Thr Ile Asp Ala Leu Lys Met Leu Ala Leu Pro Ala Gly Val Asp  
 100 105 110  
 Ile Lys Ile Lys Ala Ala  
 115

&lt;210&gt;589

&lt;211&gt;651

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;589

Ser His Glu Gly Gly Ala Thr Met Asp Trp Met Ala Gln Glu Glu Glu

1	5	10	15
Arg Gly Ile Thr	Ile Thr Ser Ala Ala Thr Thr Val Phe Trp Leu Gly		
20	25	30	
Ala Lys Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr Ile			
35	40	45	
Glu Val Glu Arg Ser Leu Arg Val Leu Asp Gly Ala Val Ala Val Phe			
50	55	60	
Asp Ala Val Ser Gly Val Glu Pro Gln Ser Glu Thr Val Trp Arg Gln			
65	70	75	80
Ala Asp Lys Tyr Gly Val Pro Arg Ile Ala Phe Val Asn Lys Met Asp			
85	90	95	
Arg Met Gly Ala Asp Tyr Phe Ala Ala Val Glu Ser Met Lys Glu Lys			
100	105	110	
Leu Gly Ala Asn Ala Phe Pro Val His Cys Pro Ile Gly Ser Glu Ser			
115	120	125	
Gln Phe Val Gly Met Val Asp Leu Ile Ser Gln Lys Ala Leu Tyr Phe			
130	135	140	
Leu Asp Asp Thr Leu Gly Ala Lys Trp Glu Glu Lys Glu Ile Ser Glu			
145	150	155	160
Asp Leu Lys Glu Arg Cys Ala Glu Leu Arg Ala Asn Leu Leu Glu Glu			
165	170	175	
Leu Ala Thr Ile Asp Glu Ser Asn Glu Ala Phe Met Met Lys Val Leu			
180	185	190	
Glu Asp Pro Asp Ser Ile Thr Glu Asp Glu Ile His Gln Val Met Arg			
195	200	205	
Lys Gly Val Ile Glu Asn Lys Ile Asn Pro Val Leu Cys Gly Thr Ala			
210	215	220	
Phe Lys Asn Lys Gly Val Gln Gln Leu Leu Asn Val Ile Val Lys Trp			
225	230	235	240
Leu Pro Ser Pro Leu Asp Arg Gly Asn Ile Arg Gly Ile Asn Leu Lys			
245	250	255	
Thr Asp Gln Glu Ile Ser Leu Glu Pro Arg Arg Asp Gly Pro Leu Ala			
260	265	270	
Ala Leu Ala Phe Lys Ile Met Thr Asp Pro Tyr Val Gly Arg Ile Thr			
275	280	285	
Phe Ile Arg Ile Tyr Ser Gly Thr Leu Lys Lys Gly Ser Ala Ile Leu			
290	295	300	
Asn Ser Thr Lys Asp Lys Lys Glu Arg Ile Ser Arg Leu Leu Glu Met			
305	310	315	320
His Ala Asn Glu Arg Thr Asp Arg Asp Glu Phe Thr Val Gly Asp Ile			
325	330	335	
Gly Ala Cys Val Gly Leu Lys Phe Ser Val Thr Gly Asp Thr Leu Cys			
340	345	350	
Asp Asp Asn Gln Glu Ile Val Leu Glu Arg Ile Glu Phe Pro Asp Pro			
355	360	365	
Val Ile Asp Met Ala Ile Glu Pro Lys Ser Lys Gly Asp Arg Glu Lys			
370	375	380	
Leu Ala Gln Ala Leu Ser Ser Leu Ser Glu Glu Asp Pro Thr Phe Arg			
385	390	395	400
Val Ser Thr Asn Glu Thr Gly Gln Thr Ile Ile Ser Gly Met Gly			
405	410	415	
Glu Leu His Leu Asp Ile Leu Arg Asp Arg Met Ile Arg Glu Phe Lys			
420	425	430	
Val Glu Ala Asn Val Gly Lys Pro Gln Val Ser Tyr Lys Glu Thr Ile			
435	440	445	
Thr Val Ser Gly Asn Ser Glu Thr Lys Tyr Val Lys Gln Ser Gly Gly			
450	455	460	
Arg Gly Gln Tyr Ala His Val Cys Leu Glu Ile Glu Pro Asn Glu Pro			
465	470	475	480
Gly Lys Gly Asn Glu Val Val Ser Lys Ile Val Gly Gly Val Ile Pro			
485	490	495	
Lys Glu Tyr Ile Pro Ala Val Ile Lys Gly Ile Glu Glu Gly Leu Asn			
500	505	510	
Thr Gly Val Leu Ala Gly Tyr Gly Leu Val Asp Val Lys Val Ser Ile			

515 520 525  
 Val Phe Gly Ser Tyr His Glu Val Asp Ser Ser Glu Met Ala Phe Lys  
 530 535 540  
 Ile Cys Gly Ser Met Ala Val Lys Asp Ala Cys Arg Lys Ala Lys Pro  
 545 550 555 560  
 Val Ile Leu Glu Pro Ile Met Lys Val Ala Val Ile Thr Pro Glu Asp  
 565 570 575  
 His Leu Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Lys Ile  
 580 585 590  
 Leu Gly Gln Glu Ser Ser Arg Gly Met Ala Gln Val Asn Ala Glu Val  
 595 600 605  
 Pro Leu Ser Glu Met Phe Gly Tyr Thr Thr Ser Leu Arg Ser Leu Thr  
 610 615 620  
 Ser Gly Arg Ala Thr Ser Thr Met Glu Pro Ala Phe Phe Ala Lys Val  
 625 630 635 640  
 Pro Gln Lys Ile Gln Glu Glu Ile Val Lys Lys  
 645 650

&lt;210&gt;590

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;590

Leu Asn Tyr Gly Glu Asn Asn Lys Phe Met Ser Asn Gln Glu Phe Asp  
 1 5 10 15  
 Leu Ser Ala Ile Arg Asn Ile Gly Ile Met Ala His Ile Asp Ala Gly  
 20 25 30  
 Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe Tyr Ala Gly Arg Thr His  
 35 40 45  
 Lys Ile Gly Glu Val Met Lys Ala Glu Leu Pro Trp Thr Gly Trp Pro  
 50 55 60  
 Arg Ser Lys Lys Glu Glu Leu Arg Leu Pro Leu Leu Gln Leu Leu Ser  
 65 70 75 80  
 Ser Gly

&lt;210&gt;591

&lt;211&gt;159

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;591

Met Tyr Met Ser Arg Arg His Ser Ala Glu Lys Arg Asp Ile Pro Gly  
 1 5 10 15  
 Asp Pro Ile Tyr Gly Ser Val Ile Leu Glu Lys Phe Ile Asn Lys Val  
 20 25 30  
 Met Met His Gly Lys Lys Ser Val Ala Arg Lys Ile Val Tyr Ser Ala  
 35 40 45  
 Leu Glu Arg Phe Gly Lys Lys Leu Asn Leu Glu Asn Val Leu Glu Gly  
 50 55 60  
 Phe Gly Glu Ala Leu Glu Asn Ala Lys Pro Ile Leu Glu Val Arg Ser  
 65 70 75 80  
 Arg Arg Val Gly Gly Ala Thr Tyr Gln Val Pro Val Glu Val Ala Ser  
 85 90 95  
 Glu Arg Arg Asn Cys Leu Ala Met Gln Trp Ile Ile Lys His Ala Arg  
 100 105 110  
 Ser Lys Pro Gly Lys Ser Met Glu Val Gly Leu Ala Thr Glu Leu Ile  
 115 120 125  
 Asp Cys Phe Asn Lys Gln Gly Ala Thr Ile Lys Lys Arg Glu Asp Thr  
 130 135 140  
 His Arg Met Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Lys Trp  
 145 150 155

&lt;210&gt;592

&lt;211&gt;146

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;592



Leu Pro Thr Lys Arg Ala Leu Leu Tyr Ile Ser Met Leu Val Val Val  
 1 5 10 15  
 Arg Leu Lys Arg Glu Glu Tyr Met Pro Thr Ile Asn Gln Leu Ile Arg  
 20 25 30  
 Lys Arg Arg Lys Ser Ser Leu Ala Arg Lys Lys Ser Pro Ala Leu Gln  
 35 40 45  
 Lys Cys Pro Gln Lys Arg Gly Val Cys Leu Gln Val Lys Thr Lys Thr  
 50 55 60  
 Pro Lys Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Trp Val Arg Leu  
 65 70 75 80  
 Ser Asn Gly Gln Glu Val Ile Ala Tyr Ile Gly Gly Glu Gly His Asn  
 85 90 95  
 Leu Gln Glu His Ser Ile Val Leu Ile Gln Gly Gly Arg Val Lys Asp  
 100 105 110  
 Leu Pro Gly Val Arg Tyr His Ile Val Arg Gly Thr Leu Asp Cys Ala  
 115 120 125  
 Ala Val Lys Asn Arg Lys Gln Ser Arg Ser Arg Tyr Gly Ala Lys Arg  
 130 135 140  
 Pro Lys  
 145

&lt;210&gt;593

&lt;211&gt;268

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;593

Gly Cys Met Trp Arg Val Val Leu Arg Phe Leu Ile Ile Phe Ile Leu  
 1 5 10 15  
 Gly Arg Ala Val Phe Pro Leu Arg Ala Ser Glu Ser Phe Ser Trp Glu  
 20 25 30  
 Thr Ser Thr Cys Leu Thr Val Leu Gly Ile Pro Phe Ile Asp Ile Ile  
 35 40 45  
 Leu Thr Thr Asn Glu Asp Phe Val Ala Gln Cys Gly Leu Gln Ile Gly  
 50 55 60  
 Thr Ile Ser Ser Thr Asn Asn Ala Lys Ile Lys Glu Ile Phe Leu Ile  
 65 70 75 80  
 Tyr Lys Glu Lys Phe Pro Glu Ala Ser Ile Ser Phe Lys Arg Lys Glu  
 85 90 95  
 Pro Leu Asn Leu Ser Gln Ser His Leu Ser Asp Leu Gly Ile Leu Cys  
 100 105 110  
 Met Arg Asn Gly Glu Thr Tyr Ala Glu Gly Met Ala Asn Lys Glu Asn  
 115 120 125  
 Gly Pro Ala Leu Lys Gln Pro Lys Asp Leu Arg Leu Val Leu Arg Cys  
 130 135 140  
 Pro Asn Gln Pro Asp Thr Leu Leu Tyr Ser Glu Lys Glu Ala Glu Lys  
 145 150 155 160  
 Gly Ile Glu Thr Asn Thr Cys Leu Cys Asn Gln Gly Tyr Thr Leu Leu  
 165 170 175  
 Asp Gly Gln Leu Ile Leu Tyr Gly Asp Ser Ile Glu Lys Phe Leu Lys  
 180 185 190  
 Glu Thr Lys Arg Lys Asn Asn His Thr Leu Val Asp Leu Cys Asp Ser  
 195 200 205  
 Gln Val Val Thr Thr Phe Leu Gly Arg Phe Trp Ser Leu Leu Asn Tyr  
 210 215 220  
 Val Gln Val Leu Phe Leu Ser Glu Asp Ser Ala Lys Xaa Leu Ala Gly  
 225 230 235 240  
 Ile Pro Asp Leu Ala Gln Xaa Arg Asn Cys Phe Pro Thr Pro Tyr Leu  
 245 250 255  
 Cys Phe Leu Phe Ile Pro Thr Ile Leu Phe Thr Ser  
 260 265

&lt;210&gt;594

&lt;211&gt;648

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;594

746

Ser Gly Lys Ser Thr Gln Leu Gln Gly Val Lys Ser Asp Ile Leu Ile  
 515 520 525  
 Pro Ser Leu Tyr Ala Glu Asp Arg Leu Gly Glu Arg Phe Leu Glu His  
 530 535 540  
 Pro Leu Pro Ala Asp Cys Cys Asp Asn Val Leu His Asp Pro Leu Thr  
 545 550 555 560  
 Asp Leu Asp Thr Gln Thr Arg Pro Trp Phe Gln Lys Tyr Tyr Leu Pro  
 565 570 575  
 Asn Leu Gln Lys Gln Glu Thr Leu Trp Arg Glu Met Leu Pro Gln Leu  
 580 585 590  
 Thr Lys Asn Ser Glu Gln Arg Leu Ser Glu Asn Ser Asn Phe Gln Ala  
 595 600 605  
 Phe Leu Ser Gln Ile Lys Ser Ser Glu Lys Thr Asp Leu Ser Tyr Gly  
 610 615 620  
 Ser Asn Asp Leu Gln Leu Glu Glu Ser Ile Asn Ile Leu Lys Asp Met  
 625 630 635 640  
 Ile Leu Leu Gln Gln Cys Arg Lys  
 645

&lt;210&gt;595

&lt;211&gt;199

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;595

Glu Asn Gly Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr  
 1 5 10 15  
 Gly Ala Ala Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala  
 20 25 30  
 Ala Ser Gly Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro  
 35 40 45  
 Gly Met Val Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln  
 50 55 60  
 Pro Ile Arg Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr  
 65 70 75 80  
 Leu Leu Val Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met  
 85 90 95  
 Phe Ile Phe His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile  
 100 105 110  
 Pro Ala Ala Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe  
 115 120 125  
 Asp Glu Ala Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala  
 130 135 140  
 Gly Val Leu Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn  
 145 150 155 160  
 Lys Ile Phe Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Xaa  
 165 170 175  
 Thr Pro Val Leu Asn Asp Gly Arg Gly Xaa Pro Val Leu Ser Pro Leu  
 180 185 190  
 Val Ser Lys Ile Ala Arg Val  
 195

&lt;210&gt;596

&lt;211&gt;556

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;596

Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser  
 1 5 10 15  
 Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu  
 20 25 30  
 Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro  
 35 40 45  
 Val Pro Met Thr Ala Lys Lys Val Arg Leu Val Arg Arg Asn Lys Gln  
 50 55 60  
 Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys Asp Lys Glu Phe Tyr  
 65 70 75 80

Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser  
 85 90 95  
 Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val  
 100 105 110  
 Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr  
 115 120 125  
 Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val  
 130 135 140  
 Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro  
 145 150 155 160  
 Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg  
 165 170 175  
 Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu  
 180 185 190  
 Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu  
 195 200 205  
 Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala Ile Cys Ile Lys Gln  
 210 215 220  
 Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile  
 225 230 235 240  
 Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp  
 245 250 255  
 Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu  
 260 265 270  
 Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr  
 275 280 285  
 Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr  
 290 295 300  
 Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val  
 305 310 315 320  
 Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser  
 325 330 335  
 Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly  
 340 345 350  
 Asp Leu Val Leu His Asp Val Val Ile Gln Asp Thr Leu Pro Ser Gly  
 355 360 365  
 Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val  
 370 375 380  
 Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys  
 385 390 395 400  
 Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala  
 405 410 415  
 Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr  
 420 425 430  
 Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp  
 435 440 445  
 Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys  
 450 455 460  
 Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu  
 465 470 475 480  
 Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys  
 485 490 495  
 Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu  
 500 505 510  
 Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala  
 515 520 525  
 Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr  
 530 535 540  
 Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr  
 545 550 555

&lt;210&gt;597

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;597

Met Lys Lys Ala Val Leu Ile Ala Ala Met Phe Cys Gly Val Val Ser  
 1 5 10 15  
 Leu Ser Ser Cys Cys Arg Ile Val Asp Cys Cys Phe Glu Asp Pro Cys  
 20 25 30  
 Ala Pro Ser Ser Cys Asn Pro Cys Glu Val Ile Arg Lys Lys Glu Arg  
 35 40 45  
 Ser Cys Gly Gly Asn Ala Cys Gly Ser Tyr Val Pro Ser Cys Ser Asn  
 50 55 60  
 Pro Cys Gly Ser Thr Glu Cys Asn Ser Gln Ser Pro Gln Val Lys Gly  
 65 70 75 80  
 Cys Thr Ser Pro Asp Gly Arg Cys Lys Gln  
 85 90

&lt;210&gt;598

&lt;211&gt;516

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;598

Met Lys Ser Leu Trp Ser Lys Asp Lys Arg Ile Met Asn Trp Glu Asn  
 1 5 10 15  
 Val Arg Val Arg Val Ala Pro Ser Pro Thr Gly Asp Pro His Val Gly  
 20 25 30  
 Thr Ala Tyr Met Ala Leu Phe Asn Glu Ile Phe Ala Lys Arg Phe Lys  
 35 40 45  
 Gly Lys Met Ile Leu Arg Ile Glu Asp Thr Asp Arg Thr Arg Ser Arg  
 50 55 60  
 Gln Asp Tyr Glu Glu Asn Ile Phe Ser Ala Leu Arg Trp Cys Gly Ile  
 65 70 75 80  
 Gln Trp Asp Glu Gly Pro Asp Val Gly Gly Pro Tyr Gly Pro Tyr Arg  
 85 90 95  
 Gln Ser Glu Arg Thr Lys Ile Tyr Gln Gly Tyr Val Glu Thr Leu Leu  
 100 105 110  
 Lys Thr Asp Cys Ala Tyr Lys Cys Phe Ala Thr Pro Gln Glu Leu Ala  
 115 120 125  
 Glu Met Arg Ala Val Ala Ser Thr Leu Gly Tyr Arg Gly Gly Tyr Asp  
 130 135 140  
 Arg Arg Tyr Arg Tyr Leu Ser Pro Glu Glu Val Ala Ser Arg Glu Ala  
 145 150 155 160  
 Ala Gly Gln Pro Tyr Thr Ile Arg Leu Lys Val Pro Leu Ser Gly Glu  
 165 170 175  
 Cys Val Phe Glu Asp Tyr Ser Lys Gly Arg Val Val Phe Pro Trp Ala  
 180 185 190  
 Asp Val Asp Asp Gln Val Leu Val Lys Ser Asp Gly Phe Pro Thr Tyr  
 195 200 205  
 His Phe Ala Asn Val Ile Asp Asp His Leu Met Gly Ile Thr His Val  
 210 215 220  
 Leu Arg Gly Glu Glu Trp Leu Ser Ser Thr Pro Lys His Leu Leu Leu  
 225 230 235 240  
 Tyr Glu Ala Phe Gly Trp Glu Pro Pro Val Phe Leu His Met Pro Leu  
 245 250 255  
 Leu Leu Asn Pro Asp Gly Thr Lys Leu Ser Lys Arg Lys Asn Pro Thr  
 260 265 270  
 Ser Ile Phe Tyr Tyr Arg Asp Ser Gly Tyr Val Lys Glu Ala Phe Val  
 275 280 285  
 Asn Phe Leu Thr Leu Met Gly Tyr Ser Met Glu Gly Asp Glu Glu Val  
 290 295 300  
 Tyr Ser Leu Glu Arg Ile Ile Glu Thr Phe Asn Pro Arg Arg Ile Gly  
 305 310 315 320  
 Lys Ser Gly Ala Val Phe Asp Ile Gln Lys Leu Asp Trp Met Asn Lys  
 325 330 335  
 His Tyr Leu Asn His Glu Gly Ser Pro Glu Cys Leu Leu Lys Glu Leu  
 340 345 350  
 Gln Gly Trp Leu Leu Asn Asp Glu Phe Phe Leu Lys Ile Leu Pro Leu  
 355 360 365

Cys Gln Ser Arg Ile Thr Thr Leu Ala Glu Phe Ile Asn Leu Thr Ser  
 370 375 380  
 Phe Phe Phe Ser Gly Leu Leu Glu Tyr Arg Val Glu Glu Leu Leu Pro  
 385 390 395 400  
 Gln Ala Leu Ser Pro Glu Lys Ala Ala Ile Leu Leu Tyr Ser Tyr Val  
 405 410 415  
 Lys Tyr Leu Glu Lys Thr Asp Gln Trp Thr Lys Glu Thr Cys Tyr Leu  
 420 425 430  
 Gly Ser Lys Trp Leu Ala Gln Ala Phe Asn Val His His Lys Lys Ala  
 435 440 445  
 Ile Ile Pro Leu Leu Tyr Val Ala Ile Thr Gly Lys Lys Gln Gly Leu  
 450 455 460  
 Pro Leu Phe Asp Ser Ile Glu Ile Leu Gly Lys Pro Arg Ala Arg Ala  
 465 470 475 480  
 Arg Leu Val Tyr Ala Glu Lys Leu Leu Gly Gly Val Pro Lys Lys Leu  
 485 490 495  
 Ala Ala Thr Val Asp Lys Phe Met Gln Arg Glu Asp Phe Glu Glu Ala  
 500 505 510  
 Thr Phe Asp Leu  
 515

&lt;210&gt;599

&lt;211&gt;181

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;599

Met Ala Cys Glu Gln His Glu Gly Cys Tyr Glu Leu Glu Glu Arg Glu  
 1 5 10 15  
 Glu Arg Glu Glu Ile Glu Asp Ile Lys Asp Ser Asp Thr Lys Trp Val  
 20 25 30  
 Ser Ile Thr Gln Ala Ala Lys Leu His Asn Val Thr Arg Gln Ala Ile  
 35 40 45  
 Tyr Val Ala Ile Lys Gln Lys Lys Leu Lys Ala Ser Lys Glu Thr Arg  
 50 55 60  
 Trp Glu Ile Asp Ile Lys Asp Leu Glu Glu Tyr Lys Arg Asn Arg Tyr  
 65 70 75 80  
 Ser Arg Lys Lys Ser Leu Tyr Gln Gly Glu Leu Val Phe Asp Asn Gly  
 85 90 95  
 Lys Gly Cys Tyr Ser Ile Asn Gln Val Ala Gln Ile Leu Gly Ile Pro  
 100 105 110  
 Val Gln Lys Val Tyr Tyr Ala Thr Arg Thr Gly Thr Ile Arg Gly Glu  
 115 120 125  
 Arg Lys Gly Ala Ala Trp Val Ile His Val Ser Glu Ile Glu Arg Tyr  
 130 135 140  
 Lys Asn Glu Tyr Leu Ser Lys Gln Ala Ala Lys Lys Leu Lys Gly Ala  
 145 150 155 160  
 Glu Pro Lys Glu His Gln Ala Pro Asn Phe Glu Pro Pro Thr Glu Ile  
 165 170 175  
 Phe Pro Glu Ser Asn  
 180

&lt;210&gt;600

&lt;211&gt;373

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;600

Met Ser Ile Ala Ile Ala Arg Glu Gln His Ala Ala Ile Leu Asp Met  
 1 5 10 15  
 His Pro Lys Pro Ser Ile Ala Met Phe Ser Ser Glu Gln Ala Arg Thr  
 20 25 30  
 Ser Trp Glu Lys Arg Gln Ala His Pro Tyr Leu Tyr Arg Leu Leu Glu  
 35 40 45  
 Ile Ile Trp Gly Val Val Lys Phe Leu Leu Gly Leu Ile Phe Phe Ile  
 50 55 60  
 Pro Leu Gly Leu Phe Trp Val Leu Gln Lys Ile Cys Gln Asn Phe Ile  
 65 70 75 80

Leu Leu Gly Ala Gly Gly Trp Ile Phe Arg Pro Ile Cys Arg Asp Ser  
 85 90 95  
 Asn Leu Leu Arg Gln Ala Tyr Ala Ala Arg Leu Phe Ser Ala Ser Phe  
 100 105 110  
 Gln Asp His Val Ser Ser Val Arg Arg Val Cys Leu Gln Tyr Asp Glu  
 115 120 125  
 Val Phe Ile Asp Gly Leu Glu Leu Arg Leu Pro Asn Ala Lys Pro Asp  
 130 135 140  
 Arg Trp Met Leu Ile Ser Asn Gly Asn Ser Asp Cys Leu Glu Tyr Arg  
 145 150 155 160  
 Thr Val Leu Gln Gly Glu Lys Asp Trp Ile Phe Arg Ile Ala Glu Glu  
 165 170 175  
 Ser Gln Ser Asn Ile Leu Ile Phe Asn Tyr Pro Gly Val Met Lys Ser  
 180 185 190  
 Gln Gly Asn Ile Thr Arg Asn Asn Val Val Lys Ser Tyr Gln Ala Cys  
 195 200 205  
 Val Arg Tyr Leu Arg Asp Glu Pro Ala Gly Pro Gln Ala Arg Gln Ile  
 210 215 220  
 Val Ala Tyr Gly Tyr Ser Leu Gly Ala Ser Val Gln Ala Glu Ala Leu  
 225 230 235 240  
 Ser Lys Glu Ile Ala Asp Gly Ser Asp Ser Val Arg Trp Phe Val Val  
 245 250 255  
 Lys Asp Arg Gly Ala Arg Ser Thr Gly Ala Val Ala Lys Gln Phe Ile  
 260 265 270  
 Gly Ser Leu Gly Val Trp Leu Ala Asn Leu Thr His Trp Asn Ile Asn  
 275 280 285  
 Ser Glu Lys Arg Ser Lys Asp Leu His Cys Pro Glu Leu Phe Ile Tyr  
 290 295 300  
 Gly Lys Asp Ser Gln Gly Asn Leu Ile Gly Asp Gly Leu Phe Lys Lys  
 305 310 315 320  
 Glu Thr Cys Phe Ala Ala Pro Phe Leu Asp Pro Lys Asn Leu Glu Glu  
 325 330 335  
 Cys Ser Gly Lys Lys Ile Pro Val Ala Gln Thr Gly Leu Arg His Asp  
 340 345 350  
 His Ile Leu Ser Asp Asp Val Ile Lys Glu Val Ala Gly His Ile Arg  
 355 360 365  
 Arg His Phe Asp Asn  
 370  
 <210>601  
 <211>564  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>601  
 Gln Tyr Lys Asn Leu Leu Trp Asp Phe Ser Pro Lys Gly Pro Cys Gly  
 1 5 10 15  
 Ile Lys Phe Met Thr Asn Ser Asp Asn Ala Ser Ala Ala Gly Leu Leu  
 20 25 30  
 Trp Ala His Pro Lys Glu Asp Pro Ala Phe Leu Gly Met Ile Ile Lys  
 35 40 45  
 Glu Phe His Leu Pro Pro Thr Val Ala Gln Ile Phe Ile Ser Arg Gly  
 50 55 60  
 Phe Gln Thr Ile Gln Glu Ile His Lys Phe Leu Tyr Ser His Leu Ser  
 65 70 75 80  
 Ser Leu Tyr Asp Pro Gly Leu Phe Leu Asp Met Ser Lys Ala Val Glu  
 85 90 95  
 Arg Leu Leu Leu Ala Arg Asp Arg Lys Glu His Val Met Ile Tyr Gly  
 100 105 110  
 Asp Ser Asp Val Asp Gly Met Thr Gly Val Ala Leu Leu Val Glu Phe  
 115 120 125  
 Leu Arg Asp Ile Asp Val His Val Ser Tyr Phe Phe Leu Gly Ala Ile  
 130 135 140  
 Leu Lys Gln His Gly Glu Thr Ser Thr Leu Ile Ala Lys Leu Lys Glu  
 145 150 155 160  
 Glu Gly Ile Thr Leu Leu Ile Thr Val Asp Cys Gly Ile Thr Ala Gly

```

165      170      175
Lys Glu Val Ser Asp Ile Thr Arg Gln Gly Ile Asp Val Ile Ile Thr
180      185      190
Asp His His Met Pro Thr Gly Lys Ile Pro His Cys Val Val Thr Leu
195      200      205
Asn Pro Lys Leu Arg Asp His Thr Tyr Pro Asn Arg Glu Leu Thr Gly
210      215      220
Val Gly Val Ala Phe Lys Leu Ala Arg Gly Val Leu Asn Ala Leu Ile
225      230      235
Ser Arg Asn Leu Val Pro Lys Ser Gln Gly Ser Leu Lys Lys Leu Leu
245      250      255
Asp Leu Val Thr Leu Gly Thr Ile Thr Asp Val Gly Val Leu Leu Gly
260      265      270
Glu Asn Arg Val Met Val Arg Tyr Gly Ile Lys Glu Ile Ala Arg Gly
275      280      285
Ala Arg Pro Gly Leu Asn Lys Leu Cys Ala Leu Cys Gly Val Glu Lys
290      295      300
Ser Glu Val Thr Ser Thr Asp Ile Val Leu Lys Ile Ala Pro Lys Leu
305      310      315
Asn Ser Leu Gly Arg Leu Asp Asp Pro Ala Lys Gly Val Glu Leu Leu
325      330      335
Leu Thr Gln Asp Asp Glu Arg Val Asp Ala Leu Ile Met Glu Leu Asp
340      345      350
Asn Ile Asn Arg Glu Arg Gln Arg Ile Glu Ala Glu Val Phe Gln Asp
355      360      365
Val Gln Glu Ile Leu Asn Ser Asn Pro Glu Ile Leu Lys Gln Ala Ala
370      375      380
Ile Val Leu Ser Ser Thr Ala Trp His Ala Arg Val Ile Pro Ile Ile
385      390      395
Ser Ala Arg Leu Ala Lys Thr Tyr Asn Lys Pro Val Val Ile Ile Ala
405      410      415
Ile Gln Arg Gly Ile Gly Lys Gly Ser Ala Arg Thr Ile Gly Ser Phe
420      425      430
Pro Leu Leu Gly Val Leu Lys Lys Cys Ser Ser Leu Leu Leu Ser Tyr
435      440      445
Gly Gly His Asp Phe Ala Ala Gly Val Ile Met Lys Glu Asp Lys Val
450      455      460
Glu Asp Phe Lys Lys Lys Phe Val His Leu Val Asn Ser Ser Leu Lys
465      470      475
Lys Gly Asp Thr Leu Pro His Leu Glu Ile Asp Ala Tyr Ala Asp Phe
485      490      495
Asp Ala Ile Asp Tyr Asp Leu Leu Ala Ser Met Glu Leu Phe Glu Pro
500      505      510
Phe Gly Lys Gly Asn Leu Met Pro Ile Phe Tyr Ser Lys Val Arg Gln
515      520      525
Val Arg Tyr Pro Lys Val Leu Pro Gly Asn His Leu Lys Leu Tyr Leu
530      535      540
Ser Gln Lys Glu Arg Asn Leu Glu Gly Val Ala Ser Val Trp Glu Asp
545      550      555
Thr Leu Met His

```

&lt;210&gt;602

&lt;211&gt;997

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;602

```

Arg Lys Arg Ser Phe Gly Cys Tyr Ile Phe Ser Pro Asn Thr Asp Cys
1      5      10      15
Lys His Phe Ser Lys Gly Ser Val Tyr Ile Leu Leu Lys Gly Leu Arg
20      25      30
Ser Ile Val Ala Lys Tyr Gln Gln Gly Gly Gly Lys Glu Leu Gln Ser
35      40      45
Phe Glu Lys Asp Leu Gln Asn Leu Tyr Asn Cys Phe Ser His Thr Glu
50      55      60

```



Ala Ile Ser Trp Thr Leu Gly Glu Asp Gln Val Leu Glu Ile Arg His  
 65 70 75 80  
 Pro Leu Gln Gln Phe Leu Asp Val Trp Gly Glu Gly Phe Val Ile Gly  
 85 90 95  
 Lys Glu Gly Cys Ala Phe Leu Glu Val Lys Asp Ile Gln Asp Arg Leu  
 100 105 110  
 Ala Thr Val Asn Gln Ile Glu Lys Asn Arg Gln Ser Asp Leu Val Arg  
 115 120 125  
 Trp His Glu Gln Tyr Arg His Ala Lys Cys Ser Met Asp Leu Gln Glu  
 130 135 140  
 Arg Leu Ser Ala Pro Ile Pro Tyr Gln Asn Leu Phe Leu Glu Asn Met  
 145 150 155 160  
 Lys Leu Asn Met Arg Lys Phe Ser Arg Gly Glu Asn Ile Leu Arg Leu  
 165 170 175  
 Gly Ile Asp Phe Val Gly Gly Arg Gln Leu Leu Leu Ser Phe Lys Asp  
 180 185 190  
 His Gln Gly Lys Gln Leu Thr Asp Lys Glu Asp Ile Leu Lys Val Ser  
 195 200 205  
 Asp Glu Leu Cys Ala Arg Leu Asn Lys Leu Gly Val Ser Glu Ile Glu  
 210 215 220  
 Leu Arg Arg Glu Gly Asp Tyr Ile His Leu Ser Val Pro Gly Ser Ser  
 225 230 235 240  
 Thr Ile Ser Ser Ser Glu Ile Leu Gly Thr Ser Lys Met Ser Phe His  
 245 250 255  
 Val Val Asn Glu Arg Phe Ser Ser Tyr Ser Ala Ser Arg Tyr Glu Val  
 260 265 270  
 Gln Arg Phe Leu Asp Tyr Leu Trp Phe Thr Ser Gln Ala Gln Gly Lys  
 275 280 285  
 Thr Ser Pro Glu Glu Ile Asn Thr Phe Ala Ser Ala Leu Phe Asn Glu  
 290 295 300  
 Glu Val Asp Val Pro Pro Ser Val His Glu Ala Ile Thr Lys Leu Lys  
 305 310 315 320  
 Ser Glu Gly Leu Ala Phe Ser Pro Ser Gly Cys Glu Thr Pro Ser Thr  
 325 330 335  
 Asp Leu Asp Thr Thr Phe Ser Met Ile Ala Ile Gly Lys Asp Ala Glu  
 340 345 350  
 Gln Lys Ala Asn Pro Leu Val Ile Val Phe Arg Asn Tyr Ala Leu Asp  
 355 360 365  
 Gly Ala Ser Leu Lys Asp Ile Arg Pro Glu Phe Ala Ala Gly Glu Gly  
 370 375 380  
 Tyr Val Leu Asn Phe Ser Val Lys Asp Thr Ser Pro Lys Lys Met Ala  
 385 390 395 400  
 Glu Lys Leu Ser Pro Thr Glu Ser Phe His Thr Trp Thr Ser Ala Tyr  
 405 410 415  
 Cys Gln Glu Gly Ile Ser Gly Thr Ala Asn Gly Gln Tyr Ser Ala Asn  
 420 425 430  
 Arg Gly Trp Arg Met Ala Val Val Ile Asp Gly Tyr Met Val Ser Ser  
 435 440 445  
 Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser Val Ser Gly Lys  
 450 455 460  
 Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp Leu Lys Ser Gly  
 465 470 475 480  
 Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu Thr Ile Ser Ser  
 485 490 495  
 Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile Ser Ala Cys Cys  
 500 505 510  
 Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr Tyr Arg Phe Gly  
 515 520 525  
 Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu Leu Leu Ile Trp  
 530 535 540  
 Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu Ser Gly Leu Ala  
 545 550 555 560  
 Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala Asn Val Leu Val  
 565 570 575

Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln Ser Leu Lys Lys  
 580 585 590  
 Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala Ile Phe Asp Ser  
 595 600 605  
 Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe Phe Leu Asp Thr  
 610 615 620  
 Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu Gly Ile Phe Ser  
 625 630 635 640  
 Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe Phe Met Leu Trp  
 645 650 655  
 Met Asn Lys Thr Gln His Thr Gln Leu His Met Met Asn Lys Phe Val  
 660 665 670  
 Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys Leu Trp Ala Val  
 675 680 685  
 Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu Gly Phe Gly Ala  
 690 695 700  
 Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly Tyr Ala Phe Thr  
 705 710 715 720  
 Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala Gln Met Arg Gly  
 725 730 735  
 Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser Ser Arg Asp Phe  
 740 745 750  
 Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys Ile Tyr Phe Ser  
 755 760 765  
 Asp Lys Ala Leu Ser Tyr Thr Lys Ala Asp Thr Ser Leu Ser Pro Lys  
 770 775 780  
 Ile Asn Asp His Glu Leu Ala Leu Ala Val Gly Leu Leu Ser Glu Thr  
 785 790 795 800  
 Gly Leu Asp Phe Ser Thr Glu Thr Leu Asn Glu Thr Gln Asn Phe Trp  
 805 810 815  
 Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr Gln Ala Thr  
 820 825 830  
 Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr Val Ser Leu  
 835 840 845  
 Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala Leu Ile His  
 850 855 860  
 Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His Phe Phe Leu  
 865 870 875 880  
 Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu Met Thr Val  
 885 890 895  
 Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp Arg Ile Arg  
 900 905 910  
 Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val Leu Val Asn  
 915 920 925  
 Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr Thr Ala Thr  
 930 935 940  
 Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly Ser Ser Val  
 945 950 955 960  
 Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu Gly Thr Leu  
 965 970 975  
 Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys  
 980 985 990  
 Glu Asn Arg Ser Lys  
 995  
 <210>603  
 <211>435  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>603  
 Ser Gly Ala Met Lys Gln Lys Val Lys Arg Asn Phe Ala Ile Ile Ile  
 1 5 10 15  
 Cys Val Phe Ala Leu Ala Leu Tyr Tyr Val Leu Pro Thr Cys Leu Tyr  
 20 25 30  
 Tyr Ala Lys Pro Leu Asp Lys Lys Ile Asp Gly Asn Glu Ala Glu His

35 40 45  
 Ile Ile Lys Ser Phe Thr Lys Gln Ala Gln Gln Val Arg Lys Asp Val  
 50 55 60  
 Ile Pro Arg Val Ser Ala Ile Leu Ser Ser Leu His Leu Arg Gly His  
 65 70 75 80  
 Ile Gln Gln His Pro Ala Ile Pro Asp Ile Val Ser Val Arg Phe Lys  
 85 90 95  
 Arg Gly Glu Asp Ala Glu Asp Phe Ile Gly Asn Leu Val His Gly Glu  
 100 105 110  
 Pro Asn Val Pro Ile Lys Ser Ala Arg Leu His Val Val Gly Tyr Ser  
 115 120 125  
 Arg Glu His Asp Asp His Val Ile Gln Val Ala Ser Ser Ile Asn Thr  
 130 135 140  
 Ser Leu Val Glu Ser Asp Phe Ser Phe Val Ser Tyr Ser Ser Glu Asn  
 145 150 155 160  
 Glu Gln Glu Met Ala Ser Ser Ile Leu Gln Arg Val Tyr Ser Ala Cys  
 165 170 175  
 Thr Cys Pro Lys Gln Lys Asp Cys Ser Cys Ser Tyr Pro Ser Ile Trp  
 180 185 190  
 Glu Thr Ala Pro Lys Glu Gln Leu Leu Gln Tyr Ala Lys Asn Leu Ser  
 195 200 205  
 Ser Gly Phe Glu Val Phe Ser Ser Arg Leu Ser Ala Phe Cys Gln Gln  
 210 215 220  
 Ser Phe Ser Ser Asn Gln Asp Arg Leu Ala Phe Leu Ser Arg Leu Ser  
 225 230 235 240  
 Ser Leu Ser Asn Asp Ala Ala Ile Asp Val Glu Asp Gln Lys Leu Leu  
 245 250 255  
 Lys Ser Val Tyr Glu Thr Leu Ser Gln Thr Ala Cys Ile Arg Ser Leu  
 260 265 270  
 Asp Cys Pro Tyr Ile Glu Gly Leu Arg Leu Asp Cys Ser Glu Ser Ser  
 275 280 285  
 Leu Phe Phe Ser Ser Ile Glu Tyr Cys Pro Lys Glu Arg Lys Ile Phe  
 290 295 300  
 Leu Thr Leu His Ser Asp Leu Leu Ala Gln Arg Thr Ser Leu Ser Lys  
 305 310 315 320  
 Glu Gln Arg Leu Asp Phe Asp Ser Arg Leu Ala Val Glu Lys Gln Lys  
 325 330 335  
 Leu Ser Lys Asn Leu Thr Val Gln Val Glu Asp Tyr Asn Asn Gly Phe  
 340 345 350  
 Ser Phe Gln Trp Met Asp Lys Asp Thr Gln Gly Lys Ile Ile Leu Gln  
 355 360 365  
 Gly Glu Arg Leu Leu Gln Gly Ile Ala Glu His Leu Thr Ala Leu Thr  
 370 375 380  
 Leu His Arg Pro Ala Ala Glu Ser Cys Asp Leu Ile Pro Glu Asn Phe  
 385 390 395 400  
 Pro Val Phe Cys Arg Gln Pro Arg Glu Ser Glu Val Leu Ala Val Thr  
 405 410 415  
 Ser Phe Leu Pro Ile Gln Ile Ala Asn Thr Phe Leu Lys Ala Pro Phe  
 420 425 430  
 Thr Ser Tyr  
 435

&lt;210&gt;604

&lt;211&gt;367

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;604

Tyr Glu Ile Ser Ser His Ile His Phe Arg Phe Asp Ser His Ser Asn  
 1 5 10 15  
 Gly His Leu Val Ala Ala Glu Xaa Gly Asn Val His Tyr Val Pro Asn  
 20 25 30  
 Ala Gln Asn Leu Pro Lys Lys Ile Leu Gly Gly Val Leu Ala Cys Phe  
 35 40 45  
 Gly Leu Ala Leu Leu Gly Cys Ala Ala Phe Ala Ala Gly Val Cys Gln  
 50 55 60

Thr Ile Phe Pro Cys Ile Gly Leu Met Ile Leu Gly Leu Val Leu Leu  
 65 70 75 80  
 Gly Phe Ala Tyr Leu Gln Tyr Ser Lys Gly Trp Ser Arg Phe Glu Arg  
 85 90 95  
 Pro Leu Phe Arg Glu Thr Lys Val Phe Glu Lys Pro Ile Asn Trp Leu  
 100 105 110  
 Gly Cys Leu Ser Leu Leu Gln Ser Trp Lys Lys Ile Arg Pro Gly Cys  
 115 120 125  
 Tyr Tyr His Pro Gly Cys Pro Gln Val Glu Ile Cys Glu Gly Ser Gln  
 130 135 140  
 Glu Ile Val Thr Lys Ile Phe Gln Lys Lys Ser Asp Arg Asn Thr Ser  
 145 150 155 160  
 Ile Phe Leu Ile Gln Glu Met Asp Gln Ile Ala Leu Arg Gln Gly Ile  
 165 170 175  
 Glu Lys Ser Ser Leu Ser Arg Lys Thr Phe Ala Ile Asp Pro Ser Val  
 180 185 190  
 Val Ser Ser Leu Leu Ser Glu Ile Gln Arg Glu Glu Gln Tyr Leu  
 195 200 205  
 Asp Pro Lys Val Ile Ser Trp Ser Ser Glu Asp Gln Ala Ser Asp Arg  
 210 215 220  
 Thr His Pro Lys Ser Ala Ile Tyr Val Asn Ile Ser Asp Ala Ala Gln  
 225 230 235 240  
 Glu Pro Gln Gly Arg Cys Tyr Ile Asp Ala Tyr Thr Lys Ala Phe Phe  
 245 250 255  
 Thr Val Leu Asp Gln Ile Gly Asp Pro Asn Ile Val Lys Lys His Thr  
 260 265 270  
 Ile Tyr Val Leu Thr Pro Ile Leu Gly Val Pro Asp Ala Leu Pro Lys  
 275 280 285  
 Glu Glu Gln Glu Asn Leu Lys Leu Leu Ser Gln Ala Ala Phe Leu Tyr  
 290 295 300  
 Ser Ala Glu Gln Val Ala Lys Arg Met Arg Glu Glu Lys Gln Asp Ser  
 305 310 315 320  
 Ile Arg Ile Lys Phe Ile Phe Thr Asp Pro Thr Ser Pro Thr Ser Leu  
 325 330 335  
 Tyr Phe Ser Pro His His Ser Ser Thr Pro His Ser Val Thr Pro Ile  
 340 345 350  
 Ser Leu Ser Gly Phe Val Gly Glu Gln Glu Ser Tyr Thr Phe Ala  
 355 360 365

&lt;210&gt;605

&lt;211&gt;261

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;605

Val Thr Tyr Ala Leu Ile Asn Asp Pro Val Asp Leu Ser Leu Ala Thr  
 1 5 10 15  
 Asn Asn Ala Glu Ser Lys Phe Pro Ser Leu Gln Arg Leu Pro Asn His  
 20 25 30  
 Val Ala Ile Ile Met Asp Gly Asn Arg Arg Trp Tyr Lys Lys His Arg  
 35 40 45  
 Glu Glu Cys Gly His Thr His Thr Ser Gly His Tyr Tyr Gly Ala Lys  
 50 55 60  
 Val Leu Pro Asn Ile Leu Asn Ala Val Leu Asp Leu Gly Ile Lys Val  
 65 70 75 80  
 Leu Thr Leu Tyr Thr Phe Ser Thr Glu Asn Phe Gly Arg Pro Lys Glu  
 85 90 95  
 Glu Ile Gln Glu Ile Phe Asn Ile Phe Tyr Thr Gln Leu Asp Lys Gln  
 100 105 110  
 Leu Pro Tyr Leu Met Glu Asn Glu Ile Cys Leu Arg Cys Ile Gly Asp  
 115 120 125  
 Leu Ser Lys Leu Pro Lys Gly Ile Gln Thr Lys Ile Asn His Val Ser  
 130 135 140  
 Arg Met Thr Ala Ser Phe Ser Arg Leu Glu Leu Val Leu Ala Val Asn  
 145 150 155 160  
 Tyr Gly Gly Lys Asp Glu Leu Val Arg Ala Phe Lys Lys Leu His Val

```

      165      170      175
Asp Ile Leu Asn Lys Lys Ile Ser Ser Asp Asp Leu Ser Glu Ser Leu
      180      185      190
Ile Ser Ser Tyr Leu Asp Thr Ser Gly Leu Thr Asp Pro Asp Leu Leu
      195      200      205
Ile Arg Thr Gly Gly Glu Met Arg Val Ser Asn Phe Leu Leu Trp Gln
      210      215      220
Ile Ala Tyr Thr Glu Leu Tyr Ile Thr Asp Thr Leu Trp Pro Asp Phe
225      230      235
Thr Pro Gln Asp Leu Phe Glu Ala Ile Asn Val Tyr Gln Gln Arg Ser
      245      250      255
Arg Arg Gly Gly Lys
      260
<210>606
<211>308
<212>PRT
<213>Chlamydia pneumoniae
<400>606
Val Leu Asn Ser Asn Lys Phe Lys Ser Lys Thr Gly Ala Tyr Gly Asp
 1      5      10      15
Leu Phe Gln Arg Val Val Val His Ser Leu Val Leu Thr Phe Leu Val
      20      25      30
Leu Leu Leu Tyr Ser Ser Leu Phe Pro Leu Thr Ser Phe Ala Leu Gly
      35      40      45
Phe Ile Thr Ala Thr Cys Gly Ala Val Gly Thr Tyr Glu Tyr Ser Ser
      50      55      60
Met Ala Lys Ala Lys Met His Tyr Pro Leu Ser Thr Phe Ser Ala Ile
      65      70      75      80
Gly Ser Phe Leu Phe Leu Ala Leu Ser Phe Leu Ser Ile Arg Trp Gly
      85      90      95
His Ser Leu Pro Gly Phe Phe Asp Ala Leu Pro Trp Thr Leu Leu Ile
      100      105      110
Val Trp Val Val Trp Ser Ile Phe Arg Val Arg Lys Ser Thr Ile Gly
      115      120      125
Ala Leu Gln Leu Ser Gly Val Thr Leu Phe Ser Ile Leu Tyr Val Gly
      130      135      140
Ile Pro Ile Arg Leu Phe Leu His Val Leu Tyr Ser Phe Ile His Thr
145      150      155      160
Gln Glu Pro Tyr Leu Gly Ile Trp Trp Ala Ser Phe Leu Ile Ala Thr
      165      170      175
Thr Lys Gly Ala Asp Ile Phe Gly Tyr Phe Phe Gly Lys Ala Phe Gly
      180      185      190
Asn Lys Lys Ile Ala Pro Gln Ile Ser Pro Asn Lys Thr Val Val Gly
      195      200      205
Phe Val Ala Gly Cys Leu Gly Ala Thr Leu Ile Ser Phe Ile Phe Phe
      210      215      220
Leu Gln Ile Pro Thr Arg Phe Ala Ser Tyr Phe Pro Met Pro Ala Ile
225      230      235      240
Leu Ile Pro Leu Gly Leu Ala Leu Gly Ile Thr Gly Phe Phe Gly Asp
      245      250      255
Ile Ile Glu Ser Ile Phe Lys Arg Asp Ala His Leu Lys Asn Ser Asn
      260      265      270
Lys Leu Lys Ala Val Gly Gly Met Leu Asp Thr Leu Asp Ser Leu Leu
      275      280      285
Leu Ser Thr Pro Ile Ala Tyr Leu Phe Leu Leu Ile Thr Gln Ser Lys
      290      295      300
Glu Phe Ile Gly
305
<210>607
<211>220
<212>PRT
<213>Chlamydia pneumoniae
<400>607
Arg Val Tyr Trp Met Ile Ile Thr Ile Asp Gly Pro Ser Gly Thr Gly

```

1 5 10 15  
 Lys Ser Thr Thr Ala Lys Ala Leu Ala Asp His Leu His Phe Asn Tyr  
 20 25 30  
 Cys Asn Thr Gly Lys Met Tyr Arg Thr Leu Ala Tyr Ala Arg Leu Gln  
 35 40 45  
 Ser Pro Trp Ala Thr Leu Pro Leu Thr Lys Phe Leu Glu Glu Pro Pro  
 50 55 60  
 Phe Ser Phe Thr Phe Ala Thr Gly Gln Pro Leu Glu Ser Phe Phe Asn  
 65 70 75 80  
 Gly His Leu Leu Thr Ser Glu Leu Thr Thr Gln Glu Val Ala Asn Ala  
 85 90 95  
 Ala Ser Glu Leu Ser Gln Leu Pro Glu Val Arg Ala Phe Met Gln Asp  
 100 105 110  
 Leu Gln Arg Arg Tyr Ala Gln Leu Gly Asn Cys Val Phe Glu Gly Arg  
 115 120 125  
 Asp Met Gly Ser Lys Val Phe Pro Asn Ala Asp Leu Lys Ile Phe Leu  
 130 135 140  
 Thr Ser Ser Pro Glu Val Arg Ala Gln Arg Arg Leu Lys Asp Leu Pro  
 145 150 155 160  
 Glu Gly Thr Leu Ser Pro Glu Gln Leu Gln Ala Glu Leu Val Lys Arg  
 165 170 175  
 Asp Ala Ala Asp Ala Gln Arg Ala His Asp Pro Leu Val Ile Pro Glu  
 180 185 190  
 Asn Gly Ile Val Ile Asp Ser Ser Asp Leu Thr Ile Arg Gln Val Leu  
 195 200 205  
 Glu Lys Ile Leu Ala Leu Leu Phe Arg Asn Glu Leu  
 210 215 220  
 <210>608  
 <211>234  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>608  
 Leu Phe Gly Phe Asp Asn Lys Thr Ser Ser Gly Glu Asn Phe Ser Phe  
 1 5 10 15  
 Thr Ile Ser Lys Arg Ala Met Ile Phe Arg Ile Cys Lys Phe Phe Thr  
 20 25 30  
 Trp Val Ala Phe Ser Leu Phe Tyr Lys Leu Lys Val Tyr Gly Val Lys  
 35 40 45  
 Lys Asn Phe Ile Lys Gly Pro Ala Ile Ile Ala Val Asn His Asn Ser  
 50 55 60  
 Phe Leu Asp Pro Ile Ala Leu His Met Cys Val His Glu Cys Ile Tyr  
 65 70 75 80  
 His Leu Ala Arg Ala Ser Leu Phe Asn Ile Pro Trp Leu Trp Lys Gln  
 85 90 95  
 Trp Gly Cys Phe Pro Val Arg Gln Asp Glu Gly Asn Ser Ala Ala Phe  
 100 105 110  
 Lys Ile Ala Ser Arg Leu Phe Asn Lys Arg Lys Lys Leu Val Ile Tyr  
 115 120 125  
 Pro Glu Gly Ala Arg Ser Pro Asp Gly Gln Leu Gln Pro Gly Lys Val  
 130 135 140  
 Gly Ile Gly Met Met Ala Ala Lys Ser Arg Val Pro Ile Ile Pro Val  
 145 150 155 160  
 Tyr Ile Arg Gly Thr Phe Glu Ala Phe Asn Arg His Gln Lys Ile Pro  
 165 170 175  
 His Val Trp Lys Thr Ile Thr Cys Val Phe Gly Thr Pro Met Tyr Phe  
 180 185 190  
 Asp Asp Ile Ile Gln Asn Pro Glu Ile Lys Asn Lys Glu Thr Tyr Gln  
 195 200 205  
 Ile Ile Thr Asn Gln Thr Met Asn Lys Ile Ala Glu Leu Lys Ala Trp  
 210 215 220  
 Tyr Glu Ser Gly Cys Lys Gly Asp Val Pro  
 225 230  
 <210>609  
 <211>580

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;609

Leu Pro Ser Ser Lys His Gly Met Asn Arg Gly Ala Lys Glu Thr Ser  
 1 5 10 15  
 Pro Lys Leu Met Ser Thr Leu Leu Ser Ile Leu Ser Val Ile Cys Ser  
 20 25 30  
 Gln Ala Ile Ala Lys Ala Phe Pro Asn Leu Glu Asp Trp Ala Pro Glu  
 35 40 45  
 Ile Thr Pro Ser Thr Lys Glu His Phe Gly His Tyr Gln Cys Asn Asp  
 50 55 60  
 Ala Met Lys Leu Ala Arg Val Leu Lys Lys Ala Pro Arg Ala Ile Ala  
 65 70 75 80  
 Glu Ala Ile Val Ala Glu Leu Pro Gln Glu Pro Phe Ser Leu Ile Glu  
 85 90 95  
 Ile Ala Gly Ala Gly Phe Ile Asn Phe Thr Phe Ser Pro Val Phe Leu  
 100 105 110  
 Asn Gln Gln Leu Glu His Phe Lys Asp Ala Leu Lys Leu Gly Phe Gln  
 115 120 125  
 Val Ser Gln Pro Lys Xaa Ile Ile Ile Asp Phe Ser Ser Pro Asn Ile  
 130 135 140  
 Ala Lys Asp Met His Val Gly His Leu Arg Ser Thr Ile Ile Gly Asp  
 145 150 155 160  
 Ser Leu Ala Arg Ile Phe Ser Tyr Val Gly His Asp Val Leu Arg Leu  
 165 170 175  
 Asn His Ile Gly Asp Trp Gly Thr Ala Phe Gly Met Leu Ile Thr Tyr  
 180 185 190  
 Leu Gln Glu Asn Pro Cys Asp Tyr Ser Asp Leu Glu Asp Leu Thr Ser  
 195 200 205  
 Leu Tyr Lys Lys Ala Tyr Val Cys Phe Thr Asn Asp Glu Glu Phe Lys  
 210 215 220  
 Lys Arg Ser Gln Gln Asn Val Val Ala Leu Gln Ala Lys Asp Pro Gln  
 225 230 235 240  
 Ala Ile Ala Ile Trp Glu Lys Ile Cys Glu Thr Ser Glu Lys Ala Phe  
 245 250 255  
 Gln Lys Ile Tyr Asp Ile Leu Asp Ile Val Val Glu Lys Arg Gly Glu  
 260 265 270  
 Ser Phe Tyr Asn Pro Phe Leu Pro Glu Ile Ile Glu Asp Leu Glu Lys  
 275 280 285  
 Lys Gly Leu Leu Thr Val Ser Asn Asp Ala Lys Cys Val Phe His Glu  
 290 295 300  
 Ala Phe Ser Ile Pro Phe Met Val Gln Lys Ser Asp Gly Gly Tyr Asn  
 305 310 315 320  
 Tyr Ala Thr Thr Asp Leu Ala Ala Met Arg Tyr Arg Ile Glu Glu Asp  
 325 330 335  
 His Ala Asp Lys Ile Ile Ile Val Thr Asp Leu Gly Gln Ser Leu His  
 340 345 350  
 Phe Gln Leu Leu Glu Ala Thr Ala Ile Ala Ala Gly Tyr Leu Gln Pro  
 355 360 365  
 Gly Ile Phe Ser His Val Gly Phe Gly Leu Val Leu Asp Pro Gln Gly  
 370 375 380  
 Lys Lys Leu Lys Thr Arg Ser Gly Glu Asn Val Lys Leu Arg Glu Leu  
 385 390 395 400  
 Leu Asp Thr Ala Ile Glu Lys Ala Glu Glu Ala Leu Arg Glu His Arg  
 405 410 415  
 Pro Glu Leu Thr Asp Glu Ala Ile Gln Glu Arg Ala Pro Val Ile Gly  
 420 425 430  
 Ile Asn Ala Ile Lys Tyr Ser Asp Leu Ser Ser His Arg Thr Ser Asp  
 435 440 445  
 Tyr Val Phe Ser Phe Glu Lys Met Leu Arg Phe Glu Gly Asn Thr Ala  
 450 455 460  
 Met Phe Leu Leu Tyr Ala Tyr Val Arg Ile Gln Gly Ile Lys Arg Arg  
 465 470 475 480  
 Leu Gly Ile Ser Gln Leu Ser Leu Glu Gly Pro Pro Glu Ile Gln Glu

485 490 495  
 Pro Ala Glu Glu Leu Leu Ala Leu Thr Leu Leu Arg Phe Pro Glu Ala  
 500 505 510  
 Leu Glu Ser Thr Ile Lys Glu Leu Cys Pro His Phe Leu Thr Asp Tyr  
 515 520 525  
 Leu Tyr Asn Leu Thr His Lys Phe Asn Gly Phe Phe Arg Asp Ser His  
 530 535 540  
 Ile Gln Asp Ser Pro Tyr Ala Lys Ser Arg Leu Phe Leu Cys Ala Leu  
 545 550 555 560  
 Ala Glu Gln Val Leu Ala Thr Gly Met His Leu Leu Gly Leu Lys Thr  
 565 570 575  
 Leu Glu Arg Leu  
 580  
 <210>610  
 <211>458  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>610  
 Met Gln Ile Ala Gln Val Phe Gly Cys Gly Arg Leu Asn Gly Glu Val  
 1 5 10 15  
 Lys Val Ser Gly Ala Lys Asn Ala Ala Thr Lys Leu Leu Val Ala Ser  
 20 25 30  
 Leu Leu Ser Asp Gln Lys Cys Thr Leu Arg Asn Val Pro Asp Ile Gly  
 35 40 45  
 Asp Val Ser Leu Thr Val Glu Leu Cys Lys Ser Leu Gly Ala His Val  
 50 55 60  
 Ser Trp Asp Lys Glu Thr Glu Val Leu Glu Ile Tyr Thr Pro Glu Ile  
 65 70 75 80  
 Gln Cys Thr Arg Val Pro Pro Thr Phe Ser Asn Val Asn Arg Ile Pro  
 85 90 95  
 Ile Leu Leu Leu Gly Ala Leu Leu Gly Arg Cys Pro Glu Gly Val Tyr  
 100 105 110  
 Val Pro Thr Val Gly Gly Asp Ala Ile Gly Glu Arg Thr Leu Asn Phe  
 115 120 125  
 His Phe Glu Gly Leu Lys Gln Leu Gly Val Gln Ile Ser Ser Asp Ser  
 130 135 140  
 Ser Gly Tyr Tyr Ala Lys Ala Pro Arg Gly Leu Lys Gly Asn Tyr Ile  
 145 150 155 160  
 His Leu Pro Tyr Pro Ser Val Gly Ala Thr Glu Asn Leu Ile Leu Ala  
 165 170 175  
 Ala Ile His Ala Lys Gly Arg Thr Val Ile Lys Asn Val Ala Leu Glu  
 180 185 190  
 Ala Glu Ile Leu Asp Leu Val Leu Phe Leu Gln Lys Ala Gly Ala Asp  
 195 200 205  
 Ile Thr Thr Asp Asn Asp Arg Thr Ile Asp Ile Phe Gly Thr Gly Gly  
 210 215 220  
 Leu Gly Ser Val Asp His Thr Ile Leu Pro Asp Lys Ile Glu Ala Ala  
 225 230 235 240  
 Ser Phe Gly Met Ala Ala Val Val Ser Gly Gly Arg Val Phe Val Arg  
 245 250 255  
 Asn Ala Lys Gln Glu Leu Leu Ile Pro Phe Leu Lys Met Leu Arg Ser  
 260 265 270  
 Ile Gly Gly Gly Phe Leu Val Ser Glu Ser Gly Ile Glu Phe Phe Gln  
 275 280 285  
 Glu Arg Pro Leu Val Gly Gly Val Val Leu Glu Thr Asp Val His Pro  
 290 295 300  
 Gly Phe Leu Thr Asp Trp Gln Gln Pro Phe Ala Val Leu Leu Ser Gln  
 305 310 315 320  
 Ala Gln Gly Ser Ser Val Ile His Glu Thr Val His Glu Asn Arg Leu  
 325 330 335  
 Gly Tyr Leu His Gly Leu Gln His Met Gly Ala Glu Cys Gln Leu Phe  
 340 345 350  
 His Gln Cys Leu Ser Thr Lys Ala Cys Arg Tyr Ala Ile Gly Asn Phe  
 355 360 365



Pro His Ser Ala Val Ile His Gly Ala Thr Pro Leu Trp Ala Ser His  
 370 375 380  
 Leu Val Ile Pro Asp Leu Arg Ala Gly Phe Ala Tyr Val Met Ala Ala  
 385 390 395 400  
 Leu Ile Ala Glu Gly Gly Gly Ser Ile Ile Glu Asn Thr His Leu Leu  
 405 410 415  
 Asp Arg Gly Tyr Thr Asn Trp Val Gly Lys Leu Arg Ser Leu Gly Ala  
 420 425 430  
 Lys Ile Gln Ile Phe Asp Met Glu Gln Glu Glu Leu Thr Thr Ser Pro  
 435 440 445  
 Lys Ser Leu Ala Leu Arg Asp Ala Ser Leu  
 450 455

&lt;210&gt;611

&lt;211&gt;96

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;611

His Asn Asp Met Pro Trp Tyr Leu Ser Thr Asp Glu Lys Ala Asp Thr  
 1 5 10 15  
 Gln Leu Pro Cys Ala Glu Asp His Glu Gly Ser Arg Gly Asp Phe His  
 20 25 30  
 Gly Gln Ser His Gly Leu Leu Lys Ile Pro Glu Pro Val Ile Val Glu  
 35 40 45  
 Leu Arg Arg Val Val Ala Ser Pro Ser Gly Thr Leu Asp Glu His Arg  
 50 55 60  
 Phe Pro Arg Gln His Leu Pro Pro Arg Gly Val Leu Glu Lys Ile Leu  
 65 70 75 80  
 Phe Pro Thr Arg Arg Pro Lys Ile Leu Arg Leu Trp Ser Ala Thr Ser  
 85 90 95

&lt;210&gt;612

&lt;211&gt;183

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;612

Ile Met Ala Ala Pro Ile Asn Gln Pro Ser Thr Thr Thr Gln Ile Thr  
 1 5 10 15  
 Gln Thr Gly Gln Thr Thr Thr Thr Thr Thr Val Gly Ser Leu Gly Glu  
 20 25 30  
 His Ser Val Thr Thr Thr Gly Ser Gly Ala Ala Ala Gln Thr Ser Gln  
 35 40 45  
 Thr Val Thr Leu Ile Ala Asp His Glu Met Gln Asp Ile Ala Ser Gln  
 50 55 60  
 Asp Gly Ser Ala Val Ser Phe Ser Ala Glu His Ser Phe Ser Thr Leu  
 65 70 75 80  
 Pro Pro Glu Thr Gly Ser Val Gly Ala Thr Ala Gln Ser Ala Gln Ser  
 85 90 95  
 Ala Gly Leu Phe Ser Leu Ser Gly Arg Thr Gln Arg Arg Asp Ser Glu  
 100 105 110  
 Ile Ser Ser Ser Ser Asp Gly Ser Ser Ile Ser Arg Thr Ser Ser Asn  
 115 120 125  
 Ala Ser Ser Gly Glu Thr Ser Arg Ala Glu Ser Ser Pro Asp Leu Gly  
 130 135 140  
 Asp Leu Asp Ser Leu Ser Gly Ser Glu Arg Ala Glu Gly Ala Glu Asp  
 145 150 155 160  
 Leu Lys Asp Leu Glu Ala Tyr Leu Lys Val Arg Phe His Ile Met Ile  
 165 170 175  
 Leu Pro Ile Lys Arg Leu Phe  
 180

&lt;210&gt;613

&lt;211&gt;550

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;613

Met Lys Pro Arg Ser Ser Phe Ile Phe Val Arg Asn Gly Asp Trp Ser

1	5	10	15
Thr Ala Glu Ser Ile Lys Val Ser Asn Ala Lys Thr Lys Glu Asn Ile			
20	25	30	
Thr Lys Pro Ala Asp Leu Glu Met Cys Ile Ala Lys Phe Cys Val Gly			
35	40	45	
Tyr Glu Thr Ile His Ser Asp Trp Thr Gly Arg Val Lys Pro Thr Met			
50	55	60	
Glu Glu Arg Ser Gly Ala Thr Gly Asn Tyr Asn His Leu Met Leu Ser			
65	70	75	80
Met Lys Phe Lys Thr Ala Val Val Tyr Gly Pro Trp Asn Ala Lys Glu			
85	90	95	
Ser Ser Ser Gly Tyr Thr Pro Ser Ala Trp Arg Arg Gly Ala Lys Val			
100	105	110	
Glu Thr Gly Pro Ile Trp Asp Asp Val Gly Gly Leu Lys Gly Ile Asn			
115	120	125	
Trp Lys Thr Thr Pro Ala Pro Asp Phe Ser Phe Ile Asn Glu Thr Pro			
130	135	140	
Gly Gly Gly Ala His Ser Thr Ser His Thr Gly Pro Gly Thr Pro Val			
145	150	155	160
Gly Ala Thr Val Val Pro Asn Val Asn Val Asn Leu Gly Gly Ile Lys			
165	170	175	
Val Asp Leu Gly Gly Ile Asn Leu Gly Gly Ile Thr Thr Asn Val Thr			
180	185	190	
Thr Glu Glu Gly Gly Gly Thr Asn Ile Thr Ser Thr Lys Ser Thr Ser			
195	200	205	
Thr Asp Asp Lys Val Ser Ile Thr Ser Thr Gly Ser Gln Ser Thr Ile			
210	215	220	
Glu Glu Asp Thr Ile Gln Phe Asp Asp Pro Gly Gln Gly Glu Asp Asp			
225	230	235	240
Asn Ala Ile Pro Gly Thr Asn Thr Pro Pro Pro Pro Gly Pro Pro Pro			
245	250	255	
Asn Leu Ser Ser Ser Arg Leu Leu Thr Ile Ser Asn Ala Ser Leu Asn			
260	265	270	
Gln Val Leu Gln Asn Val Arg Gln His Leu Asn Thr Ala Tyr Asp Ser			
275	280	285	
Asn Gly Asn Ser Val Ser Asp Leu Asn Gln Asp Leu Gly Gln Val Val			
290	295	300	
Lys Asn Ser Glu Asn Gly Val Asn Phe Pro Thr Val Ile Leu Pro Lys			
305	310	315	320
Thr Thr Gly Asp Thr Asp Pro Ser Gly Gln Ala Thr Gly Gly Val Thr			
325	330	335	
Glu Gly Gly Gly His Ile Arg Asn Ile Ile Gln Arg Asn Thr Gln Ser			
340	345	350	
Thr Gly Gln Ser Glu Gly Ala Thr Pro Thr Pro Gln Pro Thr Ile Ala			
355	360	365	
Lys Ile Val Thr Ser Leu Arg Lys Ala Asn Val Ser Ser Ser Ser Val			
370	375	380	
Leu Pro Gln Pro Gln Val Ala Thr Thr Ile Thr Pro Gln Ala Arg Thr			
385	390	395	400
Ala Ser Thr Ser Thr Thr Ser Ile Gly Thr Gly Thr Glu Ser Thr Ser			
405	410	415	
Thr Thr Ser Thr Gly Thr Gly Thr Gly Ser Val Ser Thr Gln Ser Thr			
420	425	430	
Gly Val Gly Thr Pro Thr Thr Thr Thr Arg Ser Thr Gly Thr Ser Ala			
435	440	445	
Thr Thr Thr Thr Ser Ser Ala Ser Thr Gln Thr Pro Gln Ala Pro Leu			
450	455	460	
Pro Ser Gly Thr Arg His Val Ala Thr Ile Ser Leu Val Arg Asn Ala			
465	470	475	480
Ala Gly Arg Ser Ile Val Leu Gln Gln Gly Gly Arg Ser Gln Ser Phe			
485	490	495	
Pro Ile Pro Pro Ser Gly Thr Gly Thr Gln Asn Met Gly Ala Gln Leu			
500	505	510	
Trp Ala Ala Ala Ser Gln Val Ala Ser Thr Leu Gly Gln Val Val Asn			

515 520 525  
 Gln Ala Ala Thr Ala Gly Ser Gln Pro Ser Ser Arg Arg Ser Ser Pro  
 530 535 540  
 Thr Ser Pro Arg Arg Lys  
 545 550  
 <210>614  
 <211>96  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>614  
 Asp Arg Pro Pro Cys Cys Asn Thr Ile Asp Leu Pro Ala Ala Leu Arg  
 1 5 10 15  
 Thr Lys Glu Ile Val Ala Thr Cys Leu Val Pro Glu Gly Arg Gly Ala  
 20 25 30  
 Trp Gly Val Cys Val Glu Ala Asp Asp Val Val Val Val Ala Glu Val  
 35 40 45  
 Pro Val Asp Arg Val Val Val Val Gly Val Pro Thr Pro Val Leu Cys  
 50 55 60  
 Val Glu Thr Leu Pro Val Pro Val Pro Val Leu Val Val Asp Val Leu  
 65 70 75 80  
 Ser Val Pro Val Pro Met Leu Val Val Asp Val Leu Ala Val Leu Ala  
 85 90 95  
 <210>615  
 <211>241  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>615  
 Val Glu Asp Met Ala Gly His Ser Lys Trp Ala Asn Thr Lys His Arg  
 1 5 10 15  
 Lys Glu Arg Ala Asp His Lys Lys Gly Lys Ile Phe Ser Arg Ile Ile  
 20 25 30  
 Lys Glu Leu Ile Ser Ala Val Lys Leu Gly Gly Ala Asp Pro Lys Ser  
 35 40 45  
 Asn Ala Arg Leu Arg Met Val Ile Gln Lys Ala Lys Glu Asn Asn Ile  
 50 55 60  
 Pro Asn Glu Asn Ile Glu Arg Asn Leu Lys Lys Ala Thr Ser Ala Glu  
 65 70 75 80  
 Gln Lys Asn Phe Glu Glu Val Thr Tyr Glu Leu Tyr Gly His Gly Gly  
 85 90 95  
 Val Gly Ile Ile Val Glu Ala Met Thr Asp Asn Lys Asn Arg Thr Ala  
 100 105 110  
 Ser Asp Met Arg Ile Ala Ile Asn Lys Arg Gly Gly Ser Leu Val Glu  
 115 120 125  
 Pro Gly Ser Val Leu Tyr Asn Phe Ala Arg Lys Gly Ala Cys Thr Val  
 130 135 140  
 Ala Lys Ser Ser Ile Asp Glu Glu Val Ile Phe Ser Tyr Ala Ile Glu  
 145 150 155 160  
 Ala Gly Ala Glu Asp Leu Asp Thr Glu Asp Glu Glu Asn Phe Leu Val  
 165 170 175  
 Ile Cys Ala Pro Ser Glu Leu Ala Ser Val Lys Glu Lys Leu Ile Ser  
 180 185 190  
 Gln Gly Ala Thr Cys Ser Glu Asp Arg Leu Ile Tyr Leu Pro Leu Arg  
 195 200 205  
 Leu Val Asp Cys Asp Glu Lys Asp Gly Glu Ala Asn Leu Ala Leu Ile  
 210 215 220  
 Asp Trp Leu Glu Gln Ile Glu Asp Val Asp Asp Val Tyr His Asn Met  
 225 230 235 240  
 Ser

<210>616  
 <211>195  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>616

Ser Ala Glu Arg Gly Phe Arg His Pro Ile Val Met Val Glu Thr Val  
 1 5 10 15  
 Leu His Asn Phe Gln Arg Tyr Leu Ser Lys Tyr Leu Tyr Arg Val Phe  
 20 25 30  
 Arg Phe Pro Cys Arg Gln Lys Thr Phe Leu Ser Ser His Arg Val Leu  
 35 40 45  
 Ala Arg Pro Ser Phe Pro Val Asp Tyr Cys Pro Gly Lys Ile Tyr Asp  
 50 55 60  
 Leu Gln Glu Ile Tyr Glu Glu Leu Asn Ala Gln Leu Phe Gln Gly Ala  
 65 70 75 80  
 Leu Arg Leu Gln Ile Gly Trp Phe Gly Arg Lys Ala Thr Arg Lys Gly  
 85 90 95  
 Lys Ser Val Val Leu Gly Leu Phe His Glu Asn Glu Gln Leu Ile Arg  
 100 105 110  
 Ile His Arg Ser Leu Asp Arg Gln Glu Ile Pro Arg Phe Phe Met Glu  
 115 120 125  
 Tyr Leu Val Tyr His Glu Met Val His Ser Val Val Pro Arg Glu Tyr  
 130 135 140  
 Ser Leu Ser Gly Arg Ser Ile Phe His Gly Lys Lys Phe Lys Glu Tyr  
 145 150 155 160  
 Glu Gln Arg Phe Pro Leu Tyr Asp Arg Ala Val Ala Trp Glu Lys Ala  
 165 170 175  
 Asn Ala Tyr Leu Leu Arg Gly Tyr Lys Lys Arg Val Gly Gly Gly Tyr  
 180 185 190  
 Gly Arg Ala  
 195

&lt;210&gt;617

&lt;211&gt;188

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;617

Ser Ile Phe Gly Arg Val Trp Xaa Xaa Phe Met Thr Ala Glu Lys Gln  
 1 5 10 15  
 Asn Thr Gly Ile Leu Gly Leu Glu Ile Arg Tyr Thr Leu Pro Ser Asp  
 20 25 30  
 Ala Thr Tyr Met Leu Lys Trp Leu Asn Asp Pro Lys Ile Leu Arg Gly  
 35 40 45  
 Phe Pro Ile Gln Thr Glu Ala Glu Ile Arg Glu Thr Val Asn Phe Trp  
 50 55 60  
 Val Gly Phe Tyr Arg Tyr His Ser Ser Leu Thr Ala Val Tyr Asn Gly  
 65 70 75 80  
 Asn Val Ala Gly Val Ala Thr Leu Val Leu Asn Pro Tyr Val Lys Val  
 85 90 95  
 Ser His His Ala Leu Ile Ser Ile Ile Val Gly Glu Glu Phe Arg Asn  
 100 105 110  
 Lys Gly Ile Gly Thr Ala Leu Leu Asn Asn Leu Ile His Leu Ala Lys  
 115 120 125  
 Thr Arg Phe Lys Leu Glu Val Leu Tyr Leu Glu Val Tyr Glu Gly Asn  
 130 135 140  
 Pro Ala Leu His Leu Tyr Gln Arg Phe Gly Phe Val Glu Val Gly Arg  
 145 150 155 160  
 Gln Asn Arg Phe Tyr Lys Asp Glu Ile Gly Tyr Leu Ala Lys Thr Thr  
 165 170 175  
 Met Glu Lys Gly Ser Ile Glu Arg Arg Lys Arg Phe  
 180 185

&lt;210&gt;618

&lt;211&gt;139

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;618

Asp Glu Ile Arg Pro Asn Asp Leu Arg Ile Asp Thr Phe Arg Ser Ser  
 1 5 10 15  
 Gly Ala Gly Gly Gln His Val Asn Val Thr Glu Ser Ala Val Arg Ile  
 20 25 30

Thr His Leu Pro Ser Gly Val Val Val Ser Cys Gln Asn Glu Arg Ser  
 35 40 45  
 Gln Ile Gln Asn Arg Glu Ser Cys Met Lys Met Leu Gln Ala Lys Leu  
 50 55 60  
 Tyr Gln Gln Val Leu Gln Glu Arg Leu Glu Lys Gln Ser Leu Asp Arg  
 65 70 75 80  
 Lys Asp Lys Lys Glu Ile Ala Trp Gly Ser Gln Ile Arg Asn Tyr Val  
 85 90 95  
 Phe Gln Pro Tyr Thr Leu Val Lys Asp Val Arg Thr Gly His Glu Thr  
 100 105 110  
 Gly Asn Val Gln Ala Met Leu Asp Gly Glu Leu Leu Asp Glu Phe Ile  
 115 120 125  
 Lys Ala Tyr Leu Ala Glu Phe Gly Xaa Val Ser  
 130 135

&lt;210&gt;619

&lt;211&gt;211

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;619

Leu Arg Gly Leu Phe Asp Leu Asp Lys Lys Gln Lys Glu Leu Gln Val  
 1 5 10 15  
 Leu Glu Glu Glu Ser Ser Glu Glu Asn Phe Trp Gln Asp Ser Val His  
 20 25 30  
 Ala Gly Lys Ile Ser Glu Gln Ile Val Ser Leu Arg Arg Gln Ile Gln  
 35 40 45  
 Glu Tyr Gln Glu Leu Lys Ser Lys Ile Asp Ala Ile Glu Phe Phe Leu  
 50 55 60  
 Glu Asp Ala Asp Ala Leu Glu Asp Pro Ala Ile Cys Glu Asp Leu Glu  
 65 70 75 80  
 Lys Glu Phe Leu Phe Cys Glu Lys Lys Leu Ala Val Trp Glu Thr Gln  
 85 90 95  
 Arg Leu Leu Ser Gly Glu Ala Asp Lys Asn Ser Cys Phe Leu Thr Ile  
 100 105 110  
 Asn Ala Gly Ala Gly Gly Thr Glu Ser Cys Asp Trp Val Glu Met Leu  
 115 120 125  
 Phe Arg Met Tyr Ser Arg Trp Ala Thr Lys His Gln Trp Ala Leu Glu  
 130 135 140  
 Val Val Asp Arg Leu Asp Gly Glu Val Val Gly Ile Lys His Val Thr  
 145 150 155 160  
 Val Lys Phe Ser Gly Met Tyr Ala Tyr Gly Tyr Ala Lys Ala Glu Arg  
 165 170 175  
 Gly Val His Arg Leu Val Arg Ile Ser Pro Phe Asp Ser Asn Gly Lys  
 180 185 190  
 Arg His Thr Ser Phe Ala Ser Val Asp Val Phe Pro Glu Ile Asp Xaa  
 195 200 205  
 Arg Leu Arg  
 210

&lt;210&gt;620

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;620

Glu Ser Pro Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro  
 1 5 10 15  
 Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met  
 20 25 30  
 Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His  
 35 40 45  
 Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn  
 50 55 60  
 Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met  
 65 70 75 80  
 Thr Lys Ala Leu Ser Lys His Ile Val Lys  
 85 90

&lt;210&gt;621

&lt;211&gt;218

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;621

```

Ser Ala Thr Ser His Val Pro Met Ile Lys Ser Ser Leu Ile Leu Leu
  1           5           10           15
Ser Gly Gly Gln Gly Thr Arg Phe Gly Ser Lys Ile Pro Lys Gln Tyr
           20           25           30
Leu Pro Leu Asn Gly Thr Pro Leu Val Leu His Ser Leu Lys Ile Leu
           35           40           45
Ser Ser Leu Pro Gln Ile Ala Glu Val Ile Val Val Cys Asp Pro Ser
           50           55           60
Tyr Gln Glu Thr Phe Gln Glu Tyr Pro Val Ser Phe Ala Ile Pro Gly
           65           70           75           80
Glu Arg Arg Gln Asp Ser Val Phe Ser Gly Leu Gln Gln Val Ser Tyr
           85           90           95
Pro Trp Val Ile Ile His Asp Gly Ala Arg Pro Phe Ile Tyr Pro Asp
           100          105          110
Glu Ile His Asp Leu Leu Glu Thr Ala Glu Lys Ile Gly Ala Thr Ala
           115          120          125
Leu Ala Ser Pro Ile Pro Tyr Thr Ile Lys Gln Arg Asn Pro Val Arg
           130          135          140
Thr Leu Asp Arg Asp Asn Leu Ala Ile Ile His Thr Pro Gln Cys Ile
           145          150          155          160
Lys Thr Glu Ile Leu Arg Glu Gly Leu Ala Leu Ala Lys Glu Lys Gln
           165          170          175
Leu Thr Leu Val Asp Asp Ile Glu Ala Ala Glu Ile Ile Gly Lys Pro
           180          185          190
Ser Gln Leu Val Phe Asn Lys His Pro Gln Ile Lys Ile Ser Tyr Pro
           195          200          205
Glu Asp Leu Thr Ile Ala Gln Ala Leu Leu
           210          215

```

&lt;210&gt;622

&lt;211&gt;267

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;622

```

Met Thr Lys Val Ala Leu Leu Ile Ala Tyr Gln Gly Thr Ala Tyr Ser
  1           5           10           15
Gly Trp Gln Gln Gln Pro Asn Asp Leu Ser Ile Gln Glu Val Ile Glu
           20           25           30
Ser Ser Leu Lys Lys Ile Thr Lys Thr Arg Thr Pro Leu Ile Ala Ser
           35           40           45
Gly Arg Thr Asp Ala Gly Val His Ala Tyr Gly Gln Val Ala His Phe
           50           55           60
Arg Ala Pro Asp His Pro Leu Phe Ala Asn Ala Asn Leu Thr Lys Lys
           65           70           75           80
Ala Leu Asn Ala Ile Leu Pro Lys Asp Ile Val Ile Arg Asp Val Ala
           85           90           95
Leu Phe Asp Asp Asn Phe His Ala Arg Tyr Leu Thr Ile Ala Lys Glu
           100          105          110
Tyr Arg Tyr Ser Leu Ser Arg Leu Ala Lys Pro Leu Pro Trp Gln Arg
           115          120          125
His Phe Cys Tyr Thr Pro Arg His Pro Phe Ser Thr Glu Leu Met Gln
           130          135          140
Glu Gly Ala Asn Leu Leu Ile Gly Thr His Asp Phe Ala Ser Phe Ala
           145          150          155          160
Asn His Gly Arg Asp Tyr Asn Ser Thr Val Arg Thr Ile Tyr Thr Leu
           165          170          175
Asp Ile Val Asp Lys Gly Asp Ser Leu Ser Ile Ile Cys Arg Gly Asn
           180          185          190
Gly Phe Leu Tyr Lys Met Val Arg Asn Leu Val Gly Ala Leu Leu Asp
           195          200          205

```

Val Gly Lys Gly Ala Tyr Pro Pro Glu His Leu Leu Asp Ile Leu Glu  
 210 215 220  
 Gln Lys Asn Arg Arg Glu Gly Pro Ser Ala Ala Pro Ala Tyr Gly Leu  
 225 230 235 240  
 Ser Leu His His Val Cys Tyr Ser Ser Pro Tyr Asn Asn Phe Cys Cys  
 245 250 255  
 Glu Gln Cys Ser Val Ser Thr Ser Asn Glu Gly  
 260 265

&lt;210&gt;623

&lt;211&gt;263

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;623

Glu Gly Leu Arg Trp Arg Ser Val Lys Ser Phe Leu Arg Gln Cys Trp  
 1 5 10 15  
 Ile Tyr Ser Met Leu Val Ser Asp Glu Phe Gln Leu Cys Leu Arg Ser  
 20 25 30  
 Gly Met Tyr Leu Glu Asp Tyr Asp Val Phe Phe Phe Asp Leu Asp Gly  
 35 40 45  
 Leu Leu Val Asp Thr Glu Pro Cys Phe Tyr Arg Ala Phe Leu Gln Ala  
 50 55 60  
 Cys Ala Glu Phe Ser Leu Glu Val His Trp Asp Phe Ser Thr Tyr Tyr  
 65 70 75 80  
 Ser His Thr Thr Leu Gly Thr Glu Ile Phe Ser Lys Lys Phe Ile Glu  
 85 90 95  
 Gln Tyr Pro Gln Ala Gln Glu Tyr Met Ala Glu Ile Phe Ala Lys Arg  
 100 105 110  
 Leu Gln Ile Tyr Tyr Lys Ser Leu Glu His Ala Gly Pro Ala Leu Met  
 115 120 125  
 Pro Gly Val Glu Ala Phe Ile Glu Leu Val Leu Ser Leu Asn Lys Thr  
 130 135 140  
 Phe Gly Val Val Thr Asn Ser Pro Arg Asp Ala Thr His Thr Leu Arg  
 145 150 155 160  
 Thr Met Tyr Pro Ile Leu Asn Lys Phe Leu Phe Trp Val Thr Arg Glu  
 165 170 175  
 Asn Tyr Ala Arg Pro Lys Pro Tyr Gly Asp Ser Tyr Asp Tyr Ala Tyr  
 180 185 190  
 Arg Thr Phe Ala Arg Glu Gly Met Lys Val Ile Gly Phe Glu Asp Ser  
 195 200 205  
 Val Lys Gly Leu Arg Ala Leu Ser Lys Ile Pro Ala Thr Leu Val Cys  
 210 215 220  
 Ile Asn Ser Met Ala Glu Ile Thr Pro Glu Asp Tyr Pro Glu Leu Lys  
 225 230 235 240  
 Gly Lys Glu Phe Phe Ser Tyr Pro Ser Phe Asp Val Leu Thr Glu His  
 245 250 255  
 Cys Ser Gln Gln Lys Leu Leu  
 260

&lt;210&gt;624

&lt;211&gt;291

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;624

Lys Asn Pro Asn Ala Leu Leu Lys Lys Ile Gln His Arg Leu Val Lys  
 1 5 10 15  
 Met His Asp Lys Asn Lys Val Leu Tyr Leu Gln Ala Asn His Leu Asn  
 20 25 30  
 Gln Lys Arg Lys Arg His Asn Pro Leu Asn Thr Tyr His Ser Ser Asn  
 35 40 45  
 Thr Thr Glu Thr Arg Arg Leu Pro Thr Tyr Tyr Lys Ser Asn Ile Val  
 50 55 60  
 Leu Lys Met Ile Leu Arg Ile Ser Thr Val Ser Leu Leu Thr Ser Cys  
 65 70 75 80  
 Ser Phe Ser Lys Asn Ser Arg Thr Cys Phe Val Thr Pro Glu Arg Ile  
 85 90 95

Thr Ser Gln Lys Asp Cys Pro Val Leu His Pro Lys Ser Thr Thr  
 100 105 110  
 Ile Ser Pro Leu Tyr Asp Trp Ile Ser Pro Asn Arg Glu Val Ile  
 115 120 125  
 Thr Ala Tyr Ser Phe Tyr Cys Arg Gly Gln Gly Asn Ser Ile Ile Thr  
 130 135 140  
 Pro Glu Gly Val Leu Tyr Asp Cys Asp Gly Leu His His Ser Ile Thr  
 145 150 155 160  
 Lys Glu Glu Phe Arg Tyr Ile His Pro Arg Leu Ile Glu Val Val Arg  
 165 170 175  
 Leu Leu Gln Gln Asp His Pro Lys Val Ser Ile Ile Glu Ala Phe Cys  
 180 185 190  
 Cys Pro Lys His Phe His Phe Leu Glu Ala Ser Gly Ile Ser Leu Ser  
 195 200 205  
 Gln Leu His Leu Gln Gly Thr Ala Ala Thr Phe Ala Leu Asp Pro Pro  
 210 215 220  
 Leu Pro Met Glu Lys Leu Leu Ala Thr Ile Lys Lys Leu Tyr Lys Lys  
 225 230 235 240  
 Asn Ser Asp Pro Ser Leu Ser Asn Phe Ile Val Thr Glu Ala Thr Leu  
 245 250 255  
 Thr Asn Pro Glu Leu Arg Leu Thr Gln Gln Asp Leu Gly Ser His Thr  
 260 265 270  
 Glu Ile Thr Val Glu Ile Leu Asp Asn Leu Gln Asn Lys Glu Ala Leu  
 275 280 285  
 Ser Ser Ala  
 290

&lt;210&gt;625

&lt;211&gt;123

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;625

Ile Val Leu Ser Phe Phe Leu Gly Lys Thr Lys Val Thr Pro Arg Phe  
 1 5 10 15  
 Leu Met Asn Glu Arg Thr Leu Leu Leu Leu Lys Lys Lys Lys Gly  
 20 25 30  
 Leu Phe Leu Ala Ile Leu Asp Leu Thr Gln Thr Glu Ser Ser Leu Thr  
 35 40 45  
 Thr Pro Glu Leu Glu Lys Val Leu Lys Gln Lys Lys Ile Phe Leu Ser  
 50 55 60  
 Cys Ile Asp Arg Val Asp Leu Gln Ile Lys Glu Phe Arg His Ala Phe  
 65 70 75 80  
 Ser Ser Glu Leu Pro Gln Asp Ile Gln Glu Glu Leu Glu Glu Ile Arg  
 85 90 95  
 Asp Val Ile Ile Arg Ile Leu Asp Thr Asp Lys Arg Asn Tyr Ala Gln  
 100 105 110  
 Lys Lys Lys Glu Phe Gly Ile Tyr Glu Arg Pro  
 115 120

&lt;210&gt;626

&lt;211&gt;380

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;626

Ile Arg Ile Asn Ala Thr Met His Arg Lys Lys Arg Asn Leu Val Phe  
 1 5 10 15  
 Met Asn Val Pro Asp Ser Lys Asn Leu His Pro Pro Ala Tyr Glu Leu  
 20 25 30  
 Leu Glu Ile Lys Ala Arg Ile Thr Gln Ser Tyr Lys Glu Ala Ser Ala  
 35 40 45  
 Ile Leu Thr Ala Ile Pro Asp Gly Ile Leu Leu Leu Ser Glu Thr Gly  
 50 55 60  
 His Phe Leu Ile Cys Asn Ser Gln Ala Arg Glu Ile Leu Gly Ile Asp  
 65 70 75 80  
 Glu Asn Leu Glu Ile Leu Asn Arg Ser Phe Thr Asp Val Leu Pro Asp  
 85 90 95



Thr Cys Leu Gly Phe Ser Ile Gln Glu Ala Leu Glu Ser Leu Lys Val  
 100 105 110  
 Pro Lys Thr Leu Arg Leu Ser Leu Cys Lys Glu Ser Lys Glu Lys Glu  
 115 120 125  
 Val Glu Leu Phe Ile Arg Lys Asn Glu Ile Ser Gly Tyr Leu Phe Ile  
 130 135 140  
 Gln Ile Arg Asp Arg Ser Asp Tyr Lys Gln Leu Glu Asn Ala Ile Glu  
 145 150 155 160  
 Arg Tyr Lys Asn Ile Ala Glu Leu Gly Lys Met Thr Ala Thr Leu Ala  
 165 170 175  
 His Glu Ile Arg Asn Pro Leu Ser Gly Ile Val Gly Phe Ala Ser Ile  
 180 185 190  
 Leu Lys Lys Glu Ile Ser Ser Pro Arg His Gln Arg Met Leu Ser Ser  
 195 200 205  
 Ile Ile Ser Gly Thr Arg Ser Leu Asn Asn Leu Val Ser Ser Met Leu  
 210 215 220  
 Glu Tyr Thr Lys Ser Gln Pro Leu Asn Leu Lys Ile Ile Asn Leu Gln  
 225 230 235 240  
 Asp Phe Phe Ser Ser Leu Ile Pro Leu Leu Ser Val Ser Phe Pro Asn  
 245 250 255  
 Cys Lys Phe Val Arg Glu Gly Ala Gln Pro Leu Phe Arg Ser Ile Asp  
 260 265 270  
 Pro Asp Arg Met Asn Ser Val Val Trp Asn Leu Val Lys Asn Ala Val  
 275 280 285  
 Glu Thr Gly Asn Ser Pro Ile Thr Leu Thr Leu His Thr Ser Gly Asp  
 290 295 300  
 Ile Ser Val Thr Asn Pro Gly Thr Ile Pro Ser Glu Ile Met Asp Lys  
 305 310 315 320  
 Leu Phe Thr Pro Phe Phe Thr Thr Lys Arg Glu Gly Asn Gly Leu Gly  
 325 330 335  
 Leu Ala Glu Ala Gln Lys Ile Ile Arg Leu His Gly Gly Asp Ile Gln  
 340 345 350  
 Leu Lys Thr Ser Asp Ser Ala Val Ser Phe Phe Ile Ile Ile Pro Glu  
 355 360 365  
 Leu Leu Ala Ala Leu Pro Lys Glu Arg Ala Ala Ser  
 370 375 380  
 <210>627  
 <211>216  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>627  
 Ile His Ser Phe Leu Ser Thr Arg Thr Val Cys Val Arg Gln Lys Lys  
 1 5 10 15  
 Leu Arg Lys Ile Ser Lys Glu Leu Gln Gln Arg Tyr Ser Arg Leu Gln  
 20 25 30  
 Glu Glu Lys Gln Val Lys Glu Lys Ile Leu Glu Glu Ser Met Asn His  
 35 40 45  
 Phe Ala Asp Leu Phe Glu Lys Ala Gln Lys Glu Asn Met Ala Tyr Lys  
 50 55 60  
 Lys Lys Leu Ala Asp Leu Glu Gly Ala Ala Ala Pro Thr Glu Ile Gly  
 65 70 75 80  
 Glu Asp Asp Asp Trp Val Leu Thr Asp Ser Ala Ser Leu Ser Gln Lys  
 85 90 95  
 Lys Ile Arg Glu Leu Val Glu Glu Asn Gln Glu Leu Leu Lys Ala Leu  
 100 105 110  
 Ala Phe Lys Ser Asn Glu Leu Thr Gln Leu Val Ala Asp Ala Val Glu  
 115 120 125  
 Ala Glu Lys Glu Ile Ser Lys Leu Arg Glu His Ile Glu Glu Gln Lys  
 130 135 140  
 Glu Gly Leu Arg Ala Leu Asp Lys Met His Ala Gln Ala Ile Lys Asp  
 145 150 155 160  
 Cys Glu Val Ala Gln Arg Lys Cys Cys Asp Leu Glu Ser Leu Leu Ser  
 165 170 175  
 Pro Val Arg Glu Asp Ala Gly Met Arg Phe Glu Leu Glu Val Glu Leu

180 185 190  
 Gln Arg Leu Gln Glu Glu Asn Ala Gln Leu Arg Ala Glu Val Glu Arg  
 195 200 205  
 Leu Glu Gln Glu Gln Phe Gln Gly  
 210 215  
 <210>628  
 <211>212  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>628  
 Gly Val Gly Ser Met Thr Ser Arg Arg Asp Ala Gly Arg Leu Tyr Asn  
 1 5 10 15  
 Val Phe Asn Gln Ser Gln Lys Asp Ile Gln Arg Ala His Asp Arg Glu  
 20 25 30  
 Ala Ser Gln Arg Ala Cys Glu Gly Thr Glu Met Asp Cys Ala Glu Arg  
 35 40 45  
 Gln Gln Leu Glu Lys Asp Leu Arg Arg Gln Leu Lys Ser Met Gln Glu  
 50 55 60  
 Trp Ile Glu Met Arg Gly Thr Ile His Gln Gln Glu Lys Ala Trp Arg  
 65 70 75 80  
 Lys Gln Asn Ala Lys Leu Glu Arg Leu Gln Glu Asp Leu Arg Leu Thr  
 85 90 95  
 Gly Ile Ala Phe Asp Glu Gln Ser Leu Phe Tyr Arg Glu Tyr Lys Glu  
 100 105 110  
 Lys Tyr Leu Ser Gln Lys Leu Asp Met Gln Lys Ile Leu Gln Glu Val  
 115 120 125  
 Asn Ala Glu Lys Ser Glu Lys Ala Cys Leu Glu Ser Leu Val His Asp  
 130 135 140  
 Tyr Glu Lys Gln Leu Glu Gln Lys Asp Ala Asn Leu Lys Lys Ala Ala  
 145 150 155 160  
 Ala Val Trp Glu Glu Glu Leu Gly Lys Gln Gln Gln Glu Asp Tyr Glu  
 165 170 175  
 Gln Thr Gln Glu Ile Arg Arg Leu Asn Thr Phe Ile Leu Glu Tyr Gln  
 180 185 190  
 Asp Ser Leu Arg Glu Ala Glu Lys Val Glu Lys Asp Phe Gln Arg Ala  
 195 200 205  
 Thr Thr Lys Val  
 210  
 <210>629  
 <211>290  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>629  
 Ile Ser Leu Arg Arg Lys Ile Leu Arg Pro Asn Asn Phe Ser Ile Gly  
 1 5 10 15  
 Asp Cys Ser Ser Asn Met Ala Thr Pro Ala Gln Lys Ser Pro Thr Phe  
 20 25 30  
 Gln Asp Pro Ser Phe Val Arg Glu Leu Gly Ser Asn His Pro Val Phe  
 35 40 45  
 Ser Pro Leu Thr Leu Glu Glu Arg Gly Glu Met Ala Ile Ala Arg Val  
 50 55 60  
 Gln Gln Cys Gly Trp Asn His Thr Ile Val Lys Val Ser Leu Ile Ile  
 65 70 75 80  
 Leu Ala Leu Leu Thr Ile Leu Gly Gly Gly Leu Leu Val Gly Leu Leu  
 85 90 95  
 Pro Ala Val Pro Met Phe Ile Gly Thr Gly Leu Ile Ala Leu Gly Ala  
 100 105 110  
 Val Ile Phe Ala Leu Ala Leu Ile Leu Cys Leu Tyr Asp Ser Gln Gly  
 115 120 125  
 Leu Pro Glu Glu Leu Pro Pro Val Pro Glu Pro Gln Gln Ile Gln Ile  
 130 135 140  
 Glu Asp Leu Arg Asn Glu Thr Arg Glu Val Leu Glu Gly Thr Leu Leu  
 145 150 155 160  
 Glu Val Leu Leu Lys Asp Arg Asp Ala Lys Asp Pro Ala Val Pro Gln

165 170 175  
 Val Val Val Asp Cys Glu Lys Arg Leu Gly Met Leu Asp Arg Lys Leu  
 180 185 190  
 Arg Arg Glu Glu Ile Leu Tyr Arg Ser Thr Ala His Leu Lys Asp  
 195 200 205  
 Glu Glu Arg Tyr Glu Phe Leu Leu Glu Leu Leu Glu Met Arg Ser Leu  
 210 215 220  
 Val Ala Asp Arg Leu Glu Phe Asn Arg Arg Ser Tyr Glu Arg Phe Val  
 225 230 235 240  
 Gln Gly Ile Met Thr Val Arg Ser Glu Glu Gly Glu Lys Glu Ile Ser  
 245 250 255  
 Arg Leu Gln Asp Leu Ile Ser Leu Gln Gln Gln Thr Val Gln Asp Leu  
 260 265 270  
 Arg Ser Arg Ile Asp Asp Glu Gln Lys Arg Cys Trp Thr Ala Leu Gln  
 275 280 285  
 Arg Ile  
 290  
 <210>630  
 <211>337  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>630  
 Pro Cys His Leu Arg His Glu Tyr Pro Asp Gly Ser Gly Leu Asp Leu  
 1 5 10 15  
 Ile Lys Ile Ile Lys Gln Ser Ser Pro His Thr Pro Val Leu Val Val  
 20 25 30  
 Thr Ala Tyr Gly Ser Ile Glu Asn Ala Val Glu Ala Met His Gln Gly  
 35 40 45  
 Ala Phe Asn Tyr Leu Thr Lys Pro Phe Ser Ser Glu Ala Leu Phe Ala  
 50 55 60  
 Phe Ile Ser Lys Ala Glu Glu Leu Lys Asn Leu Val His Glu Asn Leu  
 65 70 75 80  
 Phe Leu His Ser Gln Thr Thr Pro Asp Ser His Pro Leu Ile Ala Glu  
 85 90 95  
 Ser Lys Ala Met Lys Asp Leu Leu Ala Ile Ala Lys Lys Ala Ala Ser  
 100 105 110  
 Ser Ser Ala Asn Ile Phe Ile His Gly Glu Ser Gly Cys Gly Lys Glu  
 115 120 125  
 Val Leu Ser Phe Phe Ile His His Asn Ser Pro Arg Ala Asn His Pro  
 130 135 140  
 Tyr Ile Lys Val Asn Cys Ala Ala Ile Pro Glu Thr Leu Leu Glu Ser  
 145 150 155 160  
 Glu Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Thr Thr Lys  
 165 170 175  
 Lys Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Leu Leu Asp  
 180 185 190  
 Glu Ile Thr Glu Val Pro Val Asn Leu Gln Ala Lys Leu Leu Arg Ala  
 195 200 205  
 Ile Gln Glu Lys Glu Ile Glu His Leu Gly Gly Thr Lys Thr Leu Ser  
 210 215 220  
 Val Asp Val Arg Ile Leu Ala Thr Ser Asn Arg Lys Leu Lys Glu Ala  
 225 230 235 240  
 Ile Asp Asp Lys Ser Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Asn Val  
 245 250 255  
 Ile Pro Leu His Leu Pro Pro Leu Arg Asp Arg Gln Asp Asp Ile Leu  
 260 265 270  
 Pro Leu Ala Asn Tyr Phe Leu Asn Lys Phe Cys Arg Met Asn Asn Thr  
 275 280 285  
 Pro Leu Lys Thr Leu Ser Pro Lys Ala Gln Glu Leu Leu Leu Asn Tyr  
 290 295 300  
 Pro Trp Pro Gly Asn Ile Arg Glu Leu Ser Asn Val Leu Glu Arg Val  
 305 310 315 320  
 Val Ile Leu Glu Asn Thr Ser Leu Leu Thr Glu Asp Met Leu Ala Leu  
 325 330 335

Ala

&lt;210&gt;631

&lt;211&gt;223

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;631

```

Ser Tyr Gly Glu Leu Phe Ile Leu Ser Thr Leu Leu Lys His His Val
 1          5          10          15
Thr Leu Gly Asp Lys Met Arg Pro His Arg Lys His Val Ser Ser Lys
          20          25          30
Ser Leu Ala Leu Lys Gln Ser Ala Ser Thr His Val Glu Ile Thr Thr
          35          40          45
Lys Ala Phe Arg Leu Ser Met Pro Leu Lys Gln Leu Ile Leu Glu Lys
          50          55          60
Ser Asp His Leu Pro Pro Met Glu Thr Ile Arg Val Val Leu Thr Ser
          65          70          75          80
His Lys Asp Lys Leu Gly Thr Glu Val His Val Val Ala Ser His Gly
          85          90          95
Lys Glu Ile Leu Gln Thr Lys Val His Asn Ala Asn Pro Tyr Thr Ala
          100          105          110
Val Ile Asn Ala Phe Lys Lys Ile Arg Thr Met Ala Asn Lys His Ser
          115          120          125
Asn Lys Arg Lys Asp Arg Thr Lys His Asp Leu Gly Leu Ala Ala Lys
          130          135          140
Glu Glu Arg Ile Ala Ile Gln Glu Glu Gln Glu Asp Arg Leu Ser Asn
          145          150          155          160
Arg Val Ala Ser Cys Arg Arg Pro Arg Cys Leu Gly Phe Ser Lys Asn
          165          170          175
Ser Trp Val Cys Ser Arg Ile Ser Glu Lys Glu Asp Leu Gln Glu Lys
          180          185          190
Asp Glu His Ser Tyr Ala Ile Ser Arg Arg Gly Tyr Pro Pro Ala Arg
          195          200          205
Val Cys Arg Arg Lys Leu Pro Asp Leu Leu Glu Arg Ala Arg Ala
          210          215          220

```

&lt;210&gt;632

&lt;211&gt;254

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;632

```

Ser Ser Met Gln Ile Cys Val Thr Gly Val Val Leu Arg Ser Arg Pro
 1          5          10          15
Leu Gly Lys Asn His Thr Leu Thr Thr Leu Phe Thr Pro Glu Gly Leu
          20          25          30
Phe Thr Phe Phe Ala Lys Gln Gly Gln Thr Leu Gln Cys Asp Tyr Arg
          35          40          45
Glu Thr Leu Val Pro Ile Ser Leu Gly Lys Tyr Thr Leu His Arg Asn
          50          55          60
Gly Ser Arg Leu Pro Lys Leu Thr His Gly Asp Ile Leu Asn Ala Phe
          65          70          75          80
Glu Ala Ile Lys Gln Thr Tyr Ala Leu Leu Glu Ala Ser Gly Lys Met
          85          90          95
Ile Gln Ala Leu Leu Ala Ser Gln Trp Lys Glu Lys Pro Ser His Lys
          100          105          110
Leu Phe Ser Leu Phe Leu Asn Phe Leu His Arg Ile Pro Glu Ser Ser
          115          120          125
Asn Pro Glu Phe Phe Ala Ala Ile Phe Val Leu Lys Leu Leu Gln Tyr
          130          135          140
Glu Gly Ile Leu Asp Leu Thr Pro Ala Cys Ser Leu Cys Lys Ala Ser
          145          150          155          160
Leu Pro Tyr Ala Cys Tyr Arg Tyr Gln Gly His Lys Leu Cys Lys Lys
          165          170          175
His Gln His Lys Gln Ala Ile Ser Ile Glu Lys Glu Glu Glu Gln Ile
          180          185          190

```

Leu Gln Ala Ile Ile His Ala Lys Lys Phe Ser Glu Leu Leu Ala Ile  
 195 200 205  
 Ala Glu Phe Pro Ile Ala Ile Ala Glu Lys Ile Phe Tyr Leu Phe Asp  
 210 215 220  
 Ser Leu Gln Glu Glu Lys Lys Ser Glu Arg Asn Ser Ser Glu Asp Pro  
 225 230 235 240  
 Tyr His Glu Ile Leu Arg Leu Ser Lys Val Val His Pro Tyr  
 245 250

&lt;210&gt;633

&lt;211&gt;207

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;633

Leu Phe Leu Tyr Gly Asp His Asn Leu Gly Phe Ala Cys Arg Tyr Leu  
 1 5 10 15  
 Phe Phe Phe Ile Val Leu Phe Ala Ser Gly Ser Phe Gly Asn Gln Leu  
 20 25 30  
 Leu Ser Val Pro Cys Trp Leu Ser Glu Glu Ser Phe Tyr Thr His  
 35 40 45  
 Arg Phe Asp Phe Ser Lys Ser Tyr Pro Asp Met Glu Asn Met Glu Ile  
 50 55 60  
 Gln Ala Gln Arg Lys Lys Arg Val Glu Phe Asn Leu Thr Gly Glu Phe  
 65 70 75 80  
 Pro Lys Leu Glu Thr Leu Asn Tyr Gln Gly Ser Phe Gly His Leu Arg  
 85 90 95  
 Ala Lys Cys Arg Gly Val Tyr Pro Val Leu Tyr Ala Leu Asn Phe Ser  
 100 105 110  
 Cys Ser Ser Cys Lys Met Asp Met Asp Phe Arg Gly Lys Trp Asn Arg  
 115 120 125  
 Ser Ser Thr Ile Thr Ile Ser Asn Gln Lys Glu Ser Ile Asn Leu Lys  
 130 135 140  
 Leu Pro Lys Asp Val Gly Val Ile Val Asn Thr Lys Thr Ser Leu Lys  
 145 150 155 160  
 Gly Asn Val Cys Pro Gly Ser Thr Phe Ile Lys Gln Gly Trp Gly Val  
 165 170 175  
 Trp Asn Lys Ile Tyr His Asn Asp Leu Val Gly Phe Ser Glu Val Thr  
 180 185 190  
 Leu Ile Phe Asn Val Ser Ser Glu Gly Gly Thr Ile Thr Phe Ser  
 195 200 205

&lt;210&gt;634

&lt;211&gt;219

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;634

Ser Leu Ile Met Arg Cys Thr Ala Tyr Cys Thr Ala Ser Ala Tyr Asn  
 1 5 10 15  
 Leu His Val Leu Phe His Leu Leu Lys Pro Arg Tyr Pro Thr Ile Leu  
 20 25 30  
 Ser Arg Glu Tyr Val Leu Ala Asn Leu Asp Ser Thr Gln Ala Ser Asn  
 35 40 45  
 Gln Leu Ala Ile Phe Phe Pro Phe Gly Val Ala Val Phe Trp Gly Trp  
 50 55 60  
 Glu Glu Ser Glu Glu Ile Lys Leu Leu Gln Thr Ile Val Thr Ala Ser  
 65 70 75 80  
 Pro Glu Ile Leu Pro Gln Pro Glu Ile Asp Cys Tyr Asn Phe His Tyr  
 85 90 95  
 Gly Asp Lys Leu Gln Ile Arg Arg Asp Arg Leu Thr Leu Ala Asp Thr  
 100 105 110  
 Thr Leu Asn Thr Lys Leu Ala Ile Ala Phe Gly Leu Ala Gln Ser Val  
 115 120 125  
 Lys Leu Thr Thr Phe Glu Thr Thr Ile Tyr Lys Thr Ile Glu Asp Ser  
 130 135 140  
 Lys Arg Leu Pro Gln Asp Leu Ala Thr Lys Gly Lys Ile Ser Met Ser  
 145 150 155 160

Arg Lys Ala Ile Ala Lys Lys Ile Gly Lys Leu Phe Leu Asp Lys Ala  
 165 170 175  
 Ser Val Asn Leu His Ser Asp Ile Leu Asp Glu Pro Asp Phe Phe Trp  
 180 185 190  
 Asp His Pro Glu Thr Gln Ala Ile Tyr Arg Asp Val Leu Ser Cys Leu  
 195 200 205  
 Asp Ile Glu Ala Arg Ile Asn Val Leu Ile Val  
 210 215  
 <210>635  
 <211>368  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>635  
 Val Leu Gly Ala Lys Cys Met Ala Phe Lys Arg Lys Thr Arg Trp Leu  
 1 5 10 15  
 Trp Gln Val Leu Ile Leu Ser Val Gly Leu Asn Met Leu Phe Leu Leu  
 20 25 30  
 Leu Phe Tyr Ser Ala Ile Phe Arg Lys Asp Ile Tyr Lys Leu His Leu  
 35 40 45  
 Phe Ser Gly Pro Leu Ile Ala Lys Ser Ser Arg Lys Val Tyr Leu Ser  
 50 55 60  
 Glu Asp Phe Leu Asn Glu Ile Ser Gln Ala Ser Leu Asp Asp Leu Ile  
 65 70 75 80  
 Ser Leu Phe Lys Asp Glu Arg Tyr Met Tyr Gly Arg Pro Ile Lys Leu  
 85 90 95  
 Trp Ala Leu Ser Val Ala Ile Ala Ser His His Ile Asp Ile Thr Pro  
 100 105 110  
 Val Leu Ser Lys Pro Leu Thr Tyr Thr Glu Leu Lys Gly Ser Ser Val  
 115 120 125  
 Arg Trp Leu Leu Pro Asn Ile Asp Leu Lys Asp Phe Pro Val Ile Leu  
 130 135 140  
 Asp Tyr Leu Arg Cys His Lys Tyr Pro Tyr Thr Ser Lys Gly Leu Phe  
 145 150 155 160  
 Leu Leu Ile Glu Lys Met Val Gln Glu Gly Trp Val Asp Glu Asp Cys  
 165 170 175  
 Leu Tyr His Phe Cys Ser Thr Pro Glu Phe Leu Tyr Leu Arg Thr Leu  
 180 185 190  
 Leu Val Gly Ala Asp Val Gln Ala Ser Ser Val Ala Ser Leu Ala Arg  
 195 200 205  
 Met Val Ile Arg Cys Gly Ser Glu Arg Phe Phe His Phe Cys Asn Glu  
 210 215 220  
 Glu Ser Arg Thr Ser Met Ile Ser Ala Thr Gln Arg Gln Lys Val Leu  
 225 230 235 240  
 Lys Ser Tyr Leu Asp Cys Glu Glu Ser Leu Ala Ala Leu Leu Leu Leu  
 245 250 255  
 Val His Asp Ser Asp Val Val Leu His Glu Phe Cys Asp Glu Asp Leu  
 260 265 270  
 Glu Lys Val Ile Arg Leu Met Pro Gln Glu Ser Pro Tyr Ser Gln Asn  
 275 280 285  
 Phe Phe Ser Arg Leu Gln His Ser Pro Arg Arg Glu Leu Ala Cys Met  
 290 295 300  
 Ser Thr Arg Arg Val Glu Ala Pro Arg Val Gln Glu Asp Gln Asp Glu  
 305 310 315 320  
 Glu Tyr Val Val Gln Asp Gly Asp Ser Leu Trp Leu Ile Ala Lys Arg  
 325 330 335  
 Phe Gly Ile Pro Met Asp Lys Ile Ile Gln Lys Asn Gly Leu Asn His  
 340 345 350  
 His Arg Leu Phe Pro Gly Lys Val Leu Lys Leu Pro Ala Lys Gln Ser  
 355 360 365  
 <210>636  
 <211>797  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>636

Leu Arg Leu Ser Ser Met Arg Ile Pro Ile Thr Leu Leu Gln Xaa Tyr  
 1 5 10 15  
 Phe Ser Glu Pro Leu Ser Thr Lys Glu Ile Leu Glu Ala Cys Asp His  
 20 25 30  
 Ile Gly Ile Glu Xaa Glu Ile Glu Asn Thr Thr Leu Tyr Ser Phe Ala  
 35 40 45  
 Ser Val Ile Thr Ala Lys Ile Leu His Thr Ile Pro His Pro Asn Ala  
 50 55 60  
 Asp Lys Leu Arg Val Ala Thr Leu Thr Asp Gly Glu Lys Glu His Gln  
 65 70 75 80  
 Val Val Cys Gly Ala Pro Asn Cys Glu Ala Gly Leu Ile Val Ala Leu  
 85 90 95  
 Ala Leu Pro Gly Ala Lys Leu Phe Asp Ser Glu Gly Gln Ala Tyr Thr  
 100 105 110  
 Ile Lys Lys Ser Lys Leu Arg Gly Val Glu Ser Gln Gly Met Cys Cys  
 115 120 125  
 Gly Ala Asp Glu Leu Gly Leu Asp Glu Leu Gln Ile Gln Glu Arg Ala  
 130 135 140  
 Leu Leu Glu Leu Pro Glu Ala Thr Pro Leu Gly Glu Asp Leu Ala Thr  
 145 150 155 160  
 Val Leu Gly Asn Thr Ser Leu Glu Ile Ser Leu Thr Pro Asn Leu Gly  
 165 170 175  
 His Cys Ala Ser Phe Leu Gly Leu Ala Arg Glu Ile Cys His Val Thr  
 180 185 190  
 Gln Ala Asn Leu Val Ile Pro Lys Glu Phe Ser Phe Glu Asn Leu Pro  
 195 200 205  
 Thr Thr Ala Leu Asp Met Gly Asn Asp Pro Asp Ile Cys Pro Phe Phe  
 210 215 220  
 Ser Tyr Val Val Ile Thr Gly Ile Ser Ala Gln Pro Ser Pro Ile Lys  
 225 230 235 240  
 Leu Gln Glu Ser Leu Gln Ala Leu Lys Gln Lys Pro Ile Asn Ala Ile  
 245 250 255  
 Val Asp Ile Thr Asn Tyr Ile Met Leu Ser Leu Gly Gln Pro Leu His  
 260 265 270  
 Ala Tyr Asp Ala Ser His Val Ala Leu Asp Ser Leu Arg Val Glu Lys  
 275 280 285  
 Leu Ser Thr Pro Glu Ser Leu Thr Leu Leu Asn Gly Glu Thr Val Leu  
 290 295 300  
 Leu Pro Ser Gly Val Pro Val Val Arg Asp Asp His Ser Leu Leu Gly  
 305 310 315 320  
 Leu Gly Gly Val Met Gly Ala Lys Ala Pro Ser Phe Gln Glu Thr Thr  
 325 330 335  
 Thr Thr Thr Val Ile Lys Ala Ala Tyr Phe Leu Pro Glu Ala Leu Arg  
 340 345 350  
 Ala Ser Gln Lys Leu Leu Pro Ile Pro Ser Glu Ser Ala Tyr Arg Phe  
 355 360 365  
 Thr Arg Gly Ile Asp Pro Gln Asn Val Val Pro Ala Leu Gln Ala Ala  
 370 375 380  
 Ile His Tyr Ile Leu Glu Ile Phe Pro Glu Ala Thr Ile Ser Pro Ile  
 385 390 395 400  
 Tyr Ser Ser Gly Glu Ile Cys Arg Glu Leu Lys Glu Val Ala Leu Arg  
 405 410 415  
 Pro Lys Thr Leu Gln Arg Ile Leu Gly Lys Ser Phe Ser Ile Glu Ile  
 420 425 430  
 Leu Ser Gln Lys Leu Gln Ser Leu Gly Phe Ser Thr Thr Pro Gln Glu  
 435 440 445  
 Thr Ser Leu Leu Val Lys Val Pro Ser Tyr Arg His Asp Ile Asn Glu  
 450 455 460  
 Glu Ile Asp Leu Val Glu Glu Ile Cys Arg Thr Glu Ser Trp Asn Ile  
 465 470 475 480  
 Glu Thr Gln Asn Pro Val Ser Cys Tyr Thr Pro Ile Tyr Lys Leu Lys  
 485 490 495  
 Arg Glu Thr Ala Gly Phe Leu Ala Asn Ala Gly Leu Gln Glu Phe Phe  
 500 505 510

Thr Pro Asp Leu Leu Asp Pro Glu Thr Val Ala Leu Thr Arg Lys Glu  
 515 520 525  
 Lys Glu Ile Ser Leu Gln Gly Ser Lys His Thr Thr Val Leu Arg  
 530 535 540  
 Ser Ser Leu Leu Pro Gly Leu Leu Lys Ser Ala Ala Thr Asn Leu Asn  
 545 550 555 560  
 Arg Gln Ala Pro Ser Val Gln Ala Phe Glu Ile Gly Thr Val Tyr Ala  
 565 570 575  
 Lys His Gly Glu Gln Cys Gln Glu Thr Gln Thr Leu Ala Ile Leu Leu  
 580 585 590  
 Thr Glu Asp Gly Glu Ser Arg Ser Trp Leu Pro Lys Pro Ser Leu Ser  
 595 600 605  
 Phe Tyr Ser Leu Lys Gly Trp Val Glu Arg Leu Leu Tyr His His His  
 610 615 620  
 Leu Ser Ile Asp Ala Leu Thr Leu Glu Ser Ser Ala Leu Cys Glu Phe  
 625 630 635 640  
 His Pro Tyr Gln Gln Gly Val Leu Arg Ile His Lys Gln Ser Phe Ala  
 645 650 655  
 Thr Leu Gly Gln Val His Pro Glu Leu Ala Lys Lys Ala Gln Ile Lys  
 660 665 670  
 His Pro Val Phe Phe Ala Glu Leu Asn Leu Asp Leu Leu Cys Lys Met  
 675 680 685  
 Leu Lys Lys Thr Thr Lys Leu Tyr Lys Pro Tyr Ala Ile Tyr Pro Ser  
 690 695 700  
 Ser Phe Arg Asp Leu Thr Leu Thr Val Pro Glu Asp Ile Pro Ala Asn  
 705 710 715 720  
 Leu Leu Arg Gln Lys Leu Leu His Glu Gly Ser Lys Trp Leu Glu Ser  
 725 730 735  
 Val Thr Ile Ile Ser Ile Tyr Gln Asp Lys Ser Leu Glu Thr Arg Asn  
 740 745 750  
 Lys Asn Val Ser Leu Arg Leu Val Phe Gln Asp Tyr Glu Arg Thr Leu  
 755 760 765  
 Ser Asn Gln Asp Ile Glu Glu Tyr Cys Arg Leu Val Ala Leu Leu  
 770 775 780  
 Asn Glu Leu Leu Thr Asp Thr Lys Gly Thr Ile Asn Ser  
 785 790 795

&lt;210&gt;637

&lt;211&gt;328

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;637

Arg Asp Tyr Gln Phe Met Lys Gln Leu Leu Phe Cys Val Cys Val Phe  
 1 5 10 15  
 Ala Met Ser Cys Ser Ala Tyr Ala Ser Pro Arg Arg Gln Asp Pro Ser  
 20 25 30  
 Val Met Lys Glu Thr Phe Arg Asn Asn Tyr Gly Ile Ile Val Ser Gly  
 35 40 45  
 Gln Glu Trp Val Lys Arg Gly Ser Asp Gly Thr Ile Thr Lys Val Leu  
 50 55 60  
 Lys Asn Gly Ala Thr Leu His Glu Val Tyr Ser Gly Gly Leu Leu His  
 65 70 75 80  
 Gly Glu Ile Thr Leu Thr Phe Pro His Thr Thr Ala Leu Asp Val Val  
 85 90 95  
 Gln Ile Tyr Asp Gln Gly Arg Leu Val Ser Arg Lys Thr Phe Phe Val  
 100 105 110  
 Asn Gly Leu Pro Ser Gln Glu Glu Leu Phe Asn Glu Asp Gly Thr Phe  
 115 120 125  
 Val Leu Thr Arg Trp Pro Asp Asn Asn Asp Ser Asp Thr Ile Thr Lys  
 130 135 140  
 Pro Tyr Phe Ile Glu Thr Thr Tyr Gln Gly His Val Ile Glu Gly Ser  
 145 150 155 160  
 Tyr Thr Ser Phe Asn Gly Lys Tyr Ser Ser Ser Ile His Asn Gly Glu  
 165 170 175  
 Gly Val Arg Ser Val Phe Ser Ser Asn Asn Ile Leu Leu Ser Glu Glu



180 185 190  
 Thr Phe Asn Glu Gly Val Met Val Lys Tyr Thr Thr Phe Tyr Pro Asn  
 195 200 205  
 Arg Asp Pro Glu Ser Ile Thr His Tyr Gln Asn Gly Gln Pro His Gly  
 210 215 220  
 Leu Arg Leu Thr Tyr Leu Gln Gly Gly Ile Pro Asn Thr Ile Glu Glu  
 225 230 235 240  
 Trp Arg Tyr Gly Phe Gln Asp Gly Thr Thr Ile Val Phe Lys Asn Gly  
 245 250 255  
 Cys Lys Thr Ser Glu Ile Ala Tyr Val Lys Gly Val Lys Glu Gly Leu  
 260 265 270  
 Glu Leu Arg Tyr Asn Glu Gln Glu Ile Val Ala Glu Glu Val Ser Trp  
 275 280 285  
 Arg Asn Asp Phe Leu His Gly Glu Arg Lys Ile Tyr Ala Gly Gly Ile  
 290 295 300  
 Gln Lys His Glu Trp Tyr Tyr Arg Gly Arg Ser Val Ser Lys Ala Lys  
 305 310 315 320  
 Phe Glu Arg Leu Asn Ala Ala Gly  
 325

&lt;210&gt;638

&lt;211&gt;460

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;638

Trp Glu Ser Ser Arg Ser Arg Val Thr Glu Asn Leu Lys Lys Met Arg  
 1 5 10 15  
 Ala Glu Lys Val Arg Glu Asn Ile Ser Lys Val Asn Ser Glu Met Val  
 20 25 30  
 Met Leu Leu Pro Lys Asp Thr Arg Thr Trp Glu Met Glu Arg Arg Tyr  
 35 40 45  
 Met Ser Thr Tyr Glu Gln Leu Gly Ile Leu Ile Lys Ala Lys Tyr Arg  
 50 55 60  
 Lys Lys Gln Glu Ala Ser Val Lys Lys Tyr Gln Val Ala Phe Glu Glu  
 65 70 75 80  
 Lys Arg Gln Ser Pro Met Pro Thr Leu Arg His Leu Glu Met Lys Asn  
 85 90 95  
 Glu Gly Ile Cys Leu Lys Arg Leu Gln Gln Arg Val Asp Lys Met Gln  
 100 105 110  
 Arg Pro Tyr Glu Met Ala Gln Gln Ala Trp Asn Arg Ala Thr Asp Asn  
 115 120 125  
 Tyr Arg Pro Phe Leu Met Ala Leu Thr Arg Ile Glu His Glu Leu Arg  
 130 135 140  
 Leu Ala Asp Tyr Asn Asn Trp Gly Gln Pro Glu Asp Leu Cys Ile Ala  
 145 150 155 160  
 Tyr Ala Asn Val Glu Lys Arg Ala Glu Pro Tyr Lys Lys Ser Leu Leu  
 165 170 175  
 Glu Ile Arg Gln Val Leu Glu Asp Tyr Ala Lys Leu Arg Ser Ala Ile  
 180 185 190  
 Ser Phe Ile Gln Asp Lys Arg Leu Trp Ile Glu Lys Glu Ser Glu Asp  
 195 200 205  
 Leu Arg Ile Leu Ile Asn Pro Phe Phe Ser Ser Phe His Trp Glu Asp  
 210 215 220  
 Asp Ala Gly Gly Ser Arg Glu Met Asn Lys Tyr Val Pro Trp Trp Gln  
 225 230 235 240  
 Leu Ser Arg Val Thr Arg Lys Asp Leu Leu Ala Ala Leu Val Phe Gly  
 245 250 255  
 Ile Arg Ile Ala Leu Val Val Ala Gly Ile Gly Ile Thr Ile Ala Leu  
 260 265 270  
 Ala Ile Gly Ile Met Ile Gly Leu Val Ser Gly Tyr Phe Gly Gly Thr  
 275 280 285  
 Val Asp Met Ile Leu Ser Arg Phe Thr Glu Ile Trp Glu Thr Met Pro  
 290 295 300  
 Val Leu Phe Ile Leu Met Leu Val Ile Ser Ile Thr Gln Gln Lys Ser  
 305 310 315 320

Leu Leu Leu Asn Thr Val Leu Leu Gly Cys Phe Ser Trp Thr Gly Phe  
 325 330 335  
 Ser Arg Tyr Val Arg Ile Glu Val Leu Lys Gln Arg Asp Arg Gly Tyr  
 340 345 350  
 Val Leu Ala Ala Thr Asn Leu Gly Tyr Ser His Tyr Tyr Ile Met Val  
 355 360 365  
 His Gln Ile Leu Pro Asn Ala Ile Val Pro Val Ile Ser Leu Val Pro  
 370 375 380  
 Phe Ala Met Met Ala Met Ile Ser Cys Glu Ala Gly Leu Thr Phe Leu  
 385 390 395 400  
 Gly Leu Gly Glu Glu Ser Ser Ala Ser Trp Gly Asn Leu Met Arg Glu  
 405 410 415  
 Gly Val Thr Gly Phe Pro Ala Glu Ser Ala Val Leu Trp Pro Pro Ala  
 420 425 430  
 Ile Ile Leu Thr Met Leu Leu Ile Ala Ile Ala Leu Ile Gly Asp Gly  
 435 440 445  
 Val Arg Asp Ala Leu Asp Pro Arg Leu Gln Asp Ser  
 450 455 460

&lt;210&gt;639

&lt;211&gt;510

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;639

Val Leu Lys Tyr Ile Leu Lys Arg Leu Val Leu Ile Pro Leu Thr Leu  
 1 5 10 15  
 Phe Ala Ile Val Ser Ile Asn Phe Val Ile Leu Asn Ala Ala Pro Gly  
 20 25 30  
 Asp Val Leu Glu Glu Lys Ser Arg Asp Ala Leu Gly Glu Ala Gly Lys  
 35 40 45  
 Ser Asp Lys Met Arg Ser Tyr Lys Gly Pro Asp Arg Tyr Leu Gln Phe  
 50 55 60  
 Arg Glu His Tyr Gly Leu Thr Leu Pro Ile Phe Phe Asn Thr Arg Pro  
 65 70 75 80  
 Lys Ile Thr His Lys Lys Ile Gln Thr Ala Leu Gln Glu Leu Ala Asn  
 85 90 95  
 Ala Asn Asn Thr Thr Pro Ser Ala Lys Asn Ala Ala Lys Ser Leu Val  
 100 105 110  
 Tyr Trp Gly Asp Cys Ala Lys Phe Val Met Pro Ala Leu Leu Phe Glu  
 115 120 125  
 Ala Asp Asp Ala Ser Arg Asp Asp Lys Tyr Arg His Ile Ala Ala Asp  
 130 135 140  
 Leu Phe Ile Arg Gly Gly Val Leu Gln Gly Phe Val Gly Pro Asn Leu  
 145 150 155 160  
 Ser Pro Glu Gln Arg Ala Gln Asn Lys Glu Ile Ala Glu Ser Asn Ala  
 165 170 175  
 Phe Leu Val Arg Gln Leu Asn Glu Glu Asp Leu Asp Thr Lys Val Glu  
 180 185 190  
 Ala Leu Lys Gly Trp Phe Gln Asp His Gly Gly Thr Glu Val Phe Cys  
 195 200 205  
 Tyr Ser Ser Lys Gln Phe Trp Lys Thr Phe Phe Leu Glu Thr Arg Phe  
 210 215 220  
 Ala Arg Tyr Met Ser Arg Val Leu Arg Leu Asp Phe Gly Thr Leu Arg  
 225 230 235 240  
 Asn Asp Ala His Lys Thr Val Ile Ser Glu Val Ile Lys Arg Leu Arg  
 245 250 255  
 Cys Ser Leu Val Leu Ser Ile Leu Pro Met Ile Val Gly Phe Val Leu  
 260 265 270  
 Cys Gln Ile Phe Gly Met Ile Met Ala Leu Lys Arg Asn Arg Trp Ile  
 275 280 285  
 Asp His Ser Leu Asn Phe Ile Phe Leu Ile Leu Phe Ser Ile Pro Val  
 290 295 300  
 Phe Val Ala Val Pro Trp Ile Leu Asp Asn Phe Val Ile Asn Lys Thr  
 305 310 315 320  
 Ile Pro Phe Thr Thr Ile Pro Met Pro Tyr Ser Gly Leu Arg Ser Pro

325 330 335  
 Pro Glu Val Phe Asn Glu Leu Ser Thr Leu Gly Arg Ile Phe Asp Leu  
 340 345 350  
 Val Ser His Gly Phe Leu Pro Phe Cys Ala Val Ser Tyr Gly Ala Leu  
 355 360 365  
 Ala Ala Gln Ser Arg Leu Ser Arg Ser Ile Phe Leu Glu Val Leu Ser  
 370 375 380  
 Gln Asp Phe Ile Cys Ala Ala Lys Ala Arg Gly Leu Arg Trp Phe Asp  
 385 390 395 400  
 Ile Leu Tyr Lys His Val Gly Lys Asn Ala Ala Val Ser Ile Val Thr  
 405 410 415  
 Ser Leu Ala Ser Ser Phe Arg Asn Val Thr Trp Arg Gly Val Gly Cys  
 420 425 430  
 Arg Asn Pro Ile Gln Tyr Arg Trp Leu Trp Glu Leu Leu Leu Ser Gly  
 435 440 445  
 Asn Phe Lys Ser Arg Ser Gln Cys Ser Ser Ile Phe Cys Ala Cys Arg  
 450 455 460  
 Ile Gly Ser Ile Phe Ser Gly Ile Phe Ala Arg Arg Tyr Leu Leu Arg  
 465 470 475 480  
 Thr Leu Arg Ser Ser Ser Ser Ala Arg Gly Lys Glu Asp Ile Asn Ala  
 485 490 495  
 Glu Ala Ser Phe Leu Leu Ser Thr Phe Ser Ile Cys Leu Leu  
 500 505 510

&lt;210&gt;640

&lt;211&gt;713

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;640

Lys Arg Arg Glu Ser Gly His Met Tyr Lys Arg Cys Val Leu Asp Lys  
 1 5 10 15  
 Ile Leu Lys Gly Ile Val Ala Gly Ser Leu Ile Leu Leu Tyr Trp Ser  
 20 25 30  
 Ser Asp Leu Leu Glu Arg Asp Ile Lys Ser Ile Lys Gly Asn Val Arg  
 35 40 45  
 Asp Ile Gln Glu Asp Ile Arg Glu Ile Ser Arg Val Val Lys Gln Gln  
 50 55 60  
 Gln Thr Ser Gln Ala Ile Pro Ala Ala Pro Gly Val Met Leu Ala Pro  
 65 70 75 80  
 Lys Leu Val Arg Asp Glu Ala Phe Ala Leu Leu Phe Gly Asp Pro Ser  
 85 90 95  
 Tyr Pro Asn Leu Leu Ser Leu Asp Pro Tyr Lys Gln Gln Thr Leu Pro  
 100 105 110  
 Glu Leu Leu Gly Thr Asn Phe His Pro His Gly Ile Leu Arg Thr Ala  
 115 120 125  
 His Val Gly Lys Pro Glu Xaa Leu Ser Leu Leu Met Ala Leu Ile Cys  
 130 135 140  
 Arg Gly Leu Leu Arg Ser Leu Tyr Ser Ser Leu Ala Ser Pro His Val  
 145 150 155 160  
 Gly Lys Tyr Glu Glu Phe Ser Pro Asp Leu Ala Val Lys Ile Glu Glu  
 165 170 175  
 His Leu Val Glu Asp Gly Ser Gly Asp Lys Glu Phe His Ile Tyr Leu  
 180 185 190  
 Arg Pro Asn Val Phe Trp Arg Pro Ile Asp Pro Lys Ala Leu Pro Lys  
 195 200 205  
 His Val Gln Leu Asp Glu Val Phe Gln Arg Pro His Pro Val Thr Ala  
 210 215 220  
 His Asp Ile Lys Phe Phe Tyr Asp Ala Val Met Asn Pro Tyr Val Ala  
 225 230 235 240  
 Thr Met Arg Ala Val Ala Leu Arg Ser Cys Tyr Glu Asp Val Val Ser  
 245 250 255  
 Val Ser Val Glu Asn Asp Leu Lys Leu Val Val Arg Trp Lys Ala His  
 260 265 270  
 Thr Val Ile Asn Glu Glu Gly Lys Glu Glu Arg Lys Val Leu Tyr Ser  
 275 280 285

Ala Phe Ser Asn Thr Leu Ser Leu Gln Pro Leu Pro Arg Phe Val Tyr  
 290 295 300  
 Gln Tyr Phe Ala Asn Gly Lys Ile Ile Glu Asp Glu Asn Ile Asp  
 305 310 315 320  
 Thr Tyr Arg Thr Asn Ser Ile Trp Ala Gln Asn Phe Thr Met His Trp  
 325 330 335  
 Ala Asn Asn Tyr Ile Val Ser Cys Gly Ala Tyr Tyr Phe Ala Gly Met  
 340 345 350  
 Asp Asp Glu Lys Ile Val Phe Ser Arg Asn Pro Asp Phe Tyr Asp Pro  
 355 360 365  
 Leu Ala Ala Leu Ile Asp Lys Arg Phe Val Tyr Phe Lys Glu Ser Thr  
 370 375 380  
 Asp Ser Leu Phe Gln Asp Phe Lys Thr Gly Lys Ile Asp Ile Ser Tyr  
 385 390 395 400  
 Leu Pro Pro Asn Gln Arg Asp Asn Phe Tyr Ser Phe Met Lys Ser Ser  
 405 410 415  
 Ala Tyr Asn Lys Gln Val Ala Lys Gly Gly Ala Val Arg Glu Thr Val  
 420 425 430  
 Ser Ala Asp Arg Ala Tyr Thr Tyr Ile Gly Trp Asn Cys Phe Ser Leu  
 435 440 445  
 Phe Phe Gln Ser Arg Gln Val Arg Cys Ala Met Asn Met Ala Ile Asp  
 450 455 460  
 Arg Glu Arg Ile Ile Glu Gln Cys Leu Asp Gly Gln Gly Tyr Thr Ile  
 465 470 475 480  
 Ser Gly Pro Phe Ala Ser Ser Ser Pro Ser Tyr Asn Lys Gln Ile Glu  
 485 490 495  
 Gly Trp His Tyr Ser Pro Glu Glu Ala Ala Arg Leu Leu Glu Glu Glu  
 500 505 510  
 Gly Trp Ile Asp Thr Asp Gly Asp Gly Ile Arg Glu Lys Val Ile Asp  
 515 520 525  
 Gly Val Ile Val Pro Phe Arg Phe Arg Leu Cys Tyr Tyr Val Lys Ser  
 530 535 540  
 Val Thr Ala His Thr Ile Ala Asp Tyr Val Ala Thr Ala Cys Lys Glu  
 545 550 555 560  
 Ile Gly Ile Glu Cys Ser Leu Leu Gly Leu Asp Met Ala Asp Leu Ser  
 565 570 575  
 Gln Ala Phe Asp Glu Lys Asn Phe Asp Ala Leu Leu Met Gly Trp Cys  
 580 585 590  
 Leu Gly Ile Pro Pro Glu Asp Pro Arg Ala Leu Trp His Ser Glu Gly  
 595 600 605  
 Ala Met Glu Lys Gly Ser Ala Asn Val Val Gly Phe His Asn Glu Glu  
 610 615 620  
 Ala Asp Lys Ile Ile Asp Arg Leu Ser Tyr Glu Tyr Asp Leu Lys Glu  
 625 630 635 640  
 Arg Asn Arg Leu Tyr His Arg Phe His Glu Ile Ile His Glu Glu Ala  
 645 650 655  
 Pro Tyr Ala Phe Leu Phe Ser Arg His Cys Ser Leu Leu Tyr Lys Asp  
 660 665 670  
 Tyr Val Lys Asn Ile Phe Val Pro Thr His Arg Thr Asp Leu Ile Pro  
 675 680 685  
 Glu Ala Gln Asp Glu Thr Val Asn Val Thr Met Val Trp Leu Glu Lys  
 690 695 700  
 Lys Glu Asp Pro Cys Leu Ser Thr Ser  
 705 710  
 <210>641  
 <211>210  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>641  
 Gln Phe Pro Arg Ile His Ala Asp Asp Ile Ile Asn Ser Met Asp Glu  
 1 5 10 15  
 Ile Thr Pro Asn Tyr Pro Leu Leu Arg Gln Asp Ser Leu Trp Asn Arg  
 20 25 30  
 Val Arg Val Ser Trp Arg Ala Asp Leu Ser Val Ser Ser Arg Tyr Glu

```

      35      40      45
Ile Ala Ser Ala Ile Ala Ile Leu Gly Leu Leu Val Ala Phe Cys Ala
      50      55      60
Ser Ala Ala Val Ser Ile Ile Phe Thr Ala Asn Pro Ser Cys Ser Gly
      65      70      75      80
Ile Tyr Arg Trp Leu Phe Gly Phe Arg Ala Phe Thr Tyr Pro Ile Gly
      85      90      95
Tyr Arg Ser Thr Asn His Arg Asn Tyr Ser Phe Thr Leu Trp Tyr Leu
      100      105      110
Leu Val Ser Ser Thr Thr Arg Val Ile Thr Leu Ser Ile Cys Phe Tyr
      115      120      125
Thr Phe Tyr Leu Gln Ile Ile Phe Leu Phe Leu Tyr Ser Ala Trp Lys
      130      135      140
Pro Leu Arg Gln Pro Leu Phe Cys His Arg Leu Leu Ile Ile Trp Pro
      145      150      155      160
Ile Ser Gly Leu Ser Cys Arg Ile Leu Asn Lys Glu Asn Lys Asn Glu
      165      170      175
Lys Ile Asn Val Ser Pro Ser Phe Ser Ser Cys Ala Ser Cys Cys Arg
      180      185      190
Phe Cys Phe Trp Ile Arg Ile Leu Phe Ser Thr Thr Arg Arg Ser Ser
      195      200      205
Arg Phe
      210
<210>642
<211>338
<212>PRT
<213>Chlamydia pneumoniae
<400>642
Asp Ser Gly Phe Met Lys Pro Leu Gly Phe Gln Glu Asn Leu Glu Ala
      1      5      10      15
Leu Cys Asn Lys Thr Ser Arg Gln Leu Leu Lys Tyr Leu Ile Lys Gln
      20      25      30
Ile Leu Phe Val Cys Gly Ala Ser Leu Leu Ile Ala Leu Glu Phe Ser
      35      40      45
Phe Phe Leu Tyr Phe Phe Leu Phe Ser Gly Lys Thr Val Ile Pro Ala
      50      55      60
Phe Cys Leu Ala Cys Phe Phe Leu Thr Leu Phe Val Cys Leu Val Thr
      65      70      75      80
Arg Leu Tyr Leu Leu Ser Gly Lys Gly Asp Phe Phe Glu Asp Leu Ala
      85      90      95
Ser Glu Tyr Leu Gln Gly Ala Val Pro Asn Lys Arg Ser Gln Asn
      100      105      110
Ile Val Glu Glu Gln Ser His Leu Ala Ala Ala Ala Thr Lys Leu Ser
      115      120      125
Ile Asn Leu Gln Asn Gln Glu Tyr Ser Leu Leu Ser Glu Ile Phe Lys
      130      135      140
Phe Leu Pro Lys His Asp Leu Ile Arg Lys Phe Ser Cys Phe Cys Phe
      145      150      155      160
Trp Lys Asp Tyr Phe Leu Phe Arg Glu Cys Leu Leu Gln Lys Ala Ile
      165      170      175
Glu Ala Tyr Ile Lys Val Val Gln Ala Ile Pro Val Asp Leu Ser Ala
      180      185      190
His Val Ser Leu Ala Asp Ala Tyr Val Ala Leu Ser Gly Leu Tyr Ala
      195      200      205
Asp Pro Arg Lys Tyr Pro Glu Phe Asp Ala Asn Tyr Trp Ile Pro Ser
      210      215      220
Gly Arg Tyr Ser Ala Glu Ile Gln Glu Lys Phe Phe Ala Thr Ala Arg
      225      230      235      240
Arg Ala Ile Glu Glu Phe Gln Ile Leu Asn Glu Tyr Ala Pro Gly Asn
      245      250      255
Ala Trp Val His Ala Gln Leu Ala Tyr Ser Tyr His Asp Leu Gln Met
      260      265      270
Pro Met Glu Glu Ile Gln Glu Tyr Glu Ile Val Leu Lys Leu Lys Pro
      275      280      285

```

Asn Asp Val Glu Thr Met Ser Lys Leu Gly Ile Leu Tyr Phe Gln Gln  
 290 295 300  
 Gly Met Asn Ala Lys Gly Leu Arg Ile Tyr Glu Glu Ile Lys Lys Arg  
 305 310 315 320  
 Asp Tyr Lys Lys Ser Gln Lys Leu Ile Lys Phe Tyr Gly Val Glu Tyr  
 325 330 335  
 Lys Tyr

&lt;210&gt;643

&lt;211&gt;350

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;643

Trp Lys Ile Met Arg Leu Ile Val Leu Met Gln Cys Leu Val Ser Leu  
 1 5 10 15  
 Phe Leu Ala Lys Lys Val Thr Val Thr Thr Pro Ala Tyr Leu Leu Ala  
 20 25 30  
 Asn Phe Gly Gly Pro Arg His Ala Lys Asp Leu Gln Glu Phe Leu Ile  
 35 40 45  
 Ser Leu Leu Thr Asp Arg Asp Val Thr Gly Thr Phe Leu Pro Arg Val  
 50 55 60  
 Leu His Arg His Leu Phe Thr Phe Ile Ala Lys Lys Arg Val Pro Lys  
 65 70 75 80  
 Val Leu Pro Gln Tyr Gln Ser Leu Gln Asn Trp Ser Pro Ile Tyr Phe  
 85 90 95  
 Asp Thr Glu Thr Leu Ala Lys Thr Leu Ser Glu Ile Leu Arg Ala Pro  
 100 105 110  
 Val Ile Pro Phe His Arg Tyr Leu Pro Ser Thr His Glu Lys Thr Leu  
 115 120 125  
 Leu Ala Leu Arg Thr Leu His Thr Arg His Val Ile Gly Ile Pro Leu  
 130 135 140  
 Phe Pro His Phe Thr Tyr Ser Val Thr Gly Ser Ile Val Arg Phe Phe  
 145 150 155 160  
 Met Lys His Val Pro Glu Ile Pro Ile Ser Trp Ile Pro Gln Phe Gly  
 165 170 175  
 Ser Asp Ser Lys Phe Val Ser Leu Ile Thr Cys His Ile Arg Asp Phe  
 180 185 190  
 Leu Gln Lys Leu Gly Ile Leu Glu Lys Glu Cys Cys Phe Leu Phe Ser  
 195 200 205  
 Val His Gly Leu Pro Val Arg Tyr Ile Ser Gln Gly Asp Pro Tyr Ser  
 210 215 220  
 Lys Gln Cys Tyr Glu Ser Phe Ser Ala Ile Thr Thr Asn Phe Lys Gln  
 225 230 235 240  
 Ser Glu Asn Phe Leu Cys Phe Gln Ser Lys Phe Gly Pro Gly Lys Trp  
 245 250 255  
 Leu Ser Pro Ser Thr Ala Gln Leu Cys Gln Asn Ile Asp Thr Asp Lys  
 260 265 270  
 Pro Asn Val Ile Val Val Pro Phe Gly Phe Ile Ser Asp His Leu Glu  
 275 280 285  
 Thr Leu Tyr Glu Ile Glu Arg Asp Tyr Leu Pro Leu Leu Arg Ser Arg  
 290 295 300  
 Gly Tyr Arg Ala Leu Arg Ile Pro Ala Ile Tyr Ser Ser Pro Leu Trp  
 305 310 315 320  
 Val Ser Thr Leu Val Asp Ile Val Lys Glu Asn Ser Thr Val Val Ala  
 325 330 335  
 Glu Glu Leu Ile Lys Ser Gly Lys Lys His Thr Gly Ile Arg  
 340 345 350

&lt;210&gt;644

&lt;211&gt;257

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;644

Asn Ser Glu Ala Gln Leu Asn Val Lys Ile Lys Phe Ser Trp Lys Val  
 1 5 10 15

Asn Phe Leu Ile Cys Leu Leu Ala Val Gly Leu Ile Phe Phe Gly Cys  
                   20                  25                  30  
 Ser Arg Val Lys Arg Glu Val Leu Val Gly Arg Asp Ala Thr Trp Phe  
                   35                  40                  45  
 Pro Lys Gln Phe Gly Ile Tyr Thr Ser Asp Thr Asn Ala Phe Leu Asn  
                   50                  55                  60  
 Asp Leu Val Ser Glu Ile Asn Tyr Lys Glu Asn Leu Asn Ile Asn Ile  
                   65                  70                  75  
 Val Asn Gln Asp Trp Val His Leu Phe Glu Asn Leu Asp Asp Lys Lys  
                   85                  90                  95  
 Thr Gln Gly Ala Phe Thr Ser Val Leu Pro Thr Leu Glu Met Leu Glu  
                   100                  105                  110  
 His Tyr Gln Phe Ser Asp Pro Ile Leu Leu Thr Gly Pro Val Leu Val  
                   115                  120                  125  
 Val Ala Gln Asp Ser Pro Tyr Gln Ser Ile Glu Asp Leu Lys Gly Arg  
                   130                  135                  140  
 Leu Ile Gly Val Tyr Lys Phe Asp Ser Ser Val Leu Val Ala Gln Asn  
                   145                  150                  155                  160  
 Ile Pro Asp Ala Val Ile Ser Leu Tyr Gln His Val Pro Ile Ala Leu  
                   165                  170                  175  
 Glu Ala Leu Thr Ser Asn Cys Tyr Asp Ala Leu Leu Ala Pro Val Ile  
                   180                  185                  190  
 Glu Val Thr Ala Leu Ile Glu Thr Ala Tyr Lys Gly Arg Leu Lys Ile  
                   195                  200                  205  
 Ile Ser Lys Pro Leu Asn Ala Asp Gly Leu Arg Leu Ala Ile Leu Lys  
                   210                  215                  220  
 Gly Thr Asn Gly Asp Leu Leu Glu Gly Phe Asn Ala Gly Leu Val Lys  
                   225                  230                  235                  240  
 Thr Arg Arg Ser Gly Lys Tyr Asp Ala Ile Lys Gln Arg Tyr Arg Leu  
                   245                  250                  255  
 Pro

&lt;210&gt;645

&lt;211&gt;196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;645

Leu Arg Lys Leu Cys Ser Ser Arg Gly Asp Val Arg Ile Leu Ala Gly  
                   1                  5                  10                  15  
 Lys Tyr Lys Gly Lys Ser Leu Lys Thr Phe Ser Asn Pro His Ile Arg  
                   20                  25                  30  
 Pro Thr Ser Gly Leu Val Lys Glu Ala Phe Phe Ser Ile Cys Arg Glu  
                   35                  40                  45  
 Asp Ile Glu Gly Ala Ala Phe Leu Asp Leu Phe Ala Gly Met Gly Ala  
                   50                  55                  60  
 Ile Gly Phe Glu Ala Leu Ser Arg Gly Ala Ala Ser Val Val Phe Val  
                   65                  70                  75                  80  
 Asp Ile Ser Ile Lys Ala Ile Gln Leu Ile His Thr Asn Ser Ala Leu  
                   85                  90                  95  
 Leu Gly Glu Gln Leu Pro Val Val Ile Phe Arg Gln Asp Ala Gln Ser  
                   100                  105                  110  
 Ala Ile Gln Arg Leu Ile Lys Gln Lys Arg Ser Phe Asp Leu Ile Tyr  
                   115                  120                  125  
 Ile Asp Pro Pro Tyr Glu Leu Cys Asn Cys Tyr Val Glu Thr Leu Leu  
                   130                  135                  140  
 Gln Lys Ile Val Ser Gly Asn Ile Leu Asn Pro Glu Gly Thr Leu Phe  
                   145                  150                  155                  160  
 Leu Glu Asn Ala Ser Asp Glu Glu Ile Ala Cys Glu Gly Leu Thr Leu  
                   165                  170                  175  
 Arg Arg Arg Arg Lys Leu Gly Lys Thr Tyr Leu Ala Glu Tyr Ile Val  
                   180                  185                  190  
 Glu Lys Asp Pro  
                   195

&lt;210&gt;646

&lt;211&gt;262

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;646

```

Ser Ser Tyr Ser Arg Arg Gln Leu Arg Phe Tyr Thr Gly Ser Leu Gln
 1          5          10          15
Met His Ile Tyr Gly Leu Ala Asp Leu His Leu Ala Leu Gly Val Pro
          20          25          30
Glu Lys Thr Met Glu Val Phe Gly Asp Pro Trp Ile Gly Tyr His Gln
          35          40          45
Lys Ile Cys Ser Glu Trp Gln Ala Val Val His Pro Glu Asp Ile Val
          50          55          60
Leu Leu Pro Gly Asp Ile Ser Trp Ala Met Asn Leu Ser Glu Ala His
          65          70          75          80
Lys Asp Phe Ala Phe Ile Gly Asp Leu Pro Gly Thr Lys Tyr Met Ile
          85          90          95
Arg Gly Asn His Asp Tyr Trp Ser Ser Ala Ser Thr Ser Lys Ile Leu
          100          105          110
Gln Ala Leu Pro Pro Ser Leu Tyr Tyr Leu Asn Gln Gly Phe Ala Leu
          115          120          125
Leu Thr Pro His Leu Ala Val Val Gly Val Arg Leu Trp Asp Ser Pro
          130          135          140
Thr Ile Cys Val Lys Lys Glu Asn Phe Leu Thr Pro Ser Thr Gln Glu
          145          150          155          160
Gln Ser Tyr Thr Glu Gln Asp Glu Lys Ile Phe Leu Arg Glu Leu Gly
          165          170          175
Arg Leu Lys Arg Ala Phe Ala Ala Leu Pro Lys Glu Val Thr Glu Val
          180          185          190
Ile Val Met Thr His Tyr Pro Pro Ile Ser Ser Asp Gly Thr Pro Gly
          195          200          205
Pro Ile Ser Glu Phe Leu Glu Ala Asp Gly Arg Val Ser Leu Cys Leu
          210          215          220
Phe Gly His Ile His Lys Val Gln Arg Pro Ile Asp Gly Phe Gly Asn
          225          230          235          240
Ile Arg Gly Ile His Tyr Ile Leu Val Ala Ala Asp Tyr Val Asn Phe
          245          250          255
Val Pro Gln Glu Val Met
          260

```

&lt;210&gt;647

&lt;211&gt;330

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;647

```

Pro Asn Leu Val Ser Gly Tyr Ala Asp Ala Ile Arg Lys Asn Leu Leu
 1          5          10          15
Tyr Phe Glu Asp Thr Glu Ile Glu Tyr Phe Leu Ile Leu Ser Gly Asp
          20          25          30
Gln Leu Tyr Asn Met Asp Phe Arg Ser Ile Val Asp Thr Ala Ile Arg
          35          40          45
Thr His Val Asp Met Val Leu Val Ala Gln Pro Ile Pro Glu Lys Asp
          50          55          60
Ala Tyr Arg Met Gly Val Leu Asp Ile Asp Ser Glu Gly Lys Leu Ile
          65          70          75          80
Asp Phe Tyr Glu Lys Pro Gln Glu Lys Glu Val Leu Lys Arg Phe Gln
          85          90          95
Leu Ser Ser Glu Asp Arg Arg Ile His Lys Leu Thr Glu Asp Ser Gly
          100          105          110
Asp Phe Leu Gly Ser Met Gly Ile Tyr Leu Phe Arg Arg Asp Ser Leu
          115          120          125
Phe Ser Leu Leu Arg Glu Glu Glu Gly Asn Asp Phe Gly Lys His Leu
          130          135          140
Ile Gln Ala Gln Met Lys Arg Gly Gln Val Gln Thr Leu Leu Tyr Asn
          145          150          155          160
Gly Tyr Trp Ala Asp Ile Gly Thr Ile Glu Ser Tyr Tyr Glu Ala Asn

```



165 170 175  
 Ile Ala Leu Thr Gln Lys Pro His Ala Glu Lys Arg Gly Leu Asn Cys  
 180 185 190  
 Tyr Asp Asp Asn Gly Met Ile Tyr Ser Lys Asn His His Leu Pro Gly  
 195 200 205  
 Ala Ile Ile Thr Asp Ser Met Ile Ser Ser Ser Leu Leu Cys Glu Gly  
 210 215 220  
 Cys Val Ile Asn Thr Ser His Val Ser Arg Ser Val Leu Gly Ile Arg  
 225 230 235 240  
 Ser Lys Ile Gly Glu Asn Ser Val Val Asp Gln Ser Ile Ile Met Gly  
 245 250 255  
 Asn Ala Arg Tyr Gly Ser Pro Ser Met Pro Ser Leu Gly Ile Gly Lys  
 260 265 270  
 Asp Cys Glu Ile Arg Lys Ala Ile Ile Asp Glu Asn Cys Cys Ile Gly  
 275 280 285  
 Asn Gly Val Lys Leu Gln Asn Leu Lys Gly Tyr Ile Lys Tyr Asp Ser  
 290 295 300  
 Pro Asp Lys Lys Leu Phe Val Arg Asp Asn Ile Ile Ile Val Pro Gln  
 305 310 315 320  
 Gly Thr His Ile Pro Asp Asn Tyr Ile Phe  
 325 330

&lt;210&gt;648

&lt;211&gt;225

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;648

Val Ser Phe Leu Tyr Phe Val Lys Asn Gly Arg Arg Leu Trp Arg Met  
 1 5 10 15  
 Met Asn Tyr Glu Asp Ala Lys Leu Arg Gly Gln Ala Val Ala Ile Leu  
 20 25 30  
 Tyr Gln Ile Gly Ala Ile Lys Phe Gly Lys His Ile Leu Ala Ser Gly  
 35 40 45  
 Glu Glu Thr Pro Leu Tyr Val Asp Met Arg Leu Val Ile Ser Ser Pro  
 50 55 60  
 Glu Val Leu Gln Thr Val Ala Thr Leu Ile Trp Arg Leu Arg Pro Ser  
 65 70 75 80  
 Phe Asn Ser Ser Leu Leu Cys Gly Val Pro Tyr Thr Ala Leu Thr Leu  
 85 90 95  
 Ala Thr Ser Ile Ser Leu Lys Tyr Asn Ile Pro Met Val Leu Arg Arg  
 100 105 110  
 Lys Glu Leu Gln Asn Val Asp Pro Ser Asp Ala Ile Lys Val Glu Gly  
 115 120 125  
 Leu Phe Thr Pro Gly Gln Thr Cys Leu Val Ile Asn Asp Met Val Ser  
 130 135 140  
 Ser Gly Lys Ser Ile Ile Glu Thr Ala Val Ala Leu Glu Glu Asn Gly  
 145 150 155 160  
 Leu Val Val Arg Glu Ala Leu Val Phe Leu Asp Arg Arg Lys Glu Ala  
 165 170 175  
 Cys Gln Pro Leu Gly Pro Gln Gly Ile Lys Val Ser Ser Val Phe Thr  
 180 185 190  
 Val Pro Thr Leu Ile Lys Ala Leu Ile Ala Tyr Gly Lys Leu Ser Ser  
 195 200 205  
 Gly Asp Leu Thr Leu Ala Asn Lys Ile Ser Glu Ile Leu Glu Ile Glu  
 210 215 220

Ser

225

&lt;210&gt;649

&lt;211&gt;464

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;649

Met Lys Glu Glu Arg Ser Ser Glu Ile Leu Pro Arg Val Lys Glu Thr  
 1 5 10 15  
 Lys Lys His Ala Tyr Val Ser Met Gln Glu Lys Ser Cys Val Gly Glu

20 25 30  
 Cys Ala Val Val Ala Ser Glu Ser Glu Glu Ala Glu Ser Val Thr Val  
 35 40 45  
 Thr Lys Ile Ala Lys Leu Gln Arg Met Gly Ile Glu Glu Leu Asn Ile  
 50 55 60  
 Leu Ala Arg Gln Tyr Gly Val Lys Asn Ile Gly Ser Leu Thr Lys Ser  
 65 70 75 80  
 Gln Val Val Phe Glu Ile Val Lys Ala Lys Ser Glu Arg Pro Asp Glu  
 85 90 95  
 Leu Leu Ile Gly Glu Gly Val Leu Glu Val Leu Pro Asp Gly Phe Gly  
 100 105 110  
 Phe Leu Arg Ser Pro Thr Tyr Asn Tyr Leu Pro Ser Ala Glu Asp Ile  
 115 120 125  
 Tyr Val Ser Pro Ala Gln Ile Arg Arg Phe Asp Leu Lys Lys Gly Asp  
 130 135 140  
 Thr Ile Ile Gly Thr Ile Arg Ser Pro Lys Glu Lys Glu Lys Tyr Phe  
 145 150 155 160  
 Ala Leu Leu Lys Val Asp Lys Ile Asn Gly Ser Thr Pro Asp Lys Ala  
 165 170 175  
 Lys Glu Arg Val Leu Phe Glu Asn Leu Thr Pro Leu Tyr Pro Asn Gln  
 180 185 190  
 Arg Ile Val Met Glu Met Gly Lys Asp His Leu Ala Glu Arg Val Leu  
 195 200 205  
 Asp Leu Thr Ala Pro Ile Gly Lys Gly Gln Arg Gly Leu Ile Val Ala  
 210 215 220  
 Pro Pro Arg Ser Gly Lys Thr Val Ile Leu Gln Ser Ile Ala His Ala  
 225 230 235 240  
 Ile Ala Val Asn Asn Pro Asp Ile Val Leu Ile Val Leu Leu Ile Asp  
 245 250 255  
 Glu Arg Pro Glu Glu Val Thr Asp Met Ile Arg Gln Val Arg Gly Glu  
 260 265 270  
 Val Val Ala Ser Thr Phe Asp Glu Gln Pro Glu Arg His Ile Gln Val  
 275 280 285  
 Ala Glu Met Val Ile Glu Lys Ala Arg Arg Leu Val Glu His Gly Asn  
 290 295 300  
 Asp Val Val Ile Leu Leu Asp Ser Ile Thr Arg Leu Ala Arg Ala Tyr  
 305 310 315 320  
 Asn Thr Val Gln Pro His Ser Gly Lys Ile Leu Thr Gly Gly Val Asp  
 325 330 335  
 Ala Ser Ala Leu His Lys Pro Lys Arg Phe Phe Gly Ala Ala Arg Asn  
 340 345 350  
 Ile Glu Gly Gly Gly Ser Leu Thr Ile Leu Ala Thr Ala Leu Ile Asp  
 355 360 365  
 Thr Gly Ser Arg Met Asp Glu Val Ile Phe Glu Glu Phe Lys Gly Thr  
 370 375 380  
 Gly Asn Met Glu Leu Val Leu Asp Arg Arg Leu Ser Asp Arg Arg Thr  
 385 390 395 400  
 Tyr Pro Ala Ile Asp Leu Ile Lys Ser Gly Thr Arg Lys Glu Glu Leu  
 405 410 415  
 Leu Tyr His Pro Ser Glu Leu Glu Arg Val Tyr Leu Phe Arg Gln Ala  
 420 425 430  
 Ile Ala Asp Leu Thr Thr Ile Asp Ala Met His Leu Leu Leu Gly Arg  
 435 440 445  
 Leu Lys Lys Thr Asn Ser Asn Ala Glu Phe Leu Leu Ser Leu Lys Glu  
 450 455 460  
 <210>650  
 <211>238  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>650  
 Arg Arg Asn Arg Arg Asp Ala Lys Thr Ser Glu Arg Glu Asp Gly Ile  
 1 5 10 15  
 Ser Tyr Asp Phe Ile Arg Ser Tyr Ser Cys Glu Tyr Leu Asn Trp Lys  
 20 25 30

Lys Leu Gly Arg Met Leu Lys Leu Leu Lys Val Ser Ile Thr Gly Asp  
 35 40 45  
 Leu Ser Ser Gly Lys Thr Glu Ala Cys Gln Val Phe Gln Glu Leu Gly  
 50 55 60  
 Ala Tyr Val Val Ser Ala Asp Glu Ile Ser His Ser Phe Leu Ile Pro  
 65 70 75 80  
 His Thr Arg Ile Gly Arg Arg Val Ile Asp Leu Leu Gly Ser Asp Val  
 85 90 95  
 Val Val Asp Gly Ala Phe Asp Ala Gln Ala Ile Ala Ala Lys Val Phe  
 100 105 110  
 Tyr Asn Ser Val Leu Leu Gln Gly Leu Glu Ala Ile Leu His Pro Glu  
 115 120 125  
 Val Cys Arg Ile Ile Glu Glu Gln Tyr His Gln Ser Ile Gln Asp Gly  
 130 135 140  
 Asn Tyr Pro Phe Phe Val Ala Glu Val Pro Leu Leu Tyr Glu Ile His  
 145 150 155 160  
 Tyr Ala Lys Trp Phe Asp Ser Val Ile Leu Val Met Ala Asn Glu Asp  
 165 170 175  
 Ile Arg Arg Glu Arg Phe Met Lys Lys Thr Gly Arg Ser Ser Glu Asp  
 180 185 190  
 Phe Asp Gln Arg Cys Ser Arg Phe Leu Asn Val Glu Glu Lys Leu Ala  
 195 200 205  
 Gln Ala Asp Val Val Val Glu Asn Asn Gly Thr Lys Lys Glu Leu His  
 210 215 220  
 Gln Lys Ile Glu Glu Tyr Phe Tyr Ala Leu Lys Gly Ala Leu  
 225 230 235

&lt;210&gt;651

&lt;211&gt;870

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;651

Met Lys Lys Leu Phe Val Leu Asp Ala Ser Gly Phe Ile Phe Arg Ala  
 1 5 10 15  
 Tyr Phe Ala Leu Pro Glu Met Lys Asn His Gln Gly Gln Ala Thr Gln  
 20 25 30  
 Ala Val Phe Gly Phe Ile Arg Ser Leu Asn Lys Leu Ile Lys Glu Phe  
 35 40 45  
 Ser Pro Glu Tyr Met Ile Ser Val Phe Asp Gly Pro Asn Asn Lys Gln  
 50 55 60  
 Ser Arg Gln Ala Ile Tyr Ala Asp Tyr Lys Ser Asn Arg Gln Lys Lys  
 65 70 75 80  
 Phe Glu Asp Ile Pro Pro Gln Ile Ala Leu Val Lys Glu Tyr Cys Ser  
 85 90 95  
 Leu Ile Gly Leu Ala Tyr Leu Glu Lys Glu Ser Val Glu Ala Asp Asp  
 100 105 110  
 Val Ile Ala Ser Ile Ala Lys Lys Ala Arg Glu Glu Asn Tyr Lys Val  
 115 120 125  
 Tyr Val Cys Thr Ala Asp Lys Asp Leu Leu Gln Leu Val Asn Asp His  
 130 135 140  
 Val Val Ala Trp Asn Pro Trp Ala Asp Gln Gly Val Val Gly Ile Ser  
 145 150 155 160  
 Glu Val Ile Glu Arg Tyr Gly Ile Pro Pro Gly Asn Ile Pro Asp Tyr  
 165 170 175  
 Leu Ala Leu Val Gly Asp Ser Ser Asp Asn Ile Pro Gly Leu Pro Gly  
 180 185 190  
 Cys Gly Pro Lys Lys Ala Ala Ala Leu Leu Lys Gln Phe Gly Ser Val  
 195 200 205  
 Glu Gly Leu Leu Glu Asn Leu Asp Ala Val Lys Gly Leu Ser Gln Thr  
 210 215 220  
 Met Leu Ser Glu Arg Gln Glu Thr Leu Lys Leu Ser Lys Arg Leu Ala  
 225 230 235 240  
 Leu Leu Asp Ser Asn Ile Pro Ile Pro Val Pro Ile Glu Ser Leu Thr  
 245 250 255  
 Phe Pro Gln His Pro Val Asp Glu Glu Lys Leu Ile His Phe Tyr Ile

										260											265											270	
Gln	Gln	Gly	Phe	Lys	Thr	Leu	Val	Pro	Ser	Lys	Gln	Thr	Glu	Ala	Ala																		
										275											280											285	
Thr	Val	Asp	Val	Gln	Ile	Ile	Lys	Asp	Ala	Glu	Ser	Leu	Thr	Asn	Ile																		
										290											295											300	
Leu	Asn	Leu	Val	Gln	Gly	Gly	Asp	Ile	Ala	Phe	Ala	Val	Ala	Tyr	Thr																		
305											310											315											320
Gly	Asn	His	Leu	Leu	Ser	Leu	Lys	Leu	Glu	Gly	Leu	Ala	Leu	Thr	Gln																		
										325											330											335	
Gly	Ser	Gly	Val	Phe	Phe	Ile	Ala	Leu	Glu	Glu	Glu	Gly	Thr	Lys	Ile																		
										340											345											350	
Leu	Pro	Ile	Leu	Lys	Asp	Phe	Phe	Leu	Arg	Glu	Asp	Leu	Thr	Phe	Tyr																		
										355											360											365	
Gly	Tyr	Asn	Leu	Lys	Arg	Asp	Cys	His	Ala	Leu	Leu	Asn	Ala	Gly	Ile																		
370											375											380											385
Val	Ile	Arg	Glu	Ile	Ser	Tyr	Asp	Leu	Ala	Leu	Ala	Glu	His	Leu	Thr																		
385											390											395											400
Asn	Gly	Gly	Gly	Lys	Ile	Ser	Phe	Gln	Ser	Leu	Leu	Val	Asn	His	Gly																		
										405											410											415	
Phe	Thr	Glu	Thr	Ala	His	Arg	Phe	Ala	Lys	Glu	Trp	Gly	Asn	Ser	Gly																		
										420											425											430	
Leu	Pro	Ile	Gly	Arg	Leu	Pro	Glu	Gln	Pro	Glu	Gln	Tyr	Phe	Gly	Glu																		
										435											440											445	
Phe	Val	Ala	Tyr	Leu	Pro	Ile	Ile	Lys	Asp	Ala	Ile	Leu	Glu	Glu	Ile																		
450											455											460											465
Asn	Arg	Lys	Asn	Leu	Asn	His	Ile	Leu	Ser	Asp	Ile	Glu	Met	Pro	Leu																		
465											470											475											480
Glu	Lys	Val	Leu	Phe	Ser	Met	Glu	Arg	Ala	Gly	Val	Pro	Leu	Asp	Val																		
										485											490											495	
Glu	Glu	Leu	Ala	Ile	Leu	Glu	Ala	Leu	Phe	Glu	Thr	Glu	Leu	Ala	Val																		
										500											505											510	
Leu	Thr	Glu	Glu	Ile	Tyr	Asp	Leu	Ser	Gly	Arg	Pro	Phe	Asn	Ile	Lys																		
515											520											525											530
Ser	Pro	Lys	Gln	Leu	Ser	Asp	Ile	Leu	Tyr	Asn	Glu	Leu	Gly	Leu	Arg																		
530											535											540											545
Pro	Ile	Asp	Lys	Ala	Lys	Ser	Thr	Arg	Ala	Glu	Val	Leu	Glu	Ala	Leu																		
545											550											555											560
Arg	Ser	Glu	His	Pro	Ile	Ile	Glu	Lys	Leu	Leu	Ala	Phe	Arg	Thr	Ile																		
										565											570											575	
Glu	Lys	Leu	Leu	Ser	Thr	Tyr	Val	Lys	Ala	Leu	Pro	Lys	Gln	Val	Asp																		
										580											585											590	
Ser	His	Thr	Gln	Arg	Ile	His	Pro	Ser	Phe	Asp	Gln	Thr	Gly	Ala	Val																		
595											600											605											610
Thr	Gly	Arg	Leu	Ala	Cys	Arg	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile																		
610											615											620											625
Arg	Ser	Glu	Arg	Gly	Ile	Leu	Leu	Arg	Lys	Ala	Phe	Arg	Leu	Ser	Glu																		
625											630											635											640
Lys	Asn	Ser	Tyr	Phe	Leu	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg																		
										645											650											655	
Phe	Leu	Ala	His	Leu	Ser	Gln	Asp	Lys	Ser	Leu	Lys	Phe	Ala	Phe	Glu																		
										660											665											670	
Ser	Gly	Glu	Asp	Ile	His	Ala	Phe	Thr	Ala	Ser	Gln	Val	Phe	His	Val																		
										675											680											685	
Pro	Leu	Glu	Gln	Val	Ser	Lys	Glu	Gln	Arg	Met	Gln	Ala	Lys	Thr	Val																		
690											695											700											705
Asn	Phe	Gly	Ile	Val	Tyr	Gly	Gln	Gln	Ala	Phe	Gly	Leu	Ala	Lys	Val																		
705											710											715											720
Leu	Lys	Ile	Ser	Ile	Gly	Glu	Val	Gln	Glu	Leu	Ile	Gln	Ala	Tyr	Phe																		
										725											730											735	
Ser	Arg	Tyr	Pro	Glu	Ile	Ala	His	Phe	Val	Glu	Glu	Thr	Ile	Gln	Gln																		
										740											745											750	
Ala	Ala	Lys	Asp	Leu	Arg	Val	Thr	Met	Leu	Gly	Arg	Glu	Arg	Ile																			
755											760											765											770
Ile	Asp	Ser	Trp	Asn	Glu	Phe	Pro	Gly	Ser	Arg	Ala	Ala	Ser	Gly	Arg																		

```

      770              775              780
Phe Ala Val Asn Thr Arg Ile Gln Gly Ser Ala Ala Glu Leu Ile Lys
785              790              795              800
Leu Ala Met Leu Asp Ile Ser Gln Ala Ile Lys Gln Gln Gln Met Lys
      805              810              815
Ser Arg Met Leu Leu Gln Ile His Asp Glu Leu Leu Phe Glu Val Pro
      820              825              830
Glu Glu Glu Ile Glu Glu Met Gln Arg Leu Val Arg Glu Lys Met Glu
      835              840              845
Ser Ala Met Thr Leu Ser Val Pro Ile Val Val Asn Ile Leu Ile Gly
      850              855              860
Lys Asn Trp Ala Glu Cys
865              870
<210>652
<211>333
<212>PRT
<213>Chlamydia pneumoniae
<400>652
Met Lys Thr Leu Trp His Phe Val Ser Lys Ala Phe Leu Ser Ile Val
 1              5              10              15
Gly Leu Cys Cys Gly Val Val Leu Ala Phe Val Val Ile Phe Ala Leu
      20              25              30
Ile Ala Ser Ser Leu Gly Asn Gly Asp Ala Thr Phe Val Ser Leu Pro
      35              40              45
Asp Ala Gln Gly Glu Val Lys Asp Leu Gly Lys Thr Ala Pro Ile Ile
      50              55              60
Ala Val Ile Glu Met Lys Asp Val Ile Ala Ser Ser Lys Asn Thr Ala
      65              70              75              80
Lys Thr Ile Gln Asn Ile Leu Glu Gly Phe Glu Lys Ala Pro Leu Lys
      85              90              95
Asp Arg Val Lys Gly Ile Val Ile Asp Met Asp Cys Pro Gly Gly Glu
      100              105              110
Val Phe Glu Ile Asp Arg Ile Tyr Ser Met Leu Arg Phe Trp Lys Glu
      115              120              125
Arg Lys Gly Phe Pro Ile Tyr Ile Tyr Val Asn Gly Leu Cys Ala Ser
      130              135              140
Gly Gly Tyr Tyr Val Ser Cys Ala Ala Thr Lys Ile Tyr Ala Thr Ser
      145              150              155              160
Ser Ser Leu Ile Gly Ser Ile Gly Val Arg Ser Gly Pro Phe Phe Asn
      165              170              175
Val Lys Glu Gly Leu Asn Arg Tyr Gly Val Glu Ser Asp Leu Leu Thr
      180              185              190
Ala Gly Lys Asp Lys Ala Pro Met Asn Pro Tyr Thr Pro Trp Thr Ser
      195              200              205
His Asp Arg Glu Glu Arg Gln Ala Thr Leu Asp Phe Leu Tyr Gly Gln
      210              215              220
Phe Val Asp Ile Val Thr Gln Asn Arg Pro Leu Leu Thr Lys Glu Lys
      225              230              235              240
Leu Val His Thr Leu Gly Ala Arg Ile Phe Ser Pro Glu Lys Ala Lys
      245              250              255
Gln Glu Gly Tyr Ile Asp Val Val Gly Ala Thr Lys Glu Gln Val Leu
      260              265              270
Gln Asp Ile Val Ala Val Cys Lys Ile Glu Asp Asn Tyr Arg Val Ile
      275              280              285
Gly Ser Gly Gly Asp Gly Trp Trp Lys Arg Val Ala Ser Ala Ala Ala
      290              295              300
Ser Ser Pro Leu Val Thr Gly Met Ile Lys His Asp Ile Leu Pro Leu
      305              310              315              320
Ser His Asp Ala Ala Tyr Ile Pro Pro Tyr Leu Ala Leu
      325              330
<210>653
<211>551
<212>PRT
<213>Chlamydia pneumoniae

```

&lt;400&gt;653

Val Phe Ile Arg His Lys Val Gly Lys Glu Phe Met Gln Ser Ser Glu  
 1 5 10 15  
 Val Lys Pro Phe Ser Arg Leu Arg Ala Tyr Leu Cys Pro Ile Tyr Lys  
 20 25 30  
 Ser Glu Phe Ser Lys Phe Val Pro Leu Phe Leu Leu Ala Phe Phe Val  
 35 40 45  
 Gly Phe Asn Tyr Cys Leu Leu Lys Asn Met Lys Asp Thr Leu Val Ile  
 50 55 60  
 Val Gly Ser Asp Ala Gly Ala Glu Val Ile Pro Phe Leu Lys Val Trp  
 65 70 75 80  
 Gly Ile Val Pro Gly Ala Val Ile Val Thr Met Val Tyr Gly Trp Leu  
 85 90 95  
 Gly Ser Arg Tyr Pro Arg Asp Thr Val Phe Tyr Cys Phe Met Ala Ala  
 100 105 110  
 Phe Leu Gly Phe Phe Phe Leu Phe Ala Val Ile Ile Tyr Pro Val Gly  
 115 120 125  
 Asp Ser Leu His Leu Asn Ser Leu Ala Asp Lys Leu Gln Glu Leu Leu  
 130 135 140  
 Pro Gln Gly Leu Arg Gly Phe Ile Val Met Val Arg Tyr Trp Ser Tyr  
 145 150 155 160  
 Ser Ile Tyr Tyr Val Met Ser Glu Leu Trp Ser Ser Val Val Leu Ser  
 165 170 175  
 Met Leu Phe Trp Gly Leu Ala Asn Gln Ile Thr Thr Ile Thr Glu Ala  
 180 185 190  
 Gly Arg Phe Tyr Ala Leu Ile Asn Thr Gly Leu Asn Leu Ser Ser Ile  
 195 200 205  
 Cys Ala Gly Glu Ile Ser Tyr Trp Met Gly Lys Gln Thr Phe Val Ala  
 210 215 220  
 Tyr Ser Phe Ala Cys Asp Ser Trp His Ser Val Met Leu Asn Leu Thr  
 225 230 235 240  
 Met Leu Ile Thr Cys Ser Gly Leu Ile Met Ile Trp Leu Tyr Arg Arg  
 245 250 255  
 Ile His His Leu Thr Ile Asp Thr Ser Ile Pro Pro Ser Arg Arg Val  
 260 265 270  
 Leu Ala Glu Glu Gly Ala Ala Thr Ala Asn Leu Lys Glu Lys Lys Lys  
 275 280 285  
 Pro Lys Ala Lys Ala Arg Asn Leu Phe Leu His Leu Ile Gln Ser Arg  
 290 295 300  
 Tyr Leu Leu Gly Leu Ala Ile Ile Val Leu Ser Tyr Asn Leu Val Ile  
 305 310 315 320  
 His Leu Phe Glu Val Val Trp Lys Asp Gln Val Ser Gln Ile Tyr Ser  
 325 330 335  
 Ser His Val Glu Phe Asn Gly Tyr Met Ser Arg Ile Thr Thr Leu Ile  
 340 345 350  
 Gly Val Val Ser Val Leu Ala Ala Val Leu Leu Thr Gly Gln Cys Ile  
 355 360 365  
 Arg Lys Trp Gly Trp Thr Val Gly Ala Leu Val Thr Pro Leu Val Met  
 370 375 380  
 Leu Val Ser Gly Leu Leu Phe Phe Gly Thr Ile Phe Ala Ala Lys Arg  
 385 390 395 400  
 Asp Ile Ser Ile Phe Gly Gly Val Leu Gly Met Thr Pro Leu Ala Leu  
 405 410 415  
 Ala Ala Trp Thr Gly Gly Met Gln Asn Val Leu Ser Arg Gly Thr Lys  
 420 425 430  
 Phe Thr Phe Phe Asp Gln Thr Lys Glu Met Ala Phe Ile Pro Leu Ser  
 435 440 445  
 Pro Glu Asp Lys Asn His Gly Lys Ala Ala Ile Asp Gly Val Val Ser  
 450 455 460  
 Arg Ile Gly Lys Ser Gly Gly Ser Leu Ile Tyr Gln Gly Leu Leu Val  
 465 470 475 480  
 Ile Phe Ser Ser Val Ala Ala Ser Leu Asn Val Ile Ala Leu Val Leu  
 485 490 495  
 Leu Ile Ile Met Val Val Trp Ile Ala Val Val Ala Tyr Ile Gly Lys

500 505 510  
 Glu Tyr Tyr Ser Arg Ala Ala Asp Ala Val Ala Thr Leu Lys Gln Pro  
 515 520 525  
 Lys Glu Pro Ser Ser Ser Ile Val Arg Glu Ala Gln Glu Ser Val Glu  
 530 535 540  
 Gln Glu Glu Met Ala Val Leu  
 545 550  
 <210>654  
 <211>377  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>654  
 Ile Thr Leu Ala Glu Phe Ala Gly Thr Xaa Ala Tyr Leu Glu Glu Tyr  
 1 5 10 15  
 Val Asp Ile Ile Arg Ser Lys Ser Ile Leu Arg Lys Met Ile Ser Thr  
 20 25 30  
 Ala Lys Glu Ile Glu Lys Arg Ala Leu Glu Gln Pro Lys Asn Val Ala  
 35 40 45  
 Glu Ala Leu Asp Glu Ala Gln Asn Ser Phe Phe Lys Ile Ser Gln Ser  
 50 55 60  
 Thr Ser Val Ser Gln Tyr Thr Leu Val Ala Asp Lys Leu Arg Gly Leu  
 65 70 75 80  
 Thr Thr Thr Thr Asp Lys Pro Tyr Leu Val Gln Leu Gln Glu Arg Gln  
 85 90 95  
 Glu Leu Phe Leu Gln Asn Ala Gln Gly Asp Asn Lys Ser Phe Phe Thr  
 100 105 110  
 Gly Ile Pro Thr His Phe Ile Asp Leu Asp Gln Leu Ile His Gly Phe  
 115 120 125  
 Ser Pro Ser Asn Leu Met Ile Leu Ala Ala Arg Pro Ala Met Gly Lys  
 130 135 140  
 Thr Ala Leu Ala Leu Asn Ile Ala Glu Asn Leu Cys Phe Gln Asn Arg  
 145 150 155 160  
 Leu Pro Ile Gly Ile Phe Ser Leu Glu Met Thr Val Asp Gln Leu Ile  
 165 170 175  
 His Arg Met Ile Cys Ser Arg Ser Glu Val Asp Ser Lys Lys Ile Ser  
 180 185 190  
 Ile Gly Asp Leu Ser Gly His Asp Phe Gln Arg Ile Val Ser Val Ile  
 195 200 205  
 Asn Glu Met Gln Glu His Thr Leu Leu Ile Asp Asp Gln Pro Gly Leu  
 210 215 220  
 Lys Val Ser Asp Leu Arg Ala Arg Ala Arg Met Lys Glu Ser Tyr  
 225 230 235 240  
 Asp Ile Gln Phe Leu Ile Ile Asp Tyr Leu Gln Leu Leu Ser Gly Ser  
 245 250 255  
 Gly Thr Leu Arg Ala Thr Glu Ser Arg Gln Thr Glu Ile Ser Glu Ile  
 260 265 270  
 Ser Arg Met Leu Lys Thr Leu Ala Arg Glu Leu Asn Ile Pro Ile Leu  
 275 280 285  
 Cys Leu Ser Gln Leu Ser Arg Lys Val Glu Asp Arg Ala Asn His Arg  
 290 295 300  
 Pro Met Met Ser Asp Leu Arg Glu Ser Gly Ser Ile Glu Gln Asp Ser  
 305 310 315 320  
 Asp Leu Val Met Phe Leu Leu Arg Arg Glu Tyr Tyr Asp Pro Asn Asp  
 325 330 335  
 Lys Pro Gly Thr Ala Glu Leu Ile Ile Ala Lys Asn Arg His Gly Ser  
 340 345 350  
 Ile Gly Ser Val Pro Leu Val Phe Glu Lys Glu Leu Ala Arg Phe Arg  
 355 360 365  
 Asn Tyr Ser Ala Phe Glu Cys Ile Ser  
 370 375  
 <210>655  
 <211>611  
 <212>PRT  
 <213>Chlamydia pneumoniae

&lt;400&gt;655

Met Trp Thr His Pro Ile Ala Tyr Asp Val Ile Val Val Gly Ala Gly  
 1 5 10 15  
 His Ala Gly Cys Glu Ala Ala Tyr Cys Ser Ala Lys Met Gly Val Ser  
 20 25 30  
 Val Leu Met Leu Thr Ser Asn Leu Asp Thr Ile Ala Lys Leu Ser Cys  
 35 40 45  
 Asn Pro Ala Val Gly Gly Ile Gly Lys Gly His Ile Val Arg Glu Ile  
 50 55 60  
 Asp Ala Leu Gly Gly Ile Met Ala Glu Val Thr Asp Gln Ser Gly Ile  
 65 70 75 80  
 Gln Phe Arg Ile Leu Asn Gln Thr Lys Gly Pro Ala Val Arg Ala Pro  
 85 90 95  
 Arg Ala Gln Val Asp Lys Gln Leu Tyr His Ile His Met Lys Arg Leu  
 100 105 110  
 Leu Glu Asn Thr Pro Gly Leu His Ile Met Gln Ala Thr Val Glu Ser  
 115 120 125  
 Leu Leu Asp Lys Glu Gly Val Ile Ser Gly Val Thr Thr Lys Glu Gly  
 130 135 140  
 Trp Met Phe Ser Gly Lys Thr Val Val Leu Ser Ser Gly Thr Phe Met  
 145 150 155 160  
 Arg Gly Leu Ile His Ile Gly Asp Arg Asn Phe Ser Gly Gly Arg Leu  
 165 170 175  
 Gly Asp Pro Ser Ser Gln Gly Leu Ser Glu Asp Leu Lys Lys Arg Gly  
 180 185 190  
 Phe Pro Ile Ser Arg Leu Lys Thr Gly Thr Pro Pro Arg Leu Leu Ala  
 195 200 205  
 Ser Ser Ile Asn Phe Ser Cys Met Glu Glu Gln Pro Gly Asp Leu Gly  
 210 215 220  
 Val Gly Phe Val His Arg Thr Glu Pro Phe Gln Pro Pro Leu Pro Gln  
 225 230 235 240  
 Leu Ser Cys Phe Ile Thr His Thr Met Glu Lys Thr Lys Ala Ile Ile  
 245 250 255  
 Ser Ala Asn Leu His Arg Ser Ala Leu Tyr Gly Gly Cys Ile Glu Gly  
 260 265 270  
 Val Gly Pro Arg Tyr Cys Pro Ser Ile Glu Asp Lys Ile Val Lys Phe  
 275 280 285  
 Ser Asp Lys Glu Arg His His Val Phe Leu Glu Pro Glu Gly Leu His  
 290 295 300  
 Thr Gln Glu Ile Tyr Ala Asn Gly Leu Ser Thr Ser Met Pro Phe Asp  
 305 310 315 320  
 Val Gln Tyr Asp Met Ile Arg Ser Val Leu Gly Leu Glu Asn Ala Ile  
 325 330 335  
 Ile Thr Arg Pro Ala Tyr Ala Ile Glu Tyr Asp Tyr Ile His Gly Asn  
 340 345 350  
 Val Ile His Pro Thr Leu Glu Ser Lys Leu Ile Glu Gly Leu Phe Leu  
 355 360 365  
 Cys Gly Gln Ile Asn Gly Thr Thr Gly Tyr Glu Glu Ala Ala Ala Gln  
 370 375 380  
 Gly Leu Ile Ala Gly Ile Asn Ala Val Asn Lys Val Phe Asn Arg Pro  
 385 390 395 400  
 Pro Phe Ile Pro Ser Arg Gln Glu Ser Tyr Ile Gly Val Met Leu Asp  
 405 410 415  
 Asp Leu Thr Thr Gln Ile Leu Asp Glu Pro Tyr Arg Met Phe Thr Gly  
 420 425 430  
 Arg Ala Glu His Arg Leu Leu Leu Arg Gln Asp Asn Ala Cys Ala Arg  
 435 440 445  
 Leu Ser His Tyr Gly Tyr Glu Leu Gly Leu Leu Ser Glu Glu Arg Tyr  
 450 455 460  
 Glu Leu Val Lys Lys Gln Asn Gln Leu Leu Glu Glu Glu Lys Val Arg  
 465 470 475 480  
 Leu Gln Lys Thr Phe Arg Gln Tyr Gly Gln Ser Val Val Ser Leu Ala  
 485 490 495  
 Lys Ala Leu Ser Arg Pro Glu Val Ser Tyr Asp Met Leu Arg Glu Ala



500 505 510  
 Phe Pro Asn Asp Ile Arg Asp Leu Gly Ala Val Leu Asn Ala Ser Leu  
 515 520 525  
 Glu Met Glu Ile Lys Tyr Ser Gly Tyr Ile Asp Arg Gln Lys Ile Leu  
 530 535 540  
 Ile Gln Ser Leu Glu Lys Ala Glu Ser Leu Leu Ile Pro Glu Asp Leu  
 545 550 555 560  
 Asp Tyr Lys Gln Ile Thr Ala Leu Ser Leu Glu Ala Gln Glu Lys Leu  
 565 570 575  
 Ala Lys Phe Thr Pro Arg Thr Leu Gly Ser Ala Ser Arg Ile Ser Gly  
 580 585 590  
 Ile Ala Ser Ala Asp Ile Gln Val Leu Met Ile Ala Leu Lys Lys His  
 595 600 605  
 Ala His His  
 610  
 <210>656  
 <211>217  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>656  
 Lys Asn Met Pro Thr Thr Asn Cys Ile Phe Leu Asp Leu Arg Gly His  
 1 5 10 15  
 Ser Ile Leu His Gln Leu Gln Ile Glu Glu Ala Leu Leu Arg Val Ala  
 20 25 30  
 Asn Gln Asn Phe Cys Ile Ile Asn Ser Gly Ala Lys Asp Ser Ile Val  
 35 40 45  
 Leu Gly Ile Ser Arg Asn Leu Asn Gln Asp Val His Ile Ser Arg Ala  
 50 55 60  
 Gln Ala Asp His Ile Pro Ile Ile Arg Arg Tyr Ser Gly Gly Gly Thr  
 65 70 75 80  
 Val Phe Ile Asp Ser Asn Thr Leu Met Val Ser Trp Ile Met Asn Ser  
 85 90 95  
 Ser Glu Ala Ser Ala Gln Pro Gln Glu Leu Leu Ala Trp Thr Tyr Gly  
 100 105 110  
 Ile Tyr Ser Pro Leu Leu Pro Asn Thr Phe Ser Ile Arg Glu Asn Asp  
 115 120 125  
 Tyr Val Leu Gly His Lys Lys Ile Gly Gly Asn Ala Gln Tyr Ile Gln  
 130 135 140  
 Arg His Arg Trp Val His His Thr Thr Phe Leu Trp Asp Ile Asp Leu  
 145 150 155 160  
 Asp Lys Leu Ser Tyr Tyr Leu Pro Ile Pro Gln Gln Gln Pro Thr Tyr  
 165 170 175  
 Arg Asn Gln Arg Ser His Glu Glu Phe Leu Thr Thr Leu Arg Pro Trp  
 180 185 190  
 Phe Pro Ser Arg Asp Asp Phe Leu Glu Arg Ile Lys Ala Ser Gly Ser  
 195 200 205  
 Leu Leu Phe Tyr Leu Gly Arg Ile Ser  
 210 215  
 <210>657  
 <211>144  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>657  
 Met Glu Gln Thr Leu Ser Ile Ile Lys Pro Asp Ser Val Ser Lys Ala  
 1 5 10 15  
 His Ile Gly Glu Ile Leu Ser Ile Phe Glu Gln Ser Gly Leu Arg Ile  
 20 25 30  
 Ala Ala Met Lys Met Met His Leu Ser Gln Thr Glu Ala Glu Gly Phe  
 35 40 45  
 Tyr Phe Val His Arg Glu Arg Pro Phe Phe Gln Glu Leu Val Asp Phe  
 50 55 60  
 Met Val Ser Gly Pro Val Val Leu Val Leu Glu Gly Ala Asn Ala  
 65 70 75 80  
 Val Ser Arg Asn Arg Glu Leu Met Gly Ala Thr Asn Pro Ala Glu Ala

85 90 95  
 Ala Ser Gly Thr Ile Arg Ala Lys Phe Gly Glu Ser Ile Gly Val Asn  
 100 105 110  
 Ala Val His Gly Ser Asp Thr Leu Glu Asn Ala Ala Val Glu Ile Ala  
 115 120 125  
 Tyr Phe Phe Ser Lys Ile Glu Val Val Asn Ala Ser Lys Pro Leu Val  
 130 135 140  
 <210>658  
 <211>207  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>658  
 Met Tyr Asp Tyr Ile Arg Gly Thr Leu Thr Tyr Val His Thr Gly Ala  
 1 5 10 15  
 Ile Val Ile Glu Cys Gln Gly Ile Gly Tyr His Ile Ala Ile Thr Glu  
 20 25 30  
 Arg Trp Ala Ile Glu Cys Ile Arg Ala Leu His Gln Asp Phe Leu Val  
 35 40 45  
 Phe Thr His Val Ile Phe Arg Glu Thr Glu His Leu Leu Tyr Gly Phe  
 50 55 60  
 His Ser Arg Glu Glu Arg Glu Cys Phe Arg Ile Leu Ile Ser Phe Ser  
 65 70 75 80  
 Gly Ile Gly Pro Lys Leu Ala Leu Ala Ile Leu Asn Ala Leu Pro Leu  
 85 90 95  
 Lys Val Leu Cys Ser Val Val Arg Ser Glu Asp Ile Arg Ala Leu Ala  
 100 105 110  
 Ser Val Ser Gly Ile Gly Lys Lys Thr Ala Glu Lys Leu Met Val Glu  
 115 120 125  
 Leu Lys Gln Lys Leu Pro Asp Leu Leu Pro Leu Asp Ser Arg Val Glu  
 130 135 140  
 Thr Ser Gln Thr His Thr Thr Ser Ser Cys Leu Glu Glu Gly Ile Gln  
 145 150 155 160  
 Ala Leu Ala Ala Leu Gly Tyr Ser Lys Ile Ala Ala Glu Arg Met Ile  
 165 170 175  
 Ala Glu Ala Ile Lys Asp Leu Pro Glu Gly Ser Ser Leu Thr Asp Ile  
 180 185 190  
 Leu Pro Ile Ala Leu Lys Lys Asn Phe Ser Gly Val Asn Lys Asp  
 195 200 205  
 <210>659  
 <211>168  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>659  
 Val Ser Glu Leu Ile Ile Gly Val Asp Pro Gly Thr Ile Val Ala Gly  
 1 5 10 15  
 Tyr Ala Ile Ile Ala Val Glu Gln Arg Tyr Gln Leu Arg Pro Tyr Ser  
 20 25 30  
 Tyr Gly Ala Ile Arg Leu Ser Ser Asp Met Pro Leu Pro Met Arg Tyr  
 35 40 45  
 Lys Thr Leu Phe Glu Gln Leu Ser Gly Val Leu Asp Asp Thr Gln Pro  
 50 55 60  
 Asn Ala Met Val Leu Glu Thr Gln Phe Val Asn Lys Asn Pro Gln Ser  
 65 70 75 80  
 Thr Met Lys Leu Ala Met Ala Arg Gly Ile Val Leu Leu Ala Ala Ala  
 85 90 95  
 Gln Arg Asp Ile Leu Ile Phe Glu Tyr Ala Pro Asn Val Ala Lys Lys  
 100 105 110  
 Ala Val Val Gly Lys Gly His Ala Ser Lys Arg Gln Val Gln Val Met  
 115 120 125  
 Val Ser Lys Ile Leu Asn Val Pro Glu Val Leu His Pro Ser Asn Glu  
 130 135 140  
 Asp Ile Ala Asp Ala Phe Ala Leu Ala Ile Cys His Thr His Val Ala  
 145 150 155 160  
 Arg Ser Pro Leu Cys Gly Val Arg

165

&lt;210&gt;660

&lt;211&gt;323

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;660

Arg Tyr Ser Val Arg Leu Leu Ser Ile Leu Lys Leu His Leu Phe Ser  
 1 5 10 15  
 Leu Arg Ser Ser Ser Leu Ser Pro His Tyr Tyr His Ser Cys Ser  
 20 25 30  
 Arg Ser Met Leu His Leu Leu Cys Arg Trp Lys Asp Ala Asp Ile Met  
 35 40 45  
 Glu Trp Gln Gln Ile Cys Asn Ile Leu Ser Gly Val Cys Ser Arg Met  
 50 55 60  
 Ser Gly Lys Leu Val Ser Leu Gln Lys Glu Thr Gln Asp Ser Cys His  
 65 70 75 80  
 Gln Glu His Glu Arg Ile His Leu Gln Tyr Arg Glu Gln Leu Ser Ala  
 85 90 95  
 Leu Glu Glu Glu Tyr Arg Arg Arg Glu Glu Ala Lys Asn Gln Asp Leu  
 100 105 110  
 Glu Lys Leu Gln Gln Glu Asn Thr Trp Leu Gln Asn Arg Leu Ala Glu  
 115 120 125  
 Lys Leu Gln Gln Ile Arg His Gln Ser Asp Ile Ile Asp Glu Ile Lys  
 130 135 140  
 Lys Glu Leu Leu Gln Ser Val Gln Arg Thr Glu Ile Ser Glu Gly Arg  
 145 150 155 160  
 Arg Leu Cys Tyr Glu His Lys Ile Lys Gln Leu Glu Glu Gln Leu Gln  
 165 170 175  
 Arg Tyr Val Ser Gln His Gly Ala Pro Ser Ile Glu Ile Glu Glu Asp  
 180 185 190  
 Lys Ser Ser Ala Ala Tyr Ala Glu Ile Asn Arg Leu Lys Lys Ser Leu  
 195 200 205  
 Ile Asp Leu Gln Gln Glu Lys Asp Ile Tyr Ile Lys Thr Tyr His Ser  
 210 215 220  
 Glu Ile Ala Lys Leu Arg Glu Lys Leu Gln Arg Gln Glu Gly Ala Gln  
 225 230 235 240  
 Thr Ser Ser Glu Val Cys Ser Ile Glu Lys Leu Thr Glu Val Gln Thr  
 245 250 255  
 Asp Leu Ala Glu Lys Lys Lys Ala Ile Ala Leu Leu Gln Asp Ile Val  
 260 265 270  
 Glu Asp Gln Tyr Cys Gln Leu Arg Asp Leu His Lys Glu Lys Gly Met  
 275 280 285  
 Ala Met Pro Ser Asn Thr Lys Leu Asp His Leu Lys Gly Leu Leu Gly  
 290 295 300  
 Lys Glu Pro Glu Ser Glu Val Asp Val Val Phe Ser Glu Ser Lys Ser  
 305 310 315 320  
 Leu Gly Ser

&lt;210&gt;661

&lt;211&gt;282

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;661

Lys Gly Tyr Asn Tyr Val Tyr Phe Thr Arg Asp Pro Val Ile Glu Thr  
 1 5 10 15  
 Val Ile Thr Ser Arg Glu Gly Tyr Lys Leu Ser Val Arg Asn Thr Lys  
 20 25 30  
 His Phe Ser Gln Asp Pro Phe Met Val Glu Ala Ile Glu Val Ile Ser  
 35 40 45  
 Leu Gly Asn Ile Cys Phe Phe Arg Asn Cys Asp His Ser Lys Pro Phe  
 50 55 60  
 Leu Val Pro Ala Gly Asp Tyr Glu Val Met Glu Val Arg Asp Thr Lys  
 65 70 75 80  
 Ile Asn Leu Lys Ala Val Gly Leu Asp Arg Gly Val Lys Ile Ala Gly

85 90 95  
 Gly Arg Glu Ala Leu Ile Lys Leu Thr Lys Ser Thr Pro Leu Pro Val  
 100 105 110  
 Ile Asp Glu Lys Pro Leu Ala Asp Ser Pro Glu Glu Gly Thr Glu Pro  
 115 120 125  
 Thr Ser Pro Ser Lys Lys Glu Lys Lys Glu Ala Arg Lys Asp Ser Phe  
 130 135 140  
 Lys Gly Glu Lys Trp Lys Glu Lys Lys Lys Leu Ser Arg Arg Arg Asn  
 145 150 155 160  
 His Lys Glu Ile Ala Glu Val Thr Gly Ala Ser Gln Glu Ile Leu Asp  
 165 170 175  
 Thr Val Lys Glu Leu Trp Glu Glu Ser Gln Glu Asn Glu Ile Val  
 180 185 190  
 Glu Gln Lys Lys Phe Ser Leu Leu Pro Pro Pro Ala Lys Leu Ile Ser  
 195 200 205  
 Glu Val Ile Ser Gln Thr Val Val Asp Pro Val Val Thr Ser Ala Asp  
 210 215 220  
 Leu Asn Glu Ser Leu Gln Ala Leu Val Arg Glu Ser Ser Asp Leu Ile  
 225 230 235 240  
 Asn Ala Leu Leu Ser Ala Asp Asp Ala Ile His Phe Pro Glu Thr Glu  
 245 250 255  
 Glu Glu Pro Thr Ser Ala Ser Phe Glu Glu Ser Ser Ala Met Phe Phe  
 260 265 270  
 Pro Glu Thr Ser Ser Ala Thr Glu Glu  
 275 280  
 <210>662  
 <211>336  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>662  
 Ala Met Lys Val Val Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Val  
 1 5 10 15  
 Phe Arg Gln Ile Leu Lys Arg Asn Ser Ser Val Glu Val Leu Ala Ile  
 20 25 30  
 Asn Asp Leu Val Pro Gly Asp Ala Leu Thr Tyr Leu Phe Lys Phe Asp  
 35 40 45  
 Ser Thr His Gly Arg Phe Pro Glu Asp Val Arg Cys Glu Ala Asp His  
 50 55 60  
 Leu Ile Val Gly Lys Arg Lys Ile Gln Phe Leu Ser Glu Arg Asn Val  
 65 70 75 80  
 Gln Asn Leu Pro Trp Lys Asp Leu Gly Val Asp Leu Val Ile Glu Cys  
 85 90 95  
 Thr Gly Leu Phe Thr Lys Lys Glu Asp Ala Glu Lys His Ile Gln Ala  
 100 105 110  
 Gly Ala Lys Arg Val Leu Ile Ser Ala Pro Gly Lys Gly Asp Ile Pro  
 115 120 125  
 Thr Phe Val Met Gly Val Asn His Lys Thr Phe Asn Pro Glu Lys Asp  
 130 135 140  
 Phe Val Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Ile  
 145 150 155 160  
 Ala Lys Val Leu Leu Asp Asn Phe Gly Ile Thr Glu Gly Leu Met Thr  
 165 170 175  
 Thr Val His Ala Ala Thr Ala Thr Gln Leu Val Val Asp Gly Pro Ser  
 180 185 190  
 Lys Lys Asp Trp Arg Gly Gly Arg Gly Cys Leu Gln Asn Ile Ile Pro  
 195 200 205  
 Ala Ser Thr Gly Ala Ala Lys Ala Val Thr Leu Cys Leu Pro Glu Leu  
 210 215 220  
 Lys Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Ile Glu Asp Val  
 225 230 235 240  
 Ser Val Val Asp Leu Thr Val Arg Leu Asp Lys Ser Thr Thr Tyr Asp  
 245 250 255  
 Asp Ile Cys Lys Ala Met Lys Gln Ala Ser Glu Thr Asp Leu Lys Gly  
 260 265 270

Ile Leu Asp Tyr Thr Asp Glu Gln Val Val Ser Ser Asp Phe Ile Gly  
 275 280 285  
 Ser Glu Tyr Ser Ser Ile Phe Asp Ala Leu Ala Gly Ile Ala Leu Asn  
 290 295 300  
 Asp Arg Phe Phe Lys Leu Val Ala Trp Tyr Asp Asn Glu Thr Gly Tyr  
 305 310 315 320  
 Ala Thr Arg Ile Val Asp Leu Leu Glu Tyr Val Glu Lys Asn Ser Lys  
 325 330 335

&lt;210&gt;663

&lt;211&gt;129

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;663

Met Gln His Ala Arg Lys Lys Phe Arg Val Gly Arg Thr Ser Ser His  
 1 5 10 15  
 Asn Arg Cys Met Leu Ala Asn Met Leu Lys Ser Leu Ile His Tyr Glu  
 20 25 30  
 Arg Ile Glu Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg His Ala  
 35 40 45  
 Asp Lys Met Ile Thr Leu Ala Lys Lys Asn Ser Leu Ala Ala Arg Arg  
 50 55 60  
 Ile Ala Ile Gly Arg Leu Met Val Arg Tyr Asn Lys Leu Thr Ser Lys  
 65 70 75 80  
 Glu Ala Arg Gln Ala Lys Gly Gly Asp Thr Ser Val Tyr Asn Val Asp  
 85 90 95  
 Arg Leu Val Val Asn Lys Leu Phe Asp Glu Leu Gly Asn Arg Phe Val  
 100 105 110  
 Glu Arg Lys Gly Gly Tyr Thr Arg Ile Leu Lys Leu Gln Asn Arg Thr  
 115 120 125  
 Trp

&lt;210&gt;664

&lt;211&gt;337

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;664

Ala Ser Arg Lys Arg Asn Gly Pro His Phe Arg Lys Cys Ser Lys Thr  
 1 5 10 15  
 Cys Phe Ala Tyr Trp Phe Arg Ser Ser Arg Tyr Leu Ile Ser Phe Ala  
 20 25 30  
 Met Thr Gly Val Leu His Glu Tyr Met Ala Ile Glu Gly Val Ile Glu  
 35 40 45  
 Asp Val Thr Asn Ile Ile Leu Asn Leu Lys Gly Ala Leu Leu Lys Lys  
 50 55 60  
 Tyr Pro Met Gln Asp Ser Ser Leu Gly Arg Thr Thr Gln Val Leu Lys  
 65 70 75 80  
 Ala Ser Ile Ser Ile Asp Ala Ser Asp Leu Ala Ala Ala Asn Gly Gln  
 85 90 95  
 Lys Glu Val Thr Leu Gln Asp Leu Leu Gln Glu Gly Asp Phe Glu Ala  
 100 105 110  
 Val Asn Pro Asp Gln Val Ile Phe Thr Val Thr Gln Pro Ile Gln Leu  
 115 120 125  
 Glu Val Asp Leu Arg Ile Ala Phe Gly Arg Gly Tyr Thr Pro Ser Glu  
 130 135 140  
 Arg Ile Val Leu Glu Asp Lys Gly Val Tyr Glu Ile Val Leu Asp Ala  
 145 150 155 160  
 Ala Phe Ser Pro Val Thr Leu Val Asn Tyr Phe Val Glu Asp Thr Arg  
 165 170 175  
 Val Gly Gln Asp Thr Asp Phe Asp Arg Leu Val Leu Ile Val Glu Thr  
 180 185 190  
 Asp Gly Arg Val Thr Pro Lys Glu Ala Leu Ala Phe Ser Thr Gln Ile  
 195 200 205  
 Leu Thr Lys His Phe Ser Ile Phe Glu Asn Met Asp Glu Lys Lys Ile  
 210 215 220

Val Phe Glu Glu Ala Ile Ser Ile Glu Lys Glu Asn Lys Asp Asp Ile  
 225 230 235 240  
 Leu His Lys Leu Ile Leu Gly Ile Asn Glu Ile Glu Leu Ser Val Arg  
 245 250 255  
 Ser Thr Asn Cys Leu Ser Asn Ala Asn Ile Glu Thr Ile Gly Glu Leu  
 260 265 270  
 Val Ile Met Pro Glu Pro Arg Leu Leu Gln Phe Arg Asn Phe Gly Lys  
 275 280 285  
 Lys Ser Leu Cys Glu Ile Lys Asn Lys Leu Lys Glu Met Lys Leu Glu  
 290 295 300  
 Leu Gly Met Asp Leu Thr Gln Phe Gly Val Gly Leu Asp Asn Val Lys  
 305 310 315 320  
 Glu Lys Met Lys Trp Tyr Ala Glu Lys Ile Arg Ala Lys Asn Ile Lys  
 325 330 335  
 Gly

&lt;210&gt;665

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;665

Leu Pro Ala Lys Lys Lys Ala Gln Ser Val Val Leu Gly Lys Glu Lys  
 1 5 10 15  
 Gly Met Ser Asp Asn Ala His Asn Leu Leu Tyr Asp Lys Phe Glu Leu  
 20 25 30  
 Pro Glu Ala Val Lys Met Leu Pro Val Glu Gly Leu Pro Ile Asp Lys  
 35 40 45  
 His Ala Arg Phe Ile Ala Glu Pro Leu Glu Arg Gly Met Gly His Thr  
 50 55 60  
 Leu Gly Asn Ala Leu Arg Arg Ala Leu Leu Ile Gly Leu Glu Ala Pro  
 65 70 75 80  
 Gly Ile

&lt;210&gt;666

&lt;211&gt;133

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;666

Leu Val Lys Asn Gln Ala Gln Ala Lys Lys Ser Val Lys Arg Lys Gln  
 1 5 10 15  
 Leu Lys Asn Ile Pro Ser Gly Val Val His Val Lys Ala Thr Phe Asn  
 20 25 30  
 Asn Thr Ile Val Ser Ile Thr Asp Pro Ala Gly Asn Val Ile Ser Trp  
 35 40 45  
 Ala Ser Ala Gly Lys Val Gly Tyr Ser Gly Ser Xaa Lys Ser Ser Ala  
 50 55 60  
 Phe Ala Ala Thr Val Ala Ala Gln Asp Ala Ala Lys Thr Ala Met Asn  
 65 70 75 80  
 Ser Gly Leu Lys Glu Xaa Xaa Val Cys Leu Lys Gly Thr Gly Ala Gly  
 85 90 95  
 Arg Glu Ser Ala Val Arg Ala Leu Ile Ser Ala Gly Leu Val Val Ser  
 100 105 110  
 Val Ile Arg Asp Glu Thr Pro Val Pro His Asn Gly Cys Arg Pro Arg  
 115 120 125  
 Lys Arg Arg Arg Val  
 130

&lt;210&gt;667

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;667

Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys  
 1 5 10 15  
 Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu

20 25 30  
 Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu  
 35 40 45  
 Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr  
 50 55 60  
 Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg  
 65 70 75 80  
 Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu  
 85 90 95  
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly  
 100 105 110  
 Lys Arg Lys Thr Val Ala Gly Lys Lys Lys  
 115 120  
 <210>668  
 <211>462  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>668  
 Leu Phe Arg Pro Tyr Met Thr Thr Leu Arg Gln Phe Phe Leu Ile Thr  
 1 5 10 15  
 Glu Leu Arg Gln Lys Leu Phe Tyr Thr Phe Ala Leu Leu Thr Ala Cys  
 20 25 30  
 Arg Val Gly Val Phe Ile Pro Val Pro Gly Ile Asn Gly Glu Leu Ala  
 35 40 45  
 Val Ala Tyr Phe Lys Gln Leu Leu Gly Ser Gly Gln Asn Leu Phe Gln  
 50 55 60  
 Leu Ala Asp Ile Phe Ser Gly Gly Ala Phe Ala Gln Met Thr Val Ile  
 65 70 75 80  
 Ala Leu Gly Val Val Pro Tyr Ile Ser Ala Ser Ile Ile Val Gln Leu  
 85 90 95  
 Phe Leu Val Phe Met Pro Ala Leu Gln Arg Glu Met Arg Glu Ser Ser  
 100 105 110  
 Asp Gln Gly Lys Arg Arg Ile Gly Arg Leu Thr Arg Leu Phe Thr Val  
 115 120 125  
 Ala Leu Ala Val Ile Gln Ser Leu Leu Phe Ala Lys Phe Ala Leu Arg  
 130 135 140  
 Met Asn Leu Thr Ile Pro Gly Ile Val Leu Pro Thr Leu Leu Ser Ser  
 145 150 155 160  
 Lys Leu Phe Gly Val Pro Trp Ile Phe Tyr Ile Thr Thr Val Val Val  
 165 170 175  
 Met Thr Thr Gly Thr Leu Leu Leu Met Trp Ile Gly Glu Gln Ile Ser  
 180 185 190  
 Asp Lys Gly Ile Gly Asn Gly Ile Ser Leu Ile Ile Ala Leu Gly Ile  
 195 200 205  
 Leu Ser Ser Phe Pro Ser Val Leu Gly Ser Ile Val Asn Lys Leu Asn  
 210 215 220  
 Leu Gly Ser Gln Asp Ser Ser Asp Leu Gly Leu Ile Ser Ile Leu Ile  
 225 230 235 240  
 Leu Ala Leu Val Phe Val Phe Val Leu Ile Thr Thr Ile Leu Ile Ile  
 245 250 255  
 Glu Gly Val Arg Lys Ile Pro Val Gln Tyr Ala Arg Arg Val Ile Gly  
 260 265 270  
 Arg Arg Glu Val Pro Gly Gly Gly Ser Tyr Leu Pro Leu Lys Val Asn  
 275 280 285  
 Tyr Ala Gly Val Ile Pro Val Ile Phe Ala Ser Ser Leu Leu Met Phe  
 290 295 300  
 Pro Ala Thr Ile Gly Gln Phe Ile Ala Ser Glu Ser Ser Trp Met Lys  
 305 310 315 320  
 Arg Ile Ala Ala Leu Leu Ala Pro Gly Ser Leu Val Tyr Ser Ile Cys  
 325 330 335  
 Tyr Val Leu Leu Ile Ile Phe Phe Thr Tyr Phe Trp Thr Ala Thr Gln  
 340 345 350  
 Phe His Pro Glu Gln Ile Ala Ser Glu Met Lys Lys Asn Asn Ala Phe  
 355 360 365

Ile Pro Gly Ile Arg Gln Gly Lys Pro Thr Gln His Tyr Leu Glu Tyr  
 370 375 380  
 Thr Met Asn Arg Val Thr Leu Leu Gly Ala Leu Phe Leu Ala Ala Ile  
 385 390 395 400  
 Ala Ile Leu Pro Ser Leu Leu Gly Cys Leu Leu Arg Val Asp Ser Asn  
 405 410 415  
 Val Ser Tyr Phe Leu Gly Gly Thr Ala Met Leu Ile Val Val Gly Val  
 420 425 430  
 Val Leu Asp Thr Met Lys Gln Val Asp Ala Phe Leu Leu Met Arg Arg  
 435 440 445  
 Tyr Asp Ser Val Leu Lys Thr Asp Arg Thr Lys Gly Arg His  
 450 455 460

&lt;210&gt;669

&lt;211&gt;144

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;669

Met Ile Lys Leu Glu Ser Leu Phe Asp Ile Ser Glu Arg Lys Arg Arg  
 1 5 10 15  
 Lys Lys Leu Leu Gly Arg Gly Pro Ser Ser Gly His Gly Lys Thr Ser  
 20 25 30  
 Gly Arg Gly His Lys Gly Asp Gly Ser Arg Ser Gly Tyr Lys Arg Arg  
 35 40 45  
 Phe Gly Tyr Glu Gly Gly Gly Val Pro Leu Tyr Arg Arg Val Pro Thr  
 50 55 60  
 Arg Gly Phe Ser His Lys Arg Phe Asp Lys Cys Val Glu Glu Ile Thr  
 65 70 75 80  
 Thr Gly Arg Leu Ala Glu Leu Phe Gln Glu Gly Glu Ala Ile Thr Leu  
 85 90 95  
 Asp Ala Leu Lys Ala Lys Lys Ala Ile Ala Arg Gln Ala Val Arg Val  
 100 105 110  
 Lys Val Ile Leu Lys Gly Asp Leu Glu Lys Thr Phe Val Trp Gln Asp  
 115 120 125  
 Thr Ala Val Val Leu Ser Gln Gly Val Gln Asn Leu Leu Gly Ile Thr  
 130 135 140

&lt;210&gt;670

&lt;211&gt;165

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;670

Met Ser Leu Ser Lys Asn Ser His Lys Glu Asp Gln Leu Glu Glu Lys  
 1 5 10 15  
 Val Leu Val Val Asn Arg Cys Ser Lys Val Val Lys Gly Gly Arg Lys  
 20 25 30  
 Phe Ser Phe Ser Ala Leu Ile Leu Val Gly Asp Gly Lys Gly Arg Leu  
 35 40 45  
 Gly Tyr Gly Phe Ala Lys Ala Asn Glu Leu Thr Asp Ala Ile Arg Lys  
 50 55 60  
 Gly Gly Glu Ala Ala Lys Lys Asn Leu Met Lys Ile Glu Ala Leu Glu  
 65 70 75 80  
 Asp Gly Ser Ile Pro His Glu Val Leu Val His His Asp Gly Ala Gln  
 85 90 95  
 Leu Leu Leu Lys Pro Ala Lys Pro Gly Thr Gly Ile Val Ala Gly Ser  
 100 105 110  
 Arg Ile Arg Leu Ile Leu Glu Met Ala Gly Ile Lys Asp Ile Val Ala  
 115 120 125  
 Lys Ser Phe Gly Ser Asn Asn Pro Met Asn Gln Val Lys Ala Ala Phe  
 130 135 140  
 Lys Ala Leu Thr Gly Leu Ser Pro Arg Lys Asp Leu Leu Arg Arg Gly  
 145 150 155 160  
 Ala Ala Ile Asn Asp  
 165

&lt;210&gt;671

&lt;211&gt;93



&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;671

Leu Glu Trp Val Ser Glu Pro Leu Phe Lys Val His Phe Trp Ile Ser  
 1 5 10 15  
 Pro Leu Gly Phe Leu Thr Leu Gln Lys Phe Pro Ile Pro Ser Thr Leu  
 20 25 30  
 Gln Val Ser Val Glu Lys Asn Thr Leu Ile Ser Val Lys Gly Leu Asp  
 35 40 45  
 Lys Gln Leu Val Gly Glu Phe Ala Ala Ser Ile Arg Ala Lys Arg Pro  
 50 55 60  
 Pro Glu Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu Asn Glu Tyr Val  
 65 70 75 80  
 Arg Arg Lys Ala Gly Lys Ala Ala Lys Thr Gly Lys Lys  
 85 90

&lt;210&gt;672

&lt;211&gt;126

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;672

Met Ser Arg Lys Ala Arg Glu Pro Ile Leu Leu Pro Gln Gly Val Glu  
 1 5 10 15  
 Val Ser Ile Gln Asp Asp Lys Ile Ile Val Lys Gly Pro Lys Gly Ser  
 20 25 30  
 Leu Thr Gln Lys Ser Val Lys Glu Val Glu Ile Thr Leu Lys Asp Asn  
 35 40 45  
 Ser Ile Phe Val His Ala Ala Pro His Val Val Asp Arg Pro Ser Cys  
 50 55 60  
 Met Gln Gly Leu Tyr Trp Ala Leu Ile Ser Asn Met Val Gln Gly Val  
 65 70 75 80  
 His Leu Gly Phe Glu Lys Arg Leu Glu Met Ile Gly Val Gly Phe Arg  
 85 90 95  
 Ala Ser Val Gln Gly Ala Phe Leu Asp Leu Ser Ile Gly Val Ser His  
 100 105 110  
 Pro Thr Lys Ile Ser Tyr Pro Ile Tyr Ser Ser Gly Ile Ser  
 115 120 125

&lt;210&gt;673

&lt;211&gt;133

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;673

Met Gly Met Thr Ser Asp Ser Ile Ala Asp Leu Leu Thr Arg Ile Arg  
 1 5 10 15  
 Asn Ala Leu Met Ala Glu His Leu Tyr Val Asp Val Glu His Ser Lys  
 20 25 30  
 Met Arg Glu Ala Ile Val Lys Ile Leu Lys His Lys Gly Phe Val Ala  
 35 40 45  
 His Tyr Leu Val Xaa Glu Xaa Asn Xaa Lys Arg Ala Met Arg Val Phe  
 50 55 60  
 Leu Gln Tyr Ser Asp Asp Arg Lys Pro Val Ile His Gln Leu Lys Arg  
 65 70 75 80  
 Val Ser Lys Pro Ser Arg Arg Val Tyr Val Ser Ala Ala Lys Ile Pro  
 85 90 95  
 Tyr Val Phe Gly Asn Met Gly Ile Ser Val Leu Ser Thr Ser Gln Gly  
 100 105 110  
 Val Met Glu Gly Ser Leu Ala Arg Ser Lys Asn Ile Gly Gly Glu Leu  
 115 120 125  
 Leu Cys Leu Val Trp  
 130

&lt;210&gt;674

&lt;211&gt;180

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;674

Met Ser Arg Leu Lys Lys Phe Tyr Thr Glu Glu Ile Arg Lys Ser Leu  
 1 5 10 15  
 Phe Glu Lys Phe Gly Tyr Ala Asn Lys Met Gln Ile Pro Val Leu Lys  
 20 25 30  
 Lys Ile Val Leu Ser Met Gly Leu Ala Glu Ala Ala Lys Asp Lys Asn  
 35 40 45  
 Leu Phe Gln Ala His Leu Glu Leu Thr Met Ile Ser Gly Gln Lys  
 50 55 60  
 Pro Leu Val Thr Lys Ala Arg Asn Ser Ile Ala Gly Phe Lys Leu Arg  
 65 70 75 80  
 Glu Gly Gln Gly Ile Gly Ala Lys Val Thr Leu Arg Gly Ile Arg Met  
 85 90 95  
 Tyr Asp Phe Met Asp Arg Phe Cys Asn Ile Val Ser Pro Arg Ile Arg  
 100 105 110  
 Asp Phe Arg Gly Phe Ser Asn Lys Gly Asp Gly Arg Gly Cys Tyr Ser  
 115 120 125  
 Val Gly Leu Asp Asp Gln Gln Ile Phe Pro Glu Ile Asn Leu Asp Arg  
 130 135 140  
 Val Lys Arg Thr Gln Gly Leu Asn Ile Thr Trp Val Thr Thr Ala Gln  
 145 150 155 160  
 Thr Asp Asp Glu Cys Thr Thr Leu Leu Glu Leu Met Gly Leu Arg Phe  
 165 170 175  
 Lys Lys Ala Gln  
 180

&lt;210&gt;675

&lt;211&gt;111

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;675

Met Lys Lys Gln Asn Ile Arg Val Gly Asp Lys Val Phe Ile Leu Ala  
 1 5 10 15  
 Gly Asn Asp Lys Gly Lys Glu Gly Lys Val Leu Ser Leu Thr Glu Asp  
 20 25 30  
 Lys Val Val Val Glu Gly Val Asn Val Arg Ile Lys Asn Ile Lys Arg  
 35 40 45  
 Ser Gln Gln Asn Pro Lys Gly Lys Arg Ile Ser Ile Glu Ala Pro Ile  
 50 55 60  
 His Ile Ser Asn Val Arg Leu Thr Ile Ala Gly Glu Pro Ala Lys Leu  
 65 70 75 80  
 Ser Val Lys Val Thr Glu Gln Gly Arg Glu Leu Trp Gln Arg Arg Pro  
 85 90 95  
 Asp Gly Thr Ser Gln Leu Tyr Arg Leu Val Arg Gly Lys Lys Gly  
 100 105 110

&lt;210&gt;676

&lt;211&gt;79

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;676

Met Ile Gln Gln Glu Ser Gln Leu Lys Val Ala Asp Asn Thr Gly Ala  
 1 5 10 15  
 Lys Lys Val Lys Cys Phe Lys Val Leu Gly Gly Ser Arg Arg Arg Tyr  
 20 25 30  
 Ala Thr Val Gly Asp Val Ile Val Cys Ser Val Arg Asp Val Glu Pro  
 35 40 45  
 Asn Ser Ser Ile Lys Lys Gly Arg Arg Tyr Gln Ser Cys Asp Arg Ala  
 50 55 60  
 His Thr Ser Ala Tyr Tyr Lys Lys Arg Trp Val Tyr Phe Lys Ile  
 65 70 75

&lt;210&gt;677

&lt;211&gt;86

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;677

Met Ala Ser Glu Pro Arg Gly Ser Arg Lys Val Lys Ile Gly Val Val

```

      1           5           10           15
Val Ser Ala Lys Met Glu Lys Thr Val Val Val Arg Val Glu Arg Ile
      20           25           30
Phe Ser His Pro Gln Tyr Leu Lys Val Val Arg Ser Ser Lys Lys Tyr
      35           40           45
Tyr Ala His Thr Glu Leu Lys Val Ser Glu Gly Asp Lys Val Lys Ile
      50           55           60
Gln Glu Thr Arg Pro Leu Ser Lys Leu Lys Arg Trp Arg Val Ile Glu
      65           70           75           80
His Val Gly Val Val Ser
      85

```

&lt;210&gt;678

&lt;211&gt;138

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;678

```

Met Leu Met Pro Lys Arg Thr Lys Phe Arg Lys Gln Gln Xaa Gly Gln
      1           5           10           15
Phe Ala Gly Leu Ser Lys Gly Ala Thr Phe Val Asp Phe Gly Glu Tyr
      20           25           30
Ala Met Gln Thr Leu Glu Arg Gly Leu Val Thr Ser Arg Lys Ile Glu
      35           40           45
Ala Cys Arg Val Ala Ile Asn Arg Tyr Leu Lys Arg Arg Gly Lys Val
      50           55           60
Trp Ile Arg Ile Phe Pro Asp Lys Ser Val Thr Lys Lys Pro Ala Glu
      65           70           75           80
Thr Arg Met Gly Lys Gly Lys Gly Ala Pro Asp His Trp Val Ala Val
      85           90           95
Val Arg Pro Gly Arg Ile Leu Phe Glu Val Ala Asn Val Ser Lys Glu
      100           105           110
Asp Ala Gln Asp Ala Leu Arg Arg Ala Ala Lys Leu Gly Ile Lys
      115           120           125
Thr Arg Phe Val Lys Arg Val Glu Arg Val
      130           135

```

&lt;210&gt;679

&lt;211&gt;223

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;679

```

Met Gly Gln Lys Gly Cys Pro Ile Gly Phe Arg Thr Gly Val Thr Lys
      1           5           10           15
Lys Trp Arg Ser Leu Trp Tyr Gly Asn Lys Gln Glu Phe Gly Lys Phe
      20           25           30
Leu Ile Glu Asp Val Arg Ile Arg Gln Phe Leu Arg Lys Lys Pro Ser
      35           40           45
Cys Gln Gly Ala Ala Gly Phe Val Val Arg Arg Met Ser Gly Lys Ile
      50           55           60
Glu Val Thr Ile Gln Thr Ala Arg Pro Gly Leu Val Ile Gly Lys Lys
      65           70           75           80
Gly Ala Glu Val Asp Leu Leu Lys Glu Glu Leu Arg Ala Leu Thr Gly
      85           90           95
Lys Glu Val Trp Leu Glu Ile Ala Glu Ile Lys Arg Pro Glu Leu Asn
      100           105           110
Ala Lys Leu Val Ala Asp Asn Ile Ala Arg Gln Ile Glu Arg Arg Val
      115           120           125
Ser Phe Arg Arg Ala Met Lys Lys Ala Met Gln Ser Val Met Asp Ala
      130           135           140
Gly Ala Val Gly Val Lys Ile Gln Val Ser Gly Arg Leu Ala Gly Ala
      145           150           155           160
Glu Ile Ala Arg Ser Glu Trp Tyr Lys Asn Gly Arg Val Pro Leu His
      165           170           175
Thr Leu Arg Ala Asp Ile Asp Tyr Ala Thr Ala Cys Ala Glu Thr Thr
      180           185           190
Tyr Gly Ile Ile Gly Ile Lys Val Trp Ile Asn Leu Gly Glu Asn Ser

```

195 200 205  
 Ser Ser Thr Thr Pro Asn Asn Pro Ala Ala Pro Ser Ala Ala Ala  
 210 215 220  
 <210>680  
 <211>115  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>680  
 Arg Arg His Ser Met Phe Lys Ala Thr Ala Arg Tyr Ile Arg Val Gln  
 1 5 10 15  
 Pro Arg Lys Ala Arg Leu Ala Ala Gly Leu Met Arg Asn Leu Ser Val  
 20 25 30  
 Gln Glu Ala Glu Glu Gln Leu Gly Phe Ser Gln Leu Lys Ala Gly Arg  
 35 40 45  
 Cys Leu Lys Lys Val Leu Asn Ser Ala Val Ala Asn Ala Glu Leu His  
 50 55 60  
 Glu Asn Ile Lys Arg Glu Asn Leu Ser Val Thr Glu Val Arg Val Asp  
 65 70 75 80  
 Ala Gly Pro Val Tyr Lys Arg Ser Lys Ser Lys Ser Arg Gly Gly Arg  
 85 90 95  
 Ser Pro Ile Leu Lys Arg Thr Ser His Leu Thr Val Ile Val Gly Glu  
 100 105 110  
 Lys Glu Arg  
 115  
 <210>681  
 <211>284  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>681  
 Met Phe Lys Lys Phe Lys Pro Val Thr Pro Gly Thr Arg Gln Leu Val  
 1 5 10 15  
 Leu Pro Ala Phe Asp Glu Leu Thr Thr Arg Gly Glu Leu Arg Gly Thr  
 20 25 30  
 Lys Ser Lys Arg Ser Leu Arg Pro Asn Lys Lys Leu Ser Phe Phe Lys  
 35 40 45  
 Lys Ser Ser Gly Gly Arg Asp Asn Leu Gly His Ile Ser Cys Arg His  
 50 55 60  
 Arg Gly Gly Gly Ala Lys Gln Leu Tyr Arg Val Val Asp Phe Lys Arg  
 65 70 75 80  
 Asn Lys Asp Gly Ile Thr Ala Lys Val Val Thr Val Glu Tyr Asp Pro  
 85 90 95  
 Asn Arg Ser Ala Tyr Ile Ala Leu Leu Ser Tyr Glu Asp Gly Glu Lys  
 100 105 110  
 Arg Tyr Ile Leu Ala Pro Lys Gly Ile Gln Arg Gly Asp Val Val Val  
 115 120 125  
 Ser Gly Glu Gly Ser Pro Phe Lys Pro Gly Cys Cys Met Thr Leu Lys  
 130 135 140  
 Ser Ile Pro Leu Gly Leu Ser Val His Asn Ile Glu Met Arg Pro Ser  
 145 150 155 160  
 Ser Gly Gly Lys Leu Val Arg Ser Ala Gly Leu Ala Ala Gln Val Ile  
 165 170 175  
 Ala Lys Ser Pro Gly Tyr Val Thr Leu Lys Met Pro Ser Gly Glu Phe  
 180 185 190  
 Arg Met Leu Asn Glu Gly Cys Arg Ala Thr Ile Gly Glu Val Ser Asn  
 195 200 205  
 Ala Asp His Asn Leu Arg Val Asp Gly Lys Ala Gly Arg Arg Arg Trp  
 210 215 220  
 Met Gly Val Arg Pro Thr Val Arg Gly Thr Ala Met Asn Pro Val Asp  
 225 230 235 240  
 His Pro His Gly Gly Gly Glu Gly Arg His Asn Gly Tyr Ile Pro Arg  
 245 250 255  
 Thr Pro Trp Gly Lys Val Thr Lys Gly Leu Lys Thr Arg Asp Lys Asn  
 260 265 270  
 Lys Ser Asn Lys Trp Ile Val Lys Asp Arg Arg Lys

275 280

<210>682  
 <211>112  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>682

Asp Met Lys Asp Pro Tyr Asp Val Ile Lys Arg His Tyr Val Thr Glu  
 1 5 10 15  
 Lys Ala Lys Met Leu Glu His Leu Ser Ala Gly Thr Gly Glu Gly Lys  
 20 25 30  
 Lys Lys Gly Ser Phe Cys Lys Asp Pro Lys Phe Val Phe Ile Val Ser  
 35 40 45  
 His Asp Ala Thr Lys Pro Leu Ile Ala Gln Ala Leu Glu Ala Ile Tyr  
 50 55 60  
 Val Asp Lys Asn Val Lys Val Lys Ser Val Asn Thr Ile Asn Val Lys  
 65 70 75 80  
 Pro Gln Pro Ala Arg Met Phe Arg Gly Arg Arg Lys Gly Lys Thr Ser  
 85 90 95  
 Gly Phe Lys Lys Ala Ile Val Thr Phe Tyr Gln Gly His Ser Val Gly  
 100 105 110

<210>683  
 <211>224  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>683

Trp Phe Tyr Tyr Gln Asn Leu Asp Phe Ser Gly Asn Lys Ile Gly Glu  
 1 5 10 15  
 Val Glu Val Ala Asp Ser Leu Phe Ala Asp Glu Gly Asp Gly Leu Gln  
 20 25 30  
 Leu Ile Lys Asp Tyr Ile Val Ala Ile Arg Ala Asn Lys Arg Gln Trp  
 35 40 45  
 Ser Ala Cys Thr Arg Asn Arg Ser Glu Val Ser His Ser Thr Lys Lys  
 50 55 60  
 Pro Phe Lys Gln Lys Gly Thr Gly Asn Ser Arg Gln Gly Cys Leu Ala  
 65 70 75 80  
 Ser Pro Gln Phe Arg Gly Gly Gly Ile Val Phe Gly Pro Lys Pro Lys  
 85 90 95  
 Phe Asn Gln His Val Arg Ile Asn Arg Lys Glu Arg Lys Ala Ala Ile  
 100 105 110  
 Arg Leu Leu Leu Ala Gln Lys Ile Gln Thr Asn Lys Leu Thr Val Val  
 115 120 125  
 Asp Asp Thr Val Phe Val Asp Ala Leu Thr Ala Pro Lys Thr Gln Ser  
 130 135 140  
 Ala Leu Arg Phe Leu Lys Asp Cys Asn Val Glu Cys Arg Ser Ile Leu  
 145 150 155 160  
 Phe Ile Asp His Leu Asp His Val Glu Lys Asn Glu Asn Leu Arg Leu  
 165 170 175  
 Ser Leu Arg Asn Leu Thr Ala Val Lys Gly Phe Val Tyr Gly Ile Asn  
 180 185 190  
 Ile Asn Gly Tyr Asp Leu Ala Ser Ala His Asn Ile Val Ile Ser Lys  
 195 200 205  
 Lys Ala Leu Gln Glu Leu Val Glu Arg Leu Val Ser Glu Thr Lys Asp  
 210 215 220

<210>684  
 <211>235  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>684

Leu Phe Leu Gln Glu Glu Ser Lys Ser Leu Leu Leu Met Asp Lys Phe  
 1 5 10 15  
 Met Arg Ser His Ile Ser Val Met Gly Lys Lys Glu Gly Met Ile His  
 20 25 30  
 Ile Phe Asp Lys Asp Gly Ser Leu Val Ala Cys Ser Val Ile Arg Val  
 35 40 45

Glu Pro Asn Val Val Thr Gln Ile Lys Thr Lys Glu Ser Asp Gly Tyr  
 50 55 60  
 Phe Ser Leu Gln Ile Gly Ala Glu Glu Met Asn Ala Pro Ala His Thr  
 65 70 75 80  
 Ile Thr Lys Arg Val Ser Lys Pro Lys Leu Gly His Leu Arg Lys Ala  
 85 90 95  
 Gly Gly Arg Val Phe Arg Phe Leu Lys Glu Val Arg Gly Ser Glu Glu  
 100 105 110  
 Ala Leu Asn Gly Val Ser Leu Gly Asp Ala Phe Gly Leu Glu Val Phe  
 115 120 125  
 Glu Asp Val Ser Ser Val Asp Val Arg Gly Ile Ser Lys Gly Lys Gly  
 130 135 140  
 Phe Gln Gly Val Met Lys Lys Phe Gly Phe Arg Gly Gly Pro Gly Ser  
 145 150 155 160  
 His Gly Ser Gly Phe His Arg His Ala Gly Ser Ile Gly Met Arg Ser  
 165 170 175  
 Thr Pro Gly Arg Cys Phe Pro Gly Ser Lys Arg Pro Ser His Met Gly  
 180 185 190  
 Ala Glu Asn Val Thr Val Lys Asn Leu Glu Val Ile Lys Val Asp Leu  
 195 200 205  
 Glu Lys Lys Val Leu Leu Val Lys Gly Ala Ile Pro Gly Ala Arg Gly  
 210 215 220  
 Ser Ile Val Ile Val Lys His Ser Ser Arg Thr  
 225 230 235

&lt;210&gt;685

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;685

Lys Val Ala Ser Lys Lys Phe Phe Arg Ser Asp Phe Phe Lys Ile Lys  
 1 5 10 15  
 Ile Lys Leu Ala Tyr Leu Pro Asp Phe Val Phe Cys His Met Leu Tyr  
 20 25 30  
 Lys Pro Ile Pro Ala Asp Ala Ala Val Lys Ala Pro Glu Ile Ala Ala  
 35 40 45  
 Glu Gln Ala Thr Val Ile Gly Lys Gly Met Ser Leu Thr Pro Ser Thr  
 50 55 60  
 Thr Asn Ser Lys Ala Phe Ser Arg Arg Val Lys Thr Phe Leu Phe Arg  
 65 70 75 80  
 Val Ala Thr Cys Ser Leu Arg Asn Ala Leu Ser Ala Leu Arg Ile Thr  
 85 90 95  
 Ser Pro Leu Asn  
 100

&lt;210&gt;686

&lt;211&gt;334

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;686

Lys Trp Arg Leu Thr Gln Leu Asp Arg Gln Glu Val Gln Gln Val Arg  
 1 5 10 15  
 Cys Cys Cys Gln Leu Pro Lys Asn Gln Arg Leu Ser Ala Pro Leu Leu  
 20 25 30  
 Arg Lys Gly Phe Ile Val Phe Asn Asn Phe Phe Thr Asn Pro Gly Asn  
 35 40 45  
 Lys Leu Ala Lys Phe Val Gly Ala Thr Lys Ser Leu Asp Lys Cys Phe  
 50 55 60  
 Lys Leu Ser Lys Ala Val Ser Asp Cys Val Val Gly Ser Leu Glu Glu  
 65 70 75 80  
 Ala Gly Cys Thr Gly Asp Ala Leu Thr Ser Ala Arg Asn Ala Gln Gly  
 85 90 95  
 Met Leu Lys Thr Thr Arg Glu Val Val Ala Leu Ala Asn Val Leu Asn  
 100 105 110  
 Gly Ala Val Pro Ser Ile Val Asn Ser Thr Gln Arg Cys Tyr Gln Tyr  
 115 120 125

Thr Arg Gln Ala Phe Glu Leu Gly Ser Lys Thr Lys Glu Arg Lys Thr  
 130 135 140  
 Pro Gly Glu Tyr Ser Lys Met Leu Leu Thr Arg Gly Asp Tyr Leu Leu  
 145 150 155 160  
 Ala Ala Ser Arg Glu Ala Cys Thr Ala Val Gly Ala Thr Thr Tyr Ser  
 165 170 175  
 Ala Thr Phe Gly Val Leu Arg Pro Leu Met Leu Ile Asn Lys Leu Thr  
 180 185 190  
 Ala Lys Pro Phe Leu Asp Lys Ala Thr Val Gly Asn Phe Gly Thr Ala  
 195 200 205  
 Val Ala Gly Ile Met Thr Ile Asn His Met Ala Gly Val Ala Gly Ala  
 210 215 220  
 Val Gly Gly Ile Ala Leu Glu Gln Lys Leu Phe Lys Arg Ala Lys Glu  
 225 230 235 240  
 Ser Leu Tyr Asn Glu Arg Cys Ala Leu Glu Asn Gln Gln Ser Gln Leu  
 245 250 255  
 Ser Gly Asp Val Ile Leu Ser Ala Glu Arg Ala Leu Arg Lys Glu His  
 260 265 270  
 Val Ala Thr Leu Lys Arg Asn Val Leu Thr Leu Leu Glu Lys Ala Leu  
 275 280 285  
 Glu Leu Val Val Asp Gly Val Lys Leu Ile Pro Leu Pro Ile Thr Val  
 290 295 300  
 Ala Cys Ser Ala Ala Ile Ser Gly Ala Leu Thr Ala Ala Ser Ala Gly  
 305 310 315 320  
 Ile Gly Leu Tyr Ser Ile Trp Gln Lys Thr Lys Ser Gly Lys  
 325 330

&lt;210&gt;687

&lt;211&gt;321

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;687

Leu Asn Leu Lys Val Val Tyr Phe Gly Thr Pro Thr Phe Ala Ala Thr  
 1 5 10 15  
 Val Leu Gln Asp Leu Leu His His Lys Ile Gln Ile Thr Ala Val Val  
 20 25 30  
 Thr Arg Val Asp Lys Pro Gln Lys Arg Ser Ala Gln Leu Ile Pro Ser  
 35 40 45  
 Pro Val Lys Thr Ile Ala Leu Thr His Gly Leu Pro Leu Leu Gln Pro  
 50 55 60  
 Ser Lys Ala Ser Asp Pro Gln Phe Ile Glu Glu Leu Arg Ala Phe Asn  
 65 70 75 80  
 Ala Asp Val Phe Ile Val Val Ala Tyr Gly Ala Ile Leu Arg Gln Ile  
 85 90 95  
 Val Leu Asp Ile Pro Arg Tyr Gly Cys Tyr Asn Leu His Ala Gly Leu  
 100 105 110  
 Leu Pro Ala Tyr Arg Gly Ala Ala Pro Ile Gln Arg Cys Ile Met Glu  
 115 120 125  
 Gly Ala Thr Glu Ser Gly Asn Thr Val Ile Arg Met Asp Ala Gly Met  
 130 135 140  
 Asp Thr Gly Asp Met Ala Asn Ile Thr Arg Val Pro Ile Gly Pro Asp  
 145 150 155 160  
 Met Thr Ser Gly Glu Leu Ala Asp Ala Leu Ala Ser Gln Gly Ala Glu  
 165 170 175  
 Val Leu Ile Lys Thr Leu Gln Gln Ile Glu Ser Gly Gln Leu Gln Leu  
 180 185 190  
 Val Ser Gln Asp Ala Ala Leu Ala Thr Ile Ala Pro Lys Leu Ser Lys  
 195 200 205  
 Glu Glu Gly Gln Val Pro Trp Asp Lys Pro Ala Lys Glu Ala Tyr Ala  
 210 215 220  
 His Ile Arg Gly Val Thr Pro Ala Pro Gly Ala Trp Thr Leu Phe Ser  
 225 230 235 240  
 Phe Ser Glu Lys Ala Pro Lys Arg Leu Met Ile Arg Lys Ala Ser Leu  
 245 250 255  
 Leu Ala Glu Ala Gly Arg Tyr Gly Ala Pro Gly Thr Val Val Val Thr

260 265 270  
 Asp Arg Gln Glu Leu Ala Ile Ala Cys Ser Glu Gly Ala Ile Cys Leu  
 275 280 285  
 His Glu Val Gln Val Glu Gly Lys Gly Ser Thr Asn Ser Lys Ser Phe  
 290 295 300  
 Leu Asn Gly Tyr Pro Ala Lys Lys Leu Lys Ile Val Phe Thr Leu Asn  
 305 310 315 320  
 Asn

&lt;210&gt;688

&lt;211&gt;279

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;688

Met Ala Ser Ile His Pro Thr Ala Ile Ile Glu Pro Gly Ala Lys Ile  
 1 5 10 15  
 Gly Lys Asp Val Ile Glu Pro Tyr Val Val Ile Lys Ala Thr Val  
 20 25 30  
 Thr Leu Cys Asp Asn Val Val Val Lys Ser Tyr Ala Tyr Ile Asp Gly  
 35 40 45  
 Asn Thr Thr Ile Gly Lys Gly Thr Thr Ile Trp Pro Ser Ala Met Ile  
 50 55 60  
 Gly Asn Lys Pro Gln Asp Leu Lys Tyr Gln Gly Glu Lys Thr Tyr Val  
 65 70 75 80  
 Thr Ile Gly Glu Asn Cys Glu Ile Arg Glu Phe Ala Ile Ile Thr Ser  
 85 90 95  
 Ser Thr Phe Glu Gly Thr Thr Val Ser Ile Gly Asn Asn Cys Leu Ile  
 100 105 110  
 Met Pro Trp Ala His Val Ala His Asn Cys Thr Ile Gly Asn Asn Val  
 115 120 125  
 Val Leu Ser Asn His Ala Gln Leu Ala Gly His Val Gln Val Gly Asp  
 130 135 140  
 Tyr Ala Ile Leu Gly Gly Met Val Gly Val His Gln Phe Val Arg Ile  
 145 150 155 160  
 Gly Ala His Ala Met Val Gly Ala Leu Ser Gly Ile Arg Arg Asp Val  
 165 170 175  
 Pro Pro Tyr Thr Ile Gly Ser Gly Asn Pro Tyr Gln Leu Ala Gly Ile  
 180 185 190  
 Asn Lys Val Gly Leu Gln Arg Arg Gln Val Pro Phe Ala Thr Arg Leu  
 195 200 205  
 Ala Leu Ile Lys Ala Phe Lys Lys Ile Tyr Arg Ala Asp Gly Cys Phe  
 210 215 220  
 Phe Glu Ser Leu Glu Glu Thr Leu Glu Glu Tyr Gly Asp Ile Pro Glu  
 225 230 235 240  
 Val Lys Asn Phe Ile Glu Phe Cys Gln Ser Pro Ser Lys Arg Gly Ile  
 245 250 255  
 Glu Arg Ser Ile Asp Lys Gln Ala Leu Glu Glu Glu Ser Ala Asp Lys  
 260 265 270  
 Glu Gly Val Leu Ile Glu Ser  
 275

&lt;210&gt;689

&lt;211&gt;153

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;689

Met Asn Gln Pro Ser Val Ile Lys Leu Arg Glu Leu Leu Asp Leu Leu  
 1 5 10 15  
 Pro His Arg Tyr Pro Phe Leu Leu Val Asp Lys Val Leu Ser Tyr Asp  
 20 25 30  
 Ile Glu Ala Arg Ser Ile Thr Ala Gln Lys Asn Val Thr Ile Asn Glu  
 35 40 45  
 Pro Phe Phe Met Gly His Phe Pro Asn Ala Pro Ile Met Pro Gly Val  
 50 55 60  
 Leu Ile Leu Glu Ala Leu Ala Gln Ala Ala Gly Val Leu Ile Gly Leu



65 70 75 80  
 Val Leu Glu Asn Asp Arg Asn Lys Arg Ile Ala Leu Phe Leu Gly Ile  
 85 90 95  
 Gln Lys Ala Lys Phe Arg Gln Ala Val Arg Pro Gly Asp Val Leu Thr  
 100 105 110  
 Leu Gln Ala Asp Phe Ser Leu Ile Ser Ser Lys Gly Gly Lys Ala Trp  
 115 120 125  
 Ala Gln Ala Arg Val Asp Ser Gln Leu Val Thr Glu Ala Glu Leu Ser  
 130 135 140  
 Phe Ala Leu Val Asp Lys Glu Ser Ile  
 145 150

&lt;210&gt;690

&lt;211&gt;166

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;690

Ser Ile Lys Gln Val Phe Val Asn Lys Lys Ile Xaa Val Ser Ile Ala  
 1 5 10 15  
 Arg Leu Thr Arg Pro Val Tyr Tyr Gln His Gln Asp Ile Phe Leu Ala  
 20 25 30  
 Ala Phe Pro Ser Asp Glu Leu Lys Ile Ser Tyr Thr Leu His Tyr Pro  
 35 40 45  
 Gln Ser Ser Thr Ile Gly Thr Gln Tyr Lys Ser Leu Val Ile Asn Glu  
 50 55 60  
 Glu Ser Phe Arg Gln Glu Ile Ala Pro Cys Arg Thr Phe Ala Leu Tyr  
 65 70 75 80  
 Asn Glu Leu Cys Phe Leu Met Glu Lys Gly Leu Ile Gly Gly Gly Cys  
 85 90 95  
 Leu Asp Asn Ala Val Val Phe Lys Asp Asp Gly Ile Ile Ser Arg Gly  
 100 105 110  
 Gln Leu Arg Phe Ala Asp Glu Pro Val Arg His Lys Ile Leu Asp Leu  
 115 120 125  
 Ile Gly Asp Leu Ser Leu Val Gly Arg Pro Phe Val Ala His Val Leu  
 130 135 140  
 Ala Val Gly Ser Gly His Ser Ser Asn Ile Ala Phe Gly Lys Lys Ile  
 145 150 155 160  
 Leu Glu Ala Leu Glu Leu  
 165

&lt;210&gt;691

&lt;211&gt;152

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;691

Met Leu Glu Arg Thr Gln Arg Thr Leu Lys Arg Glu Val Arg Tyr Ser  
 1 5 10 15  
 Gly Val Gly Ile His Leu Gly Lys Ser Thr Leu His Leu Gln Pro  
 20 25 30  
 Ala Gln Thr Asn Thr Gly Ile Val Phe Gln Arg Gln Ser Ala Ser Gly  
 35 40 45  
 Asn Tyr Glu Asn Val Pro Ala Leu Leu Asp His Val Tyr Thr Thr Gly  
 50 55 60  
 Arg Ser Thr Thr Leu Ser Arg Gly Ser Ala Val Ile Ala Thr Val Glu  
 65 70 75 80  
 His Leu Met Ala Ala Leu Arg Ser Asn Asn Ile Asp Asn Leu Ile Ile  
 85 90 95  
 Gln Cys Ser Gly Glu Glu Ile Pro Ile Gly Asp Gly Ser Ser Asn Val  
 100 105 110  
 Phe Val Glu Leu Ile Asp Gln Ala Gly Ile Cys Glu Gln Glu Asp Xaa  
 115 120 125  
 Gly Phe His Cys Glu Thr Asn Thr Ser Cys Ile Leu Ser Thr Ser Gly  
 130 135 140  
 His Phe Phe Ser Ser Phe Ser Leu  
 145 150

&lt;210&gt;692

&lt;211&gt;541

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;692

```

Val Leu Arg Ile Phe Cys Phe Val Ile Ser Trp Cys Leu Ile Ala Phe
  1           5           10           15
Ala Gln Pro Asp Leu Ser Gly Phe Val Ser Ile Leu Gly Ala Ala Cys
          20           25           30
Gly Tyr Gly Phe Phe Trp Tyr Ser Leu Glu Pro Leu Lys Lys Pro Ser
      35           40           45
Leu Pro Leu Arg Thr Leu Phe Val Ser Cys Phe Phe Trp Ile Phe Thr
      50           55           60
Ile Glu Gly Ile His Phe Ser Trp Met Leu Ser Asp Gln Tyr Ile Gly
      65           70           75           80
Lys Leu Ile Tyr Leu Val Trp Leu Thr Leu Ile Thr Ile Leu Ser Val
          85           90           95
Leu Phe Ser Gly Phe Ser Cys Leu Leu Val Ala Ile Val Arg Gln Lys
          100          105          110
Arg Thr Ala Phe Leu Trp Ser Leu Pro Gly Val Trp Val Ala Ile Glu
          115          120          125
Met Leu Arg Phe Tyr Gly Ile Phe Ser Gly Met Ser Phe Asp Tyr Leu
          130          135          140
Gly Trp Pro Met Thr Ala Ser Ala Tyr Gly Arg Gln Phe Gly Gly Phe
          145          150          155          160
Leu Gly Trp Ala Gly Gln Ser Phe Ala Val Ile Ala Val Asn Met Ser
          165          170          175
Phe Tyr Cys Leu Leu Leu Lys Lys Pro His Ala Lys Met Leu Trp Val
          180          185          190
Leu Thr Leu Leu Leu Pro Tyr Thr Phe Gly Ala Ile His Tyr Glu Tyr
          195          200          205
Leu Lys His Ala Phe Gln Gln Asp Lys Arg Ala Leu Arg Val Ala Val
          210          215          220
Val Gln Pro Ala His Pro Pro Ile Arg Pro Lys Leu Lys Ser Pro Ile
          225          230          235          240
Val Val Trp Glu Gln Leu Leu Gln Leu Val Ser Pro Ile Gln Gln Pro
          245          250          255
Ile Asp Leu Leu Ile Phe Pro Glu Val Val Val Pro Phe Gly Lys His
          260          265          270
Arg Gln Val Tyr Pro Tyr Glu Ser Cys Ala His Leu Leu Ser Ser Phe
          275          280          285
Ala Pro Leu Pro Glu Gly Lys Ala Phe Leu Ser Asn Ser Asp Cys Ala
          290          295          300
Thr Ala Leu Ser Gln His Phe Gln Cys Pro Val Ile Ile Gly Leu Glu
          305          310          315          320
Arg Trp Val Lys Lys Glu Asn Val Leu Tyr Trp Tyr Asn Ser Ala Glu
          325          330          335
Val Ile Ser His Lys Gly Ile Ser Val Gly Tyr Asp Lys Arg Ile Leu
          340          345          350
Val Pro Gly Gly Glu Tyr Ile Pro Gly Gly Lys Phe Gly Ser Leu Ile
          355          360          365
Cys Arg Gln Leu Phe Pro Lys Tyr Ala Leu Gly Cys Lys Arg Leu Pro
          370          375          380
Gly Arg Arg Ser Gly Val Val Gln Val Arg Gly Leu Pro Arg Ile Gly
          385          390          395          400
Ile Thr Ile Cys Tyr Glu Glu Thr Phe Gly Tyr Arg Leu Gln Ser Tyr
          405          410          415
Lys Arg Gln Gly Ala Glu Leu Leu Val Asn Leu Thr Asn Asp Gly Trp
          420          425          430
Tyr Pro Glu Ser Arg Leu Pro Lys Val His Phe Leu His Gly Met Leu
          435          440          445
Arg Asn Gln Glu Phe Gly Met Pro Cys Val Arg Ala Cys Gln Thr Gly
          450          455          460
Val Thr Ala Thr Val Asp Ser Leu Gly Arg Ile Leu Lys Ile Leu Pro
          465          470          475          480

```

Tyr Asp Thr Arg Glu Thr Lys Ala Pro Ser Gly Val Leu Glu Thr Ser  
 485 490 495  
 Leu Pro Leu Phe Asn Tyr Lys Thr Leu Tyr Gly Tyr Cys Gly Asp Tyr  
 500 505 510  
 Pro Met Ile Leu Ile Ala Phe Cys Ala Val Ser Tyr Leu Gly Gly Gly  
 515 520 525  
 Phe Leu Gly Tyr Arg Leu Leu Ala Lys Lys Glu Ile Arg  
 530 535 540

&lt;210&gt;693

&lt;211&gt;155

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;693

Met Leu Lys Lys Lys Pro Val Ser Phe Ser Cys Ile Asp Gly His Ile  
 1 5 10 15  
 Tyr Lys Ile Phe Pro Asn Asp Leu Asn Ala Asn Asn Thr Val Phe Gly  
 20 25 30  
 Gly Leu Leu Met Ser Leu Leu Asp Arg Leu Ala Leu Val Val Ala Glu  
 35 40 45  
 Arg His Thr Glu Ser Val Cys Val Thr Ala Phe Val Asp Ala Leu Arg  
 50 55 60  
 Phe Tyr Ala Pro Ala Tyr Met Gly Glu Asn Leu Ile Cys Lys Ala Ala  
 65 70 75 80  
 Val Asn Arg Thr Trp Arg Thr Ser Leu Glu Val Gly Val Lys Val Trp  
 85 90 95  
 Ala Glu Asn Ile Tyr Lys Gln Glu Arg Arg His Ile Thr Ser Ala Tyr  
 100 105 110  
 Phe Thr Phe Val Ala Val Asn Glu Asp Asn Gln Pro Ile Pro Val His  
 115 120 125  
 Gln Ile Val Pro Glu Thr Pro Glu Glu Lys Arg Arg Tyr Asn Glu Ala  
 130 135 140  
 Asp Arg Arg Arg Gln Ala Arg Leu Glu Leu Lys  
 145 150 155

&lt;210&gt;694

&lt;211&gt;252

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;694

Lys Glu Ile Met Ser Leu Leu Lys Asp Thr Val Phe Thr Cys Leu Asp  
 1 5 10 15  
 Cys Glu Met Thr Gly Leu Asp Val Lys Lys Asp Arg Ile Ile Glu Ile  
 20 25 30  
 Ala Ala Val Arg Phe Thr Phe Asp Ser Val Ile Ser Ser Ile Glu Phe  
 35 40 45  
 Leu Ile Asn Pro Glu Arg Val Val Ser Ala Glu Ser Gln Arg Val His  
 50 55 60  
 His Ile Ser Asn Ala Met Leu Arg Asp Gln Pro Lys Ile Ala Glu Val  
 65 70 75 80  
 Phe Pro Gln Ile Lys Ala Phe Phe Lys Glu Gly Asp Tyr Ile Val Gly  
 85 90 95  
 His Ser Val Gly Phe Asp Leu Gln Val Leu Ala Gln Glu Met Glu Arg  
 100 105 110  
 Ile Gly Glu Thr Phe Leu Ser Lys Tyr Thr Ile Ile Asp Thr Leu Arg  
 115 120 125  
 Leu Ala Lys Glu Tyr Gly Asp Ser Pro Asn Asn Ser Leu Glu Ser Leu  
 130 135 140  
 Ala Val His Phe Asn Val Pro Tyr Asp Gly Asn His Arg Ala Met Lys  
 145 150 155 160  
 Asp Val Glu Ile Asn Ile Asn Ile Phe Lys His Leu Cys Lys Arg Phe  
 165 170 175  
 Arg Thr Leu Glu Gln Leu Lys Gln Val Leu Ala Lys Pro Ile Lys Met  
 180 185 190  
 Lys Tyr Met Pro Leu Gly Lys His Lys Gly Arg Cys Phe Ser Glu Ile  
 195 200 205

Pro Leu Ala Tyr Leu Gln Trp Ala Ser Lys Met Asp Phe Asp Ser Asp  
 210 215 220  
 Leu Leu Phe Ser Ile Arg His Glu Ile Lys His Arg Gln Lys Gly Thr  
 225 230 235 240  
 Gly Phe Ser Gln Val Asn Asn Pro Phe Met Glu Leu  
 245 250

&lt;210&gt;695

&lt;211&gt;142

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;695

Pro Met Gly Arg Tyr Arg Arg Val Ser His Ser Ser Gln Glu Thr Leu  
 1 5 10 15  
 Leu Leu Gly Thr Glu Leu Gly Gln Val Leu Val Pro Gly Ala Val Leu  
 20 25 30  
 Leu Leu Phe Gly Asp Tyr Gly Ala Gly Lys Thr Glu Phe Val Arg Gly  
 35 40 45  
 Ile Val Ser Gly Tyr Leu Gly Asp Thr Ile Ala Glu Glu Val Ala Ser  
 50 55 60  
 Pro Ser Phe Ser Ile Leu His Val Tyr Gly Asn Glu Pro Lys Arg Leu  
 65 70 75 80  
 Cys His Tyr Asp Leu Tyr Arg Ile Asp Gln Lys Asn Gln Glu Tyr Ile  
 85 90 95  
 Phe Gln Asp Ala Glu Glu Asp Asp Val Leu Cys Ile Glu Trp Ala Asp  
 100 105 110  
 Arg Leu Pro Lys Pro Arg Phe Cys Asp Thr Ile Asn Ile Tyr Ile Thr  
 115 120 125  
 Met Gln Thr Asn Met Glu Arg Glu Ile Ile Ile Glu Lys Arg  
 130 135 140

&lt;210&gt;696

&lt;211&gt;191

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;696

Phe Ser Lys Leu Xaa Glu Asp Ala Val Arg Ile Leu Glu Gln Asp Lys  
 1 5 10 15  
 Lys Ile Trp Arg Glu Thr Glu Ile Gln Ile Ser Ser Glu Lys Pro Gln  
 20 25 30  
 Val Asn Glu Asn Thr Lys Arg Ile Tyr Ile Cys Pro Phe Thr Gly Lys  
 35 40 45  
 Val Phe Ala Asp Asn Val Tyr Ala Asn Pro Gln Asp Ala Ile Tyr Asp  
 50 55 60  
 Trp Leu Ser Ser Cys Pro Gln Asn Met Glu Lys Gln Gly Gly Val Arg  
 65 70 75 80  
 Ile Lys Arg Phe Leu Val Ser Glu Asp Pro Asp Val Ile Lys Glu Tyr  
 85 90 95  
 Ala Val Pro Pro Lys Glu Pro Ile Ile Lys Thr Val Phe Ala Ser Ala  
 100 105 110  
 Ile Thr Gly Lys Leu Phe His Ser Leu Pro Pro Leu Leu Glu Asp Phe  
 115 120 125  
 Ile Ser Ser Tyr Leu Arg Pro Met Thr Leu Glu Glu Val Gln Asn Gln  
 130 135 140  
 Thr Lys Phe Gln Leu Glu Ser Ser Phe Leu Ser Leu Leu Gln Asp Ala  
 145 150 155 160  
 Leu Val Glu Asp Lys Ile Ala Ala Phe Ile Glu Ser Leu Ala Asp Asp  
 165 170 175  
 Thr Ala Phe His Val Tyr Ile Ser Gln Trp Val Asp Thr Glu Glu  
 180 185 190

&lt;210&gt;697

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;697

Met Val Lys Ile Ile Ser Ser Glu Asn Phe Asp Ser Phe Ile Ala Ser

1 5 10 15  
 Gly Leu Val Leu Val Asp Phe Phe Ala Glu Trp Cys Gly Pro Cys Arg  
 20 25 30  
 Met Leu Thr Pro Ile Leu Glu Asn Leu Ala Ala Glu Leu Pro His Val  
 35 40 45  
 Thr Ile Gly Lys Ile Asn Ile Asp Glu Asn Ser Lys Pro Ala Glu Thr  
 50 55 60  
 Tyr Glu Val Ser Ser Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Asn  
 65 70 75 80  
 Glu Val Ala Arg Val Val Gly Leu Lys Asp Lys Glu Phe Leu Thr Asn  
 85 90 95  
 Leu Ile Asn Lys His Ala  
 100

&lt;210&gt;698

&lt;211&gt;156

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;698

Met Arg Val Val Leu His Cys Pro Asp Ile Pro Gln Asn Thr Gly Asn  
 1 5 10 15  
 Ile Gly Arg Thr Cys Val Ala Leu Gly Ala Glu Leu Ile Leu Val Arg  
 20 25 30  
 Pro Leu Gly Phe Ser Leu Ala Asp Lys Phe Val Lys Arg Ala Gly Met  
 35 40 45  
 Asp Tyr Trp Asp Lys Leu Gln Leu Thr Val Val Asp Ser Ile Glu Glu  
 50 55 60  
 Ala Leu His Asp Val Pro Glu Asp Gln Ile Phe Cys Leu Cys Thr Lys  
 65 70 75 80  
 Gly Ser Ala Ser Tyr Thr Glu Phe Ser Leu Pro Ser Ser Gly Thr Tyr  
 85 90 95  
 Val Phe Gly Ser Glu Ser Lys Gly Leu Pro Lys Glu Ile Leu Lys Lys  
 100 105 110  
 Tyr Tyr Lys Asn Cys Leu Arg Ile Pro Met Gln Gln Asp Ile Arg Ser  
 115 120 125  
 Leu Asn Leu Ala Thr Ser Val Gly Ile Val Leu Tyr Glu Val Val Arg  
 130 135 140  
 Gln Lys Thr Val Ala Leu Gln Lys Asn Pro Thr Val  
 145 150 155

&lt;210&gt;699

&lt;211&gt;258

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;699

Met Asn Arg Arg Trp Asn Leu Val Leu Ala Thr Val Ala Leu Ala Leu  
 1 5 10 15  
 Ser Val Ala Ser Cys Asp Val Arg Ser Lys Asp Lys Asp Lys Asp Gln  
 20 25 30  
 Gly Ser Leu Val Glu Tyr Lys Asp Asn Lys Asp Thr Asn Asp Ile Glu  
 35 40 45  
 Leu Ser Asp Asn Gln Lys Leu Ser Arg Thr Phe Gly His Leu Leu Ala  
 50 55 60  
 Arg Gln Leu Arg Lys Ser Glu Asp Met Phe Phe Asp Ile Ala Glu Val  
 65 70 75 80  
 Ala Lys Gly Leu Gln Ala Glu Leu Val Cys Lys Ser Ala Pro Leu Thr  
 85 90 95  
 Glu Thr Glu Tyr Glu Glu Lys Met Ala Glu Val Gln Lys Leu Val Phe  
 100 105 110  
 Glu Lys Lys Ser Lys Glu Asn Leu Ser Leu Ala Glu Lys Phe Leu Lys  
 115 120 125  
 Glu Asn Ser Lys Asn Ala Gly Val Val Glu Val Gln Pro Ser Lys Leu  
 130 135 140  
 Gln Tyr Lys Ile Ile Lys Glu Gly Ala Gly Lys Ala Ile Ser Gly Lys  
 145 150 155 160  
 Pro Ser Ala Leu Leu His Tyr Lys Gly Ser Phe Ile Asn Gly Gln Val

165 170 175  
 Phe Ser Ser Ser Glu Gly Asn Asn Glu Pro Ile Leu Leu Pro Leu Gly  
 180 185 190  
 Gln Thr Ile Pro Gly Phe Ala Leu Gly Met Gln Gly Met Lys Glu Gly  
 195 200 205  
 Glu Thr Arg Val Leu Tyr Ile His Pro Asp Leu Ala Tyr Gly Thr Ala  
 210 215 220  
 Gly Gln Leu Pro Pro Asn Ser Leu Leu Ile Phe Glu Ile Asn Leu Ile  
 225 230 235 240  
 Gln Ala Ser Ala Asp Glu Val Ala Ala Val Pro Gln Glu Gly Asn Gln  
 245 250 255  
 Gly Glu

&lt;210&gt;700

&lt;211&gt;584

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;700

Met Lys Tyr Arg Thr His Arg Cys Asn Glu Leu Thr Ser Asn His Ile  
 1 5 10 15  
 Gly Glu Asn Val Gln Leu Ala Gly Trp Val His Arg Tyr Arg Asn His  
 20 25 30  
 Gly Gly Val Val Phe Ile Xaa Leu Arg Asp Arg Phe Gly Ile Thr Gln  
 35 40 45  
 Ile Val Cys Arg Glu Asp Glu Gln Pro Glu Leu His Gln Arg Leu Asp  
 50 55 60  
 Ala Val Arg Ser Glu Trp Val Leu Ser Val Arg Gly Lys Val Cys Pro  
 65 70 75 80  
 Arg Leu Ala Gly Met Glu Asn Pro Asn Leu Ala Thr Gly His Ile Glu  
 85 90 95  
 Val Glu Val Ala Ser Phe Glu Val Leu Ser Lys Ser Gln Asn Leu Pro  
 100 105 110  
 Phe Ser Ile Ala Asp Asp His Ile Asn Val Asn Glu Glu Leu Arg Leu  
 115 120 125  
 Glu Tyr Arg Tyr Leu Asp Met Arg Arg Gly Asp Ile Ile Glu Lys Leu  
 130 135 140  
 Leu Cys Arg His Gln Val Met Leu Ala Cys Arg Asn Phe Met Asp Ala  
 145 150 155 160  
 Gln Gly Phe Thr Glu Ile Val Thr Pro Val Leu Gly Lys Ser Thr Pro  
 165 170 175  
 Glu Gly Ala Arg Asp Tyr Leu Val Pro Ser Arg Ile Tyr Pro Gly Lys  
 180 185 190  
 Phe Tyr Ala Leu Pro Gln Ser Pro Gln Leu Phe Lys Gln Leu Leu Met  
 195 200 205  
 Val Gly Gly Leu Asp Arg Tyr Phe Gln Ile Ala Thr Cys Phe Arg Asp  
 210 215 220  
 Glu Asp Leu Arg Ala Asp Arg Gln Pro Glu Phe Ala Gln Ile Asp Ile  
 225 230 235 240  
 Glu Met Ser Phe Gly Asp Thr Gln Asp Leu Leu Pro Ile Ile Glu Gln  
 245 250 255  
 Leu Val Ala Thr Leu Phe Ala Thr Gln Gly Ile Glu Ile Pro Leu Pro  
 260 265 270  
 Leu Ala Lys Met Thr Tyr Gln Glu Ala Lys Asp Ser Tyr Gly Thr Asp  
 275 280 285  
 Lys Pro Asp Leu Arg Phe Asp Leu Lys Leu Lys Asp Cys Arg Asp Tyr  
 290 295 300  
 Ala Lys Arg Ser Ser Phe Ser Ile Phe Leu Asp Gln Leu Ala His Gly  
 305 310 315 320  
 Gly Thr Ile Lys Gly Phe Cys Val Pro Gly Gly Ala Thr Met Ser Arg  
 325 330 335  
 Lys Gln Leu Asp Gly Tyr Thr Glu Phe Val Lys Arg Tyr Gly Ala Met  
 340 345 350  
 Gly Leu Val Trp Ile Lys Asn Gln Glu Gly Lys Val Ala Ser Asn Ile  
 355 360 365

Ala Lys Phe Met Asp Glu Glu Val Phe His Glu Leu Phe Ala Tyr Phe  
 370 375 380  
 Asp Ala Lys Asp Gln Asp Ile Leu Leu Leu Ile Ala Ala Pro Glu Ser  
 385 390 395 400  
 Val Ala Asn Gln Ser Leu Asp His Leu Arg Arg Leu Ile Ala Lys Glu  
 405 410 415  
 Arg Glu Leu Tyr Ser Asp Asn Gln Tyr Asn Phe Val Trp Ile Thr Asp  
 420 425 430  
 Phe Pro Leu Phe Ser Leu Glu Asp Gly Lys Ile Val Ala Glu His His  
 435 440 445  
 Pro Phe Thr Ala Pro Leu Glu Glu Asp Ile Pro Leu Leu Glu Thr Asp  
 450 455 460  
 Pro Leu Ala Val Arg Ser Ser Ser Tyr Asp Leu Val Leu Asn Gly Tyr  
 465 470 475 480  
 Glu Ile Ala Ser Gly Ser Gln Arg Ile His Asn Pro Asp Leu Gln Ser  
 485 490 495  
 Gln Ile Phe Thr Ile Leu Lys Ile Ser Pro Glu Ser Ile Gln Glu Lys  
 500 505 510  
 Phe Gly Phe Phe Ile Lys Ala Leu Ser Phe Gly Thr Pro Pro His Leu  
 515 520 525  
 Gly Ile Ala Leu Gly Leu Asp Arg Leu Val Met Val Leu Thr Ala Ala  
 530 535 540  
 Glu Ser Ile Arg Glu Val Ile Ala Phe Pro Lys Thr Gln Lys Ala Ser  
 545 550 555 560  
 Asp Leu Met Met Asn Ala Pro Ser Glu Ile Met Ser Ser Gln Leu Lys  
 565 570 575  
 Glu Leu Ser Ile Lys Val Ala Phe  
 580

&lt;210&gt;701

&lt;211&gt;430

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;701

Val Thr Val Thr Leu Pro Lys Gly Val Phe Asp Ile Phe Pro Tyr Leu  
 1 5 10 15  
 Ala Asp Ala Lys Gln Leu Trp Arg His Thr Ser Leu Trp His Ser Val  
 20 25 30  
 Glu Lys Ala Ile His Thr Val Cys Met Leu Tyr Gly Phe Cys Glu Ile  
 35 40 45  
 Arg Thr Pro Ile Phe Glu Lys Ser Glu Val Phe Leu His Val Gly Glu  
 50 55 60  
 Glu Ser Asp Val Val Lys Lys Glu Val Tyr Ser Phe Leu Asp Arg Lys  
 65 70 75 80  
 Gly Arg Ser Met Thr Leu Arg Pro Glu Gly Thr Ala Ala Val Val Arg  
 85 90 95  
 Ser Phe Leu Glu His Gly Ala Ser His Arg Ser Asp Asn Lys Phe Tyr  
 100 105 110  
 Tyr Ile Leu Pro Met Phe Arg Tyr Glu Arg Gln Gln Ala Gly Arg Tyr  
 115 120 125  
 Arg Gln His His Gln Phe Gly Val Glu Ala Ile Gly Val Arg His Pro  
 130 135 140  
 Leu Arg Asp Ala Glu Val Leu Ala Leu Leu Trp Asp Phe Tyr Ser Arg  
 145 150 155 160  
 Val Gly Leu Gln His Met Gln Ile Gln Leu Asn Phe Leu Gly Gly Ser  
 165 170 175  
 Glu Thr Arg Phe Arg Tyr Asp Lys Val Leu Arg Ala Tyr Leu Lys Glu  
 180 185 190  
 Ser Met Gly Glu Leu Ser Ala Leu Ser Gln Gln Arg Phe Ser Thr Asn  
 195 200 205  
 Val Leu Arg Ile Leu Asp Ser Lys Glu Pro Glu Asp Gln Glu Ile Ile  
 210 215 220  
 Arg Gln Ala Pro Pro Ile Leu Asp Tyr Val Ser Asp Glu Asp Leu Lys  
 225 230 235 240  
 Tyr Phe Asn Glu Ile Leu Asp Ala Leu Arg Val Leu Glu Ile Pro Tyr

245 250 255  
 Ala Ile Asn Pro Arg Leu Val Arg Gly Leu Asp Tyr Tyr Ser Asp Leu  
 260 265 270  
 Val Phe Glu Ala Thr Thr Thr Phe Gln Glu Val Ser Tyr Ala Leu Gly  
 275 280 285  
 Gly Gly Gly Arg Tyr Asp Gly Leu Ile Ser Ala Phe Gly Gly Ala Ser  
 290 295 300  
 Leu Pro Ala Cys Gly Phe Gly Val Gly Leu Glu Arg Ala Ile Gln Thr  
 305 310 315 320  
 Leu Leu Ala Gln Lys Arg Ile Glu Pro Gln Phe Pro His Lys Leu Arg  
 325 330 335  
 Leu Ile Pro Met Glu Pro Asp Ala Asp Gln Phe Cys Leu Glu Trp Ser  
 340 345 350  
 Gln His Leu Arg Arg Leu Gly Ile Pro Thr Glu Val Asp Trp Ser His  
 355 360 365  
 Lys Lys Val Lys Gly Ala Leu Lys Ala Ala Ser Thr Glu Gln Val Ser  
 370 375 380  
 Phe Val Cys Leu Ile Gly Glu Arg Glu Leu Ile Ser Gln Gln Leu Val  
 385 390 395 400  
 Ile Lys Asn Met Ser Leu Arg Lys Glu Phe Phe Gly Thr Lys Glu Glu  
 405 410 415  
 Val Glu Gln Arg Leu Leu Tyr Glu Ile Gln Asn Thr Pro Leu  
 420 425 430  
 <210>702  
 <211>352  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>702  
 Met Asn Val Trp Thr Lys Phe Phe Gln Pro Pro Lys His Ile Lys Glu  
 1 5 10 15  
 Ile Glu Asp Gln Glu Val Val Lys Lys Tyr Lys Tyr Trp Arg Ile  
 20 25 30  
 Arg Ile Phe Tyr Ser Met Phe Ile Gly Tyr Ile Phe Tyr Tyr Phe Thr  
 35 40 45  
 Arg Lys Ser Phe Thr Phe Ala Met Pro Thr Leu Ile Ala Asp Leu Gly  
 50 55 60  
 Phe Asp Lys Ala Gln Leu Gly Ile Ile Gly Ser Thr Leu Tyr Phe Ser  
 65 70 75 80  
 Tyr Gly Ile Ser Lys Phe Val Ser Gly Val Met Ser Asp Gln Ser Asn  
 85 90 95  
 Pro Arg Tyr Phe Met Ala Ile Gly Leu Met Ile Thr Gly Leu Thr Asn  
 100 105 110  
 Ile Phe Phe Gly Met Ser Ser Ser Ile Val Leu Phe Ala Leu Trp Trp  
 115 120 125  
 Gly Leu Asn Gly Trp Phe Gln Gly Trp Gly Trp Pro Pro Cys Ala Arg  
 130 135 140  
 Leu Leu Thr His Trp Tyr Ala Lys Ser Glu Arg Gly Thr Trp Trp Ser  
 145 150 155 160  
 Val Trp Ser Thr Ser His Asn Ile Gly Gly Ala Leu Ile Pro Ile Leu  
 165 170 175  
 Thr Gly Phe Ile Ile Asp Tyr Ser Gly Trp Arg Gly Ala Met Tyr Val  
 180 185 190  
 Pro Gly Ile Leu Cys Ile Gly Met Gly Leu Val Leu Ile Asn Arg Leu  
 195 200 205  
 Arg Asp Thr Pro Gln Ser Leu Gly Leu Pro Pro Ile Glu Lys Tyr Lys  
 210 215 220  
 Arg Asp Pro His His Ala His His Glu Gly Lys Ser Ala Ser Glu Gly  
 225 230 235 240  
 Thr Glu Glu Ile Glu Arg Glu Leu Ser Thr Arg Glu Ile Leu Phe Thr  
 245 250 255  
 Tyr Val Leu Thr Asn Gln Trp Leu Trp Phe Leu Ala Ala Ala Ser Phe  
 260 265 270  
 Phe Ile Tyr Ile Val Arg Met Ala Val Asn Asp Trp Ser Ala Leu Phe  
 275 280 285



Leu Ile Glu Thr Lys His Tyr Ala Ala Val Lys Ala Asn Phe Cys Val  
 290 295 300  
 Ser Leu Phe Glu Ile Gly Gly Leu Phe Gly Met Leu Val Ala Gly Trp  
 305 310 315 320  
 Leu Ser Asp Lys Ile Ser Lys Gly Asn Arg Gly Pro Met Lys Arg Pro  
 325 330 335  
 Leu Leu Phe Arg Phe Ala Val Cys Tyr Phe Arg His Val Val Phe Thr  
 340 345 350

&lt;210&gt;703

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;703

Asn Val Leu Phe Ser Leu Gly Leu Leu Phe Ala Ile Leu Gly Met Trp  
 1 5 10 15  
 Phe Ser Arg Ser His Asn Gln Trp Trp Val Asp Gly Thr Leu Leu Phe  
 20 25 30  
 Val Ile Gly Phe Phe Leu Tyr Gly Pro Gln Met Met Ile Gly Leu Ala  
 35 40 45  
 Ala Ala Glu Leu Ser His Lys Lys Ala Ala Gly Thr Ala Ser Gly Phe  
 50 55 60  
 Thr Gly Trp Phe Ala Tyr Phe Gly Ala Thr Phe Ala Gly Tyr Pro Leu  
 65 70 75 80  
 Gly Lys Val Thr Asp Val Trp Gly Trp Lys Gly Phe Phe Ile Ala Leu  
 85 90 95  
 Leu Ala Cys Ala Ser Ile Ala Leu Leu Leu Phe Leu Pro Thr Trp Asn  
 100 105 110  
 Ala Thr Glu Lys Asn Thr Arg Ser Lys Ala  
 115 120

&lt;210&gt;704

&lt;211&gt;1243

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;704

Gly Phe Phe Leu Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser  
 1 5 10 15  
 Val Leu Asp Ala Met Ser Ser Ile Lys Asp Phe Val Ala Lys Gly Gln  
 20 25 30  
 Glu Phe Gly Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Tyr  
 35 40 45  
 Gly Ala Val Asp Phe Tyr Lys Glu Cys Thr Gln Lys Gly Ile Gln Pro  
 50 55 60  
 Ile Ile Gly Cys Glu Cys Tyr Ile Ala Pro Gly Ser Arg Phe Asp Lys  
 65 70 75 80  
 Lys Lys Glu Lys Arg Ser Arg Ala Ala His Leu Ile Leu Leu Cys  
 85 90 95  
 Lys Asn Glu Gln Gly Tyr Arg Asn Leu Cys Ile Leu Thr Ser Leu Ala  
 100 105 110  
 Phe Thr Glu Gly Phe Tyr Tyr Phe Pro Arg Ile Asp Lys Asp Leu Leu  
 115 120 125  
 Arg Gln Tyr Ser Glu Gly Leu Ile Cys Leu Ser Gly Cys Leu Ser Ser  
 130 135 140  
 Ser Val Ser Asp Ala Ala Leu Lys Ser Pro Glu Ala Leu Leu Leu Glu  
 145 150 155 160  
 Leu Gln Trp Phe Gln Asp Leu Phe Lys Asp Asp Tyr Phe Thr Glu Val  
 165 170 175  
 Gln Leu His Lys Met Ser Glu Glu Ser Ile Ala Gly Phe Lys Glu Glu  
 180 185 190  
 Trp Leu Lys Gln Glu Tyr Tyr Ser Leu Ile Glu Lys Gln Ile Lys Val  
 195 200 205  
 Asn Thr Ala Val Leu Glu Ala Ser Lys Arg Leu Gly Ile Pro Thr Val  
 210 215 220  
 Ala Thr Asn Asp Ile His Tyr Ile Asn Ala Asn Asp Trp Gln Ala His  
 225 230 235 240

Glu Ile Leu Leu Asn Val Gln Ser Gly Glu Thr Val Arg Ile Ala Lys  
 245 250 255  
 Gln Asn Thr His Ile Pro Asn Pro Lys Arg Lys Val Tyr Arg Ser Arg  
 260 265 270  
 Glu Tyr Tyr Phe Lys Ser Pro Ala Gln Met Ala Glu Leu Phe Lys Asp  
 275 280 285  
 Ile Pro Glu Val Ile Ser Asn Thr Leu Glu Val Ala Lys Arg Cys Asp  
 290 295 300  
 Phe Thr Phe Asp Phe Ser Lys Lys His Tyr Pro Ile Tyr Val Pro Glu  
 305 310 315 320  
 Ser Leu Lys Thr Leu Asn Ser Tyr Thr Glu Glu Asp Arg Tyr Gln Ala  
 325 330 335  
 Ser Ala Val Phe Leu Lys Gln Leu Ala Glu Glu Ala Leu Pro Lys Lys  
 340 345 350  
 Tyr Ser Ser Glu Val Leu Ala His Ile Ala Lys Lys Phe Pro His Arg  
 355 360 365  
 Asp Pro Ile Asp Ile Val Lys Glu Arg Met Asp Met Glu Met Ala Ile  
 370 375 380  
 Ile Ile Pro Lys Gly Met Cys Asp Tyr Leu Leu Ile Val Trp Asp Ile  
 385 390 395 400  
 Ile His Trp Ala Lys Ala Asn Gly Ile Pro Val Gly Pro Gly Arg Gly  
 405 410 415  
 Ser Gly Ala Gly Ser Val Leu Leu Phe Leu Leu Gly Ile Thr Glu Ile  
 420 425 430  
 Glu Pro Ile Arg Phe Asp Leu Phe Phe Glu Arg Phe Ile Asn Pro Glu  
 435 440 445  
 Arg Leu Ser Tyr Pro Asp Ile Asp Ile Asp Ile Cys Met Ala Gly Arg  
 450 455 460  
 Glu Arg Val Ile Asn Tyr Ala Ile Glu Arg His Gly Lys Asp Asn Val  
 465 470 475 480  
 Ala Gln Ile Ile Thr Phe Gly Thr Met Lys Ala Lys Met Ala Val Lys  
 485 490 495  
 Asp Val Gly Arg Thr Leu Asp Met Ala Leu Ser Lys Val Asn His Ile  
 500 505 510  
 Ala Lys His Ile Pro Asp Leu Asn Thr Thr Leu Ser Lys Ala Leu Glu  
 515 520 525  
 Thr Asp Pro Asp Leu His Gln Leu Tyr Ile Asn Asp Ala Glu Ser Ala  
 530 535 540  
 Gln Val Ile Asp Met Ala Leu Cys Leu Glu Gly Ser Ile Arg Asn Thr  
 545 550 555 560  
 Gly Val His Ala Ala Gly Val Ile Ile Cys Gly Asp Gln Leu Thr Asn  
 565 570 575  
 His Ile Pro Ile Cys Ile Ser Lys Asp Ser Thr Met Ile Thr Thr Gln  
 580 585 590  
 Tyr Ser Met Lys Pro Val Glu Ser Val Gly Met Leu Lys Val Asp Leu  
 595 600 605  
 Leu Gly Leu Lys Thr Leu Thr Ser Ile Asn Ile Ala Met Ser Ala Ile  
 610 615 620  
 Glu Lys Lys Thr Gly Gln Ser Leu Ala Met Ala Thr Leu Pro Leu Asp  
 625 630 635 640  
 Asp Ala Thr Thr Phe Ser Leu Leu His Gln Gly Lys Thr Met Gly Ile  
 645 650 655  
 Phe Gln Met Glu Ser Lys Gly Met Gln Glu Leu Ala Lys Asn Leu Arg  
 660 665 670  
 Pro Asp Leu Phe Glu Glu Ile Ile Ala Met Gly Ala Leu Tyr Arg Pro  
 675 680 685  
 Gly Pro Met Asp Met Ile Pro Ser Phe Ile Asn Arg Lys His Gly Lys  
 690 695 700  
 Glu Ile Ile Glu Tyr Asp His Pro Leu Met Glu Ser Ile Leu Lys Glu  
 705 710 715 720  
 Thr Tyr Gly Ile Met Val Tyr Gln Glu Gln Val Met Gln Ile Ala Gly  
 725 730 735  
 Ala Leu Ala Ser Tyr Ser Leu Gly Glu Gly Asp Val Leu Arg Arg Ala  
 740 745 750

Met Gly Lys Lys Asp Phe Gln Gln Met Glu Gln Glu Arg Glu Lys Phe  
 755 760 765  
 Cys Lys Arg Ala Cys Asn Asn Gly Ile Asp Pro Glu Leu Ala Thr Val  
 770 775 780  
 Ile Phe Asp Lys Met Glu Lys Phe Ala Ala Tyr Gly Phe Asn Lys Ser  
 785 790 795 800  
 His Ala Ala Ala Tyr Gly Leu Ile Thr Tyr Thr Thr Ala Tyr Leu Lys  
 805 810 815  
 Ala Asn Tyr Pro Lys Glu Trp Leu Ala Ala Leu Leu Thr Cys Asp Ser  
 820 825 830  
 Asp Asp Ile Glu Lys Ile Gly Lys Leu Ile Arg Glu Ala Gln Ser Met  
 835 840 845  
 Gly Ile Pro Ile Leu Pro Pro His Ile Asn Val Ser Ser Asn His Phe  
 850 855 860  
 Val Ala Thr Asp Glu Gly Ile Arg Phe Ala Met Gly Ala Ile Lys Gly  
 865 870 875 880  
 Ile Gly Arg Gly Leu Ile Glu Ser Ile Val Glu Glu Arg Asp His His  
 885 890 895  
 Gly Pro Tyr Glu Ser Ile Arg Asp Phe Ile Gln Arg Ser Asp Leu Lys  
 900 905 910  
 Lys Val Ser Lys Lys Ser Ile Glu Ser Leu Ile Asp Ala Gly Cys Phe  
 915 920 925  
 Asp Cys Phe Asp Ser Asn Arg Asp Leu Leu Leu Ala Ser Val Glu Pro  
 930 935 940  
 Leu Tyr Glu Ala Ile Ala Lys Asp Lys Lys Glu Ala Ala Ser Gly Val  
 945 950 955 960  
 Met Thr Phe Phe Thr Leu Gly Ala Met Asp Arg Lys Asn Glu Val Pro  
 965 970 975  
 Ile Cys Leu Pro Lys Asp Ile Pro Thr Arg Ser Lys Lys Glu Leu Leu  
 980 985 990  
 Lys Lys Glu Lys Glu Leu Leu Gly Ile Tyr Leu Thr Glu His Pro Met  
 995 1000 1005  
 Asp Thr Val Arg Asp His Leu Ser Arg Leu Ser Val Val Leu Ala Gly  
 1010 1015 1020  
 Glu Phe Glu Asn Leu Pro His Gly Ser Val Val Arg Thr Val Phe Ile  
 1025 1030 1035 1040  
 Ile Asp Lys Val Thr Lys Ile Ser Ser Lys Ala Gln Lys Lys Phe  
 1045 1050 1055  
 Ala Val Leu Arg Val Ser Asp Gly Ile Asp Ser Tyr Glu Leu Pro Ile  
 1060 1065 1070  
 Trp Pro Asp Met Tyr Glu Glu Gln Gln Glu Leu Leu Glu Glu Asp Arg  
 1075 1080 1085  
 Leu Ile Tyr Ala Ile Leu Val Leu Asp Lys Arg Ser Asp Ser Leu Arg  
 1090 1095 1100  
 Ile Ser Cys Arg Trp Met Lys Asp Leu Ser Ile Val Asn Glu Asn Ile  
 1105 1110 1115 1120  
 Ile Tyr Glu Cys Asp Gln Ala Phe Asp Arg Ile Lys Asn Gln Val Gln  
 1125 1130 1135  
 Lys Met Ser Phe Thr Met Ser Thr Ser Gly Lys Glu Thr Lys Ala Lys  
 1140 1145 1150  
 Gly Asn Lys Pro Asn Glu Asn Gly His Thr Gln Ala Leu Ala Pro Val  
 1155 1160 1165  
 Thr Leu Ser Leu Asp Leu Asn Glu Leu Arg His Ser His Leu Cys Ile  
 1170 1175 1180  
 Leu Lys Lys Ile Val Gln Lys His Pro Gly Ser Arg Thr Leu Val Leu  
 1185 1190 1195 1200  
 Val Phe Thr Gln Asp Asn Glu Arg Val Ala Ser Met Ser Pro Asp Asp  
 1205 1210 1215  
 Ala Tyr Phe Val Cys Glu Asp Ile Glu Glu Leu Arg Gln Glu Leu Val  
 1220 1225 1230  
 Thr Ala Asp Leu Pro Val Arg Val Ile Thr Val  
 1235 1240  
 <210>705  
 <211>307

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;705

```

Asn Ile Ser Leu Leu Cys Lys Ile Gln Lys Arg Tyr Phe Met Lys Lys
 1           5           10           15
Leu Ile Leu Tyr Phe Ala Ala Phe Val Ala Ser Leu Phe Cys Gly Val
      20           25           30
Phe Leu Trp Asp Arg Val Pro Cys Ala Gln Lys Ile Met Arg Leu Ala
      35           40           45
Ala Asp His Ser Ser Glu Val Phe Ser Lys Ser Cys Arg Phe Val Arg
      50           55           60
Lys Ile Ser Gly Phe Glu Glu Leu Gln Val Phe Glu Arg His Val Ser
      65           70           75           80
Pro Glu Gln Ala Leu Ala Leu Phe Pro Glu Tyr Arg Asp Gly Lys Ser
      85           90           95
Phe Val Glu Leu Ala Phe Ile Pro His Thr Leu Met His Val Arg Phe
      100          105          110
Ser Lys Glu Glu Pro Val Lys Lys His Ile Ile Ser Gln Glu Gly Glu
      115          120          125
Ile Leu Trp Ser Leu Val Asn Gly Glu Met Val Leu His Thr Gly Thr
      130          135          140
Trp Thr Cys Ser Lys Gly Phe Arg Glu Cys Leu Leu His Ala Gly
      145          150          155          160
Lys Gln Asp Met Arg Val Ile Gln Thr Leu Ala Thr Leu Gly Gly Thr
      165          170          175
Thr Ser Arg Glu Ser Leu Ala Gln Ala Leu Ala Leu Lys Asn Ile Arg
      180          185          190
Ala Glu Arg Val Ile Lys Glu Cys Gln Lys Lys Lys Leu Ile Phe Ala
      195          200          205
Ser Gly Asn Gln Ile Gly Thr His Phe Gln Gln Phe Gln Pro Ile Arg
      210          215          220
Gly Cys Thr Thr Thr Leu Asn Asn Asn Pro Val Trp Leu Gln Lys Pro
      225          230          235          240
Arg His Ala Ala Val Phe Pro Ala Gln Tyr Ser Glu Asp Arg Val Arg
      245          250          255
His Leu Val Lys Met Ile Phe Gly Asp Asn Phe Leu Ile Val Arg Ser
      260          265          270
Ser Met Val Tyr Val Pro Val Tyr Lys Ile Ser Leu Val Ser Ala Asp
      275          280          285
Asn Ser Val Arg Val Glu Tyr Ile Asn Ala Val Thr Gly Lys Ser Phe
      290          295          300
Gln Asp Leu
305

```

&lt;210&gt;706

&lt;211&gt;171

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;706

```

Trp Arg Phe Val Val Val Ser Pro Arg Leu Ile Met Lys Phe Leu Leu
 1           5           10           15
Tyr Val Pro Leu Leu Leu Val Leu Val Ser Thr Gly Cys Asp Ala Lys
      20           25           30
Pro Val Ser Phe Glu Pro Phe Ser Gly Lys Leu Ser Thr Gln Arg Phe
      35           40           45
Glu Pro Gln His Ser Ala Glu Glu Tyr Phe Ser Gln Gly Gln Glu Phe
      50           55           60
Leu Lys Lys Gly Asn Phe Arg Lys Ala Leu Leu Cys Phe Gly Ile Ile
      65           70           75           80
Thr His His Phe Pro Arg Asp Ile Leu Arg Asn Gln Ala Gln Tyr Leu
      85           90           95
Ile Gly Val Cys Tyr Phe Thr Gln Asp His Pro Asp Leu Ala Asp Lys
      100          105          110
Ala Phe Ala Ser Tyr Leu Gln Leu Pro Asp Ala Glu Tyr Ser Glu Glu
      115          120          125

```

Leu Phe Gln Met Lys Tyr Ala Ile Ala Gln Arg Phe Ala Gln Gly Lys  
 130 135 140  
 Arg Lys Arg Ile Cys Arg Leu Glu Gly Phe Pro Lys Leu Met Asn Ala  
 145 150 155 160  
 Asp Glu Asp Ala Tyr Ala Phe Met Thr Arg Phe  
 165 170

&lt;210&gt;707

&lt;211&gt;167

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;707

Arg Cys Val Arg Ile Tyr Asp Glu Ile Leu Thr Ala Phe Pro Ser Lys  
 1 5 10 15  
 Asp Leu Gly Ala Gln Ala Leu Tyr Ser Lys Ala Ala Leu Leu Ile Val  
 20 25 30  
 Lys Asn Asp Leu Thr Glu Ala Thr Lys Thr Leu Lys Lys Leu Thr Leu  
 35 40 45  
 Gln Phe Pro Leu His Ile Leu Ser Ser Glu Ala Phe Val Arg Leu Ser  
 50 55 60  
 Glu Ile Tyr Leu Gln Gln Ala Lys Lys Glu Pro His Asn Leu Gln Tyr  
 65 70 75 80  
 Leu His Phe Ala Lys Leu Asn Glu Glu Ala Met Lys Lys Gln His Pro  
 85 90 95  
 Asn His Pro Leu Asn Glu Val Val Ser Ala Asn Val Gly Ala Met Arg  
 100 105 110  
 Glu His Tyr Ala Arg Gly Leu Tyr Ala Thr Gly Arg Phe Tyr Glu Lys  
 115 120 125  
 Lys Lys Lys Ala Glu Ala Ala Asn Ile Tyr Tyr Arg Thr Ala Ile Thr  
 130 135 140  
 Asn Tyr Pro Asp Thr Leu Leu Val Ala Lys Cys Gln Lys Arg Leu Asp  
 145 150 155 160  
 Arg Ile Ser Lys His Thr Ser  
 165

&lt;210&gt;708

&lt;211&gt;212

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;708

Ile Glu Tyr Leu Ser Ile Leu Pro Lys Ile Glu Ile Asn Met Arg Leu  
 1 5 10 15  
 Phe Ser Leu Gly Thr Ile Tyr Leu Phe Phe Ser Leu Ala Leu Ser Ser  
 20 25 30  
 Cys Cys Gly Tyr Ser Ile Leu Asn Ser Pro Tyr His Leu Ser Ser Leu  
 35 40 45  
 Gly Lys Ser Leu Leu Gln Glu Arg Ile Phe Ile Ala Pro Ile Lys Glu  
 50 55 60  
 Asp Pro His Gly Gln Leu Cys Ser Ala Leu Thr Tyr Glu Leu Ser Lys  
 65 70 75 80  
 Arg Ser Phe Ala Ile Ser Gly Arg Ser Ser Cys Ala Gly Tyr Thr Leu  
 85 90 95  
 Lys Val Glu Leu Leu Asn Gly Ile Asp Lys Asn Ile Gly Phe Thr Tyr  
 100 105 110  
 Ala Pro Asn Lys Leu Gly Asp Lys Thr His Arg His Phe Ile Val Ser  
 115 120 125  
 Asn Glu Gly Arg Leu Ser Leu Ser Ala Lys Val Gln Leu Ile Asn Asn  
 130 135 140  
 Asp Thr Gln Glu Val Leu Ile Asp Gln Cys Val Ala Arg Glu Ser Val  
 145 150 155 160  
 Asp Phe Asp Phe Glu Pro Asp Leu Gly Thr Ala Asn Ala His Glu Phe  
 165 170 175  
 Ala Leu Gly Gln Phe Glu Met His Ser Glu Ala Ile Lys Ser Ala Arg  
 180 185 190  
 Arg Ile Leu Ser Ile Arg Leu Ala Glu Thr Ile Ala Gln Gln Val Tyr  
 195 200 205

Tyr Asp Leu Phe

210

&lt;210&gt;709

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;709

```

Leu Leu Asn Arg Tyr Thr Met Thr Phe Phe Glu Gly Glu Thr Val Phe
 1           5           10           15
Pro Ala Val Leu Ser Glu Leu His Ser Met Leu Asp Leu Ile Lys Arg
           20           25           30
Ala Gly Lys Gln Ser Lys Cys Pro Gln Glu Lys Leu Leu Lys Leu Glu
           35           40           45
Leu Ala Cys Glu Glu Leu Leu Val Asn Ile Ile Ser Tyr Ala Tyr Gln
           50           55           60
Gly Glu Asn Ser Pro Gly Thr Ile Ala Ile Ser Cys Ile Ser His Arg
           65           70           75           80
Gly Asp Leu Glu Val Val Ile Lys Asp His Gly Pro Ser Phe Asn Pro
           85           90           95
Leu Ala Val Ser Ile Asn Ile Gln Glu Asp Leu Pro Leu Glu Gln Arg
           100          105          110
Lys Leu Gly Gly Leu Gly Ile Phe Leu Ala Lys Ser Ser Val Asp Glu
           115          120          125
Phe Leu Tyr Ala Arg Glu Asp His Cys Asn Ile Val His Leu Lys Met
           130          135          140
Leu Asn Gly Gln His Ser
145           150

```

&lt;210&gt;710

&lt;211&gt;152

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;710

```

Arg Ile Thr Ile Asn Gln Arg Lys Tyr Thr Met Ser Leu Asp Phe Phe
 1           5           10           15
Glu Glu Phe Tyr His Gln Ser Ile Leu Asn Thr Gly Thr Ser Phe Pro
           20           25           30
Glu Gly Tyr Leu Asn Ile Ala Glu Ile Leu Ser Tyr Pro His Cys Thr
           35           40           45
Asp Ala Asn Thr Asp Phe Leu Cys Ser Gln Ser Asp Asn Asp Phe Ile
           50           55           60
Ile Ala Glu Ser Lys Asp Lys Leu Thr Leu Phe Asn Ala Asp Phe Ala
           65           70           75           80
Ile Trp Leu Val Pro Glu Leu Val Gln Gly Gln Ala Val Thr Arg Gly
           85           90           95
Tyr Ile Ala Val Ser Gln Gly Glu Gly Asn Tyr Glu Pro Glu Met Ala
           100          105          110
Phe Glu Ala Ser Gly Gln Tyr Asn Gln Ser Ser Leu Ile Leu Glu Ala
           115          120          125
Leu Gln Leu Tyr Leu Lys Asp Ile Lys Asp Thr Glu Asn Ala Leu Arg
           130          135          140
Ser Phe Arg Phe Asn Asn Asp His
145           150

```

&lt;210&gt;711

&lt;211&gt;436

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;711

```

Met Lys Arg Pro Phe Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser
 1           5           10           15
Cys Ala Ser Leu Ser Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg
           20           25           30
Gly Ala Thr Ala Ala Val Val His Ala Asp Ser Gly Lys Val Phe Tyr
           35           40           45
Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile

```

50 55 60  
 Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr  
 65 70 75 80  
 Leu Ile Lys Val Lys Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala  
 85 90 95  
 Lys Lys Gln Ser Gly Tyr Arg Ser Pro His Trp Leu Glu Thr Asp  
 100 105 110  
 Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp  
 115 120 125  
 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val  
 130 135 140  
 Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu  
 145 150 155 160  
 Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn  
 165 170 175  
 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp  
 180 185 190  
 Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly  
 195 200 205  
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly  
 210 215 220  
 Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Pro Gly Ser Thr  
 225 230 235 240  
 Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr  
 245 250 255  
 Ala Gly Lys Asn Leu Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu  
 260 265 270  
 Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro Val Ser Asp Leu Tyr Gln  
 275 280 285  
 Asp Val Ile Ala Leu Cys Glu Thr Val Phe Asn Glu Pro Leu Leu Arg  
 290 295 300  
 Lys Glu Leu Val Pro Pro Ser Asp Cys Leu Gln Leu Glu Ile Ala Asn  
 305 310 315 320  
 Leu Gly Lys Leu Ser Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe  
 325 330 335  
 Tyr Ala Ser Glu Asp Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His  
 340 345 350  
 Ala Asp Ala Phe Pro Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val  
 355 360 365  
 Phe Tyr Asp Asp Glu Gly Lys Lys Ile Ser Ser Gln Pro Phe Tyr Ala  
 370 375 380  
 Pro Cys Arg Phe Glu Arg Thr Ile Lys Pro Trp Lys Leu Tyr Met Lys  
 385 390 395 400  
 Arg Val Phe Thr Ser Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu  
 405 410 415  
 Met Tyr Phe Arg Ile Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His  
 420 425 430  
 Tyr Ser Lys Ile  
 435

&lt;210&gt;712

&lt;211&gt;371

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;712

Arg Gly Ile Leu Tyr Val Thr Met Val Pro Phe Arg Gln His His Ala  
 1 5 10 15  
 Tyr Gln Leu Leu Lys Gln Leu His Thr Ser Ala Ile Ser Glu Ala Asp  
 20 25 30  
 Arg Val Ser Tyr Tyr Phe Lys Gln Asn Arg Ser Leu Gly Ser Lys Asp  
 35 40 45  
 Arg Gln Trp Ile Gln Asn Ile Ile Phe Asn Ile Leu Arg His Arg Arg  
 50 55 60  
 Leu Leu Glu Thr Leu Ile Leu Asp Ser Gly Glu Gln Val Thr Pro Glu  
 65 70 75 80

Val 1	Pro	Leu	Ser	Met 5	Ile	Leu	Asp	Phe	Gln 10	Phe	Ser	Ile	Gly	Tyr 15	Tyr
Leu	Arg	Val 20	Leu	Glu	Leu	Ala	Ile	Arg 25	Asp	Gly	Thr	Arg	Ile 30	Leu	Ala
Tyr	Asp 35	Arg	Lys	Arg	Leu	Leu	Leu	Asp 40	Ala	Trp	Pro	Val	Asn 45	Asp	Pro
Leu 50	Pro	Thr	Asn	Tyr	Asp	Thr 55	Ser	Val	Ser	Thr	Ile 60	Arg	Gln	Val	Ile
His 65	Glu	Leu	Phe	Ser	Trp 70	Ser	Ala	Ile	Ser	Tyr 75	Ser	Ile	Ser	Ser	Arg
Leu	Leu	Ala	Ile	Ile 85	Glu	Leu	Arg	Leu	His 90	Glu	Glu	Lys	Pro 95	Gln	Thr
Gly	Trp	Leu	Tyr 100	Arg	Leu	Phe	Phe	Pro 105	Ser	Lys	Tyr	His	Ile 110	Lys	Lys
Ala	Ile 115	Val	Asp	Lys	Leu	Cys	Met 120	Phe	Lys	Ser	Leu	Ile 125	Leu	Phe	Glu
Ser 130	Lys	Arg	Pro	Val	Asp	Lys 135	Ile	Val	Gln	Ala 140	Ala	Asn	Lys	Val	Phe
Ser 145	Lys	Gly	Lys	Ser	Asn 150	Phe	Ser	Ser	Trp	Glu 155	Asp	Phe	Thr	His	Glu
Val	Thr	Val	Ser	Glu	Val	Gln	Thr	Pro	Leu	Ala	Gly	Glu	Val	Gln	Arg



165 170 175  
 Arg Leu Ala Ala Asp Ala Ser Leu Gln Met Ile Ile Glu Ala Leu Thr  
 180 185 190  
 Thr Leu Leu Glu Gly His Thr Ala Tyr Leu Pro Leu Ser Leu Glu Leu  
 195 200 205  
 Leu Asn Gln Phe Ile Gly Glu Lys Ala Gln Pro Leu Lys Thr Leu Ser  
 210 215 220  
 Glu Lys Ser Tyr Val Leu Leu Arg Glu Leu Ile Gln Leu Phe Ser Leu  
 225 230 235 240  
 Ser Ala Glu Asp Phe Gln Thr Ile Ile Met Ser Ile Ile Ser Asp Ser  
 245 250 255  
 Leu Ser Glu Val Leu Ala Asn Ser Leu Ile Gly Asn Gln Pro Leu Thr  
 260 265 270  
 Phe His Gly Lys Thr Phe Val Gly Leu Trp Gln Glu Thr Ala Leu Ala  
 275 280 285  
 Ser Pro Glu Asp Ser Lys Leu Ala Leu Gly Phe Leu Ala Glu Val Leu  
 290 295 300  
 Arg Lys Val Ile Val Glu Lys Lys Leu His Val Ser Lys Ser Asp Asn  
 305 310 315 320  
 Thr Thr Pro Glu Glu Val Gly Asn Ile Tyr Ser Ile Arg Asp Gln Asn  
 325 330 335  
 Pro Ala Leu Trp Asp Lys Met Ile Thr Met Leu Leu Met Arg Trp Leu  
 340 345 350  
 Leu Asp Tyr Asp Arg Asp Ile Gly Ile Ala Leu Arg Lys Ala Ala Glu  
 355 360 365  
 Tyr Tyr Asn Pro His Pro Ser Phe Trp Arg Gln Phe Leu Arg Leu Trp  
 370 375 380  
 Gln Arg Arg Pro  
 385

&lt;210&gt;714

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;714

Phe Thr Ser Pro Tyr Leu Gly Ala Gly Gln Cys Val Ser Val Val Asp  
 1 5 10 15  
 Asn Leu Lys Thr Tyr Asp Leu Gly Arg Asn Tyr Thr Gln Val Leu Ala  
 20 25 30  
 Cys Ala Ser Gln Ile Asp Glu Phe Ala Asp Lys Gly Glu Asn Glu Ala  
 35 40 45  
 Leu Val Met Lys Asp Ile Leu Tyr Leu Val Arg Gln Asp Arg Ser Lys  
 50 55 60  
 Glu Leu Gly Asp Phe Leu Met Met Trp Ser Glu Glu His Ala Ser Glu  
 65 70 75 80  
 Val Asn

&lt;210&gt;715

&lt;211&gt;264

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;715

Ser Met Gly Thr Pro Ile Ser Gly Asn Asp Gly Asp Arg Asn Thr Ile  
 1 5 10 15  
 Ser Asp Pro Leu Glu Glu Ser Ala Ala Glu Glu Gly Asp Ser Asp Leu  
 20 25 30  
 Glu Asp Arg Val Ser Glu Ser Ala Thr Gln Val Ile Glu Thr Ile Ala  
 35 40 45  
 Asp Thr Gly Ile Pro Glu Ala Thr Pro Ser Glu Gly Thr Asn Ser Asp  
 50 55 60  
 Leu Asn Ser Asp Leu Val Asp Arg Val Glu Tyr Glu Ala Arg Gly Ser  
 65 70 75 80  
 Leu Leu Thr Thr Met Leu Ala Arg Ile Arg Lys Ala Val Ser Gln Ile  
 85 90 95  
 Trp Met His Val Lys Thr Lys Arg His Pro Lys Glu Gln Gly Val Arg

```

      100              105              110
Ser Leu Gly Asp Ile Pro Cys Asp Leu Leu Lys Ala Thr Arg Leu Pro
      115              120              125
Lys Glu Thr Ala Glu Pro Pro Tyr Phe Tyr Ala Leu Glu Thr Ala Leu
      130              135              140
Ala Ser Cys Arg Ser Phe Phe Phe His Val Phe Leu Arg Leu Phe Thr
145              150              155
Leu Leu Arg Arg Gln His Pro Glu Ala Pro Leu Asp Leu Cys Gly Thr
      165              170              175
Asp Pro Ile Ser Pro Glu Ala Ala Val Ala Phe Ala Leu Ile Leu Arg
      180              185              190
Ser Cys Cys Lys Trp Val Ala Thr Asp Ala Val Gln Glu Gly Leu Pro
      195              200              205
Leu Glu Val Ile Glu Glu Ala Gly Met Tyr Asn Ala Phe Ser Leu Glu
      210              215              220
Ala Thr Thr Thr Val Glu Glu Val Ser Lys Arg Leu Ser Glu Leu Leu
225              230              235
Tyr Ser Asp Lys Arg Ile Asp Gly Leu Ala Asn Val Arg Gly Ile Thr
      245              250              255
Lys Ile Asn Leu Pro Leu Leu Ile
      260

<210>716
<211>385
<212>PRT
<213>Chlamydia pneumoniae
<400>716
Arg Ile Ala Met Gly Ile Asn Pro Ser Gly Asn Arg Ser Pro Asp Asp
 1              5              10              15
Val Trp Val Arg Gly Ala Gln Gly Asp Ser Ser Ser Thr Gln Gly Thr
      20              25              30
Gly Ala Thr Asn Ser Asn Leu Gly Ala His Asn Val Thr Ser Thr
      35              40              45
Ser Gln Pro Gln Val Ala Ser Lys Ala Lys Gln Leu Trp Gln Thr Val
      50              55              60
Arg Glu Phe Phe Leu Gly Lys Lys Ser Pro Asp Ser Ser Gln Gly Ala
      65              70              75              80
Ser Gly Pro Ala Met Gln Ser Pro Ser Gly Pro Thr Ile Arg Pro Thr
      85              90              95
Arg Pro Ala Pro Pro Pro Thr Thr Gly Gly Ala Asn Ala Lys Arg
      100              105              110
Pro Ala Thr His Gly Lys Gly Arg Ala Pro Gln Pro Pro Thr Ala Gly
      115              120              125
Ser Ser Ser Gly Ser Glu Gln Pro Thr Ala Met Ser Ser Glu Val Ala
      130              135              140
Lys Leu Val Ser Glu Leu Lys Asp Ala Val His Ser His Ala Glu Ser
145              150              155
Gln Lys Val Leu Lys Lys Val Ser Gln Glu Leu Gln Thr Lys Trp Thr
      165              170              175
Asp Trp Glu Asn Asn Arg Gly Pro Asp Tyr Leu Leu His Gly Tyr Arg
      180              185              190
Val Ile Ala Arg Ala Leu Gln Gln Thr Tyr Thr Glu Gln Ser Met Leu
      195              200              205
Ile Glu Gly Thr Ser Ser Thr Gly Pro Val Pro Gln Ala Val Thr Val
      210              215              220
Ala Lys Asp Ala Val Thr Gln Thr Val Arg Gly Ala Ile Lys Asn Leu
225              230              235
Glu Asn Pro Lys Pro Gly Asn Asp Pro Asp Gly Val Leu Met Gln Val
      245              250              255
Val Ile Ser Leu Gly Ile Glu Gly Pro Thr Leu Asp Pro Gly Glu Ser
      260              265              270
Ile Gln Asn Phe Leu Glu Thr Arg Val Ser Asp Phe Gly Gly Asp Asp
      275              280              285
Ser Asp Ile Asp Tyr Thr Ser Asp Ile Ala Arg Leu Gly Ser Ala Leu
      290              295              300

```

Asp Arg Val Arg Glu Asn His Pro Asn Glu Met Pro Arg Ile Trp Ile  
 305 310 315 320  
 Ala Leu Ala Arg Glu Leu Gly Ala Ala Val His Ser His Ala Thr Ser  
 325 330 335  
 Val Arg Ile Ala Asn Ala Gly Lys Asn His Thr Arg Asp Val Val Arg  
 340 345 350  
 Met Ala Asn Glu Ser Ser Arg Leu Leu Gln Gly Met Lys Val Leu Ser  
 355 360 365  
 Val Gly Ala Trp Ala Asn Thr Met Thr Val Leu Ile Gly Asp Leu Phe  
 370 375 380

Glu  
 385

<210>717

<211>216

<212>PRT

<213>Chlamydia pneumoniae

<400>717

Lys Ile Ile Met Ser Val Asn Pro Ser Gly Asn Ser Lys Asn Asp Leu  
 1 5 10 15  
 Trp Ile Thr Gly Ala His Asp Gln His Pro Asp Val Lys Glu Ser Gly  
 20 25 30  
 Val Thr Ser Ala Asn Leu Gly Ser His Arg Val Thr Ala Ser Gly Gly  
 35 40 45  
 Arg Gln Gly Leu Leu Ala Arg Ile Lys Glu Ala Val Thr Gly Phe Phe  
 50 55 60  
 Ser Arg Met Ser Phe Phe Arg Ser Gly Ala Pro Arg Gly Ser Gln Gln  
 65 70 75 80  
 Pro Ser Ala Pro Ser Ala Asp Thr Val Arg Ser Pro Leu Pro Gly Gly  
 85 90 95  
 Asp Ala Arg Ala Thr Glu Gly Ala Gly Arg Asn Leu Ile Lys Lys Gly  
 100 105 110  
 Tyr Gln Pro Gly Met Lys Val Thr Ile Pro Gln Val Pro Gly Gly Gly  
 115 120 125  
 Ala Gln Arg Ser Ser Gly Ser Thr Thr Leu Lys Pro Thr Arg Pro Ala  
 130 135 140  
 Pro Pro Pro Pro Lys Thr Gly Gly Thr Asn Ala Lys Arg Pro Ala Thr  
 145 150 155 160  
 His Gly Lys Gly Pro Ala Pro Gln Pro Pro Lys Thr Gly Gly Thr Asn  
 165 170 175  
 Ala Lys Arg Ala Ala Thr His Gly Lys Gly Pro Ala Pro Gln Pro Pro  
 180 185 190  
 Lys Gly Ile Leu Lys Gln Pro Gly Gln Ser Gly Thr Ser Gly Lys Lys  
 195 200 205  
 Arg Val Ser Trp Ser Asp Glu Asp  
 210 215

<210>718

<211>404

<212>PRT

<213>Chlamydia pneumoniae

<400>718

Gly Tyr Met Asp Lys Leu Thr Val Gln Asp Leu Ser Pro Glu Glu Lys  
 1 5 10 15  
 Lys Val Leu Val Arg Val Asp Phe Asn Val Pro Met Gln Asp Gly Lys  
 20 25 30  
 Ile Leu Asp Asp Ile Arg Ile Arg Ser Ala Met Pro Thr Ile Asn Tyr  
 35 40 45  
 Leu Leu Lys Lys His Ala Ala Val Ile Leu Met Ser His Leu Gly Arg  
 50 55 60  
 Pro Lys Gly Gln Gly Phe Gln Glu Glu Tyr Ser Leu Gln Pro Val Val  
 65 70 75 80  
 Asp Val Leu Glu Gly Tyr Leu Gly His His Val Pro Leu Ala Pro Asp  
 85 90 95  
 Cys Val Gly Glu Val Ala Arg Gln Ala Val Ala Gln Leu Ser Pro Gly  
 100 105 110

Arg Val Leu Leu Leu Glu Asn Leu Arg Phe His Ile Gly Glu Glu His  
 115 120 125  
 Pro Glu Lys Asp Pro Thr Phe Ala Ala Glu Leu Ser Ser Tyr Gly Asp  
 130 135 140  
 Phe Tyr Val Asn Asp Ala Phe Gly Thr Ser His Arg Lys His Ala Ser  
 145 150 155 160  
 Val Tyr Val Val Pro Gln Ala Phe Pro Gly Arg Ala Ala Ala Gly Leu  
 165 170 175  
 Leu Met Glu Lys Glu Leu Glu Phe Leu Gly Arg His Leu Leu Thr Ser  
 180 185 190  
 Pro Lys Arg Pro Phe Thr Ala Ile Leu Gly Gly Ala Lys Ile Ser Ser  
 195 200 205  
 Lys Ile Gly Val Ile Glu Ala Leu Leu Asn Gln Val Asp Tyr Leu Leu  
 210 215 220  
 Leu Ala Gly Gly Met Gly Phe Thr Phe Leu Gln Ala Leu Gly Lys Ser  
 225 230 235 240  
 Leu Gly Asn Ser Leu Val Glu Lys Ser Ala Leu Asp Leu Ala Arg Asn  
 245 250 255  
 Val Leu Lys Ile Ala Lys Ser Arg Asn Val Thr Ile Val Leu Pro Ser  
 260 265 270  
 Asp Val Lys Ala Ala Glu Asn Leu Gln Ser Lys Glu Tyr Ser Val Ile  
 275 280 285  
 Ser Ile Asp Gln Gly Ile Pro Pro His Leu Gln Gly Phe Asp Ile Gly  
 290 295 300  
 Pro Arg Thr Thr Glu Glu Phe Ile Arg Ile Ile Asn Gln Ser Ala Thr  
 305 310 315 320  
 Val Phe Trp Asn Gly Pro Val Gly Val Tyr Glu Val Pro Pro Phe Asp  
 325 330 335  
 Ser Gly Ser Ile Ala Ile Ala Asn Ala Leu Gly Asn His Pro Ser Ala  
 340 345 350  
 Val Thr Val Val Gly Gly Gly Asp Ala Ala Ala Val Val Ala Leu Ala  
 355 360 365  
 Gly Cys Ser Thr Lys Val Ser His Val Ser Thr Gly Gly Gly Ala Ser  
 370 375 380  
 Leu Glu Phe Leu Glu Gln Gly Phe Leu Pro Gly Thr Glu Val Leu Ser  
 385 390 395 400  
 Pro Ser Lys Ser

&lt;210&gt;719

&lt;211&gt;121

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;719

Trp Asn Lys Ala Leu Lys Ala Lys Lys Lys Ser Met Asp Asn Lys Ala  
 1 5 10 15  
 Pro Ala Gly Ser Val Ile Asn Gln Glu Ser Thr Ile Ser Leu Ile Met  
 20 25 30  
 Phe Lys Leu Met Ala Arg Ile Pro Arg Ala Lys Pro Ile Pro Lys Thr  
 35 40 45  
 Ala Pro Thr Thr Thr Cys Val Val Asp Ile Gly Ser Pro Lys Ile Glu  
 50 55 60  
 Ala Lys Ala Ile Val Asn Ala Glu Pro Ile Pro Thr Glu Asn Pro Arg  
 65 70 75 80  
 Asp Gly Val Asn Ser Val Ile Leu Gln Pro Thr Val Ser Ile Thr Arg  
 85 90 95  
 His Pro Gln Ile Ala Arg Pro Met Thr Lys Pro Met Pro Pro Asn Ala  
 100 105 110  
 Met Ser Leu Ile Asn Val Tyr Asp Val  
 115 120

&lt;210&gt;720

&lt;211&gt;428

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;720

Tyr Ser Met Leu Pro Leu Ile Ile Phe Val Leu Leu Cys Gly Phe Tyr  
 1 5 10 15  
 Thr Ser Trp Asn Ile Gly Ala Asn Asp Val Ala Asn Ala Val Gly Pro  
 20 25 30  
 Ser Val Gly Ser Gly Val Leu Thr Leu Arg Gln Ala Val Val Ile Ala  
 35 40 45  
 Ala Ile Phe Glu Phe Phe Gly Ala Leu Leu Leu Gly Asp Arg Val Ala  
 50 55 60  
 Gly Thr Ile Glu Ser Ser Ile Val Ser Val Thr Asn Pro Met Ile Ala  
 65 70 75 80  
 Ser Gly Asp Tyr Met Tyr Gly Met Thr Ala Ala Leu Leu Ala Thr Gly  
 85 90 95  
 Val Trp Leu Gln Leu Ala Ser Phe Phe Gly Trp Pro Val Ser Thr Thr  
 100 105 110  
 His Ser Ile Val Gly Ala Val Ile Gly Phe Gly Leu Val Leu Gly Lys  
 115 120 125  
 Gly Thr Ile Ile Tyr Trp Asn Ser Val Gly Ile Ile Leu Ile Ser Trp  
 130 135 140  
 Ile Leu Ser Pro Phe Met Gly Gly Cys Val Ala Tyr Leu Ile Phe Ser  
 145 150 155 160  
 Phe Ile Arg Arg His Ile Phe Tyr Lys Asn Asp Pro Val Leu Ala Met  
 165 170 175  
 Val Arg Val Ala Pro Phe Leu Ala Ala Leu Val Ile Met Thr Leu Gly  
 180 185 190  
 Thr Val Met Ile Ser Gly Gly Val Ile Leu Lys Val Ser Ser Thr Pro  
 195 200 205  
 Trp Ala Val Ser Gly Val Leu Val Cys Gly Leu Leu Ser Tyr Ile Ile  
 210 215 220  
 Thr Phe Tyr Tyr Val His Thr Lys His Cys Ser Tyr Ile Ser Asp Thr  
 225 230 235 240  
 Pro Lys Lys Gly Ser Leu Thr Tyr Arg Leu Lys Glu Arg Gly Gly Asn  
 245 250 255  
 Tyr Gly Arg Lys Tyr Leu Val Val Glu Arg Ile Phe Ala Tyr Leu Gln  
 260 265 270  
 Ile Ile Val Ala Cys Phe Met Ala Phe Ala His Gly Ser Asn Asp Val  
 275 280 285  
 Ala Asn Ala Ile Ala Pro Val Ala Gly Val Leu Arg Gln Ala Tyr Pro  
 290 295 300  
 Ala Ser Tyr Thr Ser Tyr Thr Leu Ile Arg Leu Met Ala Phe Gly Gly  
 305 310 315 320  
 Ile Gly Leu Val Ile Gly Leu Ala Ile Trp Gly Trp Arg Val Ile Glu  
 325 330 335  
 Thr Val Gly Cys Lys Ile Thr Glu Leu Thr Pro Ser Arg Gly Phe Ser  
 340 345 350  
 Val Gly Met Gly Ser Ala Leu Thr Ile Ala Leu Ala Ser Ile Leu Gly  
 355 360 365  
 Leu Pro Ile Ser Thr Thr His Val Val Val Gly Ala Val Leu Gly Ile  
 370 375 380  
 Gly Leu Ala Arg Gly Ile Arg Ala Ile Asn Leu Asn Ile Ile Lys Asp  
 385 390 395 400  
 Ile Val Leu Ser Trp Phe Ile Thr Leu Pro Ala Gly Ala Leu Leu Ser  
 405 410 415  
 Ile Leu Phe Phe Phe Ala Leu Arg Ala Leu Phe His  
 420 425

&lt;210&gt;721

&lt;211&gt;248

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;721

Asn Gly Ile Arg Ser His Lys Ser Phe Thr Arg Ser Phe Arg Gln Val  
 1 5 10 15  
 Ile Ile Ala Lys Lys Ala Ile Leu Met Gln Thr Leu Ala Arg Leu Phe  
 20 25 30  
 Gly Gln Ser Pro Phe Ala Pro Leu Gln Ala His Leu Glu Met Val Val

35 40 45  
 Ser Cys Val Glu Tyr Met Leu Pro Ile Phe Thr Ala Leu Arg Asp Gly  
 50 55 60  
 Arg Tyr Glu Glu Leu Leu Glu Met Ala Lys Leu Val Ser Asp Lys Glu  
 65 70 75 80  
 Tyr Gln Ala Asp Cys Ile Lys Asn Asp Met Arg Asn His Leu Pro Ala  
 85 90 95  
 Gly Leu Phe Met Pro Ile Ser Arg Ala Gly Ile Leu Glu Ile Ile Ser  
 100 105 110  
 Ile Gln Asp Ser Ile Ala Asp Thr Ala Glu Asp Val Ala Ile Leu Leu  
 115 120 125  
 Thr Ile Arg Arg Leu Asn Phe Tyr Pro Ser Met Glu Thr Leu Phe Phe  
 130 135 140  
 Arg Phe Leu Glu Lys Asn Leu Glu Ala Phe Glu Leu Thr Met Thr Leu  
 145 150 155 160  
 Leu His Glu Phe Asn Gln Leu Leu Glu Ser Ser Phe Gly Gly Arg Lys  
 165 170 175  
 Ala Asp Lys Ala Arg Leu Leu Val Gly Arg Val Ala Lys Ser Glu His  
 180 185 190  
 Glu Ser Asp Val Leu Gln Arg Glu Leu Met Gln Ile Phe Phe Ser Asp  
 195 200 205  
 Asp Phe Ile Ile Pro Glu Lys Glu Phe Tyr Leu Trp Leu Gln Val Ile  
 210 215 220  
 Arg Arg Thr Ala Gly Ile Ser Asp Ser Ser Glu Lys Leu Ala His Arg  
 225 230 235 240  
 Ile Asn Met Thr Leu Glu Glu Lys  
 245

&lt;210&gt;722

&lt;211&gt;161

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;722

Lys Ile Ile Glu Ile Ser Val Pro Ile Ile Phe Phe Cys Ile Glu Arg  
 1 5 10 15  
 Glu Ala Val Ser Lys Leu Trp Pro Trp Lys Leu Thr Trp Pro Glu Thr  
 20 25 30  
 Glu Asn Gly Gly Gln Gly Ser Asn Arg Arg Ile Ala Cys Ala Glu Thr  
 35 40 45  
 Asp Phe Pro Asp Pro Asp Ser Pro Met Ile Ala Lys Val Cys Pro Ser  
 50 55 60  
 Leu Ile Val Asn Asp Lys Asp Trp Thr Met Gly Tyr Cys Trp Arg Cys  
 65 70 75 80  
 Phe Ala Lys Val Met Asp Arg Ser Ser Ile Cys Lys Met Gly Leu Glu  
 85 90 95  
 Ala Ile Ser Arg Leu Gln Asp Arg Leu Gly Lys Leu Leu Leu Arg Lys  
 100 105 110  
 Arg Leu Phe Leu Cys Lys Pro Leu Leu Val Tyr Leu Ala Asn Leu His  
 115 120 125  
 Leu Leu Leu Tyr Lys Leu Ile Trp Lys Trp Trp Ser Leu Val Trp Asn  
 130 135 140  
 Thr Cys Phe Leu Tyr Ser Leu Leu Ser Glu Met Glu Asp Met Lys Asn  
 145 150 155 160  
 Tyr

&lt;210&gt;723

&lt;211&gt;344

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;723

Leu His Lys Asn Ser Leu Phe Arg Asn Asn Asn Leu Pro Lys Arg Ser  
 1 5 10 15  
 Cys Lys Arg Leu Met Ala Ser Asn Pro Ile Leu Gln Ile Glu Asp Leu  
 20 25 30  
 Ser Ile Thr Leu Ala Lys Gln Arg Gln Gln Tyr Pro Ile Val Gln Ser

35 40 45  
 Leu Ser Phe Thr Ile Asn Glu Gly Gln Thr Leu Ala Ile Ile Gly Glu  
 50 55 60  
 Ser Gly Ser Gly Lys Ser Val Ser Ala His Ala Ile Leu Arg Leu Leu  
 65 70 75 80  
 Pro Cys Pro Pro Phe Ser Val Ser Gly Gln Val Asn Phe Gln Gly His  
 85 90 95  
 Asn Leu Leu Thr Ala Ser Arg Ser Ile Gln Lys Lys Ile Ile Gly Thr  
 100 105 110  
 Glu Ile Ser Met Ile Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro Val  
 115 120 125  
 Phe Thr Ile Glu Gln Gln Phe Arg Glu Ile Ile His Thr His Leu Ala  
 130 135 140  
 Leu Thr Ala Glu Val Ala Lys Glu Lys Met Leu Tyr Ala Leu Glu Glu  
 145 150 155 160  
 Thr Gly Phe His Asp Pro Arg Leu Cys Leu Asn Leu Tyr Pro His Gln  
 165 170 175  
 Leu Ser Gly Gly Met Leu Gln Arg Ile Cys Ile Ala Met Ala Leu Leu  
 180 185 190  
 Cys Ser Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp  
 195 200 205  
 Val Ser Val Gln Tyr Gln Ile Leu Gln Leu Leu Lys Thr Leu Gln Lys  
 210 215 220  
 Lys Thr Gly Met Ser Leu Ile Ile Thr His Asn Met Gly Val Val  
 225 230 235 240  
 Ala Glu Thr Ala Asp Asp Val Leu Val Leu Tyr Ala Gly Arg Met Val  
 245 250 255  
 Glu Cys Ala Pro Ala Val Gln Met Phe His Asn Pro Ser His Pro Tyr  
 260 265 270  
 Thr Arg Asp Leu Leu Ala Ser Arg Pro Ser Leu Gln Pro Gln Gln Leu  
 275 280 285  
 Gly Ser Phe Asn Pro Ile Pro Gly Gln Pro Pro His Tyr Thr Ala Phe  
 290 295 300  
 Pro Ser Gly Cys Arg Tyr His Pro Arg Cys Ser Lys Ile Leu Asn Arg  
 305 310 315 320  
 Cys Ser Ala Glu Ala Pro Glu Ile Tyr Pro Val Arg Glu Gly His Lys  
 325 330 335  
 Val Arg Cys Trp Leu Tyr Asp Asp  
 340

&lt;210&gt;724

&lt;211&gt;324

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;724

Met Thr Thr Asn Phe Pro Gln Pro Leu Ile Gln Ala Thr Ser Leu Thr  
 1 5 10 15  
 Lys His Tyr Tyr Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile Ala  
 20 25 30  
 Ser Arg Pro Val Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg Ala  
 35 40 45  
 Val Gly Leu Ile Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala Leu  
 50 55 60  
 Ala Leu Ala Gly Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe Asn  
 65 70 75 80  
 Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu Arg  
 85 90 95  
 Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn Pro  
 100 105 110  
 Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His Lys  
 115 120 125  
 Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu Glu  
 130 135 140  
 Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln Leu  
 145 150 155 160

Ser Gly Gly Gln Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu Gly  
 165 170 175  
 Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp Leu  
 180 185 190  
 Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys  
 195 200 205  
 Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg  
 210 215 220  
 Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu  
 225 230 235 240  
 Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr  
 245 250 255  
 Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln  
 260 265 270  
 Ser Lys Pro Ile Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys  
 275 280 285  
 Ser Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu Ala  
 290 295 300  
 Cys Lys Ser Glu Ile Ile Pro Asn Gln Gly Asp Ala His His Thr Tyr  
 305 310 315 320  
 Arg Cys Ile His

&lt;210&gt;725

&lt;211&gt;143

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;725

Ala Tyr Cys Trp Arg Ala Arg Trp Arg Ala Met Gln Leu Ala Gly Ala  
 1 5 10 15  
 Thr Thr Ile Pro Val Ile Leu Lys His Val Ile Ala Asp Gly Thr Ala  
 20 25 30  
 Ala Glu Ala Thr Leu Ile Glu Asn Ile Gln Arg Val Asn Leu Asn Pro  
 35 40 45  
 Ile Glu Met Ala Glu Ala Phe Lys Arg Leu Ile His Val Phe Gly Leu  
 50 55 60  
 Thr Gln Asp Xaa Val Ala Tyr Lys Val Gly Lys Lys Arg Ser Thr Val  
 65 70 75 80  
 Ala Asn Tyr Leu Arg Leu Leu Ala Leu Ser Lys Thr Ile Gln Glu Ser  
 85 90 95  
 Leu Leu Gln Gly Gln Ile Thr Leu Gly His Ala Lys Val Ile Leu Thr  
 100 105 110  
 Leu Glu Asp Pro Ile Leu Arg Glu Lys Leu Asn Glu Ile Ile Ile Gln  
 115 120 125  
 Glu His Leu Ala Val Arg Glu Ala Glu Leu Ile Ala Asn Ser Leu  
 130 135 140

&lt;210&gt;726

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;726

Glu Lys Ser Gly Asp Ile Val Thr Glu Glu Ile Ser Lys Asp Thr Ile  
 1 5 10 15  
 Ile Glu Val Ala Ile Asp Asp Ile Arg Val Ser Pro Phe Gln Pro Arg  
 20 25 30  
 Arg Val Phe Ser Asn Glu Glu Leu Gln Glu Leu Ile Ala Ser Ile Lys  
 35 40 45  
 Ala Val Gly Leu Ile His Pro Pro Val Val Arg Glu Ile Cys Thr Gly  
 50 55 60  
 Asp Arg Val Leu Tyr Tyr Glu Leu Ile Ala Gly Glu Pro Ala Gly Gly  
 65 70 75 80  
 Pro Cys Ser Ser Gln Glu Gln Leu Arg Tyr Leu  
 85 90

&lt;210&gt;727

&lt;211&gt;238



&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;727

Arg Lys Ile His Lys Asn Leu Arg His Ala Tyr Arg Phe Ser Thr Pro  
 1 5 10 15  
 Asn Cys Arg Ser Phe Met Gln Lys Leu Val His Asn Ile Trp Lys Lys  
 20 25 30  
 Phe Tyr Ser Phe Ser Ser Ala Ile Ala Ile Cys Ile Val Leu Ala Ser  
 35 40 45  
 Phe Leu Ser Leu Lys Ile Val Ser Asn Thr Tyr Lys His Ser Gln Ala  
 50 55 60  
 Lys Arg Asn Ser Ile Leu Leu Leu Thr Arg Ala Ala Glu Val Ala Val  
 65 70 75 80  
 Ser Gln Gly Phe Leu Pro Ser Lys Ser Ala Leu Ser Ser Leu Glu Gln  
 85 90 95  
 Ala Tyr His Leu Gly Gly Glu Ser Met Lys Pro Tyr Ala Gly Phe Leu  
 100 105 110  
 Ala Ser Cys Phe Tyr Ile His Asn Glu Pro Leu Arg Gly Ala Tyr Tyr  
 115 120 125  
 Ala Gly Leu Ala Tyr Asn Asn Ser Gln Ala Leu Gln Leu Pro His Pro  
 130 135 140  
 Ile Gln Lys Leu Leu Lys Glu Ile Ser Glu Ala Gln Ala Asp Gln Leu  
 145 150 155 160  
 Tyr Asp Val Ala Leu Ser Lys Ser Tyr Gln Leu Leu Gln Thr Ala Asn  
 165 170 175  
 Ser Ser Pro Glu Tyr Pro Thr Leu Ser Phe Leu Thr Leu Leu Arg Val  
 180 185 190  
 Ile Glu Leu Lys Glu Leu Leu His Gln Asp Val Ser Gln Asp Phe Ala  
 195 200 205  
 Ala Leu Lys Ser Ser Pro Leu Phe His Gln Phe Glu Arg Met Tyr Ser  
 210 215 220  
 Asp Gly Glu Trp Thr Leu Ser Lys Arg Phe Gly Lys Lys Gly  
 225 230 235

&lt;210&gt;728

&lt;211&gt;289

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;728

Gly Arg Thr Pro Cys Glu Cys Phe Ile Leu Gly Asp Ser Cys Arg Arg  
 1 5 10 15  
 Arg Gly Ser Leu Val Lys Lys Ile Arg Val His Asp Ser Gly Leu Ile  
 20 25 30  
 Asp Leu Asp Asp Leu Glu Lys Leu Leu Asn Glu Gly Ala Gln Phe Val  
 35 40 45  
 Ser Ile Pro His Val Ser Asn Val Thr Gly Cys Val Gln Pro Leu Gln  
 50 55 60  
 Gln Val Ala Glu Leu Val His Arg Tyr Asp Ala Tyr Leu Ala Val Asp  
 65 70 75 80  
 Gly Ala Gln Gly Ala Pro His Leu Pro Ile Asp Val Gln Leu Trp Asp  
 85 90 95  
 Val Asp Phe Tyr Val Phe Ser Ser His Lys Ile Tyr Gly Pro Thr Gly  
 100 105 110  
 Ile Gly Val Leu Tyr Gly Lys Lys Asp Leu Leu Asp Gln Leu Pro Pro  
 115 120 125  
 Val Glu Gly Gly Gly Asp Met Val Ala Ile Tyr Asp His Gln Asn Pro  
 130 135 140  
 Glu Tyr Leu Pro Ala Pro Met Lys Phe Glu Ala Gly Thr Pro Asn Ile  
 145 150 155 160  
 Ala Gly Val Leu Gly Leu Gly Ala Ala Leu Asp Tyr Leu Asp Gly Leu  
 165 170 175  
 Ser Ala Lys Phe Ile Tyr Asp Lys Glu Ile Ala Leu Thr Thr Tyr Leu  
 180 185 190  
 His Lys Glu Leu Leu Glu Ile Pro Gly Val Glu Ile Leu Gly Pro Ser  
 195 200 205

Ile Glu Glu Pro Arg Gly Ala Leu Ile Gly Met Thr Ile Asp Gly Ala  
 210 215 220  
 His Pro Leu Asp Leu Gly Phe Leu Leu Asp Leu Arg Gly Ile Ala Val  
 225 230 235 240  
 Arg Thr Gly His Gln Cys Ala Gln Pro Ala Met Glu Arg Trp Asn Val  
 245 250 255  
 Gly His Val Leu Arg Val Ser Leu Gly Ile Tyr Asn Asp Glu Asp Asp  
 260 265 270  
 Ile Asp Gln Phe Ile Leu Val Leu Gln Asp Ser Leu Asp Lys Ile Arg  
 275 280 285  
 Arg

&lt;210&gt;729

&lt;211&gt;137

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;729

Ser Val Lys Asn Leu Lys Glu Asp Phe Pro Ile Phe Ala Ala Lys Ala  
 1 5 10 15  
 Lys Glu Asn Glu Pro Phe Ile Tyr Leu Asp Ser Ala Ala Thr Thr Gln  
 20 25 30  
 Lys Pro Gln Gln Val Ile Asp Ala Val Ala Asn Phe Tyr Thr Ser Ser  
 35 40 45  
 Tyr Ala Thr Val Asn Arg Ala Ile Tyr Ser Ser Ser Arg Asn Val Thr  
 50 55 60  
 Glu Ala Tyr Ala Ala Val Arg Glu Lys Val Arg Lys Trp Val Ser Ala  
 65 70 75 80  
 Ala Ser Asp Ser Glu Ile Val Phe Thr Arg Gly Thr Thr Ala Gly Leu  
 85 90 95  
 Asn Leu Leu Ala Ile Ser Val Asn Asp Leu Trp Ile Pro Lys Gly Gly  
 100 105 110  
 Val Val Leu Val Ser Glu Ala Glu His His Ala Asn Val Leu Ser Trp  
 115 120 125  
 Glu Ile Pro Val Gly Gly Glu Val Leu  
 130 135

&lt;210&gt;730

&lt;211&gt;410

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;730

Arg His Phe Leu Leu Leu Leu Arg Val Leu Leu Cys Lys Lys Leu Arg  
 1 5 10 15  
 Lys Leu Ala Thr Leu Asn Ile Ala Ser Ser Leu Leu Gln Lys Arg Cys  
 20 25 30  
 Leu Val Ala Phe Leu Gly Phe Arg Ser Phe Leu Phe Phe Leu Ile Ala  
 35 40 45  
 Asn Asn Leu Ala Thr Gly Ala Ser Glu Leu Ile Lys Gln His Trp Leu  
 50 55 60  
 His Asn Asn His Ser Leu Ala Phe Glu Cys Ile Leu Ile Asn Gly Lys  
 65 70 75 80  
 Tyr Glu Pro Ser Leu Ser Gln Leu Pro Glu Gly Val Ile Val Cys Gly  
 85 90 95  
 Ile Asp Glu Ala Arg Gly Ser Leu Ser Ser Phe Met Gln Gly Phe Asp  
 100 105 110  
 Val Asn Lys His Pro Leu Ala Phe Leu Asn Ala Val Cys Ser Glu Asp  
 115 120 125  
 Arg Gly Val Val Ile Tyr Ile Pro Glu Glu Met Gln Thr Ser Asp Pro  
 130 135 140  
 Ile Phe Val Arg His Ile Ser Phe Pro Thr Val Ser Asp His Asp Val  
 145 150 155 160  
 Ile Phe Ser Pro Arg Ile Val Val Ile Leu Gly Gln Arg Ala Ser Ala  
 165 170 175  
 Gln Ile Gln Ile Ser His Asp Val Asp Leu Glu Met Val Gly Ser Ser  
 180 185 190

Lys Thr Ile Val Asn Gly Val Thr Glu Leu Phe Val Gly Glu Gly Ala  
 195 200 205  
 Asp Leu Thr Val Phe Met Val Pro Gly Tyr Ser Glu Glu Asp Thr Leu  
 210 215 220  
 Ser Trp Ser Thr Ile Ala Thr Val Glu Lys Asp Ala Ile Cys Arg Met  
 225 230 235 240  
 Thr Gln Asn Leu Leu Glu Ser Cys Gln Gly Phe Gly Trp Phe Asp Asn  
 245 250 255  
 Thr Ser Tyr Ile Val Gly Lys Lys Gly His Ala Glu Ser Leu Val Leu  
 260 265 270  
 Val Gln Ser Pro Arg Lys Thr Trp Val Asn Asn Leu Met Ser His Asp  
 275 280 285  
 Ala Glu Glu Thr Val Ser Arg Gln Asn Ile Lys Ser Ile Leu Tyr Ser  
 290 295 300  
 Gly His Phe Leu Phe Glu Gly Thr Ile Ser Ile Ser Ser Gln Gly Asp  
 305 310 315 320  
 Leu Ser Asp Ala Asn Gln Lys His Asp Thr Leu Leu Leu Ser Ser Glu  
 325 330 335  
 Ala Arg Val Ser Thr Phe Pro Arg Leu Glu Ile Glu Thr Asp Glu Val  
 340 345 350  
 Lys Ala Ser His Gly Ala Thr Val Gly Pro Leu Asp Pro Gln Gln Ile  
 355 360 365  
 Phe Tyr Met Arg Ser Arg Gly Met Thr Glu Ala Glu Ala Gln Glu Lys  
 370 375 380  
 Leu Ile His Gly Phe Leu Lys Gln Gly Leu Val Ser Asp Thr Phe Leu  
 385 390 395 400  
 Gly Ser Ser Phe Gln Leu Asn Gln Thr Ser  
 405 410

&lt;210&gt;731

&lt;211&gt;256

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;731

Met Leu Lys Ile Lys His Leu His Ala Ser Cys Asn Asp Val Lys Ile  
 1 5 10 15  
 Leu Asp Asp Phe Asn Leu Asn Ile Gln Pro Gly Xaa Met His Val Ile  
 20 25 30  
 Met Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Ala Lys Ile Leu Ala  
 35 40 45  
 Gly Asp Glu Ser Val Leu Val Ser Ser Gly Glu Ile Ala Leu Gln Glu  
 50 55 60  
 Gln Asn Leu Leu Ser Met Leu Pro Glu Glu Arg Ser Arg Ala Gly Leu  
 65 70 75 80  
 Phe Val Gly Phe Gln Met Pro Pro Glu Ile Pro Gly Val Asn Asn Lys  
 85 90 95  
 Met Phe Leu Arg Asp Ala Tyr Asn Ala Arg Arg Arg Ala Asn Gln Glu  
 100 105 110  
 Gly Asp Ile Ser Ile Asp Glu Phe Asn Thr Leu Leu Ser Thr Val Leu  
 115 120 125  
 Glu Thr Tyr Glu Tyr Asn Ala Thr Thr Asp Leu Phe Leu Asp Arg Asn  
 130 135 140  
 Val Asn Glu Gly Phe Ser Gly Gly Glu Arg Lys Arg Asn Glu Ile Cys  
 145 150 155 160  
 Gln Met Leu Val Leu Glu Pro Glu Met Val Leu Leu Asp Glu Pro Asp  
 165 170 175  
 Ser Gly Leu Asp Val Asp Ala Leu Arg Leu Ile Cys Arg Val Leu Glu  
 180 185 190  
 Lys Tyr Arg Glu Leu His Pro Thr Ser Ser Leu Cys Ile Val Thr His  
 195 200 205  
 Asn Pro Lys Leu Gly Asn Leu Ile Arg Pro Asp Val Val His Leu Leu  
 210 215 220  
 Leu Asp Gly Arg Val Ala Leu Ser Gly Asp Val Ser Leu Met His Glu  
 225 230 235 240  
 Leu Glu Ala Lys Ser Tyr Gln Glu Val Thr Lys Arg Val Ala Trp Arg

245                      250                      255  
 <210>732  
 <211>484  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>732  
 Met Gly Glu Ser Val Lys Val Phe Leu Glu Glu Arg Glu Asp Tyr Pro  
   1                      5                      10                      15  
 Tyr Gly Phe Val Thr Pro Ile Glu Ser Gln Gly Leu Thr Arg Gly Leu  
                     20                      25                      30  
 Ser Glu Glu Thr Ile Glu Glu Ile Ala Ala Leu Arg Asn Glu Pro Gln  
                     35                      40                      45  
 Phe Ile Ile Asp Phe Arg Leu Gln Ala Tyr Arg Tyr Trp Lys Gln Leu  
                     50                      55                      60  
 His Glu Pro Ala Trp Ala Arg Leu His Tyr Gly Pro Ile Ala Tyr Asp  
   65                      70                      75                      80  
 Asp Ile Val Tyr Phe Ser Ser Pro Lys Gln Lys Lys Pro Leu Gly Arg  
                     85                      90                      95  
 Leu Glu Asp Ala Asp Pro Glu Ile Leu Asp Thr Phe Lys Lys Leu Gly  
                     100                      105                      110  
 Ile Pro Leu Asp Glu Gln Lys Arg Leu Leu Asn Val Glu Asn Val Ala  
                     115                      120                      125  
 Val Asp Leu Val Phe Asp Ser Val Ser Ile Gly Thr Thr Phe Lys Glu  
   130                      135                      140  
 Ala Leu Glu Lys Ala Gly Val Ile Phe Cys Ser Leu Gly Glu Ala Ile  
   145                      150                      155                      160  
 Gln Glu His Pro Asn Leu Val Lys Lys Tyr Leu Gly Ser Val Val Ser  
                     165                      170                      175  
 His Arg Asp Asn Phe Phe Ala Ala Leu Asn Ala Ala Val Phe Ser Asp  
                     180                      185                      190  
 Gly Ser Phe Val Tyr Val Pro Lys Gly Val Lys Cys Pro Met Asp Ile  
                     195                      200                      205  
 Ser Thr Tyr Phe Arg Ile Asn Asn Lys Glu Ala Gly Gln Phe Glu Arg  
   210                      215                      220  
 Thr Leu Ile Val Val Glu Asp Gly Gly Tyr Ala Ser Tyr Leu Glu Gly  
   225                      230                      235                      240  
 Cys Thr Ala Pro Ala Tyr Ser Ser Asn Gln Leu His Ala Ala Val Val  
                     245                      250                      255  
 Glu Leu Val Ala His Glu His Ala Val Ile Arg Tyr Ser Thr Val Gln  
                     260                      265                      270  
 Asn Trp Tyr Ala Gly Asp Lys Lys Thr Gly Lys Gly Gly Ile Tyr Asn  
                     275                      280                      285  
 Phe Val Thr Lys Arg Gly Leu Cys Ala Gly Tyr Arg Ser Lys Ile Ser  
   290                      295                      300  
 Trp Ser Gln Val Glu Val Gly Ala Ala Ile Thr Trp Lys Tyr Pro Ser  
   305                      310                      315                      320  
 Cys Ile Leu Lys Gly Asp Glu Ser Val Gly Glu Phe Tyr Ser Val Ala  
                     325                      330                      335  
 Leu Thr Ser Gly Lys Met Gln Ala Asp Thr Gly Thr Lys Met Leu His  
                     340                      345                      350  
 Val Gly Lys Arg Thr Thr Ser Thr Val Ile Ser Lys Gly Ile Ser Ser  
                     355                      360                      365  
 Asp Glu Ser Lys Asn Thr Phe Arg Ser Leu Val Ser Leu Gly Lys Lys  
   370                      375                      380  
 Ala Glu His Ser Ser Asn Tyr Thr Gln Cys Asp Ser Met Leu Ile Gly  
   385                      390                      395                      400  
 Lys Ala Ser Gly Ala Tyr Thr Asp Pro Lys Ile Val Val Glu Asn Ser  
                     405                      410                      415  
 Thr Ser Ser Ile Glu His Glu Ala Thr Thr Ser Lys Leu Arg Glu Asp  
                     420                      425                      430  
 Gln Leu Leu Tyr Leu Arg Ser Arg Gly Leu Ser Pro Glu Glu Ala Val  
                     435                      440                      445  
 Ser Leu Val Ile His Gly Phe Cys Arg Glu Ile Ile Glu Gln Leu Pro  
   450                      455                      460

Leu Glu Phe Ala Gln Glu Ala Ser Lys Leu Leu Leu Ile Lys Leu Glu  
 465 470 475 480  
 Asn Ser Val Gly

&lt;210&gt;733

&lt;211&gt;351

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;733

Leu Arg Ser Thr Asn His Val Leu Gly Glu Ile Ser Met Glu Glu Ala  
 1 5 10 15  
 Ala Lys His Leu Ala Lys Glu Phe Leu Cys Ser Gly Ile Asn Leu Phe  
 20 25 30  
 Leu Ser Gly Glu Tyr Glu Gln Ala Glu Lys Arg Leu Lys Glu Thr Leu  
 35 40 45  
 Glu Leu Asp Ser Thr Ala Ala Leu Ala Tyr Cys Tyr Leu Gly Ile Ile  
 50 55 60  
 Ala Leu Glu Thr Gly Arg Val Ser Glu Ala Leu Asn Trp Cys Ser Lys  
 65 70 75 80  
 Gly Leu Ala Ser Glu Pro Gly Asp Ser Tyr Leu Arg Tyr Cys Tyr Gly  
 85 90 95  
 Val Ala Leu Asp Arg Gly Asn Gln Tyr Glu Ala Ala Ile Glu Gln Tyr  
 100 105 110  
 Ser Ala Tyr Val Ala Leu His Pro Asp Asp Val Glu Cys Trp Phe Ser  
 115 120 125  
 Leu Gly Ser Val Tyr His Arg Leu Lys Arg Leu Gln Glu Ala Leu Asp  
 130 135 140  
 Cys Phe Asp Lys Ile Leu Ala Leu Asp Pro Trp Asn Pro Gln Ser Leu  
 145 150 155 160  
 Tyr Asn Lys Ala Val Ile Leu Ser Glu Met Asp Asp Glu Ala Glu Ser  
 165 170 175  
 Ile Arg Leu Leu Glu Val Ala Val Ala Lys Asn Pro Leu Tyr Trp Lys  
 180 185 190  
 Ala Trp Val Lys Leu Gly Phe Leu Leu Ser Arg Ser Lys Arg Trp Asp  
 195 200 205  
 Lys Ala Thr Glu Ala Tyr Glu Arg Val Val Gln Leu Arg Pro Asp Leu  
 210 215 220  
 Ser Asp Gly His Tyr Asn Leu Gly Leu Cys Tyr Leu Thr Leu Asp Lys  
 225 230 235 240  
 Thr Arg Leu Ala Leu Lys Ala Phe Gln Glu Ala Leu Phe Leu Asn Ala  
 245 250 255  
 Glu Asp Ala Asp Ala His Phe Tyr Val Gly Leu Ala His Leu Asp Leu  
 260 265 270  
 Lys Gln Met Arg Glu Ala Tyr Glu Ala Phe Asn Ser Ala Leu Ser Ile  
 275 280 285  
 Asn Leu Glu His Glu Arg Ala His Tyr Leu Leu Gly Tyr Leu His His  
 290 295 300  
 Met Gln Gly Glu Thr Asp Lys Ala Thr Lys Glu Leu Leu Phe Leu Gln  
 305 310 315 320  
 Lys Lys Asp Ser Thr Phe Ala Pro Leu Leu Gln Lys Thr Val Val Ser  
 325 330 335  
 Asp Pro Ser Ser Met Gln Phe Glu Arg Arg Leu Asp Thr Ile Ser  
 340 345 350

&lt;210&gt;734

&lt;211&gt;660

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;734

Leu Pro Leu Thr Phe Asp Cys Phe Leu Asp Phe Leu Phe Pro Glu Asn  
 1 5 10 15  
 Ser Val Ile Lys Leu Gln Leu Lys Arg Asn Ser Phe Val Gly Gln Ala  
 20 25 30  
 Ile Glu Val Gln Asn Leu Val Thr Arg Leu Leu Ser Leu Phe Pro Tyr  
 35 40 45

Glu Glu Gly Thr Cys Pro Cys Ser Ala Ile Phe Asp Ala Val Phe Pro  
 50 55 60  
 Asn Glu Glu Gly His Ile Leu Ile Gln Glu Val Ile Ser Leu Gln Glu  
 65 70 75 80  
 Gln Lys Trp Ile Met Glu Cys Leu Asn Gln His Lys Ala Asp Ile Glu  
 85 90 95  
 Glu Leu Lys Glu Ala Leu Asp Gln Val Phe Asn Glu Leu Pro Ala Asn  
 100 105 110  
 Tyr Asp Lys Ile Leu Tyr Thr Asp Ile Leu Arg Leu Ile Val Asp Pro  
 115 120 125  
 Glu Arg Phe Ser Pro Val Leu Pro Ser Glu Val His Arg Leu Ser Leu  
 130 135 140  
 Ser Glu Phe Thr Glu Leu Gln Gly Arg Tyr Val Val Leu Arg Ser Ala  
 145 150 155 160  
 Phe Ser Thr Ile Leu Glu Asp Ala Phe Ile Glu Val His Phe Lys Ser  
 165 170 175  
 Trp Arg Lys Ser Glu Phe Leu Gln Tyr Leu Ala Ala Lys Arg Gln Glu  
 180 185 190  
 Glu Ala Leu Arg Lys Gln Arg Tyr Pro Thr Pro Tyr Val Asp Tyr Leu  
 195 200 205  
 Glu Glu Glu Lys Thr Arg Gln Tyr Lys Met Phe Cys Gln Glu His Leu  
 210 215 220  
 Asp Thr Phe Leu Ala Tyr Leu Phe Ser Lys Thr Pro Tyr Lys Glu Gly  
 225 230 235 240  
 Leu Glu Pro Tyr Tyr Asp Ile Leu Asp Leu Trp Ile Asn Glu Leu Asp  
 245 250 255  
 Asn Gly Ala His Arg Ala Leu Ser Trp Asn Glu His Tyr Leu Phe Leu  
 260 265 270  
 Lys Glu Arg Val Ser His Leu Ser Glu His Leu Pro Ala Leu Phe Ser  
 275 280 285  
 Thr Phe Arg Glu Phe Asn Glu Leu Gln Arg Pro Leu Leu Gly Lys Tyr  
 290 295 300  
 Pro Ile Ser Ile Val Arg Asn Lys Arg Gln Thr Glu Gln Asp Leu Ala  
 305 310 315 320  
 Ala Ser Phe Tyr Pro Val Tyr Gly Tyr Gly Tyr Leu Arg Pro His Ala  
 325 330 335  
 Tyr Gly Gln Ala Ala Thr Leu Gly Ser Ile Phe Lys Leu Val Ser Ala  
 340 345 350  
 Tyr Ser Val Leu Ser Gln Arg Ile Leu Trp Gly His Asn Glu Glu Pro  
 355 360 365  
 Ala Asn Pro Leu Val Ile Ile Asp Lys Asn Ser Phe Gly Tyr Arg Ser  
 370 375 380  
 Ser Lys Pro His Val Gly Phe Phe Lys Asp Gly Thr Pro Ile Pro Thr  
 385 390 395 400  
 Phe Phe Arg Gly Gly Ser Leu Pro Gly Asn Asp Phe Met Gly Arg Gly  
 405 410 415  
 Phe Ile Asp Leu Val Ser Ala Leu Glu Met Ser Ser Asn Pro Tyr Phe  
 420 425 430  
 Ser Leu Leu Val Gly Glu Gly Leu Gly Asp Pro Glu Asp Leu Ala Asp  
 435 440 445  
 Ala Ala Ser Leu Phe Gly Phe Gly Glu Lys Thr Gly Leu Gly Leu Pro  
 450 455 460  
 Gly Glu Tyr Ala Gly Arg Val Pro His Asp Leu Ala Tyr Asn Arg Ser  
 465 470 475 480  
 Gly Leu Tyr Ala Thr Ala Ile Gly Gln His Thr Leu Val Val Thr Pro  
 485 490 495  
 Leu Gln Thr Ala Val Met Leu Ala Ser Leu Val Asn Gly Gly Val Val  
 500 505 510  
 Tyr Val Pro Lys Leu Leu Leu Gly Glu Trp Glu Gly Glu His Val Ser  
 515 520 525  
 Tyr Leu Ser Ser Lys Lys Lys Arg Thr Ile Phe Met Pro Asp Ala Val  
 530 535 540  
 Val Glu Val Leu Lys Thr Gly Met Arg Asn Val Ile Trp Gly Gln Tyr  
 545 550 555 560

Gly Thr Ala Arg Ala Ile Gln Ser Gln Phe Pro Pro Gln Leu Leu Ser  
 565 570 575  
 Arg Ile Ile Gly Lys Thr Ser Thr Ala Glu Ser Ile Met Arg Val Gly  
 580 585 590  
 Leu Asp Arg Glu Tyr Gly Thr Met Lys Met Lys Asp Ile Trp Phe Ala  
 595 600 605  
 Ala Val Gly Phe Ser Asp Gln Asp Leu Ser Leu Pro Thr Ile Val Val  
 610 615 620  
 Ile Val Tyr Leu Arg Leu Gly Glu Phe Gly Arg Asp Ala Ala Pro Met  
 625 630 635 640  
 Ala Val Lys Met Ile Asp Met Trp Glu Lys Ile Gln Gln Arg Glu Ser  
 645 650 655  
 Phe Leu Arg Gly  
 660

&lt;210&gt;735

&lt;211&gt;139

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;735

Glu Lys Trp Val Leu Arg His Cys Trp Asp Ser Lys Leu Arg Gly Lys  
 1 5 10 15  
 Ile Gly Lys Lys Pro Ile Leu Val Asp Arg Arg Gly Asn Phe Ile Gln  
 20 25 30  
 Glu Met Glu Gly Ala Val Pro Glu Ala Pro Gly Thr Lys Leu Gln Leu  
 35 40 45  
 Thr Leu Ser Ala Glu Leu Gln Ala Tyr Ala Asp Ala Leu Leu Leu Glu  
 50 55 60  
 Tyr Glu Lys Thr Glu Thr Phe Arg Ser Ala Lys Ser Leu Lys Lys Arg  
 65 70 75 80  
 Glu Lys Leu Pro Pro Leu Phe Pro Trp Ile Lys Gly Gly Ala Ile Ile  
 85 90 95  
 Ala Leu Asp Pro Asn Asn Gly Glu Ile Leu Ala Met Ala Ser Ser Pro  
 100 105 110  
 Arg Tyr Arg Asn Asn Asp Phe Val Asn Ala Lys Val Ala Glu Asp Ser  
 115 120 125  
 Lys Ala Val Arg Ser Ser Ile Tyr Leu Asp Gly  
 130 135

&lt;210&gt;736

&lt;211&gt;286

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;736

Phe Ser Asp Glu Ser Glu Ala His Asn Ile His Ser Met Lys Arg Pro  
 1 5 10 15  
 Lys Lys Phe Pro Ile Tyr Leu Ser Ile Ala Gln Lys Thr Asn Arg Leu  
 20 25 30  
 Leu Ser Gly Ile Val Ile Ala Phe Ala Val Ile Ala Leu Arg Leu Trp  
 35 40 45  
 Tyr Leu Ala Val Val Glu His Glu Gln Lys Leu Glu Glu Ala Tyr Lys  
 50 55 60  
 Pro Gln Ile Arg Val Leu Pro Gln Tyr Val Glu Arg Ala Thr Ile Cys  
 65 70 75 80  
 Asp Arg Phe Gly Lys Thr Leu Ala Val Asn Gln Leu Gln Tyr Asp Val  
 85 90 95  
 Ser Val Ala Tyr Gly Ala Ile Arg Asp Leu Pro Thr Arg Ala Trp Arg  
 100 105 110  
 Val Asp Glu His Gly His Lys Gln Leu Ile Pro Val Arg Lys His Tyr  
 115 120 125  
 Ile Met Cys Leu Ser Glu Leu Leu Ser Gln Glu Leu His Leu Asp Arg  
 130 135 140  
 Glu Ala Ile Glu Asp Ala Ile His Ala Lys Ala Ser Val Leu Gly Ser  
 145 150 155 160  
 Val Pro Tyr Leu Val Ala Ala Asn Val Ser Glu Arg Thr Tyr Leu Lys  
 165 170 175

Leu Lys Met Leu Ser Lys Asp Trp Pro Gly Leu His Val Glu Ala Val  
 180 185 190  
 Val Arg Arg His Tyr Pro Gln Glu Ser Val Ala Ser Asp Ile Leu Gly  
 195 200 205  
 Tyr Val Gly Pro Ile Ser Leu Gln Glu Tyr Lys Arg Val Thr Gln Glu  
 210 215 220  
 Leu Ser Gln Leu Arg Glu Cys Val Arg Ala Tyr Glu Glu Gly Glu Asp  
 225 230 235 240  
 Pro Lys Leu Pro Glu Gly Leu Ala Ser Ile Asp Gln Val Arg Ala Leu  
 245 250 255  
 Leu Glu Ser Val Glu Ser Asn Ala Tyr Ser Leu Asn Ala Leu Val Gly  
 260 265 270  
 Lys Met Gly Val Glu Ala Leu Leu Gly Leu Lys Ile Thr Arg  
 275 280 285  
 <210>737  
 <211>391  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>737  
 Val Ser Met Lys Lys Leu Leu Lys Ser Ala Leu Leu Ser Ala Ala Phe  
 1 5 10 15  
 Ala Gly Ser Val Gly Ser Leu Gln Ala Leu Pro Val Gly Asn Pro Ser  
 20 25 30  
 Asp Pro Ser Leu Leu Ile Asp Gly Thr Ile Trp Glu Gly Ala Ala Gly  
 35 40 45  
 Asp Pro Cys Asp Pro Cys Ala Thr Trp Cys Asp Ala Ile Ser Leu Arg  
 50 55 60  
 Ala Gly Phe Tyr Gly Asp Tyr Val Phe Asp Arg Ile Leu Lys Val Asp  
 65 70 75 80  
 Ala Pro Lys Thr Phe Ser Met Gly Ala Lys Pro Thr Gly Ser Ala Ala  
 85 90 95  
 Ala Asn Tyr Thr Thr Ala Val Asp Arg Pro Asn Pro Ala Tyr Asn Lys  
 100 105 110  
 His Leu His Asp Ala Glu Trp Phe Thr Asn Ala Gly Phe Ile Ala Leu  
 115 120 125  
 Asn Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Ser Asn  
 130 135 140  
 Gly Tyr Ile Arg Gly Asn Xaa Tyr Arg Phe Asn Leu Val Gly Leu Phe  
 145 150 155 160  
 Gly Val Lys Gly Thr Thr Val Asn Ala Asn Xaa Leu Pro Asn Val Ser  
 165 170 175  
 Leu Ser Asn Gly Val Val Glu Leu Tyr Thr Asp Thr Ser Phe Ser Trp  
 180 185 190  
 Ser Val Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr Leu  
 195 200 205  
 Gly Ala Glu Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu Glu Leu  
 210 215 220  
 Asn Val Ile Cys Asn Val Ser Gln Phe Ser Val Asn Lys Pro Lys Gly  
 225 230 235 240  
 Tyr Lys Gly Val Ala Phe Pro Leu Pro Thr Asp Ala Gly Val Ala Thr  
 245 250 255  
 Ala Thr Gly Thr Lys Ser Ala Thr Ile Asn Tyr His Glu Trp Gln Val  
 260 265 270  
 Gly Ala Ser Leu Ser Tyr Arg Leu Asn Ser Leu Val Pro Tyr Ile Gly  
 275 280 285  
 Val Gln Trp Ser Arg Ala Thr Phe Asp Ala Asp Asn Ile Arg Ile Ala  
 290 295 300  
 Gln Pro Lys Leu Pro Thr Ala Val Leu Asn Leu Thr Ala Trp Asn Pro  
 305 310 315 320  
 Ser Leu Leu Gly Asn Ala Thr Ala Leu Ser Thr Thr Asp Ser Phe Ser  
 325 330 335  
 Asp Phe Met Gln Ile Val Ser Cys Gln Ile Asn Lys Phe Lys Ser Arg  
 340 345 350  
 Lys Ala Cys Gly Val Thr Val Gly Ala Thr Leu Val Asp Ala Asp Lys



355 360 365  
 Trp Ser Leu Thr Ala Glu Ala Arg Leu Ile Asn Glu Arg Ala Ala His  
 370 375 380  
 Val Ser Gly Gln Phe Arg Phe  
 385 390  
 <210>738  
 <211>292  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>738  
 Met Pro Leu Leu Thr Tyr Ser Asn Phe Glu Ile Glu Val Gln Ser Leu  
 1 5 10 15  
 Glu Ser Gln Ser Cys Lys Leu Thr Ile Lys Asp Leu Met Ser Ala Gly  
 20 25 30  
 Ala His Phe Gly His Gln Thr Arg Arg Trp Asn Pro Lys Met Lys Leu  
 35 40 45  
 Tyr Ile Phe Glu Glu Lys Asn Gly Leu Tyr Ile Ile Asn Leu Ala Lys  
 50 55 60  
 Thr Leu Gln Gln Leu Arg Asn Ala Leu Pro His Ile Arg Lys Val Ile  
 65 70 75 80  
 Gln Asp Asn Lys Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Lys  
 85 90 95  
 Cys Val Ile Arg Glu Ala Ala Ile Glu Ala Gly Glu Phe Phe Ile Ala  
 100 105 110  
 Glu Arg Trp Leu Gly Gly Met Leu Thr Asn Met Thr Thr Ile Arg Asn  
 115 120 125  
 Ser Ile Lys Thr Leu Asp Lys Ile Glu Lys Asp Leu Ser Arg Asn Gln  
 130 135 140  
 Ala Tyr Leu Thr Lys Lys Glu Ala Ala Leu Leu Ala Lys Arg His Gln  
 145 150 155 160  
 Lys Leu Leu Arg Asn Leu Glu Gly Ile Arg Tyr Met Lys Lys Ala Pro  
 165 170 175  
 Gly Leu Leu Val Val Val Asp Pro Ser Tyr Glu Lys Ile Ala Val Ala  
 180 185 190  
 Glu Ala Lys Lys Leu Gly Ile Pro Val Leu Ala Leu Val Asp Thr Asn  
 195 200 205  
 Cys Asp Pro Thr Pro Ile Asp His Val Ile Pro Cys Asn Asp Asp Ser  
 210 215 220  
 Leu Lys Ser Ile Arg Leu Ile Ile Asn Val Ile Lys Glu Asn Ile Ile  
 225 230 235 240  
 Glu Ala Lys His Lys Leu Gly Ile Glu Ile Val Ser Pro Val Lys Ser  
 245 250 255  
 Leu Glu Val Pro Asp Leu Ser Ala Phe Glu Ser Ser Gln Asp Asp Glu  
 260 265 270  
 Ser Asp Glu Glu Asn Arg Glu Glu Asp Leu Leu Ala Lys Lys Phe Asp  
 275 280 285  
 Gly Glu Ala Asn  
 290  
 <210>739  
 <211>282  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>739  
 Met Ser Asp Phe Ser Met Glu Thr Leu Lys Thr Leu Arg Gln Gln Thr  
 1 5 10 15  
 Gly Val Gly Leu Thr Lys Cys Lys Glu Ala Leu Glu Ala Cys Gly Gly  
 20 25 30  
 Asn Leu Glu Glu Ala Val Val Tyr Leu Arg Lys Leu Gly Leu Ala Ser  
 35 40 45  
 Ala Gly Lys Lys Glu His Arg Glu Thr Lys Glu Gly Ile Ile Ala Ala  
 50 55 60  
 Lys Thr Asp Ala Asn Gly Thr Ala Leu Ile Glu Val Asn Val Glu Thr  
 65 70 75 80  
 Asp Phe Val Ala Asn Asn Ala Val Phe Arg Glu Phe Val Ser Asn Leu

85 90 95  
 Leu Asn Asp Ile Leu Lys Tyr Lys Val Asp Thr Val Glu Ala Leu Ser  
 100 105 110  
 Gln Ala Ala Ser Ser Gln Asp Pro Ser Leu Ser Val Asp Glu Leu Arg  
 115 120 125  
 Ala Val Thr Met Gln Thr Val Gly Glu Asn Ile Arg Ile Ser Arg Val  
 130 135 140  
 Ala Tyr Phe Pro Lys Ala Thr Asn Ser Thr Val Gly Ile Tyr Ser His  
 145 150 155 160  
 Gly Asn Gly Lys Thr Val Ala Leu Thr Met Leu Ser Gly Ser Ser Thr  
 165 170 175  
 Ala Asp Ser Leu Ala Lys Asp Ile Ala Met His Val Val Ala Ala Gln  
 180 185 190  
 Pro Gln Phe Leu Ser Lys Glu Ser Val Pro Ala Glu Ala Ile Ala Lys  
 195 200 205  
 Glu Lys Glu Val Ile Ala Ser Gln Ile Gln Gly Lys Pro Gln Glu Val  
 210 215 220  
 Ile Glu Lys Ile Val Thr Gly Lys Leu Asn Thr Phe Phe Gln Glu Ala  
 225 230 235 240  
 Cys Leu Leu Glu Gln Pro Phe Ile Lys Asn Ala Asp Leu Ser Ile Gln  
 245 250 255  
 Ser Leu Ile Asp Asp Phe Ser Lys Thr Ser Gly Ser Ser Val Ala Ile  
 260 265 270  
 Glu Gln Phe Ile Leu Trp Lys Ile Gly Ala  
 275 280

&lt;210&gt;740

&lt;211&gt;248

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;740

Met Ala Lys Gln Thr Arg Arg Val Leu Phe Lys Ile Ser Gly Glu Ala  
 1 5 10 15  
 Leu Ser Lys Asp Ser Ser Asn Arg Ile Asp Glu Met Arg Leu Ser Arg  
 20 25 30  
 Leu Val Ser Glu Leu Arg Ala Val Arg Asn Asn Asp Ile Glu Ile Ala  
 35 40 45  
 Leu Val Ile Gly Gly Gly Asn Ile Leu Arg Gly Leu Ala Glu Gln Lys  
 50 55 60  
 Glu Leu Gln Ile Asn Arg Val Ser Ala Asp Gln Met Gly Met Leu Ala  
 65 70 75 80  
 Thr Leu Ile Asn Gly Met Ala Val Ala Asp Ala Leu Lys Ala Glu Asp  
 85 90 95  
 Ile Pro Cys Leu Leu Thr Ser Thr Leu Ser Cys Pro Gln Leu Ala Asp  
 100 105 110  
 Leu Tyr Thr Pro Gln Lys Ser Ile Glu Ala Leu Asp Gln Gly Lys Ile  
 115 120 125  
 Leu Ile Cys Thr Thr Gly Ala Gly Ser Pro Tyr Leu Thr Thr Asp Thr  
 130 135 140  
 Gly Ala Ala Leu Arg Ala Cys Glu Leu Asn Val Asp Val Leu Ile Lys  
 145 150 155 160  
 Ala Thr Met His Val Asp Gly Val Tyr Asp Lys Asp Pro Arg Leu Phe  
 165 170 175  
 Pro Asp Ala Val Lys Tyr Asp Phe Val Ser Tyr Lys Asp Phe Leu Ser  
 180 185 190  
 Asn Gln Leu Gly Val Met Asp Ala Ser Ala Ile Ser Leu Cys Met Asp  
 195 200 205  
 Ser His Ile Pro Ile Arg Val Phe Ser Phe Leu Gln His Ser Leu Glu  
 210 215 220  
 Lys Ala Leu Phe Asp Pro Thr Ile Gly Thr Leu Val Ser Glu Asp Val  
 225 230 235 240  
 Asn His Val Cys Ser Pro Arg His  
 245

&lt;210&gt;741

&lt;211&gt;180

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;741

```

Met Ser Val Leu Gln Asp Thr Glu Lys Lys Met Ala Ala Ala Leu Asp
 1           5           10           15
Phe Phe His Lys Glu Val Lys Ser Phe Arg Thr Gly Lys Ala His Pro
      20           25           30
Ala Leu Val Glu Thr Val Val Val Asp Val Tyr Gly Thr Thr Met Arg
      35           40           45
Leu Ser Asp Ile Ala Ser Ile Ser Val Ala Asp Leu Arg Gln Leu Val
      50           55           60
Ile Ser Pro Tyr Asp Gly Asn Asn Ala Ser Ala Ile Ala Lys Gly Ile
      65           70           75           80
Ile Ala Ala Asn Leu Asn Leu Gln Pro Glu Val Glu Gly Ser Ile Ile
      85           90           95
Arg Ile Lys Val Pro Glu Pro Thr Ala Asp Tyr Arg Gln Glu Met Ile
      100           105           110
Lys Gln Leu Arg Arg Lys Cys Glu Glu Ala Lys Ile Asn Val Arg Asn
      115           120           125
Ile Arg Arg Glu Ala Asn Asp Lys Leu Lys Lys Asp Ser Ala Leu Thr
      130           135           140
Glu Asp Val Val Lys Gly Asn Glu Lys Lys Ile Gln Glu Leu Thr Asp
      145           150           155           160
Lys Phe Cys Lys Gln Leu Asp Glu Leu Thr Lys Gln Lys Glu Ala Glu
      165           170           175
Ile Ala Ser Ile
      180

```

&lt;210&gt;742

&lt;211&gt;172

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;742

```

Leu Met Val His Ser Pro Thr His Gln Cys Tyr His Cys Gln Gln Pro
 1           5           10           15
Ala Thr Ile Cys Tyr Thr Glu Ile Asp Lys Asp Lys Val Ile Arg Ser
      20           25           30
Tyr Val Cys Ala Thr Cys Pro Cys Pro Ser His Tyr Tyr Asn Asn Glu
      35           40           45
His Leu Ser Leu Ser Lys Gly Val Gly Val Leu Thr Leu Glu Cys Gly
      50           55           60
Asn Cys Lys Thr Val Trp His Ser Lys Gln Asp Asp Glu Gln Leu Leu
      65           70           75           80
Gly Cys His Gln Cys Tyr Thr Asn Phe Lys Asn Gln Ile Thr Ser Lys
      85           90           95
Leu Lys Ser Glu Arg Val Val Ser Ser Ser Phe Thr Met Glu Lys Gly
      100           105           110
Gln Gly Ser Leu His Ile Gly Arg Ala Pro Gly Glu Ala Ser Asn Thr
      115           120           125
Asn Pro Leu Leu Lys Leu Ile Ala Leu Asn Glu Ala Leu Gln Asp Thr
      130           135           140
Leu Glu Arg Glu Asp Tyr Glu Gln Ala Ala Val Ile Arg Asp Gln Ile
      145           150           155           160
Asn His Leu Lys Thr Lys Asn Pro Asp Asp Pro Ser
      165           170

```

&lt;210&gt;743

&lt;211&gt;358

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;743

```

Met Thr Leu Pro Asn Asp Leu Leu Glu Thr Leu Val Lys Arg Lys Glu
 1           5           10           15
Ser Pro Gln Ala Asn Lys Val Trp Pro Val Thr Thr Phe Ser Leu Ala
      20           25           30
Arg Asn Leu Ser Val Ser Lys Phe Leu Pro Cys Leu Ser Lys Glu Gln

```

35 40 45  
 Lys Leu Glu Ile Leu Gln Phe Ile Thr Ser His Phe Asn His Ile Glu  
 50 55 60  
 Gly Phe Gly Glu Phe Ile Val Leu Pro Leu Lys Asp Thr Pro Leu Trp  
 65 70 75 80  
 Gln Lys Glu Phe Leu Leu Glu His Phe Leu Pro Tyr Asp Leu Val  
 85 90 95  
 Gly Asn Pro Glu Gly Glu Ala Leu Val Ser Arg Ser Gly Asp Phe  
 100 105 110  
 Leu Ala Ala Ile Asn Phe Gln Asp His Leu Val Leu His Gly Ile Asp  
 115 120 125  
 Phe Gln Gly Asn Val Glu Lys Thr Leu Asp Gln Leu Val Gln Leu Asp  
 130 135 140  
 Ser Tyr Leu His Ser Lys Leu Ser Phe Ala Phe Ser Ser Glu Phe Gly  
 145 150 155 160  
 Phe Leu Thr Thr Asn Pro Lys Asn Cys Gly Thr Gly Leu Lys Ser Gln  
 165 170 175  
 Cys Phe Leu His Ile Pro Ala Leu Leu Tyr Ser Lys Glu Phe Thr Asn  
 180 185 190  
 Leu Ile Asp Glu Glu Val Glu Ile Ile Thr Ser Ser Leu Leu Leu Gly  
 195 200 205  
 Val Thr Gly Phe Pro Gly Asn Ile Val Val Leu Ser Asn Arg Cys Ser  
 210 215 220  
 Leu Gly Leu Thr Glu Glu Leu Leu Ser Ser Leu Arg Ile Thr Ala  
 225 230 235 240  
 Ser Lys Leu Ser Val Ala Glu Val Ala Ala Lys Lys Arg Leu Ser Glu  
 245 250 255  
 Glu Asn Ser Gly Asp Leu Lys Asn Leu Ile Leu Arg Ser Leu Gly Leu  
 260 265 270  
 Leu Thr His Ser Cys Gln Leu Glu Leu Lys Glu Thr Leu Asp Ala Leu  
 275 280 285  
 Ser Trp Ile Gln Leu Gly Ile Asp Leu Gly Leu Ile Lys Val Thr Glu  
 290 295 300  
 Asn His Pro Leu Trp Asn Pro Leu Phe Trp Gln Ile Arg Arg Ala His  
 305 310 315 320  
 Leu Ala Leu Gln Lys Gln Ala Glu Asn Ser Arg Asp Leu Gln Lys Asp  
 325 330 335  
 Thr Ile Ser His Leu Arg Ala Ser Val Leu Lys Glu Leu Thr Lys Gly  
 340 345 350  
 Leu Ser Pro Glu Ser Phe  
 355

&lt;210&gt;744

&lt;211&gt;561

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;744

Ser Cys Cys Gly Tyr Pro Ser Val Pro Ser Leu Gln Arg Gln Pro Ser  
 1 5 10 15  
 Ala Ala Val Asn Ile Ile Gln Pro Leu Leu Ser His Asp Ala Ile Val  
 20 25 30  
 Ser Ala Ser Glu Ala Thr Arg His Val Ile Ile Ser Asp Ile Ala Gly  
 35 40 45  
 Asn Val Asp Lys Val Ser Asp Leu Leu Ala Ala Leu Asp Cys Pro Gly  
 50 55 60  
 Thr Ser Val Asp Met Thr Glu Tyr Glu Val Lys Tyr Ala Asn Pro Ala  
 65 70 75 80  
 Ala Leu Val Ser Tyr Cys Gln Asp Val Leu Gly Thr Leu Ala Glu Asp  
 85 90 95  
 Asp Ala Phe Gln Met Phe Ile Gln Pro Gly Thr Asn Lys Ile Phe Val  
 100 105 110  
 Val Ser Ser Pro Arg Leu Ala Asn Lys Ala Glu Gln Leu Lys Ser  
 115 120 125  
 Leu Asp Val Pro Glu Met Ala His Thr Leu Asp Asp Pro Ala Ser Thr  
 130 135 140

Ala Leu Ala Leu Gly Gly Thr Gly Thr Thr Ser Pro Lys Ser Leu Arg  
 145 150 155 160  
 Phe Phe Met Tyr Lys Leu Lys Tyr Gln Asn Gly Glu Val Ile Ala Asn  
 165 170 175  
 Ala Leu Gln Asp Ile Gly Tyr Asn Leu Tyr Val Thr Thr Ala Met Asp  
 180 185 190  
 Glu Asp Phe Ile Asn Thr Leu Asn Ser Ile Gln Trp Leu Glu Val Asn  
 195 200 205  
 Asn Ser Ile Val Ile Ile Gly Asn Gln Gly Asn Val Asp Arg Val Ile  
 210 215 220  
 Gly Leu Leu Asn Gly Leu Asp Leu Pro Pro Lys Gln Val Tyr Ile Glu  
 225 230 235 240  
 Val Leu Ile Leu Asp Thr Ser Leu Glu Lys Ser Trp Asp Phe Gly Val  
 245 250 255  
 Gln Trp Val Ala Leu Gly Asp Glu Gln Ser Lys Val Ala Tyr Ala Ser  
 260 265 270  
 Gly Leu Leu Asn Asn Thr Gly Ile Ala Thr Pro Thr Lys Ala Thr Val  
 275 280 285  
 Pro Pro Gly Thr Pro Asn Pro Gly Ser Ile Pro Leu Pro Thr Pro Gly  
 290 295 300  
 Gln Leu Thr Gly Phe Ser Asp Met Leu Asn Ser Ser Ala Phe Gly  
 305 310 315 320  
 Leu Gly Ile Ile Gly Asn Val Leu Ser His Lys Gly Lys Ser Phe Leu  
 325 330 335  
 Thr Leu Gly Gly Leu Leu Ser Ala Leu Asp Gln Asp Gly Asp Thr Val  
 340 345 350  
 Ile Val Leu Asn Pro Arg Ile Met Ala Gln Asp Thr Gln Gln Ala Ser  
 355 360 365  
 Phe Phe Val Gly Gln Thr Val Pro Tyr Gln Thr Thr Asn Thr Ile Ile  
 370 375 380  
 Gln Glu Thr Gly Thr Val Thr Gln Asn Ile Asp Tyr Glu Asp Ile Gly  
 385 390 395 400  
 Val Asn Leu Val Val Thr Ser Thr Val Ala Pro Asn Asn Val Val Thr  
 405 410 415  
 Leu Gln Ile Glu Gln Thr Ile Ser Glu Leu His Ser Ala Ser Gly Ser  
 420 425 430  
 Leu Thr Pro Val Thr Asp Lys Thr Tyr Ala Ala Thr Arg Leu Gln Ile  
 435 440 445  
 Pro Asp Gly Cys Phe Leu Val Met Ser Gly His Ile Arg Asp Lys Thr  
 450 455 460  
 Thr Lys Val Val Ser Gly Val Pro Leu Leu Asn Ser Ile Pro Leu Ile  
 465 470 475 480  
 Arg Gly Leu Phe Ser Arg Thr Ile Asp Gln Arg Gln Lys Arg Asn Ile  
 485 490 495  
 Met Met Phe Ile Lys Pro Lys Val Ile Ser Ser Phe Glu Glu Gly Thr  
 500 505 510  
 Arg Val Thr Asn Lys Glu Gly Tyr Arg Tyr Asn Trp Glu Ala Asp Glu  
 515 520 525  
 Gly Ser Met Gln Val Ala Pro Arg His Ala Pro Glu Cys Gln Gly Pro  
 530 535 540  
 Pro Ser Leu Gln Ala Glu Ser Asp Phe Lys Ile Ile Glu Ile Glu Ala  
 545 550 555 560  
 Gln

&lt;210&gt;745

&lt;211&gt;381

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;745

Leu Lys Lys Asn Pro Val Lys Thr Val Ile Leu Asn Ile Gly Arg Lys  
 1 5 10 15  
 Ile Leu Gln Gly Ile Lys Lys Xaa Lys Lys Ile Gly Ile Xaa Ser  
 20 25 30  
 Gly Leu Phe Phe Leu Asp Leu Val Leu Leu Gly Val Ser Xaa Gln Arg

```

      35      40      45
Pro Thr Glu Thr Ser Ala Asn Val Lys His Asn Leu Arg Asp Glu Lys
      50      55      60
Leu Ala Ala Cys Pro Lys Asn Ser Ala Ala Ser Leu Ser Ala Lys Lys
      65      70      75      80
Ser His Thr Lys Lys Thr Thr Pro Gly Ser Ile Pro Ser Lys Val Phe
      85      90      95
Ser Lys Phe Asp Ala Thr Gln Asp Lys Thr Phe Gln Lys Thr Ser Gly
      100      105      110
Ser Ala Phe Pro Ala Lys Pro Thr Thr Leu Lys Glu Leu Glu Glu Arg
      115      120      125
Lys Lys Pro Arg Pro Glu Arg Arg Thr Thr Ala Asp Val Lys Arg Ser
      130      135      140
Pro Arg Phe Leu Pro Thr Gln Glu Val Glu Glu Pro Val Pro Ala Ala
      145      150      155      160
Ser Lys Glu Gln Leu Asp Ser Ile Gln Val Trp Glu Glu Lys Gln Asn
      165      170      175
Tyr Ala Arg Arg Ala Val Asn Ala Ile Asn Leu Ser Ile Lys Lys Gln
      180      185      190
Leu Glu Glu Gln Thr Ser Thr Val Thr Glu Lys Asp Val Gln Pro Lys
      195      200      205
Thr Gln Ala Thr Pro His Ala Ser Lys Lys Asn Val Ala Ser Pro Ser
      210      215      220
Thr Ser Met Pro Gly Ile Glu Lys Ala Ala Thr Thr Val Ala Val Pro
      225      230      235      240
Gln Asp Lys Ser Glu Glu Glu Lys Val Lys Glu Arg Leu Thr Lys Arg
      245      250      255
Glu Leu Thr Cys Glu Asp Leu Lys Asp Asn Gly Tyr Thr Val Asn Phe
      260      265      270
Glu Asp Ile Ser Ile Leu Glu Leu Leu Gln Phe Val Ser Lys Ile Ser
      275      280      285
Gly Thr Asn Phe Val Phe Asp Ser Asn Asp Leu Gln Phe Asn Val Thr
      290      295      300
Ile Val Ser His Asp Pro Thr Ser Val Asp Asp Leu Ser Thr Ile Leu
      305      310      315      320
Leu Gln Val Leu Lys Met His Asp Leu Lys Val Val Glu Gln Gly Asn
      325      330      335
Asn Val Leu Ile Tyr Arg Asn Pro His Leu Ser Lys Leu Ser Thr Val
      340      345      350
Val Thr Asp Ser Ser Leu Lys Glu Thr Cys Glu Ala Val Val Val Thr
      355      360      365
Arg Val Phe Arg Leu Tyr Ser Val Ser Pro Leu Gln Gln
      370      375      380

```

&lt;210&gt;746

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;746

```

Phe Cys Phe Ser Ser Gln Thr Cys Ile Leu Ser Asn Cys Ser Leu Glu
  1      5      10      15
Ala Ala Gly Thr Gly Ser Ser Thr Ser Cys Val Gly Lys Lys Arg Gly
      20      25      30
Asp Leu Phe Thr Ser Ala Val Val Leu Arg Ser Gly Arg Gly Phe Phe
      35      40      45
Leu Ser Ser Ser Ser Phe Arg Val Val Gly Phe Ala Gly Asn Ala Asp
      50      55      60
Pro Glu Val Phe Trp Lys Val Leu Ser Trp Val Ala Ser Asn Leu Glu
      65      70      75      80
Lys Thr Leu Leu Gly Ile Glu Pro Gly Val Val Phe Leu Val
      85      90

```

&lt;210&gt;747

&lt;211&gt;502

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;747

```

Met Asp Cys Arg Gly Gly Ile Pro Leu Pro Glu Pro Gln Val Ile Gly
 1          5          10          15
Gly Tyr His Val Lys Lys Ile Leu Ser Lys Lys Leu Arg Ser Arg Val
          20          25          30
Val His Gly Leu His Pro Glu Thr Arg His Ser Thr Val Ile Lys Val
          35          40          45
Phe Ser Pro Ser Pro Ser Phe Thr Ser Arg Ser Val Tyr Asn Phe Leu
          50          55          60
Lys Glu Ala Gln Ser Leu His Gln Ile Thr His Pro Asn Ile Val Lys
          65          70          75          80
Phe His Arg Tyr Gly Lys Trp Gln Asp Cys Leu Tyr Ile Ala Met Glu
          85          90          95
Tyr Ile Glu Gly Ile Ser Leu Arg Glu Tyr Ile Leu Ala Gln Phe Ile
          100          105          110
Ser Leu Pro Gln Ala Ile Asp Ile Ile Phe Asp Ile Ala Gln Ala Leu
          115          120          125
Glu His Leu His Ser Arg Asn Ile Leu His Lys Asp Ile Lys Pro Glu
          130          135          140
Asn Ile Leu Ile Thr Pro Gln Gly Lys Ile Lys Leu Ile Asp Phe Gly
          145          150          155          160
Leu Ala Asp Trp Asp Thr Glu Ile Gln Arg Ala His Pro Ser Val Ile
          165          170          175
Gly Thr Pro Tyr Tyr Met Ser Pro Glu Gln Arg Gln Gly Glu Ser His
          180          185          190
Ser Pro Ala Ser Asp Ile Tyr Ala Leu Gly Leu Leu Ala Tyr Glu Leu
          195          200          205
Ile Leu Gly His Leu Ser Leu Gly Arg Val Phe Leu Ser Leu Val Pro
          210          215          220
Glu Arg Ile Ser Lys Ile Leu Ala Lys Ala Leu Gln Pro Ser Pro Asn
          225          230          235          240
Asn Arg Tyr Ser Ser Thr Arg Glu Phe Ile Gln Asp Ile His His Tyr
          245          250          255
Arg Met Ser Gly Asp Met Gln Glu Asp Leu Arg Ile Lys Asp His Thr
          260          265          270
Val Ala Leu Tyr Glu Gln Leu Gln Thr Gln Arg Phe Trp Leu Ala Pro
          275          280          285
Glu Thr Leu Arg Phe Pro Asp Phe Ile Ser Gly Val Leu Tyr His Gln
          290          295          300
Gly Tyr Pro Leu Tyr Pro His Ala Tyr Asp Thr Leu Leu Glu Gly Asp
          305          310          315          320
Val Phe Asn Leu Trp Leu Gly Tyr Ser Pro Ile Ser Asn Ala Thr Ile
          325          330          335
Ala Leu Ser Val Val Lys Ser Leu Val Cys Gln Gln Asp Leu Gln Arg
          340          345          350
Pro Leu Leu Asp Arg Val Cys Glu Ile Asn Glu Cys Leu Ile Arg Met
          355          360          365
Lys Ile Pro Ile Asp Glu Met Gly Ile Ser Ile Leu Cys Leu Glu Ile
          370          375          380
Ser Lys Glu Asn Lys Glu Leu Ser Trp Ile Ala Cys Gly Lys Thr Val
          385          390          395          400
Phe Trp Ile Lys Arg Gln Gly Arg Val Val Gln Asp Phe Glu Ser Phe
          405          410          415
Ser Pro Gly Leu Gly Lys Ile Thr Ser Leu Gln Ile Arg Glu Thr Lys
          420          425          430
Val Ala Trp Glu Ile Gly Asp Glu Ala Val Val Cys Thr Leu Glu Leu
          435          440          445
Glu Glu Ser Val Ala Ser Leu Lys Thr Leu Ser Leu Ala Glu Leu Gln
          450          455          460
Asp Arg Arg Gln Lys Ala Ile Phe Cys Pro Ile Glu Ser Ile His Gly
          465          470          475          480
Gly Ile Gln Ser Arg Gln His Gly Ser Asn Ser Pro Ser Thr Leu Ile
          485          490          495
Ser Leu Lys Arg Ile Arg

```

500

&lt;210&gt;748

&lt;211&gt;374

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;748

```

Arg Tyr Phe Met Ala Val Ala Ala Asp Ser Ser Ala Ser Trp Leu Lys
 1           5           10           15
Ser Arg Asn Asn Phe Leu Ser Ser Leu Gly Lys Thr Glu Glu Gln Val
          20           25           30
Ala Ala Pro Glu Phe Pro Lys Glu Leu Cys Gln His Lys Ile Arg Glu
          35           40           45
Lys Phe Arg Leu Glu Asp Val Gln Val Ser Ile Lys Phe Arg Gly Ser
          50           55           60
Ile Thr Ala Val Glu Ala Thr Lys Glu Phe Gly Val His Leu Leu Ile
          65           70           75           80
Gln Pro Met Val Val Gln Pro Trp Glu Val Glu Asn Leu Leu Phe Leu
          85           90           95
Thr Ser Glu Glu Asp Leu Gln Glu Leu Met Val Ala Val Phe Asp Asp
          100          105          110
Ala Ser Leu Ala Ser Tyr Phe Tyr Glu Lys Asp Lys Leu Leu Gly Phe
          115          120          125
His Tyr Tyr Phe Val Ala Glu Ala Cys Lys Leu Phe Glu Glu Leu Gln
          130          135          140
Trp Val Pro Ser Leu Ser Ala Lys Val Gly Gly Asp Ala Ile Phe Thr
          145          150          155          160
Ala Thr Ser Leu Gln Gly Ser Phe Gln Val Val Asp Ile Ser Leu Arg
          165          170          175
Leu Asp Gly Lys Asn Val Arg Cys Arg Leu Leu Leu Pro Glu Asp Thr
          180          185          190
Phe Gln Ser Cys Gln Lys Phe Phe Ser Gly Leu His Asp Glu Ser Asp
          195          200          205
Leu His Asn Ile Asp Gln Thr Gln Gln Ile Ser Leu Ser Val Glu Val
          210          215          220
Gly Tyr Ser Gln Leu Thr Gln Glu Glu Trp His Gln Val Val Pro Gly
          225          230          235          240
Ser Phe Ile Met Leu Asp Ser Cys Leu Tyr Asp Pro Glu Thr Glu Glu
          245          250          255
Ser Gly Ala Leu Leu Thr Val Gln Lys His Gln Phe Phe Gly Gly Arg
          260          265          270
Phe Leu Thr Pro Ser Ser Gly Glu Phe Lys Ile Thr Ser Tyr Pro Asn
          275          280          285
Leu Thr His Glu Asp Pro Pro Leu Pro Glu Asn Pro Gln Ala Ser Ala
          290          295          300
Ala Pro Leu Pro Gly Tyr Ser Arg Leu Val Val Glu Val Ala Arg Tyr
          305          310          315          320
Ser Leu Ala Val Ser Glu Phe Ile Lys Leu Asn Leu Gly Ser Ile Leu
          325          330          335
Ser Leu Gly Asn His Pro Ala Tyr Gly Val Asp Ile Ile Leu Asp Gly
          340          345          350
Ala Lys Val Gly Arg Gly Glu Ile Ile Ala Leu Gly Asp Val Leu Gly
          355          360          365
Ile Arg Val Leu Glu Val
          370

```

&lt;210&gt;749

&lt;211&gt;281

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;749

```

Phe Met Glu Leu Lys Lys Thr Ala Glu Ser Leu Tyr Ser Ala Lys Thr
 1           5           10           15
Asp Asn His Thr Val Tyr Gln Asn Ser Pro Glu Pro Arg Asp Ser Arg
          20           25           30
Asp Val Lys Val Phe Ser Leu Glu Gly Lys Gln Thr Arg Gln Glu Lys

```



35 40 45  
 Thr Thr Ser Ser Lys Gly Asn Thr Arg Thr Glu Ser Arg Lys Phe Ala  
 50 55 60  
 Asp Glu Glu Lys Arg Val Asp Asp Glu Ile Ala Glu Val Gly Ser Lys  
 65 70 75 80  
 Glu Glu Glu Gln Glu Ser Gln Glu Phe Cys Leu Ala Glu Asn Ala Phe  
 85 90 95  
 Ala Gly Met Ser Leu Ile Asp Ile Ala Ala Gly Ser Ala Glu Ala  
 100 105 110  
 Val Val Glu Val Ala Pro Ile Ala Val Ser Ser Ile Asp Thr Gln Trp  
 115 120 125  
 Ile Glu Asn Ile Ile Leu Ser Thr Val Glu Ser Met Val Ile Ser Glu  
 130 135 140  
 Ile Asn Gly Glu Gln Leu Val Glu Leu Val Leu Asp Ala Ser Ser Ser  
 145 150 155 160  
 Val Pro Glu Ala Phe Val Gly Ala Asn Leu Thr Leu Val Gln Ser Gly  
 165 170 175  
 Gln Asp Leu Ser Val Lys Phe Ser Ser Phe Val Asp Ala Thr Gln Met  
 180 185 190  
 Ala Glu Ala Ala Asp Leu Val Thr Asn Asn Pro Ser Gln Leu Ser Ser  
 195 200 205  
 Leu Val Ser Ala Leu Lys Gly His Gln Leu Thr Leu Lys Glu Phe Ser  
 210 215 220  
 Val Gly Asn Leu Leu Val Gln Leu Pro Lys Ile Glu Glu Val Gln Thr  
 225 230 235 240  
 Pro Leu His Met Ile Ala Ser Thr Ile Arg His Arg Glu Glu Lys Asp  
 245 250 255  
 Gln Arg Asp Gln Asn Gln Lys Gln Lys Gln Asp Asp Lys Glu Gln Asp  
 260 265 270  
 Ser Tyr Lys Ile Glu Glu Ala Arg Leu  
 275 280

&lt;210&gt;750

&lt;211&gt;174

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;750

Tyr Ala Val Ala Lys Tyr Pro Leu Glu Pro Val Leu Ala Ile Lys Lys  
 1 5 10 15  
 Asp Arg Val Asp Arg Ala Glu Lys Val Val Lys Glu Lys Arg Arg Leu  
 20 25 30  
 Leu Glu Ile Glu Gln Glu Lys Leu Arg Glu Lys Glu Ala Glu Arg Asp  
 35 40 45  
 Lys Val Lys Asn His Tyr Met Gln Lys Ile Gln Gln Leu Arg Asp Leu  
 50 55 60  
 Leu Asp Glu Gly Thr Thr Ser Asp Ala Val Leu Gln Ile Lys Ser Tyr  
 65 70 75 80  
 Ile Lys Val Val Ala Val Gln Leu Ser Glu Glu Glu Glu Lys Val Asn  
 85 90 95  
 Lys Gln Lys Glu Val Val Leu Ala Ala Ser Lys Glu Leu Glu Lys Ala  
 100 105 110  
 Glu Val Asn Leu Ala Lys Arg Arg Lys Glu Glu Glu Lys Thr Arg Leu  
 115 120 125  
 His Lys Glu Glu Trp Met Lys Glu Ala Leu Lys Glu Glu Val Ala Leu  
 130 135 140  
 Lys Lys Lys Asn Lys Thr Arg Trp Gly Ser Cys Phe Ser Asn Cys Ala  
 145 150 155 160  
 Arg Lys Lys Asn Val Asn Gln Gly Glu Ala Ser Ser Trp Asn  
 165 170

&lt;210&gt;751

&lt;211&gt;442

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;751

Met Asp Gln Leu Thr Thr Asp Phe Asp Thr Leu Met Ser Gln Leu Gly

1 5 10 15  
 Asp Val Asn Leu Thr Thr Val Val Gly Arg Ile Thr Glu Val Val Gly  
 20 25 30  
 Met Leu Ile Lys Ala Val Val Pro Asn Val Arg Val Gly Glu Val Cys  
 35 40 45  
 Leu Val Lys Arg Asn Gly Met Glu Pro Leu Val Thr Glu Val Val Gly  
 50 55 60  
 Phe Thr Gln Ser Phe Ala Phe Leu Ser Pro Leu Gly Glu Leu Ser Gly  
 65 70 75 80  
 Val Ser Pro Ser Ser Glu Val Ile Pro Thr Gly Leu Pro Leu His Ile  
 85 90 95  
 Arg Ala Gly Asn Gly Leu Leu Gly Arg Val Leu Asn Gly Leu Gly Glu  
 100 105 110  
 Pro Ile Asp Val Glu Thr Lys Gly Pro Leu Gln Asn Val Asp Gln Thr  
 115 120 125  
 Phe Pro Ile Phe Arg Ala Pro Asp Pro Leu His Arg Ala Lys Leu  
 130 135 140  
 Arg Gln Ile Leu Ser Thr Gly Val Arg Cys Ile Asp Gly Met Leu Thr  
 145 150 155 160  
 Val Ala Arg Gly Gln Arg Ile Gly Ile Phe Ala Gly Ala Gly Val Gly  
 165 170 175  
 Lys Ser Ser Leu Leu Gly Met Ile Ala Arg Asn Ala Glu Glu Ala Asp  
 180 185 190  
 Val Asn Val Ile Ala Leu Ile Gly Glu Arg Gly Arg Glu Val Arg Glu  
 195 200 205  
 Phe Ile Glu Gly Asp Leu Gly Glu Glu Gly Met Lys Arg Ser Val Ile  
 210 215 220  
 Val Val Ser Thr Ser Asp Gln Ser Ser Gln Leu Arg Leu Asn Ala Ala  
 225 230 235 240  
 Tyr Val Gly Thr Ala Ile Ala Glu Tyr Phe Arg Asp Gln Gly Lys Thr  
 245 250 255  
 Val Val Leu Met Met Asp Ser Val Thr Arg Phe Ala Arg Ala Leu Arg  
 260 265 270  
 Glu Val Gly Leu Ala Ala Gly Glu Pro Pro Ala Arg Ala Gly Tyr Thr  
 275 280 285  
 Pro Ser Val Phe Ser Thr Leu Pro Arg Leu Leu Glu Arg Ser Gly Ala  
 290 295 300  
 Ser Asp Lys Gly Thr Ile Thr Ala Phe Tyr Thr Val Leu Val Ala Gly  
 305 310 315 320  
 Asp Asp Met Asn Glu Pro Val Ala Asp Glu Val Lys Ser Ile Leu Asp  
 325 330 335  
 Gly His Ile Val Leu Ser Asn Ala Leu Ala Gln Ala Tyr His Tyr Pro  
 340 345 350  
 Ala Ile Asp Val Leu Ala Ser Ile Ser Arg Leu Leu Thr Ala Ile Val  
 355 360 365  
 Pro Glu Glu Gln Arg Arg Ile Ile Gly Lys Ala Arg Glu Val Leu Ala  
 370 375 380  
 Lys Tyr Lys Ala Asn Glu Met Leu Ile Arg Ile Gly Glu Tyr Arg Arg  
 385 390 395 400  
 Gly Ser Asp Arg Glu Ile Asp Phe Ala Ile Asp His Ile Asp Lys Leu  
 405 410 415  
 Asn Arg Phe Leu Lys Gln Asp Ile His Glu Lys Thr Asn Tyr Glu Glu  
 420 425 430  
 Ala Ala Gln Gln Leu Arg Ala Ile Phe Arg  
 435 440

&lt;210&gt;752

&lt;211&gt;235

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;752

Ala Phe Lys Thr Val Lys Arg Phe Phe Cys Phe Met Ile Asp Pro Val  
 1 5 10 15  
 Glu Cys Phe Pro Asn Leu Asp Gly Asp Ala Glu Ala Gln Ser Ile Thr  
 20 25 30

Gln Asn Ser Gly Thr Pro Leu Ala Ser Glu Leu Lys Lys Asp Ile Ser  
 35 40 45  
 Pro Phe Ala Leu Gly Ser Tyr Ala Ala Pro Lys Asp Thr Thr Leu Val  
 50 55 60  
 Gln Gly Phe Lys Pro Asn Pro Met Ala Met Met Gln Asp Gln Asn Ser  
 65 70 75 80  
 Asn Leu Ile Asp Pro Glu Leu Gln Glu Ala Leu Glu Ser Glu Glu Leu  
 85 90 95  
 Gln Glu Gln Ile Asn Asn Leu Lys Gly Arg Leu Trp Asp Phe Arg Ser  
 100 105 110  
 Thr Phe Glu Asp Ser Gln Thr Thr Ala Gln Phe Ala Asp Glu His Phe  
 115 120 125  
 Gln Ala Val Gly Val Ile Ile Asp Leu Ile Asn Glu Asp Leu Asn Thr  
 130 135 140  
 Ile Ala Glu His Thr Gln Asp Ala Arg Lys Glu Asp Lys Glu Glu  
 145 150 155 160  
 Gly Ser Val Thr Arg Lys Ile Ile Asp Trp Val Ser Ser Gly Glu Glu  
 165 170 175  
 Val Leu Asn Arg Ala Leu Leu Tyr Phe Ser Asp Arg Asp Gly Asn Arg  
 180 185 190  
 Glu Ser Leu Ala Asn Phe Leu Lys Val Gln Tyr Ala Val Gln Arg Ala  
 195 200 205  
 Thr Gln Arg Ala Glu Leu Phe Ala Ser Ile Val Gly Thr Ser Val Ser  
 210 215 220  
 Ser Val Lys Thr Ile Met Thr Thr Gln Leu Gly  
 225 230 235

&lt;210&gt;753

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;753

Arg Ser Arg Gly Glu Lys Ser Met Ala Thr Asn Lys Ser Cys Thr Ala  
 1 5 10 15  
 Phe Asp Phe Asn Lys Met Leu Asp Gly Val Cys Thr Tyr Val Lys Gly  
 20 25 30  
 Val Gln Gln Tyr Leu Thr Glu Leu Glu Thr Ser Thr Gln Gly Thr Val  
 35 40 45  
 Asp Leu Gly Thr Met Phe Asn Leu Gln Phe Arg Met Gln Ile Leu Ser  
 50 55 60  
 Gln Tyr Met Glu Ser Val Ser Asn Ile Leu Thr Ala Val Asn Thr Glu  
 65 70 75 80  
 Met Ile Thr Met Ala Arg Ala Val Lys Gly Ser  
 85 90

&lt;210&gt;754

&lt;211&gt;102

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;754

Thr Thr Ile Asn Asn Gln Val Leu Gly Phe Ile Asn Tyr Leu Tyr Leu  
 1 5 10 15  
 Gly Arg Tyr Ser Met Phe Asn Met Glu Asn Thr Ala Lys Glu Glu Lys  
 20 25 30  
 Asn Ser Gln Pro Leu Leu Asp Leu Glu Gln Asp Met Gln Asp His Asp  
 35 40 45  
 Arg Ala Gln Glu Leu Lys Ala Ser Val Gln Asp Lys Val His Lys Leu  
 50 55 60  
 His Ala Leu Leu Arg Glu Gly Ser Asp Lys Glu Ser Phe Gly Gln Gln  
 65 70 75 80  
 Gln Ser Leu Leu Ala Gly Tyr Val Ala Leu Gln Lys Val Leu Gly Arg  
 85 90 95  
 Ile Asn Arg Lys Met Ile  
 100

&lt;210&gt;755

&lt;211&gt;440

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;755

Pro Glu Leu Ile Phe Gly Ala Glu Phe His Leu Asp Ser Gly Lys Thr  
 1 5 10 15  
 Tyr Ile Leu Gly Thr Asp Pro Thr Thr Cys Asp Ile Val Phe Asn Asp  
 20 25 30  
 Leu Ser Val Ser His Gln His Ala Lys Ile Thr Val Gly Asn Asp Gly  
 35 40 45  
 Gly Ile Leu Ile Glu Asp Leu Asp Ser Lys Asn Gly Val Ile Val Glu  
 50 55 60  
 Gly Arg Lys Ile Asp Lys Thr Ser Thr Leu Ser Ser Asn Gln Val Val  
 65 70 75 80  
 Ala Leu Gly Thr Thr Leu Phe Leu Leu Ile Asp His His Ala Pro Ala  
 85 90 95  
 Asp Thr Ile Val Ala Ser Leu Ser Pro Asp Asp Tyr Ser Leu Phe Gly  
 100 105 110  
 Arg Gln Gln Asp Ala Glu Ala Leu Glu Arg Gln Glu Ala Gln Glu Glu  
 115 120 125  
 Glu Glu Lys Gln Lys Arg Ala Thr Leu Pro Ala Gly Ser Phe Ile Leu  
 130 135 140  
 Thr Leu Phe Val Gly Gly Leu Ala Ile Leu Phe Gly Ile Gly Thr Ala  
 145 150 155 160  
 Ser Leu Phe His Thr Lys Glu Val Val Pro Leu Glu Asn Ile Asp Tyr  
 165 170 175  
 Gln Glu Asp Leu Ala Gln Val Ile Asn Gln Phe Pro Thr Val Arg Tyr  
 180 185 190  
 Thr Phe Asn Lys Thr Asn Ser Gln Leu Phe Leu Ile Gly His Val Lys  
 195 200 205  
 Asn Ser Thr Asp Lys Ser Glu Leu Leu Tyr Lys Val Asp Ala Leu Ser  
 210 215 220  
 Phe Val Lys Ser Val Asp Asp Asn Val Ile Asp Asp Glu Ala Val Trp  
 225 230 235 240  
 Gln Glu Met Asn Ile Leu Leu Ser Lys Arg Pro Glu Phe Lys Gly Ile  
 245 250 255  
 Ser Met His Ser Pro Glu Pro Gly Lys Phe Ile Ile Thr Gly Tyr Val  
 260 265 270  
 Lys Thr Glu Glu Gln Ala Ala Cys Leu Val Asp Tyr Leu Asn Ile His  
 275 280 285  
 Phe Asn Ser Leu Ser Leu Leu Glu Asn Lys Val Val Val Xaa Thr Xaa  
 290 295 300  
 Met Leu Lys Ala Ile Ala Gly His Leu Leu Gln Gly Gly Phe Ala Asn  
 305 310 315 320  
 Ile His Val Ala Phe Val Asn Gly Glu Val Ile Leu Thr Gly Tyr Val  
 325 330 335  
 Asn Asn Asp Asp Ala Glu Lys Phe Arg Ala Val Val Gln Glu Leu Ser  
 340 345 350  
 Gly Ile Pro Gly Val Arg Leu Val Lys Asn Phe Ala Val Leu Leu Pro  
 355 360 365  
 Ala Glu Glu Gly Ile Ile Asp Leu Asn Leu Arg Tyr Pro Asn Arg Tyr  
 370 375 380  
 Arg Val Thr Gly Tyr Ser Arg Tyr Gly Glu Ile Ser Ile Asn Val Val  
 385 390 395 400  
 Val Asn Gly Arg Ile Leu Thr Arg Gly Asp Val Ile Asp Gly Met Thr  
 405 410 415  
 Val Thr Ser Ile Gln Pro Asn Ala Ile Phe Leu Glu Lys Xaa Gly Leu  
 420 425 430  
 Lys Tyr Lys Ile Asp Tyr Asn Lys  
 435 440

&lt;210&gt;756

&lt;211&gt;202

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;756

Arg Thr Ser Pro Arg Gln Asp Pro Gln Pro Lys Ser Ala Glu Pro Ser  
 1 5 10 15  
 Leu Lys Asn Thr Ala Arg Asp Glu Thr Pro Leu Lys Glu Asn Lys Pro  
 20 25 30  
 Val Glu Glu Lys Ala Asn Lys Lys Ala Thr Pro Asp Ser Pro Glu Lys  
 35 40 45  
 Lys Asp Gln Pro Glu Glu Gly Ser Lys Lys Glu Gly Ser Lys Ile Glu  
 50 55 60  
 Ala Thr Pro Leu Asp Ser Gln Lys Glu Ser Glu Asp Lys Glu Ala Glu  
 65 70 75 80  
 Glu Ala Phe Val Gln Glu Glu Glu Glu Asn Leu Thr Glu Asp Asn Lys  
 85 90 95  
 Glu Asp Ser Asp Ser Ala Ala Asp Ala Asn Asp Asp Thr Ala Ser Asp  
 100 105 110  
 His Thr Ala Glu Asp Asn Lys Glu Thr Pro Lys Lys Val Glu Asn Glu  
 115 120 125  
 Lys Ser Ala Val Leu Ser Pro Phe His Val Gln Asp Leu Phe Arg Phe  
 130 135 140  
 Asp Gln Thr Ile Phe Pro Ala Glu Ile Asp Asp Ile Ala Lys Lys Asn  
 145 150 155 160  
 Ile Ser Val Asp Leu Thr Gln Pro Ser Arg Phe Leu Leu Lys Val Leu  
 165 170 175  
 Ala Gly Ala Asn Ile Trp Ser Arg Val Pro Phe Arg Leu Arg Lys Asn  
 180 185 190  
 Leu Tyr Phe Arg Tyr Gly Ser Tyr Asn Leu  
 195 200

&lt;210&gt;757

&lt;211&gt;255

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;757

Met Ala Val Arg Leu Ile Val Asp Glu Gly Pro Leu Ser Gly Val Ile  
 1 5 10 15  
 Phe Val Leu Glu Asp Gly Ile Ser Trp Ser Ile Gly Arg Asp Ser Ser  
 20 25 30  
 Ala Asn Asp Ile Pro Ile Glu Asp Pro Lys Leu Gly Ala Ser Gln Ala  
 35 40 45  
 Ile Ile Asn Lys Thr Asp Gly Ser Tyr Tyr Ile Thr Asn Leu Asp Asp  
 50 55 60  
 Thr Ile Pro Ile Val Val Asn Gly Val Ala Ile Gln Glu Thr Thr Gln  
 65 70 75 80  
 Leu Lys Asn Glu Asp Thr Ile Leu Leu Gly Ser Asn Gln Tyr Ser Phe  
 85 90 95  
 Leu Ser Asp Glu Phe Asp Pro Gln Asp Leu Val Tyr Asp Phe Asp Ile  
 100 105 110  
 Pro Glu Glu Asn Phe Ser Asn Asp Ser Gly Asp Leu Ser Asp Ser Asn  
 115 120 125  
 Glu Gln Gly Lys Asp Leu Glu Pro Arg Gln Thr Ser Glu Thr Asn His  
 130 135 140  
 Ser Pro Lys Pro Lys Glu Lys Leu Thr Lys Asp Gln Gly Ser Ser Asp  
 145 150 155 160  
 Pro Ile Thr Ser Gly Asp Gln Glu Leu Ala Asp Ala Phe Leu Ala Ser  
 165 170 175  
 Ala Lys Ala Glu Lys Asn Gln Pro Arg Ala Lys Val Ala Lys Lys Gly  
 180 185 190  
 Leu Lys Glu Ser Ser Asn Glu Ser Leu Asn Pro Lys Glu Gln Asn Ala  
 195 200 205  
 Lys Asp Ser Pro Lys Gly Glu Glu Arg Thr Asn Lys Pro Gln Asn Ala  
 210 215 220  
 Ile Met Glu Asp Asn Gly Leu Arg Leu Gly Lys Ile Arg Asn Gln Ser  
 225 230 235 240  
 Gln Gln Asn Pro Leu Leu Lys Thr Gln Pro Gly Met Arg Leu Pro  
 245 250 255

&lt;210&gt;758

&lt;211&gt;162

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;758

Leu Asp Leu Lys Glu Glu Lys Ala Gly Phe Arg Asn Glu Ile Val Ser  
 1 5 10 15  
 Ile Pro Gln Gly Thr Lys Thr Thr Ile Ala Ala Leu Glu Asn Thr Ser  
 20 25 30  
 Met Leu Glu Lys Leu Ile Lys Asn Phe Ala Thr Tyr Met Gly Ile Thr  
 35 40 45  
 Ser Thr Leu Glu Leu Asp Ala Asp Gly Ala Tyr Val Leu Pro Ile Ser  
 50 55 60  
 Glu Val Val Lys Val Arg Ala Gln Gln Asn Ala Asp Asn Glu Ile Val  
 65 70 75 80  
 Leu Ser Ala Ser Leu Gly Ala Leu Pro Pro Ser Ala Asp Thr Ala Lys  
 85 90 95  
 Leu Tyr Leu Gln Met Met Ile Gly Asn Leu Phe Gly Arg Glu Thr Gly  
 100 105 110  
 Gly Ser Ala Leu Gly Leu Asp Ser Glu Gly Asn Val Val Met Val Arg  
 115 120 125  
 Arg Phe Ser Gly Asp Thr Thr Tyr Asp Asp Phe Val Arg His Val Glu  
 130 135 140  
 Ser Phe Met Asn Phe Ser Glu Thr Trp Leu Ser Asp Leu Gly Leu Gly  
 145 150 155 160  
 Lys Gln

&lt;210&gt;759

&lt;211&gt;341

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;759

Val Leu Met Val Leu Gly Val Val Gly Ile Ser Tyr Arg Glu Ala Ala  
 1 5 10 15  
 Leu Lys Glu Arg Glu Arg Ala Ile Gln Tyr Leu Gln Ser Phe Glu Lys  
 20 25 30  
 Asn Leu Phe Leu Ala Gln Arg Phe Leu Gly Lys Gly Gly Ala Phe Ile  
 35 40 45  
 Pro Leu Leu Thr Cys His Arg Ala Glu Leu Tyr Tyr Ser Glu Ser  
 50 55 60  
 Pro Glu Ile Ala Gln Ala Ala Leu Leu Ser Glu Leu Thr Ser Gln Gly  
 65 70 75 80  
 Ile Arg Pro Tyr Arg His Arg Gly Leu Ser Cys Phe Thr His Leu Phe  
 85 90 95  
 Gln Val Thr Ser Gly Ile Asp Ser Leu Ile Phe Gly Glu Thr Glu Ile  
 100 105 110  
 Gln Gly Gln Val Lys Arg Ala Tyr Leu Lys Gly Ser Lys Glu Arg Glu  
 115 120 125  
 Leu Pro Phe Asp Leu His Phe Leu Phe Gln Lys Ala Leu Lys Glu Gly  
 130 135 140  
 Lys Glu Tyr Arg Ser Arg Ile Gly Phe Pro Asp His Gln Val Thr Ile  
 145 150 155 160  
 Glu Ser Val Val Gln Glu Ile Leu Leu Ser Tyr Asp Lys Ser Ile Tyr  
 165 170 175  
 Thr Asn Phe Leu Phe Val Gly Tyr Ser Asp Ile Asn Arg Lys Val Ala  
 180 185 190  
 Ala Tyr Leu Tyr Gln His Gly Tyr His Arg Ile Thr Phe Cys Ser Arg  
 195 200 205  
 Gln Gln Val Thr Ala Pro Tyr Arg Thr Leu Ser Arg Glu Thr Leu Ser  
 210 215 220  
 Phe Arg Gln Pro Tyr Asp Val Ile Phe Phe Gly Ser Ser Glu Ser Ala  
 225 230 235 240  
 Ser Gln Phe Ser Asp Leu Ser Cys Glu Ser Leu Ala Ser Ile Pro Lys  
 245 250 255  
 Arg Ile Val Phe Asp Phe Asn Val Pro Arg Thr Phe Leu Trp Lys Glu

```

                260                265                270
Thr Pro Thr Gly Phe Val Tyr Leu Asp Ile Asp Phe Ile Ser Glu Cys
                275                280                285
Val Gln Lys Arg Leu Gln Cys Thr Lys Glu Gly Val Asn Lys Ala Lys
                290                295                300
Leu Leu Leu Thr Cys Ala Ala Lys Lys Gln Trp Glu Ile Tyr Glu Lys
305                310                315                320
Lys Ser Ser His Ile Thr Gln Arg Gln Ile Ser Ser Pro Arg Ile Pro
                325                330                335
Ser Val Leu Ser Tyr
                340
<210>760
<211>426
<212>PRT
<213>Chlamydia pneumoniae
<400>760
Met Ala Ala Tyr Thr Glu Ala Ser Ile Leu Ser Leu Ala Ser Leu Asp
 1                5                10                15
His Ile Arg Leu Arg Ala Gly Met Tyr Ile Gly Arg Leu Gly Asn Gly
                20                25                30
Ser Gln Lys Glu Asp Gly Ile Tyr Thr Leu Phe Lys Glu Val Val Asp
                35                40                45
Asn Gly Ile Asp Glu Phe Ile Met Gly His Gly Lys Ser Leu Lys Ile
 50                55                60
Ser Ala Ser Asp Lys Gln Ile Ser Ile Gln Asp Gln Gly Arg Gly Ile
 65                70                75                80
Pro Leu Gly Lys Leu Ile Asp Cys Val Ser Lys Ile Asn Thr Gly Ala
                85                90                95
Lys Tyr Thr Gln Asp Val Phe His Phe Ser Val Gly Leu Asn Gly Val
                100                105                110
Gly Leu Lys Ala Val Asn Ala Leu Ser Glu Ile Phe Ser Val Arg Ser
                115                120                125
Val Arg Lys Lys Lys Tyr His Leu Ala Thr Phe His Arg Gly Val Leu
                130                135                140
Gln Glu Ser Lys Gln Gly Ser Thr Lys Asp Pro Asp Gly Thr Phe Val
145                150                155                160
Ser Phe Thr Pro Asp Pro Ser Ile Phe Pro Glu Phe Thr Phe Asn His
                165                170                175
Asp Phe Leu Lys Asp Lys Ile Arg Gln Tyr Thr Tyr Leu His Ser Gly
                180                185                190
Leu Glu Ile Arg Phe Asn Asp Glu Val Phe Ile Ser His Asn Gly Leu
                195                200                205
Lys Asp Leu Phe Asp Ala Glu Ile Thr Glu Pro Pro Leu Tyr Ser Pro
                210                215                220
Leu Phe Phe Gln Asn Glu Asp Leu Thr Phe Ile Phe Ser His Leu Glu
225                230                235                240
Gly Asn Thr Glu Arg Tyr Phe Ser Phe Val Asn Gly Gln Glu Thr Leu
                245                250                255
Asp Gly Gly Thr His Leu Thr Ala Phe Lys Glu Ala Ile Val Lys Gly
                260                265                270
Val Asn Glu Phe Phe Gly Lys Thr Phe Val Ser Asn Asp Ile Arg Glu
                275                280                285
Gly Ile Val Gly Cys Ile Ala Ile Lys Ile Ala Ser Pro Ile Phe Glu
290                295                300
Ser Gln Thr Lys Asn Lys Leu Gly Asn Thr Gln Ile Arg Ser Ser Leu
305                310                315                320
Ile Lys Asp Val Lys Glu Ala Ile Val Gln Ala Leu Arg Lys Asp Lys
                325                330                335
Val Ala Pro Glu Leu Leu Leu Glu Lys Ile Lys Phe Asn Glu Lys Thr
                340                345                350
Arg Lys Asn Ile Gln Phe Ile Lys Gln Asp Leu Lys Ser Lys Gln Lys
                355                360                365
Lys Val His Tyr Lys Ile Pro Lys Leu Arg Asp Cys Lys Phe His Tyr
                370                375                380

```

Asn Asp Arg Ser Leu Tyr Gly Glu Ala Ser Ser Ile Phe Leu Thr Glu  
 385 390 395 400  
 Gly Ser Leu Arg Pro His Gln Phe Leu Leu Gln Glu Ile Pro Ser His  
 405 410 415  
 Lys Leu Ser Phe His Phe Glu Glu Ser Leu  
 420 425

&lt;210&gt;761

&lt;211&gt;125

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;761

Trp Thr Phe Phe Cys Leu Leu Leu Arg Ser Cys Phe Ile Asn Trp Ile  
 1 5 10 15  
 Phe Phe Arg Val Phe Ser Leu Asn Phe Ile Phe Ser Lys Arg Ser Ser  
 20 25 30  
 Gly Ala Thr Leu Ser Leu Arg Arg Ala Cys Thr Ile Ala Ser Phe Thr  
 35 40 45  
 Ser Leu Ile Lys Glu Asp Arg Ile Cys Val Phe Pro Ser Leu Phe Phe  
 50 55 60  
 Val Cys Asp Ser Lys Ile Gly Glu Ala Ile Phe Ile Ala Met Gln Pro  
 65 70 75 80  
 Thr Met Pro Ser Arg Met Ser Leu Glu Thr Asn Val Phe Pro Lys Asn  
 85 90 95  
 Ser Leu Thr Pro Phe Thr Met Ala Ser Leu Lys Ala Val Arg Cys Val  
 100 105 110  
 Pro Pro Ser Arg Val Ser Cys Pro Leu Thr Lys Glu Lys  
 115 120 125

&lt;210&gt;762

&lt;211&gt;210

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;762

Gly Leu Phe Asp Phe Pro Tyr Arg Arg Glu Ser Ala Ser Ala Ser Ile  
 1 5 10 15  
 Leu Ala Ser Arg Asn Pro Leu Thr Gln Ala Val Phe Ser Leu Arg Gly  
 20 25 30  
 Lys Pro Met Asn Val Phe Ser Leu Glu Glu Thr Lys Met Tyr Lys Asn  
 35 40 45  
 Asp Glu Leu Phe Tyr Leu Ala Thr Ala Leu Gly Ile Thr Gln Asn Glu  
 50 55 60  
 Ile Gln His Leu Arg Tyr Asn Lys Val Ile Leu Ala Thr Asp Ala Asp  
 65 70 75 80  
 Val Asp Gly Met His Ile Arg Asn Leu Leu Ile Thr Phe Phe Leu Lys  
 85 90 95  
 Thr Leu Leu Pro Leu Val Glu Asn Asn His Leu Phe Ile Leu Glu Thr  
 100 105 110  
 Pro Leu Phe Lys Val Arg Asn Lys Thr Thr Thr Leu Tyr Tyr Ser  
 115 120 125  
 Glu Gln Glu Lys Met Gln Ala Leu Gln Gln Phe Gly Lys Lys Asp Ser  
 130 135 140  
 Ser Leu Glu Ile Thr Arg Phe Lys Gly Leu Gly Glu Ile Ser Pro Lys  
 145 150 155 160  
 Glu Phe Ala Ala Phe Ile Gly Pro Glu Ile Arg Leu Thr Pro Val Thr  
 165 170 175  
 Ile Thr Ser Leu Glu Ser Ile Ser Ser Ile Leu Gln Phe Tyr Met Gly  
 180 185 190  
 Lys Asn Thr Lys Glu Arg Lys Gln Phe Ile Met Asp Asn Leu Ile Thr  
 195 200 205

Asp Phe

210

&lt;210&gt;763

&lt;211&gt;479

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae



&lt;400&gt;763

Phe Met Arg Asp Val Ser Glu Leu Phe Arg Thr His Phe Met His Tyr  
 1 5 10 15  
 Ala Ser Tyr Val Ile Leu Glu Arg Ala Ile Pro His Ile Leu Asp Gly  
 20 25 30  
 Leu Lys Pro Val Gln Arg Arg Leu Leu Trp Thr Leu Phe Leu Met Asp  
 35 40 45  
 Asp Gly Lys Met His Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala  
 50 55 60  
 Leu His Pro His Gly Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu  
 65 70 75 80  
 Ala Asn Lys Gly Tyr Leu Ile Asp Thr Gln Gly Asn Phe Gly Asn Pro  
 85 90 95  
 Leu Thr Gly Asp Pro His Ala Ala Ala Arg Tyr Ile Glu Ala Arg Leu  
 100 105 110  
 Ser Pro Leu Ala Arg Glu Thr Leu Phe Asn Thr Asp Leu Ile Ala Phe  
 115 120 125  
 His Asp Ser Tyr Asp Gly Arg Glu Lys Glu Pro Asp Ile Leu Pro Ala  
 130 135 140  
 Lys Leu Pro Val Leu Leu Leu His Gly Val Asp Gly Ile Ala Val Gly  
 145 150 155 160  
 Met Thr Thr Lys Ile Phe Pro His Asn Phe Ala Glu Leu Leu Lys Ala  
 165 170 175  
 Gln Ile Ala Ile Leu Asn Asp Lys Lys Phe Thr Val Phe Pro Asp Phe  
 180 185 190  
 Pro Ser Gly Gly Leu Met Asp Pro Ser Glu Tyr Gln Asp Gly Leu Gly  
 195 200 205  
 Ser Ile Thr Leu Arg Ala Ser Ile Asp Ile Ile Asn Asp Lys Thr Leu  
 210 215 220  
 Val Val Lys Gln Ile Cys Pro Gln Ser Thr Thr Glu Thr Leu Ile Arg  
 225 230 235 240  
 Ser Ile Glu Asn Ala Ala Lys Arg Gly Thr Ile Lys Ile Asp Thr Ile  
 245 250 255  
 Gln Asp Phe Ser Thr Asp Val Pro His Ile Glu Ile Lys Leu Pro Lys  
 260 265 270  
 Gly Ser Arg Ala Lys Glu Met Leu Pro Leu Leu Phe Glu His Thr Glu  
 275 280 285  
 Cys Gln Val Ile Leu Tyr Ser Lys Pro Thr Val Ile Tyr Glu Asn Lys  
 290 295 300  
 Pro Val Glu Cys Ser Ile Ser Glu Ile Leu Lys Leu His Thr Thr Ala  
 305 310 315 320  
 Leu Gln Gly Tyr Leu Glu Lys Glu Leu Leu Leu Leu Gln Glu Gln Leu  
 325 330 335  
 Thr Leu Asp His Tyr His Lys Thr Leu Glu Tyr Ile Phe Ile Lys His  
 340 345 350  
 Lys Leu Tyr Asp Ser Val Arg Glu Val Leu Ala Ile Asn Lys Lys Ile  
 355 360 365  
 Ser Ala Asp Asp Leu His Gln Ala Val Leu His Ala Leu Glu Pro Trp  
 370 375 380  
 Leu His Glu Leu Ala Thr Pro Val Thr Lys Gln Asp Thr Ser Gln Leu  
 385 390 395 400  
 Ala Ser Leu Thr Ile Lys Lys Ile Leu Cys Phe Asn Glu Glu Ala Cys  
 405 410 415  
 Thr Lys Glu Leu Leu Ala Ile Glu Lys Lys Gln Ala Ala Ile Gln Lys  
 420 425 430  
 Asp Leu Gly Arg Ile Lys Glu Val Thr Val Lys Tyr Leu Lys Gly Leu  
 435 440 445  
 Leu Glu Arg His Gly His Leu Gly Glu Arg Lys Thr Gln Ile Thr Asn  
 450 455 460  
 Phe Lys Thr Ala Lys Thr Ser Ile Leu Lys Gln Gln Thr Leu Ile  
 465 470 475

&lt;210&gt;764

&lt;211&gt;109

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;764

Arg Ala Val Met Ser Phe Thr Tyr Phe Leu Ala Leu Pro Val Asp Arg  
 1 5 10 15  
 Leu Met Gln Glu Arg Phe Leu Cys Ser Pro Lys Arg Trp Ala Pro Phe  
 20 25 30  
 Ile Asn Ser Pro Leu Tyr Leu Thr Leu Ile Ala Asp His Asp Thr Pro  
 35 40 45  
 Tyr Leu Ala Lys Asn Leu Asp Lys Phe Pro Leu Pro Val Glu Gln Trp  
 50 55 60  
 Glu Lys Thr Val Leu His Val Ser Ser Leu Leu Lys Ser Ile Phe Leu  
 65 70 75 80  
 Cys Ser Asp Leu Ser Ser Leu Arg Leu Leu Ala Cys Thr Lys Phe Glu  
 85 90 95  
 Ile Leu Thr Leu Asn Asp Leu Tyr Cys Ala Gln Asn Ile  
 100 105

&lt;210&gt;765

&lt;211&gt;325

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;765

Met Lys Thr Val Thr Ser Phe Thr Val Cys Lys Glu Asn Ser Gly Arg  
 1 5 10 15  
 Leu Asp Lys Tyr Leu Thr Glu Val His Pro Lys Tyr Ser Arg Ala Phe  
 20 25 30  
 Tyr Gln Glu His Ile Leu Ser Gly Leu Val Gln Ile Asn Gly Gln Ile  
 35 40 45  
 Asn Thr Arg Val Ala Thr Arg Leu Asn Cys Gly Asp Ile Val Thr Ile  
 50 55 60  
 Asp Ile Gln Glu Lys Glu Glu Leu Leu Glu Leu Pro Glu Ala Ile  
 65 70 75 80  
 Pro Leu Asp Lys Val Tyr Glu Asp Gly Met Ile Leu Val Ile Asn Lys  
 85 90 95  
 Pro Arg Asp Met Val Val His Pro Ala Pro Gly His Phe His Gly Thr  
 100 105 110  
 Leu Val His Ala Leu Leu His Glu Ile Gly Glu Arg Leu Lys Glu Glu  
 115 120 125  
 Phe Pro Glu Glu Pro Trp Arg Pro Gly Ile Val His Arg Leu Asp Lys  
 130 135 140  
 Asp Thr Ser Gly Leu Ile Thr Ala Lys Thr Arg Gln Ala Lys Lys  
 145 150 155 160  
 Val Phe Ser Glu Leu Phe Ser Thr Lys Arg Leu Lys Lys Ser Tyr Leu  
 165 170 175  
 Ala Val Cys Ile Gly Lys Pro Arg Ser Thr Thr Ile His Thr His Ile  
 180 185 190  
 Ser Arg His Gln Asn Lys Arg Lys Glu Met Thr Val Ser Ser Gln Gly  
 195 200 205  
 Lys Glu Ala Val Thr His Cys Gln Val Leu Ala Phe Asn Gly Lys Leu  
 210 215 220  
 Ser Phe Val Ala Leu Ser Pro Glu Thr Gly Arg Thr His Gln Leu Arg  
 225 230 235 240  
 Val His Met Lys His Leu Gly Thr Pro Ile Leu Gly Asp Pro Val Tyr  
 245 250 255  
 Gly Ile Pro Ser Met Asn Ser Ser Tyr Gly Leu Asp Lys Gln Gln Leu  
 260 265 270  
 His Ala Tyr Ser Val Asp Phe Thr His Pro Glu Thr Arg Gln Phe Cys  
 275 280 285  
 Ser Leu Lys Ala Gly Leu Pro Glu Asp Met Arg Ser Leu Leu Ile Lys  
 290 295 300  
 Glu Phe Arg Asn Glu Thr Thr Ile Leu Asn Lys Asn Leu Leu Glu Ser  
 305 310 315 320  
 Ile Leu Lys Glu Gln  
 325

&lt;210&gt;766

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;766

Leu Arg Ile Thr Met Lys Glu Phe Leu Ala Tyr Ile Ile Lys Asn Leu  
 1 5 10 15  
 Val Asp Arg Pro Glu Glu Val Arg Ile Lys Glu Val Gln Gly Thr His  
 20 25 30  
 Thr Ile Ile Tyr Glu Leu Ser Val Ala Lys Pro Asp Ile Gly Lys Ile  
 35 40 45  
 Ile Gly Lys Glu Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val  
 50 55 60  
 Ser Val Ala Ser Arg Asn Asn Val Arg Val Ser Leu Glu Ile Met Glu  
 65 70 75 80  
 Glu Lys

&lt;210&gt;767

&lt;211&gt;273

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;767

Lys Arg Met Val Met Phe Asn Asn Lys Met Ile Leu Ile Ala Gly Pro  
 1 5 10 15  
 Cys Val Ile Glu Gly Glu Asp Ile Thr Leu Glu Ile Ala Gly Lys Leu  
 20 25 30  
 Gln Ser Ile Leu Ala Pro Tyr Ser Asp Arg Ile Gln Trp Phe Phe Lys  
 35 40 45  
 Ser Ser Tyr Asp Lys Ala Asn Arg Ser Ser Leu Asn Ser Phe Arg Gly  
 50 55 60  
 Pro Gly Leu Thr Glu Gly Leu Arg Ile Leu Ala Lys Val Lys Glu Thr  
 65 70 75 80  
 Phe Gly Val Gly Ile Leu Thr Asp Val His Thr Pro Gln Asp Ala Tyr  
 85 90 95  
 Ala Ala Ala Glu Val Cys Asn Ile Leu Gln Val Pro Ala Phe Leu Cys  
 100 105 110  
 Xaa Gln Thr Asp Leu Leu Val Ala Thr Ala Glu Thr Gly Ala Ile Val  
 115 120 125  
 Asn Leu Lys Lys Gly Gln Phe Leu Ser Pro Trp Asp Met Glu Gly Pro  
 130 135 140  
 Ile Asn Lys Val Leu Ser Thr Gly Asn Asn Lys Ile Leu Leu Thr Glu  
 145 150 155 160  
 Arg Gly Cys Ser Phe Gly Tyr Asn Asn Leu Val Ser Asp Met Arg Ser  
 165 170 175  
 Ile Pro Val Leu Ser Arg Ser Gly Phe Pro Val Ile Phe Asp Ala Thr  
 180 185 190  
 His Ser Val Gln Leu Pro Gly Ala Leu Ser Thr Glu Ser Gly Gly Leu  
 195 200 205  
 Thr Glu Phe Val Pro Thr Leu Ser Arg Ala Ala Leu Ala Ala Gly Ala  
 210 215 220  
 His Gly Leu Phe Ile Glu Thr His Thr Asn Pro Lys Ile Ala Lys Ser  
 225 230 235 240  
 Asp Ala Ala Ser Met Leu Ser Leu Glu Glu Phe Ala Ala Leu Leu Pro  
 245 250 255  
 Thr Trp Asp Gln Leu Phe Thr Cys Val Ser Ser Phe Asp Met Val Ser  
 260 265 270  
 Ala

&lt;210&gt;768

&lt;211&gt;162

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;768

Met Thr Lys Phe Leu Tyr Cys Gly Leu Phe Tyr Ser Leu Gly Leu Leu  
 1 5 10 15

Val Leu Ala Phe Gly Thr Met Val Ala Ile Ile Gln Val Asp Gln Ile  
                   20                  25                  30  
 Cys Asp Val Ser Cys Met Asn Lys His Phe Gln Glu Ser Pro Pro Phe  
                   35                  40                  45  
 Leu Lys Ile Lys Lys Val Asn Val Ser Lys Gln Ile Cys Ser Pro Glu  
                   50                  55                  60  
 Glu Arg Phe Phe His Cys Lys Ile Asp Lys Ser Cys Met Glu Leu His  
                   65                  70                  75                  80  
 Phe Pro Gln Ser Ser Tyr Ser Cys Lys Glu Tyr Leu Thr Arg Ile Ser  
                   85                  90                  95  
 Gly His Ile Leu Thr Gln Asn Phe Glu Lys Gln Met Gln Phe Arg Gly  
                   100                  105                  110  
 Asn Ser Gly Leu Leu Asn Tyr Gln Asp Gly Ser Leu His Val Tyr Asp  
                   115                  120                  125  
 Cys Arg Phe Gln Val Asp Pro Val Pro Gly Tyr Gly Ser Pro Asp Lys  
                   130                  135                  140  
 Glu Asp Ser Ser Ser Gly Met Lys Thr Leu Tyr Leu Ser Leu Phe  
                   145                  150                  155                  160  
 Arg Asn

&lt;210&gt;769

&lt;211&gt;240

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;769

Met Pro Ile Leu Ser Val Cys Asn Leu Val Lys Lys Tyr Asn Lys Lys  
   1                  5                  10                  15  
 Pro Val Thr Asn Asp Val Ser Phe Gln Ile Asn Pro Gly Glu Ile Val  
                   20                  25                  30  
 Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Ala Phe Tyr Leu  
                   35                  40                  45  
 Thr Val Gly Leu Ile Arg Pro Asp Ser Gly Lys Ile Ile Phe Lys Asn  
                   50                  55                  60  
 Val Asp Val Thr Lys Lys Thr Met Asp His Arg Ala Arg Leu Gly Ile  
                   65                  70                  75                  80  
 Gly Tyr Leu Ala Gln Glu Pro Thr Ile Phe Lys Glu Leu Thr Val Gln  
                   85                  90                  95  
 Asp Asn Leu Ile Cys Ile Leu Glu Ile Ile Tyr Lys Ala Arg Lys Gln  
                   100                  105                  110  
 Gln Ser His Leu Leu Asn Thr Leu Val Asp Asp Leu Gln Leu Gly Ser  
                   115                  120                  125  
 Cys Leu His Lys Lys Ala Gly Thr Leu Ser Gly Gly Glu Arg Arg Arg  
                   130                  135                  140  
 Leu Glu Ile Ala Cys Val Leu Ala Leu Asn Pro Ser Val Leu Leu Leu  
                   145                  150                  155                  160  
 Asp Glu Pro Phe Ala Asn Val Asp Pro Leu Val Ile Gln Asn Val Lys  
                   165                  170                  175  
 Tyr Leu Ile Lys Ile Leu Ala Gly Arg Gly Ile Gly Ile Leu Ile Thr  
                   180                  185                  190  
 Asp His Asn Ala Lys Glu Leu Leu Ser Ile Ala Asp Arg Cys Tyr Leu  
                   195                  200                  205  
 Ile Ile Asp Gly Lys Ile Phe Phe Glu Gly Ser Ser Ser Gln Met Ile  
                   210                  215                  220  
 Ser Asn Pro Met Val Lys Gln His Tyr Leu Gly Asp Ser Phe Ser Tyr  
                   225                  230                  235                  240

&lt;210&gt;770

&lt;211&gt;299

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;770

Arg Thr Ser Thr Arg Leu Asp Tyr Arg Ser Gly Cys Ile Leu Ser Lys  
   1                  5                  10                  15  
 Ile Leu Pro Phe Pro Glu Leu Trp Lys Met Leu Leu Gly Phe Leu Cys  
                   20                  25                  30

Asp Cys Pro Cys Ala Ser Trp Gln Cys Ala Ala Val Ala Asn Cys Tyr  
 35 40 45  
 Asp Ser Val Phe Met Ser Arg Pro Glu His Lys Pro Asn Ile Pro Tyr  
 50 55 60  
 Ile Thr Lys Ala Thr Arg Arg Gly Leu Arg Met Lys Thr Leu Ala Tyr  
 65 70 75 80  
 Leu Ala Ser Leu Lys Asp Ala Arg Gln Leu Ala Tyr Asp Phe Leu Lys  
 85 90 95  
 Asp Pro Gly Ser Leu Ala Arg Leu Ala Lys Ala Leu Ile Ala Pro Lys  
 100 105 110  
 Glu Ala Leu Gln Glu Gly Asn Leu Phe Phe Tyr Gly Cys Ser Asn Ile  
 115 120 125  
 Glu Asp Ile Leu Glu Glu Met Arg Arg Pro His Arg Ile Leu Leu Leu  
 130 135 140  
 Gly Phe Ser Tyr Cys Gln Lys Pro Lys Ala Cys Pro Glu Gly Arg Phe  
 145 150 155 160  
 Asn Asp Ala Cys Arg Tyr Asp Pro Ser His Pro Thr Cys Ala Ser Cys  
 165 170 175  
 Ser Ile Gly Thr Met Met Arg Leu Asn Ala Arg Arg Tyr Thr Thr Val  
 180 185 190  
 Ile Ile Pro Thr Phe Ile Asp Ile Ala Lys His Leu His Thr Leu Lys  
 195 200 205  
 Lys Arg Tyr Pro Gly Tyr Gln Ile Leu Phe Ala Val Thr Ala Cys Glu  
 210 215 220  
 Leu Ser Leu Lys Met Phe Gly Asp Tyr Ala Ser Val Met Asn Leu Lys  
 225 230 235 240  
 Gly Val Gly Ile Arg Leu Thr Gly Arg Ile Cys Asn Thr Phe Lys Ala  
 245 250 255  
 Phe Lys Leu Ala Glu Arg Gly Val Lys Pro Gly Val Thr Ile Leu Glu  
 260 265 270  
 Glu Asp Gly Phe Glu Val Leu Ala Arg Ile Leu Thr Glu Tyr Ser Ser  
 275 280 285  
 Ala Pro Phe Pro Arg Asp Phe Cys Glu Ile His  
 290 295

&lt;210&gt;771

&lt;211&gt;438

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;771

Val Tyr Lys Ser Leu Val Thr Phe Lys Cys Gly Glu His Leu Gly Ala  
 1 5 10 15  
 Ile Trp Ala Tyr Phe Thr Ala Ser Thr Val Val Ala Leu Asn Pro Thr  
 20 25 30  
 Ala Thr Met Asp His Val Lys Ala Ala Ile Leu Glu Glu Ala Lys Glu  
 35 40 45  
 Leu Asp Asn Ser Ser Phe Gln Leu Ala Ser Ser Ile Lys Ser Ala Met  
 50 55 60  
 Thr Ser Ile Val Asn Ser Ser Gly Ser Phe Ser Val Thr Val Asn Ser  
 65 70 75 80  
 Ser Thr Leu Gln Tyr Thr Ile Tyr Ser Glu Lys Asn Gly Lys Val Glu  
 85 90 95  
 Ile Asn Gln Ile Leu Leu Asn Tyr Gly Ser Thr Gly Phe Leu Pro Glu  
 100 105 110  
 Ile Thr Lys Leu Ala Lys Thr Asn Ala Glu Ser Thr Ala Arg Ser Tyr  
 115 120 125  
 Phe Arg Phe Lys Ala Leu Ala Ala Val Glu Ser Glu Asn Val Gln Asn  
 130 135 140  
 Lys Ile Glu Asp Leu Gln Ser Gln Leu Gln Gln Phe Thr Asn Met Lys  
 145 150 155 160  
 Thr Glu Leu Phe Asp Gly Gln Leu Leu Ser Gln Ala Ser Glu Leu Arg  
 165 170 175  
 Ala Leu Pro Leu Leu Ser Ala Val Ala Ser Val Leu Ile Asp Arg Tyr  
 180 185 190  
 Met Pro Lys Glu Val Asp Tyr Leu Asn Glu Ile Tyr Lys Lys Leu Tyr

195 200 205  
 Tyr Ser Asn Leu Gly Ser Ser Val Gly Asn Ser Ile Ile Asp Ala Ile  
 210 215 220  
 Ser Gln Tyr Val Asn Gly Ala Thr Tyr Phe Asn Phe Ala Ser Tyr Val  
 225 230 235 240  
 Gly Gln Gln Pro Ala Val Gly Ala Gly Gly Ala Asn Ala Phe Pro Gly  
 245 250 255  
 Ser Gln Glu Ser Ala Gln Ala Lys Leu Asp Gln Glu Arg Lys Gln Ala  
 260 265 270  
 Ala Leu Tyr Leu Gln Glu Thr Arg Gly Ala Leu Thr Val Ile Glu Glu  
 275 280 285  
 Gln Arg Ala Arg Val Leu Lys Asp Asp Lys Ile Thr Asn Glu Gln Arg  
 290 295 300  
 Ser Thr Ile Leu Asp Ser Leu Arg Asn Tyr Glu Asp Asn Ile Asn Ser  
 305 310 315 320  
 Ile Ser Gly Ser Leu Val Leu Leu Gln Asn Tyr Leu Gln Pro Leu Ser  
 325 330 335  
 Ile Ala Gly Gly Ser Val Ala Gly Thr Phe Glu Val Lys Glu Gly Gln  
 340 345 350  
 Glu Gln Trp Gln Ala Arg Leu Gln Ile Leu Glu Glu Ala Leu Val Ser  
 355 360 365  
 Gly Leu Val Gly Asn Met Ile Asn Gly Gly Met Phe Pro Leu Gln Ser  
 370 375 380  
 Thr Ile Gln Ser Asp Gln Gln Ser Phe Ala Asp Met Gly Gln Asn Phe  
 385 390 395 400  
 Gln Leu Asp Leu Gln Met His Leu Thr Ser Met Gln Gln Glu Trp Thr  
 405 410 415  
 Val Val Ala Thr Ser Leu Gln Leu Leu Asn Gln Met Tyr Leu Ser Leu  
 420 425 430  
 Ala Arg Ser Leu Thr Gly  
 435

&lt;210&gt;772

&lt;211&gt;422

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;772

Ala Asp Ile Asp Met Ile Tyr Ser Thr Ser Ile Ser Thr Phe Tyr Lys  
 1 5 10 15  
 Lys Leu Ser Leu Val Ser Ser Met His Ser Phe Ala Gln Arg His Arg  
 20 25 30  
 Glu Ser Leu Glu His Ile Ala Asn Tyr Glu Lys Thr Thr Ala Glu Arg  
 35 40 45  
 Asp Ile Leu Lys Arg Leu Ile Glu Val Leu Asp Gln Arg Ala Ser Glu  
 50 55 60  
 Arg Tyr Arg Ser Ala Val Glu Lys Leu His Lys Tyr Glu Val Glu Arg  
 65 70 75 80  
 Ala Thr Val Ala Lys Ser Ile Pro Val Ala Ala Ile His Glu Lys Pro  
 85 90 95  
 Leu Ser Ser Thr His Ala Ser Val Gln Val Thr Ala Ser Thr Pro Ala  
 100 105 110  
 Ala Thr Gly Ser Gly Val Gly Ala Tyr Tyr Asn Ala Val Lys Gln Lys  
 115 120 125  
 Trp Ala Gln Asp Leu Ile Val Glu Leu Asn Thr Val Met Thr Thr Ile  
 130 135 140  
 Met Ala Ser Val Asn Ser Lys Asn Pro Ala Asn Lys Asp Val Phe Asp  
 145 150 155 160  
 Lys Leu Asn Thr Glu Leu Gln Ala Leu Val Ala Ala Gly Asn Asn Leu  
 165 170 175  
 Thr Glu Glu Asn Phe Gln Thr Leu Tyr Asn Phe Pro Glu Glu Ile Phe  
 180 185 190  
 Thr Ala Ile Gln Arg Ala Asp Thr Phe Thr Gly Gly Met Lys Thr Asp  
 195 200 205  
 Phe Thr Asn Gln Leu Ala Gly Lys Tyr Gly Asn Gln Ala Thr Leu Thr  
 210 215 220

Gln Thr Phe Ala Asp Gly Arg Val Glu Gly Phe Lys Asp Ile Leu Thr  
 225 230 235 240  
 Ala Val Gln Gly Val Leu Thr Pro Glu Gln Phe Thr Ile Phe Ala Glu  
 245 250 255  
 Ile Ala Thr Glu Leu Gln Ala Leu Ala Asp His Val Gly Asn Phe Asp  
 260 265 270  
 Glu Ala Gly Leu Gln Arg Ile Glu Asp Ala Gly Glu Lys Leu Ala Ala  
 275 280 285  
 Val Ile Asn Ser Ser Asp Leu Thr Arg Asn Asp Lys Ile Met Phe Cys  
 290 295 300  
 Gln His Ile Thr Asp Leu Tyr Ser Asp Gln Val Ala Ala Leu Gly Ser  
 305 310 315 320  
 Phe Asp Thr Val Leu Asp Ala Ser Ile Tyr Val Asn Gln His Gln Gly  
 325 330 335  
 Thr Met Phe Ser Asn Leu Ser Ser Phe Val Gly Ser Leu Ile Gly Thr  
 340 345 350  
 Phe Ala Pro Ile Asp Leu Ser Ser Ser Gln Gly Asp Ile Ser Ser Ala  
 355 360 365  
 Ala Leu Ala Gly Ala Leu Gln Thr Ala Arg Gly Leu Asn Ser Arg Phe  
 370 375 380  
 Asn Glu Leu Thr Ala Glu Gln Gln Lys Leu Ile Asn Glu Cys Ile Asn  
 385 390 395 400  
 Leu Trp Leu Pro Leu Ser Val Val Ser Thr Leu Val Leu Ser Gly Leu  
 405 410 415  
 Ile Leu Gln His Leu Leu  
 420

&lt;210&gt;773

&lt;211&gt;645

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;773

Lys Tyr Tyr Leu Phe Ser Met Ser Thr Phe Ser Ile Gln Asn Arg Leu  
 1 5 10 15  
 Arg Thr Ile Ser Gly Glu Ser Thr Arg Ile Ile Lys Leu Asp His Lys  
 20 25 30  
 Tyr Ser Gly Phe Asp Pro Arg Ser Val Pro Ala Ile Asn Leu Glu Glu  
 35 40 45  
 Leu Asn Ser Gly Ile Tyr Ala Leu Arg His Leu Met Asn Ala Leu Gln  
 50 55 60  
 Ser Glu Asn Thr Asn Val Ala Ala Leu Leu Asn Pro Asn Asn Thr Ile  
 65 70 75 80  
 Phe Pro Thr Thr Ser Trp Thr Asp Tyr Lys His Ser Arg Pro Gln Ala  
 85 90 95  
 Ser Ser Pro Arg Ala Pro Ser Ser Gln Thr Pro Thr Asp Ile Val Ser  
 100 105 110  
 Ala Ala Ala Leu Ala Leu Val Leu Val Ile Asp Gly Gly Leu Ala Glu  
 115 120 125  
 Leu Val Ala Ser Val Thr Glu Ile Asp Leu Gly Ala Leu Ser Thr Ile  
 130 135 140  
 Ser Thr Val Arg Gln Leu Met Ala Ser Tyr Leu Gly Leu Thr Thr Leu  
 145 150 155 160  
 Thr Ala Glu Gln Glu Lys Val Val Phe Ser Ser Tyr Val Pro Ser  
 165 170 175  
 Glu Lys Asn Leu Leu Glu His Val Lys Gln Glu Lys Ala Ala Glu Ile  
 180 185 190  
 Gln Ala Lys Gln Glu Glu Ile Lys Ala Val Leu Glu Ala Lys Gly Val  
 195 200 205  
 Ser Thr Glu Glu Ile Glu Ala Ile Leu Lys Glu Tyr Pro Asp Ile Tyr  
 210 215 220  
 Ala Ala Asp Phe Phe Lys Glu Phe Ile Glu Glu Pro Leu His Thr Tyr  
 225 230 235 240  
 Arg Ala Lys Val Gly Ala Pro Ile Gln Glu Met Asn Glu Asn Ala Ile  
 245 250 255  
 Gln Leu Leu Pro Thr Pro Pro Ala Ile Thr Pro Asp Asn Val Asn Glu

260 265 270  
 Val Asn Gly Met Asn Thr Leu Ser Thr Ile Leu Gln Ala Ile Asp Asp  
 275 280 285  
 Ala Ile Lys Gln Ala Pro Ala Leu Gly Gly Asp Gln Glu Ile Ile Thr  
 290 295 300  
 Ile Leu Gln Thr Leu Val Pro Leu Val Asp Lys Thr Thr Phe Thr Lys  
 305 310 315 320  
 Ala Glu Phe Asp Leu Ile Tyr Thr Ala Thr Gln Leu Pro Asn Thr Ala  
 325 330 335  
 Ser Leu Lys Leu Tyr Leu Thr Asp Arg Gln Ile Ala Glu Tyr Arg Gly  
 340 345 350  
 Lys Ile Thr Lys Val Tyr Gln Asn Ser Ile Gln Asn Leu Ser Glu Thr  
 355 360 365  
 Lys Arg Val Val Glu Asn Asn Arg Ser Met Leu Glu Thr Gln Leu Ser  
 370 375 380  
 Met Phe Gln Gln Ala Gln Asn Cys Phe Val Thr Trp Ile Ser Gln Ala  
 385 390 395 400  
 Asn Ala Leu Asn Ile Ala Ile Thr Asn Lys Tyr Ile Ser Ala Val Leu  
 405 410 415  
 Thr Thr Ser Met Glu Met Tyr Gly Gly Leu Leu Cys Leu Ser Tyr Met  
 420 425 430  
 Tyr Glu Arg Leu Ala Asp Asp Glu Lys Ala Ile Phe Asp Lys Ser Val  
 435 440 445  
 Asn Glu Tyr Leu Pro Ile His Ile Val Val Gly Gly Ser Trp Val Asn  
 450 455 460  
 Gly Trp Ile Ala Lys Met Ala Ala Tyr Gln Glu Leu Ala Glu Tyr Ser  
 465 470 475 480  
 Leu Gly Thr Ala Val Thr Ser Gln Asp Gln Ile Lys Ala Tyr Leu Gln  
 485 490 495  
 Thr Arg Gly Asn Glu Phe Lys Ala Thr Arg His Phe Phe His Asn Ile  
 500 505 510  
 Gly Asp Gln Met Tyr Gln Phe Ala Asn Glu Thr Val Phe Gly Asn Cys  
 515 520 525  
 Leu Thr Thr Ala Asn Gly Ala Ile Gln Pro Asp Leu Gly Gly Phe Ile  
 530 535 540  
 Arg Glu Ala Met Thr Asn Val Gly Thr Val Glu Ala Asp Tyr Val Ser  
 545 550 555 560  
 Asn Ala Gln Arg Ile Leu Asn Glu Phe Asn Thr Ala Ala Thr Ala His  
 565 570 575  
 Val Leu Gln Leu Gln Leu Gln Ile Ala Glu Leu Gln Lys Lys Ala Asp  
 580 585 590  
 Asp Leu Asp Pro Gly Lys Ala Ser Phe Thr Glu Asn Arg Lys Phe Ala  
 595 600 605  
 Val Ala Ala Leu Asp His Ile Gly Glu Leu Arg Arg Cys Phe Asn Phe  
 610 615 620  
 Tyr Asp Phe Xaa Leu Ser Ala Thr Lys Ala Arg Gly Phe Phe Lys Thr  
 625 630 635 640  
 Phe Asp Arg Arg Asn  
 645

&lt;210&gt;774

&lt;211&gt;284

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;774

Thr Gln Glu Lys Pro Leu Ser Leu Arg Thr Val Asn Leu Leu Leu Pro  
 1 5 10 15  
 Leu Trp Ile Thr Ser Glu Ser Leu Gly Asp Ala Leu Ile Ser Met Ile  
 20 25 30  
 Xaa Asn Ser Gln Leu Pro Lys Gln Glu Ala Phe Leu Lys Pro Leu Ile  
 35 40 45  
 Glu Glu Ile Asn Phe Asn Asn Leu Ala Ala Asn Ala Leu Asn Ser Leu  
 50 55 60  
 Leu Gln Ile Thr Asn Glu Phe Ser Thr Thr Ser Val Tyr Tyr Ser Leu  
 65 70 75 80



Ser Ser Tyr Leu Val Gln Ser Lys Thr Gly Gln Asn Leu Phe Ala Gly  
 85 90 95  
 Asp Tyr Tyr Glu Thr Leu Leu Ala Ala Ala Arg Glu Arg Glu Tyr Ile  
 100 105 110  
 Tyr Arg Asp Thr Ala Arg Cys Lys Gln Ala Ile Asn Leu Val Asn Gly  
 115 120 125  
 Leu Leu Gln Lys Ile Asn Ser Leu Pro Gly Ala Thr Ser Ala Gln Lys  
 130 135 140  
 Gln Glu Met Leu Asn Ala Thr Thr Tyr Tyr Gln Tyr Ser Leu Ser Val  
 145 150 155 160  
 Thr Leu Asn Gln Leu Thr Val Leu Glu Ser Leu Leu Ala Gly Leu Lys  
 165 170 175  
 Met Thr Leu Gln Thr Thr Ser Asn Asn Lys Tyr Asp Lys Ser Val Phe  
 180 185 190  
 Lys Ile Glu Ser Phe Asp Asp Trp Ile Pro Thr Leu Ala Ala Leu Glu  
 195 200 205  
 Ser Phe Leu Thr Ser Gly Phe Pro Asn Ile Ser Ala Thr Gly Gly Leu  
 210 215 220  
 Gly Pro Leu Phe Thr Gln Val Gln Ser Asp Gln Gln Thr Tyr Thr Ser  
 225 230 235 240  
 Gln Gly Gln Thr Gln Gln Leu Asn Leu Gln Asn Gln Met Thr Thr Ile  
 245 250 255  
 Gln Gln Glu Trp Thr Leu Val Ser Thr Ser Met Gln Val Leu Asn Gly  
 260 265 270  
 Ile Leu Ser Gln Leu Ala Gly Ala Ile Tyr Ser Asn  
 275 280

&lt;210&gt;775

&lt;211&gt;212

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;775

Asp Arg Ser Leu Leu Leu Leu Phe Val Ser Ala Gly Val Pro Pro Ala  
 1 5 10 15  
 Ala Ala Ser Ser Ile Gly Ser Ser Val Asn Gln Leu Tyr Lys Thr Ser  
 20 25 30  
 Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly Tyr Asp  
 35 40 45  
 Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn Asp Ala  
 50 55 60  
 Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr Arg Ser  
 65 70 75 80  
 Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr Asp Gln  
 85 90 95  
 Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly Asp Val  
 100 105 110  
 Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile Gln Ser  
 115 120 125  
 Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr Ser Ala  
 130 135 140  
 Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu Ser Asn  
 145 150 155 160  
 Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe Ala Glu  
 165 170 175  
 Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu Thr Asn  
 180 185 190  
 Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu Tyr Ser  
 195 200 205  
 Gly Tyr Leu Gln  
 210

&lt;210&gt;776

&lt;211&gt;478

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;776

Val Phe Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu  
 1 5 10 15  
 Arg Thr Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala  
 20 25 30  
 Ala Asn Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys  
 35 40 45  
 Pro Lys Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg  
 50 55 60  
 Ser Ala Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala  
 65 70 75 80  
 Ser Ser Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser  
 85 90 95  
 Thr Thr Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr  
 100 105 110  
 Lys Thr Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser  
 115 120 125  
 Leu Ala Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr  
 130 135 140  
 Asn Ile Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala  
 145 150 155 160  
 Glu Trp Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile  
 165 170 175  
 Thr Glu Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser  
 180 185 190  
 Leu Gly Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln  
 195 200 205  
 Ser Val Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln  
 210 215 220  
 Asp Asn Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu  
 225 230 235 240  
 Val Asp Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn  
 245 250 255  
 Ala Ile Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val  
 260 265 270  
 Glu Asn Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys  
 275 280 285  
 Ala Ala Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys  
 290 295 300  
 Phe Pro Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln  
 305 310 315 320  
 Ala Glu Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val  
 325 330 335  
 Pro Asn Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser  
 340 345 350  
 Ile Gly Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu  
 355 360 365  
 Thr Ala Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe  
 370 375 380  
 Asn Thr Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala  
 385 390 395 400  
 Gln Ala Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala  
 405 410 415  
 Leu Ala Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly  
 420 425 430  
 Gln Gln Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala  
 435 440 445  
 Val Cys Glu Arg Arg Ser Ser Ser Arg Cys Ser Lys Phe Tyr Arg Val  
 450 455 460  
 Ile Cys Lys Pro Ala Leu Gln Asp Leu Lys Ile Tyr Arg Phe  
 465 470 475  
 <210>777  
 <211>438  
 <212>PRT  
 <213>Chlamydia pneumoniae

&lt;400&gt;777

Pro Ala Trp Ser Ser Val Ser Thr Leu Asn Ile Asp Thr Lys Asp Thr  
 1 5 10 15  
 Met Lys Lys Gln Val Tyr Gln Trp Leu Ala Ser Val Val Leu Leu Ala  
 20 25 30  
 Leu Thr Ile Ser Gly Tyr Ala Glu Leu Pro Leu Ser Glu Gln Lys Val  
 35 40 45  
 Lys Ser His Thr Tyr Thr Thr Leu Asp Glu Val Lys Asp Tyr Leu Ser  
 50 55 60  
 Lys Arg Gly Phe Val Glu Thr Arg Lys Gln Asp Gly Val Leu Arg Ile  
 65 70 75 80  
 Ala Gly Asp Val Arg Ala Arg Trp Leu Tyr Phe Arg Glu Asp Ile Lys  
 85 90 95  
 Asn Pro Ser Asp Lys Asp Lys Tyr Asn Pro Leu Pro Val Asn Arg Tyr  
 100 105 110  
 Arg Ser Glu Phe Tyr Leu Tyr Ile Asp Tyr Arg Ala Glu Arg Asn Trp  
 115 120 125  
 Leu Ser Ser Lys Met Asn Trp Thr Ala Ile Ala Gly Gly Glu Asn Thr  
 130 135 140  
 Ala Ala Gly Val Asp Ile Asn Arg Ala Phe Leu Gly Tyr Arg Phe Tyr  
 145 150 155 160  
 Lys Asn Pro Glu Thr Arg Thr Asp Phe Phe Met Glu Ile Gly Arg Ser  
 165 170 175  
 Gly Leu Gly Asp Leu Phe Glu Ser Glu Val Gln Phe Gln Ser Asn Phe  
 180 185 190  
 Asp Gly Leu His Ile Tyr Trp Thr Arg Glu Leu Ser Lys Asp Tyr Pro  
 195 200 205  
 Tyr Gln Val Ile Val His Gly Gly Pro Phe Val Val Asn Met Thr Lys  
 210 215 220  
 Lys His Tyr Ala Trp Val Val Glu Gly Ile Leu Asn Arg Leu Pro Lys  
 225 230 235 240  
 Gln Phe Phe Val Lys Cys Ser Val Val Asp Trp Asn Thr Phe Val Pro  
 245 250 255  
 Ser Glu Thr Ser Thr Thr Glu Lys Ala Ala Thr Asn Ala Met Lys Tyr  
 260 265 270  
 Lys Tyr Cys Val Trp Gln Trp Leu Val Gly Lys His Ser Gln Val Pro  
 275 280 285  
 Trp Ile Asn Gly Gln Lys Lys Pro Leu Tyr Leu Tyr Gly Ala Phe Leu  
 290 295 300  
 Met Asn Pro Leu Ala Lys Ala Thr Lys Thr Thr Leu Asn Gly Lys Glu  
 305 310 315 320  
 Asn Leu Ala Trp Phe Ile Gly Gly Thr Leu Gly Gly Leu Arg Lys Ala  
 325 330 335  
 Gly Asp Trp Ser Ala Thr Val Arg Tyr Glu Tyr Val Glu Ala Leu Ser  
 340 345 350  
 Val Pro Glu Ile Asp Val Ser Gly Ile Gly Arg Gly Asn Leu Leu Lys  
 355 360 365  
 Phe Trp Phe Ala Gln Ala Ile Ala Ala Asn Tyr Asp Pro Lys Glu Ala  
 370 375 380  
 Asn Gly Phe Thr Asn Tyr Lys Gly Phe Ser Ala Leu Tyr Met Tyr Gly  
 385 390 395 400  
 Ile Thr Asp Ser Leu Ser Phe Arg Ala Tyr Gly Ala Tyr Ser Lys Pro  
 405 410 415  
 Ala Asn Asp Lys Leu Gly Ser Asp Phe Thr Phe Arg Lys Phe Asp Leu  
 420 425 430  
 Gly Ile Ile Ser Ala Phe  
 435

&lt;210&gt;778

&lt;211&gt;321

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;778

Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser Ile Phe  
 1 5 10 15

Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val His Glu  
                   20                  25                  30  
 Ile Gly Pro Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln Leu Pro  
                   35                  40                  45  
 Ile His Leu Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro Ala Ile  
                   50                  55                  60  
 Ser Arg Cys Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys Leu Met  
                   65                  70                  75                  80  
 Lys Phe Val Leu Thr Leu Thr Met Ser Val Met Ile Ile Met Thr Ala  
                   85                  90                  95  
 Gly Leu Leu Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr Glu His  
                   100                  105                  110  
 Gly Leu Phe Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val Leu Arg  
                   115                  120                  125  
 Gly Tyr Gly Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu Val Ser  
                   130                  135                  140  
 Val Leu Phe Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe Ile Gly  
                   145                  150                  155                  160  
 Ile Gly Thr Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu Gly Arg  
                   165                  170                  175  
 Trp Val Leu Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser Ile Thr  
                   180                  185                  190  
 Ala Trp Val Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys Arg Leu  
                   195                  200                  205  
 Pro Met Tyr Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser Ile Lys  
                   210                  215                  220  
 Val Met Gly Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly Leu Asn  
                   225                  230                  235                  240  
 Ile Leu Thr Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu Thr Pro  
                   245                  250                  255  
 Leu Ala Trp Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala Phe Leu  
                   260                  265                  270  
 Ser Glu Ser Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu  
                   275                  280                  285  
 Leu Arg Val Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg  
                   290                  295                  300  
 Gly Gln Arg Gly Leu Leu Gln Arg Gln His Val Met Gln Asp Thr Gln  
                   305                  310                  315                  320  
 Asn

&lt;210&gt;779

&lt;211&gt;225

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;779

Met Ser Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn  
                   1                  5                  10                  15  
 Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu  
                   20                  25                  30  
 Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe  
                   35                  40                  45  
 Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly  
                   50                  55                  60  
 Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala  
                   65                  70                  75                  80  
 Gln Ser Leu Asp Arg Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu  
                   85                  90                  95  
 Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu  
                   100                  105                  110  
 Trp Val Val Leu Gln Tyr Val Glu Gly Thr Tyr Asp Met Ile Leu  
                   115                  120                  125  
 Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn  
                   130                  135                  140  
 Val Asn Gly Ala Leu Leu His Cys Glu Asn Lys Phe Phe Gly Val Gly

869

35 40 45  
 Leu Gln Leu Glu Glu Lys Gln Lys Leu Lys Ala Cys Tyr Gly Met Ile  
 50 55 60  
 Met Glu Lys Gln Leu Val Lys Ala Phe Lys Glu Val Ile His Lys Gln  
 65 70 75 80  
 Gly Asn Val Ala Gln Met Phe Leu Glu Arg Phe Glu Cys Arg Leu Asp  
 85 90 95  
 Asn Met Val Tyr Arg Met Gly Phe Ala Lys Thr Ile Phe Ala Ala Gln  
 100 105 110  
 Gln Leu Val Ala His Gly His Ile Leu Val Asn Gly Arg Arg Val Asp  
 115 120 125  
 Arg Arg Ser Phe Phe Leu Arg Pro Gly Met Gln Ile Ser Leu Lys Arg  
 130 135 140  
 Lys Asn Leu Asn Asp Phe Ser Leu  
 145 150  
 <210>782  
 <211>324  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>782  
 Met Glu Lys Lys Tyr Tyr Ala Leu Ala Tyr Tyr Tyr Ile Thr Arg Val  
 1 5 10 15  
 Asp Asn Pro His Glu Glu Ile Ala Leu His Lys Lys Phe Leu Glu Asp  
 20 25 30  
 Leu Asp Val Ser Cys Arg Ile Tyr Ile Ser Glu Gln Gly Ile Asn Gly  
 35 40 45  
 Gln Phe Ser Gly Tyr Glu Pro His Ala Glu Leu Tyr Met Gln Trp Leu  
 50 55 60  
 Lys Glu Arg Pro Asn Phe Ser Lys Ile Lys Phe Lys Ile His His Ile  
 65 70 75 80  
 Lys Glu Asn Ile Phe Pro Arg Ile Thr Val Lys Tyr Arg Lys Glu Leu  
 85 90 95  
 Ala Ala Leu Gly Cys Glu Val Asp Leu Ser Lys Gln Ala Lys His Ile  
 100 105 110  
 Ser Pro Gln Glu Trp His Glu Lys Leu Gln Glu Asn Arg Cys Leu Ile  
 115 120 125  
 Leu Asp Val Arg Asn Asn Tyr Glu Trp Lys Ile Gly His Phe Asp Asn  
 130 135 140  
 Ala Thr Leu Pro Asp Ile Gln Thr Phe Arg Glu Phe Pro Glu Tyr Ala  
 145 150 155 160  
 Glu Lys Leu Ala Gln Glu Cys Asp Pro Glu Thr Thr Pro Val Met Met  
 165 170 175  
 Tyr Cys Thr Gly Gly Ile Arg Cys Glu Leu Tyr Ser Pro Val Leu Leu  
 180 185 190  
 Glu Lys Gly Phe Lys Glu Val Tyr Gln Leu Asp Gly Gly Val Ile Ala  
 195 200 205  
 Tyr Gly Gln Gln Val Gly Thr Gly Lys Trp Leu Gly Lys Leu Phe Val  
 210 215 220  
 Phe Asp Asp Arg Leu Ala Ile Pro Ile Asp Glu Ser Asp Pro Asp Val  
 225 230 235 240  
 Ala Pro Ile Ala Glu Cys Cys His Cys Gln Thr Pro Ser Asp Ala Tyr  
 245 250 255  
 Tyr Asn Cys Ala Asn Thr Asp Cys Asn Ala Leu Phe Leu Cys Cys Asp  
 260 265 270  
 Glu Cys Ile His Gln His Gln Gly Cys Cys Gly Glu Glu Cys Ser Gln  
 275 280 285  
 Ser Pro Arg Val Arg Lys Phe Asp Ser Ser Arg Gly Asn Lys Pro Phe  
 290 295 300  
 Arg Arg Ala His Leu Cys Glu Ile Ser Glu Asn Ser Glu Ser Ala Ser  
 305 310 315 320  
 Cys Cys Leu Ile

&lt;210&gt;783

&lt;211&gt;222

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;783

Met Leu Met Met Leu Met Met Ile Ile Gly Ile Thr Gly Gly Ser Gly  
 1 5 10 15  
 Ala Gly Lys Thr Thr Leu Thr Gln Asn Ile Lys Glu Ile Phe Gly Glu  
 20 25 30  
 Asp Val Ser Val Ile Cys Gln Asp Asn Tyr Tyr Lys Asp Arg Ser His  
 35 40 45  
 Tyr Thr Pro Glu Glu Arg Ala Asn Leu Ile Trp Asp His Pro Asp Ala  
 50 55 60  
 Phe Asp Asn Asp Leu Leu Ile Ser Asp Ile Lys Arg Leu Lys Asn Asn  
 65 70 75 80  
 Glu Ile Val Gln Ala Pro Val Phe Asp Phe Val Leu Gly Asn Arg Ser  
 85 90 95  
 Lys Thr Glu Ile Glu Thr Ile Tyr Pro Ser Lys Val Ile Leu Val Glu  
 100 105 110  
 Gly Ile Leu Val Phe Glu Asn Gln Glu Leu Arg Asp Leu Met Asp Ile  
 115 120 125  
 Arg Ile Phe Val Asp Thr Asp Ala Asp Glu Arg Ile Leu Arg Arg Met  
 130 135 140  
 Val Arg Asp Val Gln Glu Gln Gly Asp Ser Val Asp Cys Ile Met Ser  
 145 150 155 160  
 Arg Tyr Leu Ser Met Val Lys Pro Met His Glu Lys Phe Ile Glu Pro  
 165 170 175  
 Thr Arg Lys Tyr Ala Asp Ile Ile Val His Gly Asn Tyr Arg Gln Asn  
 180 185 190  
 Val Val Thr Asn Ile Leu Ser Gln Lys Ile Lys Asn His Leu Glu Asn  
 195 200 205  
 Ala Leu Glu Ser Asp Glu Thr Tyr Tyr Met Val Asn Ser Lys  
 210 215 220

&lt;210&gt;784

&lt;211&gt;503

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;784

Leu Arg Leu Ala Gly Ser Leu Ala Asp Arg Phe Gln Lys Arg Asn Ile  
 1 5 10 15  
 Ile Leu Ala Thr Arg Phe Ile Glu Ile Leu Cys Thr Ile Leu Gly Thr  
 20 25 30  
 Tyr Phe Phe Phe Ile Gln Ser Val Val Gly Gly Tyr Val Val Leu Ile  
 35 40 45  
 Leu Met Ala Cys His Thr Thr Ile Phe Gly Pro Ala Lys Leu Gly Ile  
 50 55 60  
 Leu Pro Glu Met Leu Pro Ser Glu Gln Leu Ser Gln Ala Asn Gly Ile  
 65 70 75 80  
 Met Thr Ala Ala Thr Tyr Thr Gly Ser Ile Leu Gly Ser Cys Leu Ala  
 85 90 95  
 Pro Leu Leu Val Asp Val Thr His Arg Leu Gly Val Asn Ser Tyr Val  
 100 105 110  
 Trp Pro Thr Leu Met Cys Val Ile Val Ser Ile Ile Ser Thr Leu Ile  
 115 120 125  
 Ser Phe Cys Ile Arg Pro Ser Asn Val Lys Asn Val Lys Gln Lys Ile  
 130 135 140  
 Thr Leu Val Ser Phe Lys Asp Leu Trp Lys Val Leu Lys Asp Thr Arg  
 145 150 155 160  
 Met Ile His Tyr Leu Thr Val Ser Ile Phe Leu Gly Ser Phe Phe Leu  
 165 170 175  
 Leu Ile Gly Ala Tyr Thr Gln Leu Glu Ile Ile Pro Phe Val Glu Phe  
 180 185 190  
 Ile Leu Lys Tyr Pro Lys His Tyr Gly Ala Tyr Leu Phe Pro Ile Val  
 195 200 205  
 Ala Leu Gly Val Gly Thr Gly Ser Tyr Ile Thr Gly Lys Ile Ser Gly  
 210 215 220

Lys Asp Ile Lys Ile Gly Tyr Val Pro Leu Ala Ala Ile Gly Leu Ala  
 225 230 235 240  
 Leu Val Phe Met Gly Leu Tyr Ala Phe Ala Cys Ser Ile Leu Phe Val  
 245 250 255  
 Leu Phe Phe Leu Leu Ala Leu Gly Phe Leu Gly Gly Val Tyr Gln Val  
 260 265 270  
 Pro Leu His Ala Tyr Val Gln Tyr Ala Ser Pro Glu His Lys Arg Gly  
 275 280 285  
 Gln Ile Leu Ala Ala Asn Asn Phe Leu Asp Phe Phe Gly Val Leu Val  
 290 295 300  
 Ala Ala Gly Val Ile Arg Val Leu Gly Ser Asn Leu Gly Leu Ser Pro  
 305 310 315 320  
 Glu Thr Ser Phe Phe Tyr Ile Gly Trp Phe Val Leu Ala Val Ser Ile  
 325 330 335  
 Trp Thr Leu Trp Ile Trp Arg Glu His Val Tyr Arg Leu Leu Leu Gly  
 340 345 350  
 Ile Ile Leu Arg Arg Gln Leu Gly Tyr Tyr Leu Lys Ile His Gln Ser  
 355 360 365  
 Ser Ser Pro Lys Cys Tyr Phe Val Ala Val Gln Ser Tyr Arg Glu Ile  
 370 375 380  
 Arg Arg Val Leu Ala Ala Leu Thr Lys Thr Val Arg Ser Arg Val Ile  
 385 390 395 400  
 Ile Leu Asp Gln Lys Leu Val Pro Gly Trp Arg Ala Trp Leu Leu Ser  
 405 410 415  
 Trp Cys Val Pro Thr Val Val Ser Ser Val Arg Asp Asn Asp Ser Glu  
 420 425 430  
 Ala Gln Asp Ala Trp Ala Val Leu Gln Ala Asn His Leu Lys Thr Ser  
 435 440 445  
 Leu Lys Lys Phe Pro Asp Val Ser Val Val Cys Leu Gly Leu Pro Lys  
 450 455 460  
 Asn Val Glu Arg Phe Thr Ser Ile Leu Gln Glu Gln Gly Ile Asp Leu  
 465 470 475 480  
 His Pro Ile Gln Leu Val Gln Lys Glu Gly Lys Lys Arg Val Ile Tyr  
 485 490 495  
 Thr Leu Val Phe Pro His Ala  
 500

&lt;210&gt;785

&lt;211&gt;644

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;785

Ile His Gly Leu Lys Ile Ser Glu Ile Lys Ile Leu Leu Leu Ser Ser  
 1 5 10 15  
 Ile Leu Gln Thr Gln Gly Asp Leu His Tyr Ile Leu Gln Leu Leu Thr  
 20 25 30  
 His Pro Gln Leu Gln Gln Pro Ile Asp Gln Asn Lys Val Pro Tyr Leu  
 35 40 45  
 Ile Lys Lys Leu Ser Ser Glu Trp Gly Lys Ile Ser Ser Lys Glu Arg  
 50 55 60  
 Ala Ser Gly Gln Gln Met Lys Ala Leu Gly Asp Leu Ile Leu Glu Glu  
 65 70 75 80  
 Tyr Pro Phe His Gln Glu Gly Gly Arg Val Ser Gln Val Glu Val Trp  
 85 90 95  
 Glu Thr Thr Val Pro Leu Ile Tyr Phe Ile Gln Glu Arg Ile Asn Leu  
 100 105 110  
 Tyr Leu Ser Ser Ser Gln His Ser Tyr Glu Asp Leu Phe Gln Asn Val  
 115 120 125  
 Phe Ser Cys Leu Glu Lys Ile Phe Val Leu Ser Pro Glu Glu Thr Ser  
 130 135 140  
 Phe Ile Thr Thr Leu Arg Asn Ser Leu Phe Pro Thr Phe Ala Thr Ser  
 145 150 155 160  
 Ser Cys Ser Leu Leu Phe Phe Thr Asp Phe Cys Leu Asp Phe Leu Leu  
 165 170 175  
 His Phe His Lys Pro Ser Pro Leu Tyr Asp Lys Pro Gly Pro Tyr Ile



180 185 190  
 Gly Ser Leu Ser Ser Leu Ser Leu Ile Pro Lys Gly Tyr Val Phe Ile  
 195 200 205  
 Leu Gly Ala Asn Lys Thr Thr Ser Ser Asp Ile Phe Asp Leu Leu Asn  
 210 215 220  
 Arg Thr Thr Thr His Glu Glu Leu Ala Phe Ser Ser Thr Glu Asp Glu  
 225 230 235 240  
 Glu Asn Phe His Phe Leu Gln Ile Leu Val Ser Thr Lys His Glu Leu  
 245 250 255  
 His Ile Ser Tyr Ile Ser Ser Ala Ala Gln Phe Asn Leu Pro Ser Pro  
 260 265 270  
 Phe Leu Asn His Ile Lys Asp Thr Leu Asp Leu Pro Val Glu Thr Leu  
 275 280 285  
 Pro Thr Gln Pro Tyr Leu Ser Ala Phe Phe Lys Asn Lys Ala Cys Leu  
 290 295 300  
 His Thr Ser Gln Glu Tyr Asn Tyr Ser Leu Ala His Ala Phe Tyr Ser  
 305 310 315 320  
 Lys Lys Ala Leu Leu Pro Ser Leu Phe Ile Pro Thr Val Lys Gln Val  
 325 330 335  
 Asn Leu Pro Gln His Leu Ser Leu Asn Glu Ile Ile Lys Gly Ile Phe  
 340 345 350  
 Ser Pro Leu Asp Leu Phe Leu Lys Thr Asn Tyr Asn Leu Arg Ile Ser  
 355 360 365  
 Tyr Pro Glu His Leu Lys Lys Gln Gln Lys Leu Phe Pro Thr Lys His  
 370 375 380  
 Gln Ile Glu Asp Phe Trp Asn Glu Cys Phe Val Asp Lys Glu His Asp  
 385 390 395 400  
 Leu Ile Pro Ser Ile Ser Pro His Ala Glu Glu Leu Phe Thr Tyr Tyr  
 405 410 415  
 Arg Glu Lys Thr Ile Leu Leu Arg Asn Gly Leu Asp Lys Asp Pro Lys  
 420 425 430  
 His Ser Pro Tyr Thr Val Thr Phe Ser Ser Ser Ile Phe Glu Glu Arg  
 435 440 445  
 Pro Tyr His Glu Ser Tyr Leu Phe Pro Pro Leu Ser Leu Ser Phe Gln  
 450 455 460  
 Gly Asn Pro Val Gln Ile His Gly Thr Ile His Gly Val Cys Asn Glu  
 465 470 475 480  
 Gly Leu Tyr Leu Cys Ser Ile Asp Pro Arg Asp Ser Leu Lys Lys Thr  
 485 490 495  
 Thr Arg Thr Leu Gly Ser Leu Pro Glu Thr Ser Ser Glu Gln Lys Gln  
 500 505 510  
 Leu Leu Glu Arg Tyr Val Ala Leu Ala Val Leu Gln Met Ser Gln His  
 515 520 525  
 Leu Ser Ser Asp Ser Ala Leu Ile Lys Leu Thr Ser Phe Asn Thr Lys  
 530 535 540  
 Glu Asn His His Pro Pro Phe Ser Asp Pro Glu Gly Tyr Leu Arg Lys  
 545 550 555 560  
 Val Leu Glu Val Tyr His Leu Met Ser Ser Gln Pro Ile Pro Leu Leu  
 565 570 575  
 Ser Pro Leu Cys Trp Lys Thr Leu Asp Asp Glu Glu Lys Phe His Gln  
 580 585 590  
 Ala Val Leu Ser Ala Ile Ser Glu Glu Ala Lys Asn Pro Ser Leu Pro  
 595 600 605  
 Ile Phe Trp Gln Phe His Asn Arg Asn Ile Glu Glu Ile Leu Asn His  
 610 615 620  
 Val Gly Ala Ser Glu Arg Leu Lys Ile Leu Ser Leu Phe Arg Gly Pro  
 625 630 635 640  
 Cys Glu Ala Val

&lt;210&gt;786

&lt;211&gt;439

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;786

Pro Val Lys Pro Phe Asn Ile Phe Asp Ser Asn Ser Ser Ile Gln Gly  
 1 5 10 15  
 Lys Phe Phe Leu Glu Ala Ser Ala Gly Thr Gly Lys Thr Phe Thr Ile  
 20 25 30  
 Glu Gln Ile Val Leu Arg Ala Leu Ile Glu Gly Ser Leu Thr His Val  
 35 40 45  
 Glu His Ala Leu Ala Ile Thr Phe Thr Asn Ala Ser Thr Asn Glu Leu  
 50 55 60  
 Lys Val Arg Ile Lys Asp Asn Leu Ala Gln Thr Leu Arg Glu Leu Lys  
 65 70 75 80  
 Ala Val Leu Asn Ser Gln Pro Ala Ser Leu Pro Thr Tyr Leu Asp Ile  
 85 90 95  
 Asn Cys Asn Val Lys Gln Ile Tyr Met Gln Val Arg Asn Ala Leu Ala  
 100 105 110  
 Thr Leu Asp Gln Met Ser Leu Phe Thr Ile His Gly Phe Cys Asn Phe  
 115 120 125  
 Val Leu Glu Gln Tyr Phe Pro Lys Thr Arg Leu Ile His Lys Asn Pro  
 130 135 140  
 Ala Leu Thr His Ser Gln Leu Val Leu His His Ile Thr Asn Tyr Leu  
 145 150 155 160  
 Lys Gln Asp Leu Trp Lys Asn Val Leu Phe Gln Glu Gln Phe His Leu  
 165 170 175  
 Leu Ala Val Arg Tyr Asn Val Thr Ser Lys His Thr Ser Ser Leu Val  
 180 185 190  
 Asp Lys Leu Leu Ala Ser Tyr Thr Gln Pro Ile Ser Ser Tyr Phe Ser  
 195 200 205  
 Ser Arg Val Glu Arg Leu Glu Gln Ile Ser Leu Trp His Gln Gln Ile  
 210 215 220  
 Tyr Asn Ser Leu Leu Glu Ile Pro Lys Gln Val Phe Leu Asp Gln Leu  
 225 230 235 240  
 Thr Ala His Ile Ser Gly Phe Lys Lys Gln Pro Phe Ser Ile Leu Asp  
 245 250 255  
 Asp Leu His His Phe Val Asp Leu Leu Tyr Thr Ser Glu Thr His Ser  
 260 265 270  
 Ser Leu Phe Ser Phe Phe Lys Ile Ala Glu Thr Phe Asn Phe Lys His  
 275 280 285  
 Arg Leu Ala Arg Tyr Lys Pro Cys Ala Ala Phe Thr Val Leu Glu Asn  
 290 295 300  
 Met Ser Trp Val Glu Arg Thr Leu Glu Phe Cys Asn Leu Asp Arg Ile  
 305 310 315 320  
 Phe Asn Thr Leu Leu Val Asp Leu Gln Glu Tyr Leu Lys Gln Asn Tyr  
 325 330 335  
 Thr Pro Trp Leu Ser Pro Asp Glu Ser Val Phe Ala Leu Glu Lys Leu  
 340 345 350  
 Leu Ser Ser Ser Glu Ala Gln Pro Val Val Gln Ala Leu Arg Glu Gln  
 355 360 365  
 Tyr Gln Leu Val Leu Ile Asp Glu Phe Gln Asp Thr Asp Lys Gln Gln  
 370 375 380  
 Trp Ser Ile Phe Ser Asn Leu Phe Ile Ser Pro Lys Phe Thr Gly Ser  
 385 390 395 400  
 Leu Phe Leu Ile Gly Asp Pro Lys Gln Ser Ile Tyr Glu Trp Arg Ser  
 405 410 415  
 Ala Asp Leu Pro Thr Tyr Leu Thr Ala Lys Ser Ser Phe Ser Glu Asp  
 420 425 430  
 Lys Gln Leu Gln Leu Val Asn  
 435

&lt;210&gt;787

&lt;211&gt;489

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;787

Leu Met Asn Phe Lys Ile Gln Thr Ser Asn Asn Gly Ala Ser Phe Arg  
 1 5 10 15  
 Ile Ser Leu Phe Leu Arg Asn Leu Gln Asp Arg Tyr Phe Leu Ser Glu

20 25 30  
 Thr Pro Ser Asn Leu Phe Met Asn Gly Glu Val Arg Ile Phe Leu Pro  
 35 40 45  
 Ile Leu Gln Pro Asn Leu Arg Phe Gln Lys Thr Ser Asn Tyr Ser Leu  
 50 55 60  
 Ser Ile Asn Tyr Arg Ser Thr Pro Lys Leu Met Glu Ala Ile Asn Gln  
 65 70 75 80  
 Ile Phe Gly Lys Ile Ser Pro Phe Leu Glu Ile Pro Gly Tyr Leu Pro  
 85 90 95  
 Ile Glu Tyr His Ala Leu Asn Pro Gln Ser Ser Glu Thr Phe Glu Asn  
 100 105 110  
 Pro Pro His Ala Pro Ile His Phe Phe Phe Tyr Glu Thr Ile Lys Asp  
 115 120 125  
 Gln Ala Leu Trp Ile Phe Ser Glu Ala Leu Arg Leu Gln Lys Glu Gln  
 130 135 140  
 Lys Ile Pro Leu Gly Asn Met Val Val Leu Val Ser Asp Ser Asn Gln  
 145 150 155 160  
 Ala Phe Glu Leu Ile Ser Tyr Ala Thr Ile Pro Val Ser Phe Ser Lys  
 165 170 175  
 Asn Lys Ser Ile Phe His Leu Thr Glu Thr His Ile Leu Thr Thr Ala  
 180 185 190  
 Leu Leu Glu Ala Ile Leu His Pro Glu Asn Tyr Glu Lys Ile Ser Lys  
 195 200 205  
 Ile Leu Phe Ser Ser Leu Phe Gly Leu Ser Leu Asp Glu Val Thr Thr  
 210 215 220  
 Lys Lys Glu Asp Phe Thr Ile Tyr Phe Gln Ser Leu His Ser Tyr Ile  
 225 230 235 240  
 Ser His His Gly Leu Leu Ala Thr Phe Tyr Arg Val Met Thr Thr Gln  
 245 250 255  
 Gly Asn Val Leu Phe Ser Ser Pro Arg Gly Asp Leu Ile Phe Gln Glu  
 260 265 270  
 Met Glu Lys Leu Cys Gly Tyr Leu Asp Thr Ile Ser Ser Tyr Pro Tyr  
 275 280 285  
 His Gln Leu Leu His Leu Lys Asn Phe Ser Glu Thr Gly Arg Trp Glu  
 290 295 300  
 Glu Glu Leu Ala Ile Ser Ser Tyr Ser Glu Asp Leu Glu Thr Leu Lys  
 305 310 315 320  
 Ile Thr Thr Ile His Ser Ser Lys Gly Leu Glu Tyr Asp Ile Val Phe  
 325 330 335  
 Cys Pro Gly Ile Glu Lys Ser Lys Lys Asn Lys Ser Ser Ser Glu Leu  
 340 345 350  
 Leu Arg Glu Met Tyr Val Ala Cys Thr Arg Ala Lys Lys Gln Leu Tyr  
 355 360 365  
 Leu Pro Ile Ser Thr Gln Pro Pro Ser Leu Gln Arg Ser Ser Ala Leu  
 370 375 380  
 Thr Asn Tyr Val Lys Leu Glu Gly Thr Gln Ser Ser Ala Tyr Asp Leu  
 385 390 395 400  
 Ala Ile His Leu His Gln Glu His Pro Asp Leu Phe Ser Tyr Ser Leu  
 405 410 415  
 Pro Lys Asp His Gly His Ala Thr Thr Val Leu Asn Leu Pro Leu Leu  
 420 425 430  
 Glu Thr Phe Ala Leu Lys Val Thr Pro Pro Lys Thr Ile Phe Ser Phe  
 435 440 445  
 Ser Ser Thr Lys Phe Leu Leu Asp Thr His Lys Asp Ser Gln Ser Ile  
 450 455 460  
 Pro Tyr Ser Asn Ser Arg Phe Gln Asn Asn Ser Phe Leu Trp Glu Lys  
 465 470 475 480  
 Lys Gln Glu Phe Leu Tyr Thr Lys Phe  
 485

&lt;210&gt;788

&lt;211&gt;260

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;788

Gly Pro Trp Thr Cys Tyr His Ser Val Glu Ser Ala Thr Phe Arg Asp  
 1 5 10 15  
 Val Arg Ser Lys Ser Asp Thr Pro Glu Asn Tyr Phe Phe Leu Leu Ile  
 20 25 30  
 Tyr Lys Ile Pro Ile Gly His Ser Gln Arg Leu Ala Ile Asp Pro Ile  
 35 40 45  
 Phe Gln Leu Pro Ile Ser Lys Gln Gln Leu Pro Leu Gly Glu Lys Thr  
 50 55 60  
 Gly Ile Leu Ile His Lys Ile Leu Glu Ser Ile Gln Phe Ser Leu Leu  
 65 70 75 80  
 Gln Asp Thr Glu Tyr Leu Met Ser Thr Ile Met Arg Phe Ile Lys His  
 85 90 95  
 Thr His Leu Glu Gly Phe Glu Glu Thr Ile Leu Lys Leu Leu Ser Lys  
 100 105 110  
 Thr Phe Phe Ser Pro Leu Thr Phe Ser Ser Gln Thr Phe Ser Leu Ser  
 115 120 125  
 Gln Val Leu Pro Asn Lys Ile Phe Arg Glu Thr Ser Phe Leu Phe Leu  
 130 135 140  
 Glu Asn Gln Glu Leu Trp Gln Gly Val Ile Asp Leu Phe Phe Glu His  
 145 150 155 160  
 Glu Gly Lys Tyr Tyr Ile Ile Asp Trp Lys Thr Ser Phe Leu Gly Glu  
 165 170 175  
 Thr Asn Ser Asp Tyr Ser Lys Ser Asn Leu Ser Ile Tyr Ile Lys Gln  
 180 185 190  
 Glu Lys Leu Asp Tyr Gln Gly Arg Ile Tyr Val Lys Ala Val Arg Lys  
 195 200 205  
 Phe Leu Asn Gln Phe Glu Ile Asp Asp Asp Val Glu Leu Gly Val Ile  
 210 215 220  
 Phe Ile Arg Gly Ile Asp Thr Gln Gly Asn Gly Phe Phe Ala Leu Asn  
 225 230 235 240  
 Ser Ser Glu Asp Ile Pro Asn Phe Asn Pro Lys Ala Ile Gln Lys Cys  
 245 250 255  
 Gln Ala Tyr His  
 260

&lt;210&gt;789

&lt;211&gt;344

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;789

Cys Lys Val Leu Phe Lys Leu Met Ser Tyr Ser Leu Arg Asn Lys Lys  
 1 5 10 15  
 Thr Lys Ile Cys Val Tyr Ile Ile Ile Ala Leu Gly Ile Leu Ser Phe  
 20 25 30  
 Arg Ser Ile Pro Gln Glu Val Tyr Asp Lys Ile Arg Ser Phe Val  
 35 40 45  
 Ser Leu His Val Lys Phe Phe Pro Lys Ile Lys Gln Ala Pro Ser Ser  
 50 55 60  
 His Leu Ala Asn Leu Glu Leu Glu Asn Leu Val Leu Lys Glu Arg Val  
 65 70 75 80  
 Ala Ser Leu Glu Glu Lys Leu Lys Leu Tyr Glu Val Ser Asn His Thr  
 85 90 95  
 Pro Pro Leu Phe Pro Glu Ile Leu Thr Pro Tyr Phe His Lys Leu Val  
 100 105 110  
 Glu Gly Lys Val Val Tyr Arg Asp Tyr Thr His Trp Ser Ser Cys  
 115 120 125  
 Trp Val Asn Val Gly Lys Thr His Gly Ile Lys Lys Asn Ser Pro Val  
 130 135 140  
 Leu Ser Gly Asn Val Leu Val Gly Leu Val Asp Tyr Val Gly Glu His  
 145 150 155 160  
 Gln Ser Arg Ile Arg Leu Ile Thr Asp Val Gly Met Lys Pro Ser Val  
 165 170 175  
 Val Ala Met Arg Gly Asp Ile Gln Ser Trp Trp Ile Lys His Ser Leu  
 180 185 190  
 Arg Glu Leu Ile Arg Gln Val Glu Gln Ile Ser His Ala Tyr Ile Leu

195 200 205  
 Glu Lys Asp Lys Tyr Glu Lys Ile Ser Gln Leu Gln Glu Leu Asp Ser  
 210 215 220  
 Leu Ile Gln Gly Glu Gly Glu Asn Gln Ala Leu Leu Arg Gly Ile Leu  
 225 230 235 240  
 Ser Gly Val Gly Gly Ala Leu Trp Lys Glu Gly Ser Leu Cys Leu Glu  
 245 250 255  
 Gly Glu Gly Phe Tyr Phe Ser Glu Gly Lys Thr Leu Leu Pro Gly Asp  
 260 265 270  
 Ile Leu Val Thr Thr Gly Leu Asp Gly Val Phe Pro Pro Gly Leu Leu  
 275 280 285  
 Val Ala Arg Val Thr Lys Val Lys Ala Pro Arg Asp Gly Ala Cys Thr  
 290 295 300  
 Phe Lys Ile Glu Ala Gln Ser Leu Glu Glu Lys Leu Met Glu Leu Asp  
 305 310 315 320  
 Gln Leu Phe Ile Leu Pro Pro Leu Glu Phe Asn Pro Asn Asp Arg Pro  
 325 330 335  
 Asp Ile Phe Gly Leu Leu Trp Asp  
 340

&lt;210&gt;790

&lt;211&gt;395

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;790

Met Ser Phe Phe Asn His Ile Pro Thr Phe Ser Pro Asp Ala Ile Leu  
 1 5 10 15  
 Gly Leu Gln Asn Val Phe Phe Ala Asp Lys Arg Pro Glu Lys Val Asn  
 20 25 30  
 Leu Val Ile Gly Val Tyr Glu His Pro Gln Lys Arg Tyr Gly Gly Leu  
 35 40 45  
 Ser Cys Ile Arg Lys Ala Gln Thr Val Ile Leu Glu Glu Glu Gln Asn  
 50 55 60  
 Lys Ser Tyr Leu Pro Ile Ser Gly Leu Gln Ile Phe Leu Asp Glu Met  
 65 70 75 80  
 Arg Glu Leu Val Phe Gly Ala Val Asp Pro Ser Ala Ile Val Gly Phe  
 85 90 95  
 Gln Ser Leu Gly Gly Thr Gly Ala Leu His Leu Gly Ala Arg Leu Leu  
 100 105 110  
 Ser Val Ala Lys Gly Ser Gly Lys Val Tyr Val Pro Glu Gln Thr Trp  
 115 120 125  
 Ser Asn His Ile Arg Ile Phe Ser Gln Glu Gly Leu Glu Val Ile Arg  
 130 135 140  
 Tyr Pro Tyr Tyr Ser Lys Glu Gln Lys Gln Leu Leu Phe Glu Pro Leu  
 145 150 155 160  
 Ile Ala Phe Leu Lys Glu Val Glu Lys Asn Ser Val Ile Leu Leu His  
 165 170 175  
 Gly Cys Cys His Asn Pro Thr Gly Val Asp Phe Thr Glu Asp Met Trp  
 180 185 190  
 Lys Glu Leu Ala Ile Leu Met Lys Glu Arg Glu Leu Ile Pro Phe Phe  
 195 200 205  
 Asp Thr Ala Tyr Gln Gly Phe Ala His Gly Ile Glu Leu Asp Arg Lys  
 210 215 220  
 Pro Ile Glu Ile Phe Ile Ser Glu Gly Asn Thr Val Leu Val Ala Ala  
 225 230 235 240  
 Ser Ser Ser Lys Asn Phe Ala Leu Tyr Gly Glu Arg Val Gly Tyr Phe  
 245 250 255  
 Ala Val His Ser Thr Phe Thr Asp Glu Leu Val Lys Ile His Ser Phe  
 260 265 270  
 Leu Glu Glu Lys Ile Arg Gly Glu Tyr Ser Ser Pro Gln Arg Trp Gly  
 275 280 285  
 Val Glu Ile Val Ser Thr Ile Leu Ser Asn Pro Tyr Leu Lys Glu Glu  
 290 295 300  
 Trp Gln Ser Glu Leu Asn Phe Ile Arg Glu Ser Leu Gly Lys Met Arg  
 305 310 315 320

Thr Arg Phe Val Gln Ala Leu Arg Lys Val Ala Gly His Thr Phe Asp  
 325 330 335  
 Phe Leu Leu Ser Gln His Gly Phe Phe Ala Tyr Pro Gly Phe Ser Asp  
 340 345 350  
 Lys Gln Val Leu Phe Leu Arg Glu Gln His Ala Val Tyr Thr Thr Ala  
 355 360 365  
 Gly Gly Arg Met Asn Leu Asn Gly Ile Thr Glu Lys Asn Ile Asp His  
 370 375 380  
 Val Val Gln Ser Phe Ile Gln Ala Tyr Glu Leu  
 385 390 395  
 <210>791  
 <211>733  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>791  
 Glu Tyr Ile Phe Arg Leu Lys Thr Gly Asp Ile Val Asp Tyr Leu Glu  
 1 5 10 15  
 Lys Leu Gln Val Leu Ile Glu Glu Gly Gln Ser Ala Asn Phe Leu Ser  
 20 25 30  
 Leu Trp Glu Glu Tyr Cys Phe Asn Asp Val Val Arg Gly Arg Glu Leu  
 35 40 45  
 Val Glu Ile Leu Glu Lys Val Lys Ser Ser Ser Leu Ala Ser Leu Phe  
 50 55 60  
 Gly Lys Ile Val Asp Thr Val Val Pro Leu Trp Glu Lys Ile Pro Glu  
 65 70 75 80  
 Gly Lys Asp Lys Asp Arg Val Leu Gln Leu Ile Leu Asp Leu Gln Thr  
 85 90 95  
 Ser Asn Ser Gln Met Phe Phe Asp Ile Ala Thr Glu Tyr Val Asn Lys  
 100 105 110  
 Lys Tyr Ser Gly Glu Glu Asn Phe Asn Glu Ala Leu Arg Val Val Gly  
 115 120 125  
 Leu Arg Asp Gly Arg Asp Phe Gln Phe Ser Leu Ser Arg Phe Asp Phe  
 130 135 140  
 Leu Met His Met His Lys Gly Asn Phe Val Phe His Gln Gly Gly Trp  
 145 150 155 160  
 Gly Val Gly Glu Val Met Gly Val Ser Phe Leu Gln Gln Lys Val Leu  
 165 170 175  
 Ile Glu Phe Glu Gly Ile Met Ser Ala Lys Asp Ile Ser Phe Glu Thr  
 180 185 190  
 Ala Phe Lys Ser Leu Thr Pro Leu Ser Gly Asp His Phe Leu Ser Arg  
 195 200 205  
 Arg Phe Gly Asp Pro Asp Gly Phe Glu Ala Phe Ala Lys Glu Asn Pro  
 210 215 220  
 Ile Glu Val Val Glu Ile Leu Leu Arg Asp Leu Gly Pro Lys Thr Ala  
 225 230 235 240  
 Lys Glu Ile Lys Asp Glu Leu Val Asp Leu Val Ile Pro Glu Ala Asp  
 245 250 255  
 Trp Asn Arg Trp Trp Gln Ser Ala Lys Thr Lys Ile Lys Lys Gly Thr  
 260 265 270  
 Arg Ile Ile Ser Pro Asp Asn Pro Lys Glu Pro Tyr Val Leu Ser Asp  
 275 280 285  
 Ala Gly Cys Ser His Met Gly Gln Leu Glu Arg Lys Leu Gly Leu Ser  
 290 295 300  
 Leu Asn Ser Ala Glu Lys Ile Ser Leu Ile Tyr His Phe Ile Arg Asp  
 305 310 315 320  
 Leu His Ser Glu Leu Lys Asn Ile Glu Ile Arg Lys Ser Leu Val Lys  
 325 330 335  
 Ala Leu Gln Asp Leu Asp Val Glu Glu Gly Asn Lys Ser Leu Ile Leu  
 340 345 350  
 Gln Arg Glu Leu Leu Leu Ser Glu Tyr Leu Gly Ile Lys Asp Ala Ser  
 355 360 365  
 Ile Asp Lys Glu Tyr Ile Thr Ser Leu Ser Glu Asp Asp Thr Ser Arg  
 370 375 380  
 Leu Leu Glu Asn Met Pro Ile Val Ala Leu Gln Lys Ser Phe Leu Ser

385 390 395 400  
 Leu Val Arg Lys Tyr Ser Ser Phe Trp Gln Gln Val Phe Met Gln Ile  
 405 410 415  
 Leu Leu Tyr Thr Thr Ser Pro Thr Met Arg Asp Phe Val Tyr Lys Thr  
 420 425 430  
 Ile Lys Asn Asp Pro Ser Ser Val Glu Val Leu Lys Lys Arg Leu Leu  
 435 440 445  
 Asp Ser Ala His Gln Pro Met Met Phe Pro Glu Leu Phe Val Trp Phe  
 450 455 460  
 Phe Leu Lys Leu Gly Asn His Glu Asp Gly Leu Phe Asp Pro Glu Asp  
 465 470 475 480  
 Lys Glu Val Leu Arg Leu Phe Leu Glu Ser Ala Leu Asn Phe Met Tyr  
 485 490 495  
 Gln Val Ala Ser Thr Pro His Lys Glu Leu Gly Lys Lys Leu His His  
 500 505 510  
 Tyr Leu Val Gly Gln Arg Tyr Leu Ala Val Arg Gln Met Ile Glu Gly  
 515 520 525  
 Ala Ser Leu Pro Phe Leu Lys Glu Leu Leu Leu Leu Ser Thr Lys Cys  
 530 535 540  
 Pro Gln Phe Ser Ser Ser Asp Leu Asn Val Leu Gln Ser Leu Ala Glu  
 545 550 555 560  
 Val Val Gln Pro Thr Leu Lys Lys His Lys Ser Asn Val Glu Glu Glu  
 565 570 575  
 Asn Val Leu Trp Ser Thr Ser Glu Ser Phe Ser Arg Met Lys Ala Lys  
 580 585 590  
 Leu Gln Ser Leu Val Gly Lys Glu Met Val Asp Asn Ala Lys Glu Ile  
 595 600 605  
 Glu Asp Ala Arg Ser Leu Gly Asp Leu Arg Glu Asn Ser Glu Tyr Lys  
 610 615 620  
 Phe Ala Leu Glu Lys Arg Ala Arg Leu Gln Glu Glu Ile Arg Val Leu  
 625 630 635 640  
 Ser Glu Glu Ile Asn Arg Ala Arg Ile Leu Thr Lys Asp Leu Val Phe  
 645 650 655  
 Thr Asp Lys Val Gly Val Gly Cys Lys Val Thr Leu Lys Gly Asp Ala  
 660 665 670  
 Gly Glu Val Val Glu Tyr Thr Ile Leu Gly Pro Trp Asp Ala Asp Pro  
 675 680 685  
 Asp Ser Cys Ile Leu Ser Leu Gln Ser Lys Leu Ala Gln Asn Met Leu  
 690 695 700  
 Gly Lys Lys Leu Asn Asp Val Val Ile Leu Gln Gly Lys Glu Tyr Lys  
 705 710 715 720  
 Ile Ser Arg Ile Gln Ser Ile Trp Glu Glu His Gly Ala  
 725 730

&lt;210&gt;792

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;792

Thr Lys Met Met Val Ile Val Met Asn Ser Lys Ser Ala Gln Lys Ile  
 1 5 10 15  
 Ile Asp Ser Ile Lys Gln Ile Leu Thr Ile Tyr Asn Ile Asp Phe Asp  
 20 25 30  
 Pro Ser Phe Gly Ser Ser Leu Ser Asp Ser Asp Ala Asp Tyr Glu  
 35 40 45  
 Tyr Leu Ile Thr Lys Thr Gln Glu Lys Ile Gln Glu Leu Asp Lys Arg  
 50 55 60  
 Ala Gln Glu Ile Leu Thr Gln Thr Gly Met Ser Lys Glu Gln Met Glu  
 65 70 75 80  
 Val Phe Ala Asn Asn Pro Asp Asn Phe Ser Pro Glu Glu Trp Leu Ala  
 85 90 95  
 Leu Glu Lys Val Arg Ser Ser Cys Asp Glu Tyr Arg Lys Glu Thr Glu  
 100 105 110  
 Asn Leu Ile Asn Glu Ile Thr Leu Asp Leu His Pro Thr Lys Glu Ser  
 115 120 125

Lys Arg Pro Lys Gln Lys Leu Ser Ser Thr Lys Lys Asn Lys Lys Lys  
 130 135 140  
 Asn Trp Ile Pro Leu  
 145  
 <210>793  
 <211>469  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>793  
 Ile Phe Met Lys Ile Thr Val Asn Arg Gly Leu Asp Leu Ser Leu Gln  
 1 5 10 15  
 Gly Ser Pro Lys Glu Ser Gly Phe Tyr Asn Lys Ile Asp Pro Glu Phe  
 20 25 30  
 Val Ser Ile Asp Leu Arg Pro Phe Gln Pro Leu Ser Leu Lys Leu Lys  
 35 40 45  
 Val Glu Gln Gly Asp Ala Val Cys Ser Gly Ala Pro Ile Ala Glu Tyr  
 50 55 60  
 Lys His Phe Pro Asn Thr Tyr Ile Thr Ser His Val Ser Gly Val Val  
 65 70 75 80  
 Thr Ala Ile Arg Arg Gly Asn Lys Arg Ser Leu Leu Asp Val Ile Ile  
 85 90 95  
 Lys Lys Thr Pro Gly Pro Thr Ser Thr Glu Tyr Thr Tyr Asp Leu Gln  
 100 105 110  
 Thr Leu Ser Arg Ser Asp Leu Ser Glu Ile Phe Lys Glu Asn Gly Leu  
 115 120 125  
 Phe Ala Leu Ile Lys Gln Arg Pro Phe Asp Ile Pro Ala Ile Pro Thr  
 130 135 140  
 Gln Thr Pro Arg Asp Val Phe Ile Asn Leu Ala Asp Asn Arg Pro Phe  
 145 150 155 160  
 Thr Pro Ser Pro Glu Lys His Leu Ala Leu Phe Ser Ser Arg Glu Glu  
 165 170 175  
 Gly Phe Tyr Val Phe Val Val Gly Val Arg Ala Ile Ala Lys Leu Phe  
 180 185 190  
 Gly Leu Arg Pro His Ile Val Phe Arg Asp Arg Leu Thr Leu Pro Thr  
 195 200 205  
 Gln Glu Leu Lys Thr Ile Ala His Leu His Thr Val Ser Gly Pro Phe  
 210 215 220  
 Pro Ser Gly Ser Pro Ser Ile His Ile His Ser Val Ala Pro Ile Thr  
 225 230 235 240  
 Asn Glu Lys Glu Val Val Phe Thr Leu Ser Phe Gln Asp Val Leu Thr  
 245 250 255  
 Ile Gly His Leu Phe Leu Lys Gly Arg Ile Leu His Glu Gln Val Thr  
 260 265 270  
 Ala Leu Ala Gly Thr Ala Leu Lys Ser Ser Leu Arg Arg Tyr Val Ile  
 275 280 285  
 Thr Thr Lys Gly Ala Ser Phe Ser Ser Leu Ile Asn Leu Asn Asp Ile  
 290 295 300  
 Ser Asp Asn Asp Thr Leu Ile Ser Gly Asp Pro Leu Thr Gly Arg Leu  
 305 310 315 320  
 Cys Lys Lys Glu Glu Glu Pro Phe Leu Gly Phe Arg Asp His Ser Ile  
 325 330 335  
 Ser Val Leu His Asn Pro Thr Lys Arg Glu Leu Phe Ser Phe Leu Arg  
 340 345 350  
 Ile Gly Phe Asn Lys Pro Thr Phe Thr Lys Thr Tyr Leu Ser Gly Phe  
 355 360 365  
 Phe Lys Lys Lys Arg Thr Tyr Thr Asn Pro Asp Thr Asn Leu His Gly  
 370 375 380  
 Glu Thr Arg Pro Ile Ile Asp Thr Asp Ile Tyr Asp Lys Val Met Pro  
 385 390 395 400  
 Met Arg Ile Pro Val Val Pro Leu Ile Lys Ala Val Ile Thr Lys Asn  
 405 410 415  
 Phe Asp Leu Ala Asn Glu Leu Gly Phe Leu Glu Val Cys Gly Glu Asp  
 420 425 430  
 Phe Ala Leu Pro Thr Leu Ile Asp Pro Ser Lys Thr Glu Met Leu Thr



435 440 445  
 Ile Val Lys Glu Ser Leu Ile Glu Tyr Ala Lys Glu Ser Gly Ile Leu  
 450 455 460  
 Thr Pro His Gln Asp  
 465  
 <210>794  
 <211>313  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>794  
 Glu Met Ser Ser Leu Thr Leu Ser Arg Arg Pro Arg Arg Asn Arg Lys  
 1 5 10 15  
 Thr Ala Ala Ile Arg Asp Leu Leu Ala Glu Thr His Leu Ser Pro Lys  
 20 25 30  
 Asp Leu Ile Ala Pro Phe Phe Val Lys Tyr Gly Asn Asn Ile Lys Glu  
 35 40 45  
 Glu Ile Pro Ser Leu Pro Gly Val Phe Arg Trp Ser Leu Asp Leu Leu  
 50 55 60  
 Leu Lys Glu Ile Glu Arg Leu Cys Thr Tyr Gly Leu Arg Ala Val Met  
 65 70 75 80  
 Leu Phe Pro Ile Ile Pro Asp Asp Leu Lys Asp Ala Tyr Gly Ser Tyr  
 85 90 95  
 Ser Ser Asn Pro Lys Asn Ile Leu Cys His Ser Ile His Glu Ile Lys  
 100 105 110  
 Asn Ala Phe Pro His Leu Cys Leu Ile Ser Asp Ile Ala Leu Asp Pro  
 115 120 125  
 Tyr Thr Thr His Gly His Asp Gly Ile Phe Leu Asn Gly Glu Val Leu  
 130 135 140  
 Asn Asp Glu Ser Val Arg Ile Phe Gly Asn Ile Ala Thr Leu His Ala  
 145 150 155 160  
 Glu Met Gly Ala Asp Ile Val Ala Pro Ser Asp Met Met Asp Gly Arg  
 165 170 175  
 Ile Gly Tyr Ile Arg Ser Lys Leu Asp Gln Ser Gly Tyr Ser Lys Thr  
 180 185 190  
 Ser Ile Met Ser Tyr Ser Val Lys Tyr Ala Ser Cys Leu Tyr Ser Pro  
 195 200 205  
 Phe Arg Asp Ala Leu Ser Ser His Val Thr Ser Gly Asp Lys Lys Gln  
 210 215 220  
 Tyr Gln Met Asn Pro Lys Asn Val Leu Glu Ala Leu Leu Glu Ser Ser  
 225 230 235 240  
 Leu Asp Glu Glu Glu Gly Ala Asp Ile Leu Met Val Lys Pro Ala Gly  
 245 250 255  
 Leu Tyr Leu Asp Val Ile Tyr Arg Ile Arg Gln Asn Thr Cys Leu Pro  
 260 265 270  
 Leu Ala Ala Tyr Gln Val Ser Gly Glu Tyr Ala Met Ile Leu Ser Ala  
 275 280 285  
 Phe Gln Gln Gly Trp Leu Asp Lys Glu Thr Leu Phe His Glu Ser Leu  
 290 295 300  
 Ile Ala Ile Lys Arg Leu Ala Gln Ile  
 305 310  
 <210>795  
 <211>128  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>795  
 Phe Ser Gly Arg Cys Pro Phe Ser Phe Glu Val Phe Met Leu Gly Lys  
 1 5 10 15  
 Glu Glu Glu Phe Thr Cys Lys Gln Lys Gln Cys Leu Ser His Phe Val  
 20 25 30  
 Thr Asn Leu Thr Ser Asp Val Phe Ala Leu Lys Asn Leu Pro Glu Val  
 35 40 45  
 Val Lys Gly Ala Leu Phe Ser Lys Tyr Ser Arg Ser Val Leu Gly Leu  
 50 55 60  
 Arg Ala Leu Leu Leu Lys Glu Phe Leu Ser Asn Glu Glu Asp Gly Asp

65 70 75 80  
 Val Cys Asp Glu Ala Tyr Asp Phe Glu Thr Asp Val Gln Lys Ala Ala  
 85 90 95  
 Asp Phe Tyr Gln Arg Val Leu Asp Asn Phe Gly Asp Asp Ser Val Gly  
 100 105 110  
 Glu Leu Gly Gly Ala Pro Gly Tyr Gly Lys Cys Leu Tyr Phe Gly Cys  
 115 120 125  
 <210>796  
 <211>431  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>796  
 Glu Ser Leu Ala Glu His Leu Ala Met Glu Asn Val Ser Ile Leu Ala  
 1 5 10 15  
 Ala Lys Val Leu Glu Asp Ala Arg Ile Gly Gly Ser Pro Leu Glu Lys  
 20 25 30  
 Ser Thr Arg Tyr Val Tyr Phe Asp Gln Lys Val Arg Gly Glu Tyr Leu  
 35 40 45  
 Tyr Tyr Arg Asp Pro Ile Leu Met Thr Ser Ala Phe Lys Asp Met Phe  
 50 55 60  
 Leu Gly Thr Cys Asp Phe Leu Phe Asp Thr Tyr Ser Ala Leu Ile Pro  
 65 70 75 80  
 Gln Val Arg Ala Tyr Phe Glu Lys Leu Tyr Pro Lys Asp Ser Lys Thr  
 85 90 95  
 Pro Ala Ser Ala Tyr Ala Thr Ser Leu Arg Ala Lys Val Leu Asp Cys  
 100 105 110  
 Ile Arg Gly Leu Leu Pro Ala Ala Thr Leu Thr Asn Leu Gly Phe Phe  
 115 120 125  
 Gly Asn Gly Arg Phe Trp Gln Asn Leu Ile His Lys Leu Gln Gly His  
 130 135 140  
 Asn Leu Ala Glu Leu Arg Arg Leu Gly Asp Glu Ser Leu Thr Glu Leu  
 145 150 155 160  
 Met Lys Val Ile Pro Ser Phe Val Ser Arg Ala Glu Pro His His His  
 165 170 175  
 His His Gln Ala Met Met Gln Tyr Arg Arg Ala Leu Lys Glu Gln Leu  
 180 185 190  
 Lys Gly Leu Ala Glu Gln Ala Thr Phe Ser Glu Glu Met Ser Ser Ser  
 195 200 205  
 Pro Ser Val Gln Leu Val Tyr Gly Asp Pro Asp Gly Ile Tyr Lys Val  
 210 215 220  
 Ala Ala Gly Phe Leu Phe Pro Tyr Ser Asn Arg Ser Leu Thr Asp Leu  
 225 230 235 240  
 Ile Asp Tyr Cys Lys Lys Met Pro His Glu Asp Leu Val Gln Ile Leu  
 245 250 255  
 Glu Ser Ser Val Ser Ala Arg Glu Asn Arg Arg His Lys Ser Pro Arg  
 260 265 270  
 Gly Leu Glu Cys Val Glu Phe Gly Phe Asp Ile Leu Ala Asp Phe Gly  
 275 280 285  
 Ala Tyr Arg Asp Leu Gln Arg His Arg Thr Leu Thr Gln Glu Arg Gln  
 290 295 300  
 Leu Leu Ser Thr His His Gly Tyr Asn Phe Pro Val Glu Leu Leu Asp  
 305 310 315 320  
 Thr Pro Met Glu Lys Ser Tyr Arg Glu Ala Met Glu Arg Ala Asn Glu  
 325 330 335  
 Thr Tyr Asn Glu Ile Val Gln Glu Phe Pro Glu Glu Ala Gln Tyr Met  
 340 345 350  
 Val Pro Met Ala Tyr Asn Ile Arg Trp Phe Phe His Val Asn Ala Arg  
 355 360 365  
 Ala Leu Gln Trp Ile Cys Glu Leu Arg Ser Gln Pro Gln Gly His Gln  
 370 375 380  
 Asn Tyr Arg Thr Ile Ala Thr Gly Leu Val Arg Glu Val Val Lys Phe  
 385 390 395 400  
 Asn Pro Met Tyr Glu Leu Phe Phe Lys Phe Val Asp Tyr Ser Asp Ile  
 405 410 415

Asp Leu Gly Arg Leu Asn Gln Glu Met Arg Lys Glu Pro Thr Thr  
 420 425 430

&lt;210&gt;797

&lt;211&gt;292

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;797

Gly Thr Leu Val Leu His Ala Leu Asp Thr Tyr Arg Pro Ser Ile Glu  
 1 5 10 15  
 Ser Ala Ile Glu Lys Ala Leu Glu Gly Phe Gly Pro Ile Gly His Pro  
 20 25 30  
 Ile Arg Ser Pro Val Glu Tyr Ala Leu Gln Gly Gly Lys Arg Leu  
 35 40 45  
 Arg Pro Gly Leu Val Cys Met Met Ala Gln Gly Leu Gly Leu Asn His  
 50 55 60  
 Asp Val Met Asp Ser Ala Leu Ala Val Glu Phe Val His Thr Ser Thr  
 65 70 75 80  
 Leu Ile Ala Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Glu Arg Arg  
 85 90 95  
 Gly Arg Pro Thr Val His Lys Ala Phe Asp Glu Ala Thr Ala Leu Leu  
 100 105 110  
 Ala Ser Tyr Ala Leu Ile Pro Ala Ala Tyr Ser His Leu Arg Leu Asn  
 115 120 125  
 Ala Lys Lys Leu Lys Glu Gln Gly Cys Asp Pro Arg Glu Ile Asp Ile  
 130 135 140  
 Ala Tyr Asn Ile Ile Gly Asp Ile Thr Asp Lys Asn Ile Gly Cys Ser  
 145 150 155 160  
 Gly Val Leu Gly Gly Gln Tyr Asp Asp Met Phe Phe Ser Asn Arg Gly  
 165 170 175  
 Gln Glu His Val Gln Ser Ile Met Ile Lys Lys Thr Gly Ser Leu Phe  
 180 185 190  
 Glu Ile Ala Cys Ile Ser Gly Trp Leu Phe Gly Gly Gly Asp Pro Gln  
 195 200 205  
 Phe Ala Pro Ile Ile Thr Ser Phe Ser Asn Asn Phe Gly Leu Leu Phe  
 210 215 220  
 Gln Ile Lys Asp Asp Phe Ser Asp Leu Gln Lys Asp Ser Gln Gln Ile  
 225 230 235 240  
 Gly Leu Asn Tyr Ala Leu Leu Phe Gly Glu Lys Ala Ala Leu Glu Leu  
 245 250 255  
 Leu Ala Arg Ser Gln Asn Asn Cys Leu Glu Leu Leu Asp Arg Leu Ser  
 260 265 270  
 Ala Gly Gly Leu Lys Asn Ser Ser Glu Phe Glu Thr Ile Ile Ser Ser  
 275 280 285  
 Leu Gly Ser Phe  
 290

&lt;210&gt;798

&lt;211&gt;208

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;798

Met Thr Tyr Leu Ala Ser Ser Ile Phe Ser Pro Glu Asp Phe Leu Tyr  
 1 5 10 15  
 Pro Glu Ile Ile Ser Lys Ala His Tyr Thr Trp Asp Ile Leu Asp Leu  
 20 25 30  
 Met Asp Gln Met Leu Glu Asn His Val Phe Ser Gly Ile His Gly Thr  
 35 40 45  
 Val Glu Ser Gly Val Thr Leu Lys Asn Ile Glu Lys Ile Glu Ile Ala  
 50 55 60  
 Glu Asp Ala Tyr Val Glu Ser Gly Ala Tyr Ile Val Gly Pro Cys Ile  
 65 70 75 80  
 Leu Gly Ser Gln Thr Glu Val Arg His Gly Ala Tyr Leu Arg Gly Asn  
 85 90 95  
 Val Ile Thr Gly Ser Arg Cys Val Val Gly His Cys Thr Glu Ile Lys  
 100 105 110

Asn Ser Tyr Leu Gly His His Thr Lys Ala Ala His Phe Ala Tyr Leu  
 115 120 125  
 Gly Asp Ser Val Leu Ser Ser Glu Val Asn Leu Gly Ala Gly Val Arg  
 130 135 140  
 Cys Ala Asn Phe Arg Leu Asp Gly Arg Asn Ile Tyr Val Arg Ser Thr  
 145 150 155 160  
 Ser Asp Lys Ser Lys Lys Ile Asp Thr Gly Arg Arg Lys Leu Gly Ala  
 165 170 175  
 Phe Leu Gly Lys Gly Val Ala Ile Gly Cys Asn Val Val Ile Asn Pro  
 180 185 190  
 Gly Gln His Ile Leu Pro His Thr Arg Ile Arg Pro Gly Gln Val Ile  
 195 200 205

&lt;210&gt;799

&lt;211&gt;241

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;799

Asn Leu Phe Cys Phe His Met Ile Gly Asp Lys Ile Ile Leu Phe Val  
 1 5 10 15  
 Thr Glu Asp Leu Ser Leu Ser Ser Gln Leu Lys Asp Leu Ala Ser Gln  
 20 25 30  
 Arg Ser Asp Tyr Gln Ile Leu Val Ser Pro Val Phe Pro Thr Ser Phe  
 35 40 45  
 Glu Ser Val Ala Ile Phe Cys Glu Tyr Leu Leu Leu Pro Glu Gln Ile  
 50 55 60  
 Phe Ser Pro Gly Ile Phe Pro Glu Glu Asp Leu Ile Val Leu Phe Asp  
 65 70 75 80  
 Thr Phe Gln Glu Glu Ala Ile Thr Lys Val Leu Asn Gln Gly Ala Thr  
 85 90 95  
 Gly Tyr Leu Leu Arg Pro Ile Thr Ala Lys Val Leu Asp Ala Val Ile  
 100 105 110  
 Arg Ala Phe Leu Arg Gln His Glu Val Leu Glu His Ser Ile Pro Asp  
 115 120 125  
 Thr Met Thr Phe Gly Asp His Thr Phe Arg Val Leu Asn Leu Val Ile  
 130 135 140  
 Glu Ser Pro Glu Gly Ser Val Tyr Leu Thr Pro Ser Glu Ala Gly Ile  
 145 150 155 160  
 Leu Lys Lys Leu Leu Ile Asn Arg Gly His Leu Cys Leu Arg Lys Asn  
 165 170 175  
 Leu Leu Ala Glu Ile Lys Gly Asn Thr Lys Glu Ile Ile Ala Arg Asn  
 180 185 190  
 Val Asp Val His Ile Ala Ser Leu Arg Lys Lys Leu Gly Pro Tyr Gly  
 195 200 205  
 Ser Lys Ile Val Thr Ile Arg Gly Val Gly Tyr Leu Phe Ser Asp Ala  
 210 215 220  
 Asp Ser Ile Pro Leu Gln Asn His Asp Asn Thr Ala His Pro Ile Glu  
 225 230 235 240  
 Glu

&lt;210&gt;800

&lt;211&gt;609

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;800

Met Phe Arg Cys Ile Leu Phe Gly Ile Phe Leu Leu Thr Cys Phe Ser  
 1 5 10 15  
 Ser Gly Gly Val Leu Tyr Tyr Leu Phe Cys Ser His Asp Phe Ser Ile  
 20 25 30  
 Gly Pro Lys Glu Lys Ser Arg Ser Val Trp Ile Glu Glu Glu Lys Glu  
 35 40 45  
 Phe Thr Asp Ser Val Leu His His Leu Pro Ser Gln His Gln His Leu  
 50 55 60  
 His Ile Leu Cys Phe Gln Gly Phe Leu Leu Gln Lys Gln Gln Lys Phe  
 65 70 75 80

Ser Gln Ala Glu Lys Ile Phe Ser Lys Val Tyr Asp Glu Ala Gln Asp  
 85 90 95  
 Gly Pro Phe Leu Phe Lys Glu Glu Ile Leu Gly Ser Arg Leu Ile Asn  
 100 105 110  
 Ser Phe Phe Leu Glu Lys Thr Asp Val Met Glu Thr Ile Leu Cys Leu  
 115 120 125  
 Leu Asn Gln Arg Cys Pro Asn Ser Pro Tyr Tyr His Leu Phe Lys Ala  
 130 135 140  
 Leu Val Cys Tyr Lys Gln Lys Leu Tyr Arg Glu Val Ile Glu Gln Leu  
 145 150 155 160  
 Ala Tyr Trp Gln Glu Glu Lys Thr Arg Ala Leu Ala Pro Leu Leu Asn  
 165 170 175  
 Ile Ser Ile Glu Gln Leu Leu Thr Asp Phe Leu Leu Asp Tyr Ile Ser  
 180 185 190  
 Ala His Ser Leu Ile Glu Gln Lys Met Phe Pro Glu Gly Arg Val Ile  
 195 200 205  
 Leu Asn Arg Asn Ile Asn Arg Leu Leu Lys His Glu Cys Glu Trp Asn  
 210 215 220  
 Ala Lys Thr Tyr Asp Arg Ile Ala Ile Leu Leu Ser Arg Ser Tyr Phe  
 225 230 235 240  
 Leu Glu Leu Val Glu Ser Lys Ser Ala Asp Ile Tyr Phe Asp Tyr Tyr  
 245 250 255  
 Glu Met Val Leu Phe Tyr Leu Lys Lys Ile Tyr Ile Leu Glu Gln Cys  
 260 265 270  
 Pro Tyr Ala Glu Leu Leu Pro Glu Glu Glu Leu Val Ser Leu Ile Met  
 275 280 285  
 Glu His Val Phe Ile Leu Pro Lys Asp Lys Leu Tyr Pro Leu Ile Gln  
 290 295 300  
 Leu Leu Glu Met Trp Gln Lys His Tyr Val His Pro Asn Ser Ser Leu  
 305 310 315 320  
 Val Val Gln Ile Leu Val Asp Arg Phe Ser Thr His Met Glu Gly Ala  
 325 330 335  
 Ile Arg Phe Cys Glu Ala Leu Val Ser Phe Ser Gly Leu Glu Glu Leu  
 340 345 350  
 His Gln Gln Ile Ile Thr Thr Phe Glu Glu Leu Leu Ser Asn Lys Val  
 355 360 365  
 Gln Gln Ile Lys Thr Glu Glu Ala Lys Gln Cys Val Ala Leu Leu His  
 370 375 380  
 Ile Leu Asp Pro Ser Ile Ser Ile Ser Glu Lys Leu Ala Leu Ser Ser  
 385 390 395 400  
 Asp Thr Leu Gln Asn Ile Val Ser Gly Asp Asp Glu Gln His Thr Lys  
 405 410 415  
 Leu Arg Asn Tyr Leu Asp Leu Trp Glu Ala Ile Gln Ser Tyr Asp Ile  
 420 425 430  
 Asp Arg Gln Gln Leu Val His His Leu Val Tyr Gly Ala Lys Asp Leu  
 435 440 445  
 Trp Lys Lys Gly Gly Ser Asp Glu Lys Ala Leu Asn Leu Leu Gln Leu  
 450 455 460  
 Val Leu Arg Phe Thr Ser Tyr Asp Ile Glu Cys Glu Ser Val Val Phe  
 465 470 475 480  
 Leu Phe Ile Lys Gln Ala Tyr Lys Gln Ala Leu Ser Ser His Ala Ile  
 485 490 495  
 Ala Arg Leu Leu Lys Leu Glu Lys Phe Ile Ser Glu Ala Asn Ile Pro  
 500 505 510  
 Ser Ile Val Ile Ser Glu Ala Glu Lys Ala Asn Phe Leu Ala Asp Ala  
 515 520 525  
 Glu Tyr Leu Phe Ala His Glu Asp Tyr Asp Lys Cys Tyr Leu Tyr Ser  
 530 535 540  
 Met Trp Leu Thr Lys Val Ala Pro Ser Pro Gln Ser Tyr Arg Leu Ala  
 545 550 555 560  
 Gly Leu Cys Leu Met Glu Asn Lys Arg Tyr Asp Glu Ala Leu Glu Phe  
 565 570 575  
 Leu Cys Met Leu Ser Pro Asn Asp Ser Ile Asn Asp Tyr Lys Thr Gln  
 580 585 590

Lys Ala Leu Ala Phe Cys Gln Lys His Gln Ser Lys Asp Arg Ala Ala  
 595 600 605  
 Ser

&lt;210&gt;801

&lt;211&gt;295

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;801

Gly Trp Ala Leu His Thr Glu Phe Ala Pro Phe Leu Glu Asp Leu Val  
 1 5 10 15  
 His Gln Gln Val Ile Ser Pro Leu Asp Ile Ala Phe Ala Ser Lys His  
 20 25 30  
 Ile Ser Ser Asp Phe Glu Glu Ser Phe Val Phe Leu Ala Val Ser Ser  
 35 40 45  
 Ala Leu Trp Arg Tyr Gly His Pro Phe Leu Ser Leu Glu Glu Asn Arg  
 50 55 60  
 Ile Arg Pro Ser Leu Gly Gly Ile Ser Glu Thr Asp Leu Tyr Arg Gly  
 65 70 75 80  
 Phe His Asn Leu Pro Lys Glu Val Arg Asp Lys Leu Phe Val Val Val  
 85 90 95  
 Ser Gly Arg Leu Tyr Leu Arg Ser Leu Tyr Thr Ile Arg Ser Lys Leu  
 100 105 110  
 Leu Asp Lys Leu Ser Leu Leu Cys Ser Ala Thr Pro Asn Tyr Phe Pro  
 115 120 125  
 Pro Ser Ile Asp Ser Ser Ile Leu Ser Glu Glu Gln Asn Phe Ile Phe  
 130 135 140  
 Asn Lys Ile Thr Gln Gly Cys Phe Ser Ile Val Ser Gly Gly Pro Gly  
 145 150 155 160  
 Thr Gly Lys Thr Phe Leu Ala Ala Gln Leu Ile Leu Ser Leu Val Lys  
 165 170 175  
 Gln Gln Pro Lys Leu Arg Ile Ala Ile Val Ser Pro Thr Gly Lys Ala  
 180 185 190  
 Thr Ser His Ile Arg Gln Ile Leu Met Lys Tyr Asn Ile Phe Asp Asp  
 195 200 205  
 Met Val Leu Met Gln Thr Val His His Phe Leu Gln Glu Tyr Ala Tyr  
 210 215 220  
 Arg Arg Tyr Asn Ser Ile Asp Val Leu Leu Val Asp Glu Gly Ser Met  
 225 230 235 240  
 Val Thr Phe Asp Leu Leu Tyr Ser Leu Val Gln Thr Leu Gln Gly Tyr  
 245 250 255  
 Glu Lys Asp Lys Lys Leu Tyr Thr Ser Ser Leu Ile Ile Leu Gly Asp  
 260 265 270  
 Thr Asn Gln Leu Pro Pro Ile Gly Ile Gly Val Gly Asn Pro Leu Gln  
 275 280 285  
 Asp Leu Ile Gly Tyr Phe Pro  
 290 295

&lt;210&gt;802

&lt;211&gt;205

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;802

Asp Ile Ser His Glu Asn Thr Phe Phe Leu Lys Thr Ser His Arg Ala  
 1 5 10 15  
 Lys Thr Gly Val Val Asp Gln Leu Thr Gln Ser Val Leu Arg Gly Glu  
 20 25 30  
 Met Ile Ser Phe Ser Pro Leu Pro Ser Ile Ser Ser Ala Ile Glu Val  
 35 40 45  
 Leu Lys Asn Arg Phe Val Lys Ser Leu Arg Gln Ser Glu Ala Arg Leu  
 50 55 60  
 Cys Val Leu Thr Pro Met Arg His Gly Pro Trp Gly Val Leu Asn Leu  
 65 70 75 80  
 Asn Thr Met Ile His Gln Arg Leu Ala Arg Ser Asp Pro Asp Leu Arg  
 85 90 95

```

Ile Pro Ile Met Val Thr Ser Arg Tyr Glu Thr Trp Gly Leu Phe Asn
      100      105      110
Gly Asp Thr Gly Leu Leu Cys Leu Lys Thr Gln Lys Leu His Phe Pro
      115      120      125
Gln His Glu Pro Ile Asp Ser Arg Ala Leu Ser Gln Tyr Val Tyr Asn
      130      135      140
Tyr Val Met Ser Val His Lys Ser Gln Gly Ser Glu Tyr Asp Glu Val
145      150      155      160
Ile Val Ile Ile Pro Lys Gly Ser Glu Val Phe Gly Val Ser Ile Leu
      165      170      175
Tyr Thr Ala Ile Thr Arg Ala Lys Tyr Arg Val Ser Val Trp Arg Asp
      180      185      190
Pro Glu Thr Leu His Lys Thr Ile Lys Lys Ser Asn Tyr
      195      200      205

```

&lt;210&gt;803

&lt;211&gt;283

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;803

```

Ile Met Ala Thr Ala His Leu Gly Arg Gln Ala Leu Leu His Leu Arg
 1      5      10      15
Ser Trp Thr Pro Ala Ile Arg Ala Ser Gly Asn Leu Phe Arg Gln Gln
      20      25      30
Ser Met Ser Leu His Asn Asn Val Leu Phe Ala Gly Asp Ile Val Gly
      35      40      45
Ala Ile Lys Asn Ser Thr Ala Ile Ser Arg His Ala Leu Gly Ser Ser
      50      55      60
His Tyr Ala His Ala Ala Leu Gln Lys Thr Glu Gly Phe Leu Gly Ala
65      70      75      80
Ala Asp Gly Val Asn Thr Ala Val Ala Gly Ala Met Leu Trp Gly Gln
      85      90      95
Leu Leu Asn Gly Ser Met Ile Phe Glu Thr Asp Glu Glu Thr Gly Glu
      100      105      110
Leu Arg Arg Cys Asn Glu Ala Asp Ala Glu Gly Cys Met Thr Gln Lys
      115      120      125
Leu Gln Arg Arg Ser Ala Leu Thr Ile Thr Gly Lys Val Ala Arg Leu
      130      135      140
Ala Ser Lys Thr Leu Gly Thr Ala Thr Phe Leu His Glu Met Asp Val
145      150      155      160
Val Ser Leu Gly Ala Asn Ala Asn Lys Ile Gly Cys Lys Val Thr Ser
      165      170      175
Cys Leu Asn Leu Val Ala Thr Gly Cys Ser Leu Thr Glu Ser Ser Ile
      180      185      190
Ser Leu Tyr Arg Ile Leu Ser Thr Arg Pro Glu Thr Ile Ser Asp Pro
      195      200      205
Glu Asn Arg Asn Lys Pro Ser Ala Glu Phe Ala Ala Arg Ser Lys Ala
      210      215      220
Ile Arg Asn Ala Phe Ile Ala Trp Leu Gly Asp Val Val Asp Leu Val
225      230      235      240
Cys Asp Ala Leu Gly Thr Leu Ser Leu Phe Leu Pro Ala Ile Leu Gly
      245      250      255
Val His Ala Val Leu Ile Met Ala Ile Leu Gly Leu Ile Ser Cys Val
      260      265      270
Ile Asn Phe Val Lys Asp Tyr Ala Lys Ile Gly
      275      280

```

&lt;210&gt;804

&lt;211&gt;88

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;804

```

Tyr Thr Lys Lys Thr Ser Ala Glu Lys Arg Ile Leu Thr Ala Gln Lys
 1      5      10      15
Arg Glu Leu Ile Asn His Ser Phe Lys Ser Lys Val Lys Thr Ile Val
      20      25      30

```

Lys Lys Phe Glu Ala Ser Leu Lys Leu Asp Asp Thr Gln Ala Thr Leu  
                   35                  40                  45  
 Ser Asn Leu Gln Ser Val Tyr Ser Val Val Asp Lys Ala Val Lys Arg  
                   50                  55                  60  
 Gly Ile Phe Lys Asp Asn Lys Ala Ala Arg Ile Lys Ser Lys Ala Thr  
                   65                  70                  75                  80  
 Leu Lys Val Asn Ala Arg Ala Ser  
                                   85

&lt;210&gt;805

&lt;211&gt;407

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;805

Tyr Lys Asp Leu Phe Phe Met Leu Leu Val Arg Lys Trp Leu His Thr  
   1                  5                  10                  15  
 Cys Phe Lys Tyr Trp Ile Tyr Phe Leu Pro Val Val Thr Leu Leu Leu  
                   20                  25                  30  
 Pro Leu Val Cys Tyr Pro Phe Leu Ser Ile Ser Gln Lys Ile Tyr Gly  
                   35                  40                  45  
 Tyr Phe Val Phe Thr Thr Ile Ser Ser Leu Gly Trp Phe Phe Ala Leu  
                   50                  55                  60  
 Arg Arg Arg Glu Asn Gln Leu Lys Thr Ala Ala Val Gln Leu Leu Gln  
                   65                  70                  75                  80  
 Thr Lys Ile Arg Lys Leu Thr Glu Asn Asn Glu Gly Leu Arg Gln Ile  
                   85                  90                  95  
 Arg Glu Ser Leu Lys Glu His Gln Gln Glu Ser Ala Gln Leu Gln Ile  
                   100                  105                  110  
 Gln Ser Gln Lys Leu Lys Asn Ser Leu Phe His Leu Gln Gly Leu Leu  
                   115                  120                  125  
 Val Lys Thr Lys Gly Glu Gly Gln Lys Leu Glu Thr Leu Leu Leu His  
                   130                  135                  140  
 Arg Thr Glu Glu Asn Arg Cys Leu Lys Met Gln Val Asp Ser Leu Ile  
  145                  150                  155                  160  
 Gln Glu Cys Gly Glu Lys Thr Glu Glu Val Gln Thr Leu Asn Arg Glu  
                   165                  170                  175  
 Leu Ala Glu Thr Leu Ala Tyr Gln Gln Ala Leu Asn Asp Glu Tyr Gln  
                   180                  185                  190  
 Ala Thr Phe Ser Glu Gln Arg Asn Met Leu Asp Lys Arg Gln Ile Tyr  
                   195                  200                  205  
 Ile Gly Lys Leu Glu Asn Lys Val Gln Asp Leu Met Tyr Glu Ile Arg  
                   210                  215                  220  
 Asn Leu Leu Gln Leu Glu Ser Asp Ile Ala Glu Asn Ile Pro Ser Gln  
  225                  230                  235                  240  
 Glu Ser Asn Ala Val Thr Gly Asn Ile Ser Leu Gln Leu Ser Ser Glu  
                   245                  250                  255  
 Leu Lys Lys Ile Ala Phe Lys Ala Glu Asn Ile Glu Ala Ala Ser Ser  
                   260                  265                  270  
 Leu Thr Ala Ser Arg Tyr Leu His Thr Asp Thr Ser Val His Asn Tyr  
                   275                  280                  285  
 Ser Leu Glu Cys Arg Gln Leu Phe Asp Ser Leu Arg Glu Glu Asn Leu  
                   290                  295                  300  
 Gly Met Leu Phe Val Tyr Ala Arg Gln Ser Gln Arg Ala Val Phe Ala  
  305                  310                  315                  320  
 Asn Ala Leu Phe Lys Thr Trp Thr Gly Tyr Cys Ala Glu Asp Phe Leu  
                   325                  330                  335  
 Lys Phe Gly Ser Asp Ile Val Ile Ser Gly Gly Lys Gln Trp Met Glu  
                   340                  345                  350  
 Asp Leu His Ser Ser Arg Glu Glu Cys Ser Gly Arg Leu Val Ile Lys  
                   355                  360                  365  
 Thr Lys Ser Arg Gly His Leu Pro Phe Arg Tyr Cys Leu Met Ala Leu  
                   370                  375                  380  
 Asn Lys Gly Pro Leu Cys Tyr His Val Leu Gly Val Leu Tyr Pro Leu  
  385                  390                  395                  400  
 His Lys Glu Val Leu Gln Ser



405

&lt;210&gt;806

&lt;211&gt;591

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;806

```

Leu Thr Lys Leu Ser Ser Lys Ala Arg Asn Pro Leu Val Leu Phe Gln
 1          5          10          15
Val Arg Lys Leu Phe Met Asn Thr Gln Asn Ser Gln Ala Thr Glu Val
          20          25          30
Ser Ser Glu Glu Glu Ser Gln Lys Lys Leu Glu Glu Leu Val Ala Leu
          35          40          45
Ala Lys Glu Gln Gly Phe Ile Thr Tyr Glu Glu Ile Asn Glu Ile Leu
          50          55          60
Pro Met Ser Phe Asp Thr Pro Glu Gln Ile Asp Gln Val Leu Ile Phe
          65          70          75          80
Leu Thr Gly Met Asp Ile Gln Val Leu Asn Gln Ile Asp Val Glu Arg
          85          90          95
Gln Lys Glu Lys Lys Lys Glu Ala Lys Glu Leu Glu Gly Leu Ala Arg
          100          105          110
Arg Thr Glu Gly Thr Pro Asp Asp Pro Val Arg Met Tyr Leu Lys Glu
          115          120          125
Met Gly Thr Val Pro Leu Leu Thr Arg Glu Glu Glu Val Glu Ile Ser
          130          135          140
Lys Arg Ile Glu Lys Ala Gln Val Gln Ile Glu Arg Ile Ile Leu Arg
          145          150          155          160
Phe Arg Tyr Ser Ala Lys Glu Ala Ile Ser Ile Ala His Tyr Leu Ile
          165          170          175
Ser Gly Lys Glu Arg Phe Asp Lys Ile Ser Glu Lys Glu Val Glu
          180          185          190
Asp Lys Thr His Phe Leu Lys Leu Leu Pro Lys Leu Ile Thr Leu Leu
          195          200          205
Lys Glu Glu Asp Thr Tyr Leu Glu Asn Leu Leu Leu Ser Leu Lys Gln
          210          215          220
Pro Asp Leu Ser Lys Gln Glu Ala Ala Lys Leu Asn Asp Ser Leu Glu
          225          230          235          240
Lys Cys Arg Ile Arg Thr Gln Ala Tyr Leu Arg Cys Phe His Cys Arg
          245          250          255
His Asn Val Thr Glu Asp Phe Gly Glu Val Val Phe Lys Ala Tyr Asp
          260          265          270
Ser Phe Leu His Leu Glu Gln Gln Ile Asn Asp Leu Lys Val Arg Ala
          275          280          285
Glu Arg Asn Lys Phe Ala Ala Ala Lys Leu Ala Ala Ala Lys Arg Lys
          290          295          300
Leu Tyr Lys Arg Glu Val Ala Ala Gly Arg Thr Leu Glu Glu Phe Lys
          305          310          315          320
Lys Asp Val Arg Met Leu Gln Arg Trp Met Asp Lys Ser Gln Glu Ala
          325          330          335
Lys Lys Glu Met Val Glu Ser Asn Leu Arg Leu Val Ile Ser Ile Ala
          340          345          350
Lys Lys Tyr Thr Asn Arg Gly Leu Ser Phe Leu Asp Leu Ile Gln Glu
          355          360          365
Gly Asn Met Gly Leu Met Lys Ala Val Glu Lys Phe Glu Tyr Arg Arg
          370          375          380
Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Val
          385          390          395          400
Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile Pro Val His
          405          410          415
Met Ile Glu Thr Ile Asn Lys Val Leu Arg Gly Ala Lys Lys Leu Met
          420          425          430
Met Glu Thr Gly Lys Glu Pro Thr Pro Glu Glu Leu Ala Glu Glu Leu
          435          440          445
Gly Leu Thr Pro Asp Arg Val Arg Glu Ile Tyr Lys Ile Ala Gln His
          450          455          460

```

Pro Ile Ser Leu Gln Ala Glu Val Gly Glu Gly Ser Glu Ser Ser Phe  
 465 470 475 480  
 Gly Asp Phe Leu Glu Asp Thr Ala Val Glu Ser Pro Ala Glu Ala Thr  
 485 490 495  
 Gly Tyr Ser Met Leu Lys Asp Lys Met Lys Glu Val Leu Lys Thr Leu  
 500 505 510  
 Thr Asp Arg Glu Arg Phe Val Leu Ile His Arg Phe Gly Leu Leu Asp  
 515 520 525  
 Gly Lys Pro Lys Thr Leu Glu Glu Val Gly Ser Ala Phe Asn Val Thr  
 530 535 540  
 Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg Lys Met Arg  
 545 550 555 560  
 His Pro Ile Arg Ser Lys Gln Leu Arg Ala Phe Leu Asp Leu Leu Glu  
 565 570 575  
 Glu Glu Lys Thr Gly Thr Ser Lys Val Lys Ser Leu Lys Ser Lys  
 580 585 590

&lt;210&gt;807

&lt;211&gt;142

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;807

Pro Cys Ile Lys Asn Ile Ala Leu Val Ile Ala Ile Glu Arg Tyr Gln  
 1 5 10 15  
 Leu Ile Ile Ser Lys Phe Arg Met Trp Leu Phe Leu Gly Cys Ser Val  
 20 25 30  
 Glu Glu Arg His Phe Lys Gln Pro Val Leu Ile Ser Val Thr Phe Ser  
 35 40 45  
 Tyr Asn Glu Val Pro Ser Ala Cys Leu Ser Asp Lys Leu Ser Asp Ala  
 50 55 60  
 Cys Cys Tyr Leu Glu Val Thr Ser Leu Ile Glu Glu Ile Ala Asn Thr  
 65 70 75 80  
 Lys Pro Tyr Ala Leu Ile Glu His Leu Ala Asn Glu Leu Phe Asp Ser  
 85 90 95  
 Leu Val Ile Ser Phe Gly Asp Lys Ala Ser Lys Ile Asp Leu Glu Val  
 100 105 110  
 Glu Lys Glu Arg Pro Pro Val Pro Asn Leu Leu Asn Pro Ile Lys Phe  
 115 120 125  
 Thr Ile Ser Lys Glu Leu Cys Pro Ser Pro Val Leu Ser Ala  
 130 135 140

&lt;210&gt;808

&lt;211&gt;452

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;808

Arg Ala Met Ser Glu Pro Arg Phe Val Cys Leu Ser Leu Gly Ser Asn  
 1 5 10 15  
 Leu Gly Asn Arg Phe Lys Asn Leu Gln Ile Ala Arg Thr Leu Leu Gly  
 20 25 30  
 Glu Gln Ala Val Leu Gly Leu Arg Ser Ser Val Ile Leu Glu Thr Glu  
 35 40 45  
 Ala Leu Leu Leu Pro Gly Ser Pro Pro Glu Trp Asp Leu Pro Tyr Phe  
 50 55 60  
 Asn Ser Val Leu Val Gly Thr Thr Leu Ser Leu Arg Glu Leu Leu  
 65 70 75 80  
 Val Thr Ile Lys Gln Ile Glu Lys Val Val Gly Arg Ala Glu Glu Ser  
 85 90 95  
 Pro Pro Trp Ser Pro Arg Thr Ile Asp Val Asp Ile Leu Leu Tyr Gly  
 100 105 110  
 Asp Glu Ser Phe Cys Cys Asp His Thr Glu Ile Thr Ile Pro Leu Ser  
 115 120 125  
 Asn Leu Leu Ser Arg Pro Phe Leu Ile Ala Leu Ile Ala Ser Leu Cys  
 130 135 140  
 Pro Tyr Arg Arg Phe Cys Thr Gln Gly Ser Pro Tyr His Asn Phe Thr  
 145 150 155 160

Phe Gly Glu Leu Ala His His Leu Pro Ser Pro Pro Gly Met Ile Arg  
 165 170 175  
 Arg Ser Leu Ser Pro Asp Thr Met Leu Met Gly Val Val Asn Val Thr  
 180 185 190  
 Asn Asp Ser Met Ser Asp Gly Gly Met Phe Leu Asp Pro Glu Lys Ala  
 195 200 205  
 Val Ala Gln Ala Glu Lys Leu Phe Thr Glu Gly Ala Ala Val Ile Asp  
 210 215 220  
 Phe Gly Ala Gln Ala Thr Asn Pro Lys Val Lys Gln Phe Leu Ser Val  
 225 230 235 240  
 Asp Gln Glu Trp Glu Arg Leu Glu Pro Val Leu Arg Leu Leu Lys Glu  
 245 250 255  
 Thr Trp Ser Asn Arg Lys Gln Tyr Pro Ile Ile Ser Leu Asp Thr Phe  
 260 265 270  
 Tyr Pro Glu Ile Ile Leu Arg Ala Met Asp Ile Tyr Pro Ile Gln Trp  
 275 280 285  
 Ile Asn Asp Val Ser Gly Gly Ser Gln Ser Met Ala Glu Val Ala Arg  
 290 295 300  
 Asp Cys Glu Leu Ser Leu Val Met Asn His Ser Ser Ser Leu Pro Val  
 305 310 315 320  
 Asp Pro Lys Asn Ile Leu Ser Phe Ser Val Pro Ile Gly Glu Gln Leu  
 325 330 335  
 Leu Ser Trp Gly Glu Lys Gln Leu Lys Met Phe Ser Asp Val Gly Leu  
 340 345 350  
 Asn Ala Asn Gln Val Ile Phe Asp Pro Gly Ile Gly Phe Gly Lys Gly  
 355 360 365  
 Ala Ala Gln Ser Leu Ala Thr Leu Tyr Glu Ile Ala Lys Phe Lys Arg  
 370 375 380  
 Leu Gly Cys Pro Ile Leu Ile Gly His Ser Arg Lys Ser Phe Leu Ser  
 385 390 395 400  
 Leu Phe Gly Asn His Asp Pro Lys Asp Arg Asp Trp Glu Thr Val Gly  
 405 410 415  
 Leu Ser Ile Leu Leu Gln Gln Gln Gly Val Asp Tyr Leu Arg Val His  
 420 425 430  
 Asn Val Ala Ala His Gln Lys Ala Leu Ser Val Ala Ala Cys Glu Ala  
 435 440 445  
 Cys Ala Pro Ile  
 450

&lt;210&gt;809

&lt;211&gt;186

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;809

Val Lys Pro Val His Pro Ser Asn Phe Glu Asn Pro Leu Gly Val Glu  
 1 5 10 15  
 Met Cys Lys Asn Arg Gly Val Arg Gly Ile Val Ala Cys Asp Pro Arg  
 20 25 30  
 Gly Val Ile Gly Leu Glu Gly Lys Leu Pro Trp His Tyr Pro Glu Asp  
 35 40 45  
 Leu Gln Phe Phe Ser Glu Thr Ile Gln Lys Phe Pro Ile Val Met Gly  
 50 55 60  
 Arg Lys Thr Trp Glu Thr Leu Pro Arg Lys Tyr Phe Val Asp Arg Ala  
 65 70 75 80  
 Val Val Val Phe Ser His Glu Lys Arg Gln Gly Val His Gly Glu Ile  
 85 90 95  
 Trp Val Thr Ser Leu Glu Glu Phe Leu Leu Leu Asp Leu Ser Ser Pro  
 100 105 110  
 Thr Phe Leu Ile Gly Gly Gly Glu Leu Tyr Ser Leu Phe Leu Glu Asn  
 115 120 125  
 Gln Ile Val Arg Asp Phe Phe Ile Ser His Ile Lys Lys Glu Tyr Ala  
 130 135 140  
 Gly Asp Thr Phe Phe Pro Leu Ser Leu Leu Glu Thr Trp Thr Lys Thr  
 145 150 155 160  
 Val Leu Arg Asp Thr Gln Lys Ile Thr Thr Cys Tyr Tyr Glu Asn His

165 170 175  
 His Ser Gln Asn Thr Lys Asn Ile Ser Leu  
 180 185  
 <210>810  
 <211>264  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>810  
 Arg His Gly Pro Lys Leu Cys Leu Glu Ile Pro Lys Arg Ser Gln Arg  
 1 5 10 15  
 Val Thr Met Lys Ile Thr Thr Val Lys Thr Pro Lys Ile Tyr Pro Tyr  
 20 25 30  
 Asp Asp Leu Tyr Ser Ile Leu Glu Ser Ser Leu Pro Lys Leu Asn Glu  
 35 40 45  
 Arg Ser Ile Val Val Ile Thr Ser Lys Ile Val Ser Leu Cys Glu Gly  
 50 55 60  
 Ala Val Val Glu Leu Glu Lys Val Ser Lys Asp Glu Leu Ile Lys Gln  
 65 70 75 80  
 Glu Ala Asp Ala Tyr Val Phe Val Glu Lys Tyr Gly Ile Tyr Leu Thr  
 85 90 95  
 Lys Lys Trp Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn  
 100 105 110  
 Val Glu Gly Tyr Phe Val Leu Tyr Pro Arg Asp Val Leu Leu Ser Val  
 115 120 125  
 Asn Thr Leu Gly Asp Trp Leu Arg Asn Phe Tyr His Leu Glu His Cys  
 130 135 140  
 Gly Ile Ile Ile Ser Asp Ser His Thr Thr Pro Leu Arg Arg Gly Thr  
 145 150 155 160  
 Met Gly Leu Gly Leu Cys Trp Asn Gly Phe Phe Pro Leu Tyr Asn Tyr  
 165 170 175  
 Val Gly Lys Pro Asp Cys Phe Gly Arg Ala Leu Lys Met Thr Tyr Ser  
 180 185 190  
 Asn Leu Leu Asp Gly Leu Ser Ala Ala Ala Val Leu Cys Met Gly Glu  
 195 200 205  
 Gly Asp Glu Gln Thr Pro Ile Ala Ile Ile Glu Glu Ala Pro Lys Ile  
 210 215 220  
 Thr Phe His Ser Ser Pro Thr Thr Leu Gln Asp Met Ser Thr Leu Ala  
 225 230 235 240  
 Ile Ala Glu Asp Glu Asp Leu Tyr Gly Pro Leu Leu Gln Ser Met Ala  
 245 250 255  
 Trp Glu Thr Pro Ala Pro Thr Ser  
 260

<210>811  
 <211>226  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>811  
 Gly Ile Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp  
 1 5 10 15  
 Gln His Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys  
 20 25 30  
 Leu Glu Lys Gln Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr Leu His  
 35 40 45  
 Ile Lys Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp  
 50 55 60  
 Asp Leu Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu  
 65 70 75 80  
 Ala Gly Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser  
 85 90 95  
 Leu Gly Val Ser Glu Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala  
 100 105 110  
 Ala Gln Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln  
 115 120 125  
 Leu Ala Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro

130 135 140  
 Gln Val Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val  
 145 150 155 160  
 Ser Ala Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile  
 165 170 175  
 Lys His Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg  
 180 185 190  
 Glu Asn Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr  
 195 200 205  
 Leu Trp Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser  
 210 215 220  
 Cys Lys  
 225  
 <210>812  
 <211>361  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>812  
 Met Glu Thr Lys Arg Ser Ile Tyr Met Asn Leu Pro Asp Arg Lys Lys  
 1 5 10 15  
 Ala Leu Glu Ala Val Ala Tyr Ile Glu Lys Gln Phe Gly Ala Gly  
 20 25 30  
 Ser Ile Met Ser Leu Gly Arg His Ser Ala Thr His Glu Ile Ser Thr  
 35 40 45  
 Ile Lys Thr Gly Ala Leu Ser Leu Asp Leu Ala Leu Gly Ile His Gly  
 50 55 60  
 Val Pro Lys Gly Arg Val Ile Glu Ile Phe Gly Pro Glu Ser Ser Gly  
 65 70 75 80  
 Lys Thr Thr Leu Ala Thr His Ile Val Ala Asn Ala Gln Lys Met Gly  
 85 90 95  
 Gly Val Ala Ala Tyr Ile Asp Ala Glu His Ala Leu Asp Pro Ser Tyr  
 100 105 110  
 Ala Ser Leu Ile Gly Val Asn Ile Asp Asp Leu Met Ile Ser Gln Pro  
 115 120 125  
 Asp Cys Gly Glu Asp Ala Leu Ser Ile Ala Glu Leu Leu Ala Arg Ser  
 130 135 140  
 Gly Ala Val Asp Val Ile Val Ile Asp Ser Val Ala Ala Leu Val Pro  
 145 150 155 160  
 Lys Ser Glu Leu Glu Gly Asp Ile Gly Asp Val His Val Gly Leu Gln  
 165 170 175  
 Ala Arg Met Met Ser Gln Ala Leu Arg Lys Leu Thr Ala Thr Leu Ser  
 180 185 190  
 Arg Ser Gln Thr Cys Ala Val Phe Ile Asn Gln Ile Arg Glu Lys Ile  
 195 200 205  
 Gly Val Ser Phe Gly Asn Pro Glu Thr Thr Thr Gly Gly Arg Ala Leu  
 210 215 220  
 Lys Phe Tyr Ser Ser Ile Arg Leu Asp Ile Arg Arg Ile Gly Ser Ile  
 225 230 235 240  
 Lys Gly Ser Asp Asn Ser Asp Ile Gly Asn Arg Ile Lys Val Lys Val  
 245 250 255  
 Ala Lys Asn Lys Leu Ala Pro Pro Phe Arg Ile Ala Glu Phe Asp Ile  
 260 265 270  
 Leu Phe Asn Glu Gly Ile Ser Ser Ala Gly Cys Ile Leu Asp Leu Ala  
 275 280 285  
 Val Glu Tyr Asn Ile Ile Glu Lys Lys Gly Ser Trp Phe Asn Tyr Gln  
 290 295 300  
 Glu Lys Lys Leu Gly Gln Gly Arg Glu Phe Val Arg Glu Glu Leu Lys  
 305 310 315 320  
 Arg Asn Arg Lys Leu Phe Glu Glu Ile Glu Lys Arg Ile Tyr Asp Val  
 325 330 335  
 Ile Ala Ala Asn Lys Thr Pro Ser Val His Ala Asn Glu Thr Pro Gln  
 340 345 350  
 Glu Val Pro Ala Gln Thr Val Glu Ala  
 355 360

&lt;210&gt;813

&lt;211&gt;180

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;813

```

Met Thr Asp Pro Lys Ile Glu Lys Ser Ala Leu Arg Lys Leu Phe Ile
 1           5           10           15
Ser Ile Arg Arg Asp Leu Ser Glu Glu Arg Lys His Glu Ala Ser Ser
          20           25           30
Ala Val Ala Ser Phe Val Arg Ser Phe Ser Lys Glu Ser Val Val Leu
          35           40           45
Ser Phe Val Ser Phe Asn His Glu Ile Asp Met Gln Glu Ala Asn Arg
          50           55           60
Ile Leu Ile Gln Lys Cys Thr Leu Ala Leu Pro Lys Ile Asp Gln Glu
65           70           75           80
Asn Leu Tyr Pro Val Leu Ile Pro Ser Ile Asp Asp Leu Ile Ser Val
          85           90           95
Val His Pro Lys Asp Pro Phe Ser Lys Gln Thr Pro Ile Ser Ser Asp
          100          105          110
Lys Ile Thr His Val Leu Val Pro Gly Leu Ala Phe Asp Gln Gln Gly
          115          120          125
Tyr Arg Leu Gly Tyr Gly His Gly Phe Tyr Asp Arg Trp Leu Ala Gln
130          135          140
His Pro Tyr Pro Ser Ile Arg Thr Ile Gly Ile Gly Tyr Cys Glu Gln
145          150          155          160
Lys Ile Asp Arg Leu Pro Gln Glu Ser His Asp Ile Pro Leu Ser Gln
          165          170          175

Ile Tyr Leu Cys
          180

```

&lt;210&gt;814

&lt;211&gt;428

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;814

```

Met Asp Ile Lys Lys Leu Phe Cys Leu Phe Leu Cys Ser Ser Leu Ile
 1           5           10           15
Ala Met Ser Pro Ile Tyr Gly Lys Thr Gly Asp Tyr Glu Lys Leu Thr
          20           25           30
Leu Thr Gly Ile Asn Ile Ile Asp Arg Asn Gly Leu Ser Glu Thr Ile
          35           40           45
Cys Ser Lys Glu Lys Leu Lys Lys Tyr Thr Lys Val Asp Phe Leu Ala
          50           55           60
Pro Gln Pro Tyr Gln Lys Val Met Arg Met Tyr Lys Asn Lys Arg Gly
65           70           75           80
Asp Asn Val Ser Cys Leu Thr Ala Tyr His Thr Asn Gly Gln Ile Lys
          85           90           95
Gln Tyr Leu Glu Cys Leu Asn Asn Arg Ala Tyr Gly Arg Tyr Arg Glu
          100          105          110
Trp His Val Asn Gly Asn Ile Lys Ile Gln Ala Glu Val Ile Gly Gly
          115          120          125
Ile Ala Asp Leu His Pro Ser Ala Glu Ser Gly Trp Leu Phe Asp Gln
130          135          140
Thr Thr Phe Ala Tyr Asn Asp Glu Gly Ile Leu Glu Ala Ala Ile Val
145          150          155          160
Tyr Glu Lys Gly Leu Leu Glu Gly Ser Ser Val Tyr Tyr His Thr Asn
          165          170          175
Gly Asn Ile Trp Lys Glu Cys Pro Tyr His Lys Gly Val Pro Gln Gly
          180          185          190
Lys Phe Leu Thr Tyr Thr Ser Ser Gly Lys Leu Leu Lys Glu Gln Asn
          195          200          205
Tyr Gln Gln Gly Lys Arg His Gly Leu Ser Ile Arg Tyr Ser Glu Asp
210          215          220
Ser Glu Glu Asp Val Leu Ala Trp Glu Glu Tyr His Glu Gly Arg Leu
225          230          235          240

```

Leu Lys Ala Glu Tyr Leu Asp Pro Gln Thr His Glu Ile Tyr Ala Thr  
 245 250 255  
 Ile His Glu Gly Asn Gly Ile Gln Ala Ile Tyr Gly Lys Tyr Ala Val  
 260 265 270  
 Ile Glu Thr Arg Ala Phe Tyr Arg Gly Glu Pro Tyr Gly Lys Val Thr  
 275 280 285  
 Arg Phe Asp Asn Ser Gly Thr Gln Ile Val Gln Thr Tyr Asn Xaa Leu  
 290 295 300  
 Gln Gly Ala Lys His Gly Glu Glu Phe Ser Phe Ile Leu Arg Gln Gly  
 305 310 315 320  
 Asn Pro Ser Cys Phe Leu Asn Trp His Glu Gly Ile Leu Asn Gly Ile  
 325 330 335  
 Val Lys Thr Trp Tyr Pro Gly Gly Thr Leu Glu Ser Cys Lys Glu Leu  
 340 345 350  
 Val Asn Asn Lys Lys Ser Gly Leu Thr Ile Tyr Tyr Pro Glu Gly  
 355 360 365  
 Gln Ile Met Ala Thr Glu Glu Tyr Asp Asn Asp Leu Leu Ile Lys Gly  
 370 375 380  
 Glu Tyr Phe Arg Pro Gly Asp Arg His Pro Tyr Ser Lys Ile Asp Arg  
 385 390 395 400  
 Gly Cys Gly Thr Ala Val Phe Phe Ser Ser Ala Gly Thr Ile Thr Lys  
 405 410 415  
 Lys Ile Pro Tyr Gln Asp Gly Lys Pro Leu Leu Asn  
 420 425

&lt;210&gt;815

&lt;211&gt;151

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;815

Thr Thr Ile Tyr Ile Lys Leu Leu Gly Arg Leu Met Lys Lys Trp Ile  
 1 5 10 15  
 Ser Ile Leu Ile Leu Ser Phe Leu Ser Leu Leu Ser Ile Leu Pro Val  
 20 25 30  
 Leu Ala Ile Thr Ile Asn His Val Lys Ile Ser Gln Arg Trp Ser Asp  
 35 40 45  
 Leu Asn Ser Gln Ile Leu Thr Leu Lys Val Ile Arg Asp His Glu Asp  
 50 55 60  
 Gln Val Ile Lys His Asn Ala Arg Ile Ser Lys Asp Arg Asn Asn Leu  
 65 70 75 80  
 Ser Ile Glu Ser Leu Asn Ala Ser Cys Lys Gln Leu Arg Pro Leu Ser  
 85 90 95  
 Lys Glu Arg Glu Arg Leu Asn Lys Leu Asn Ser Asn Ser Leu Leu Ala  
 100 105 110  
 Gln Ser Lys Glu Val Trp Glu Arg Lys Arg Ala Leu Glu Lys Ser Asn  
 115 120 125  
 His Gln Leu Val Trp Asn Cys Glu Gln Met His Asn Asp Phe Ala Phe  
 130 135 140  
 Cys Ala Ser Arg Ala Ser Tyr  
 145 150

&lt;210&gt;816

&lt;211&gt;464

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;816

Ala Met Asn Phe Lys Leu Pro Val Tyr His Ile Gly Leu Thr Lys Ala  
 1 5 10 15  
 Glu Asn Asn Thr Ile Lys Ile Ala Ile Leu Gln Lys Thr Cys Lys Gly  
 20 25 30  
 Trp Ile Val Cys His Cys Glu Gln Ile Pro Glu Gly Lys Thr Trp Ser  
 35 40 45  
 Leu Pro Lys Lys Tyr Phe Ala Ala Pro Thr Thr Phe Ser Leu Gln Gly  
 50 55 60  
 Ser Asp Ile Leu Val Lys Ser Ser Ser Ser Ser Leu Lys Asn Arg Lys  
 65 70 75 80

Asn Ile Leu Lys Val Ala Leu Thr Asn Leu Glu Ala Ser Leu Ala Leu  
                                     85                                    90                                    95  
 Pro Trp Glu Ser Leu Ile Val Gln Pro Gln Leu Gly Lys Pro Thr Asp  
                                     100                                    105                                    110  
 Arg Gly Glu Thr Pro Leu Thr Leu Trp Ile Ala Gln Lys Asn Thr Leu  
                                     115                                    120                                    125  
 Lys Lys Glu Leu Ser Phe Leu Ser Gln Ala Gln Ile Phe Pro Asp Lys  
                                     130                                    135                                    140  
 Leu Ser Cys Arg Ala Ala Asp Ile Phe Phe Leu Ala Glu Gln Ser Pro  
                                     145                                    150                                    155                                    160  
 Leu Lys Ser Leu Pro Ala Tyr Leu Leu Ile Tyr Gly Gly Ser Glu Glu  
                                     165                                    170                                    175  
 Val Thr Cys Ile Phe Val Lys Asn His Ala Ile Ala Val Ala Arg Ser  
                                     180                                    185                                    190  
 Phe Ser Asn His Ser Thr Lys Lys Ser Cys Asp Asp Ile His Ala Thr  
                                     195                                    200                                    205  
 Leu Gln Tyr Ile Gln Glu Thr Phe Pro Gln Thr Val Leu Pro Ala Ile  
                                     210                                    215                                    220  
 His Val Ala Gln Ile Ser Pro Asn Leu Gln Xaa Ile Leu Glu Gln Lys  
                                     225                                    230                                    235                                    240  
 Leu Ser Leu Pro Leu Val Val Cys Gln Ser Met Thr Tyr Gly Val Glu  
                                     245                                    250                                    255  
 Asp Glu Asp Trp Glu Ile Tyr Gly Asp Thr Ile Ala Ala Ala His His  
                                     260                                    265                                    270  
 Gly Ala Ser Arg Arg Pro Leu Thr Phe Pro Tyr Asp Ala Thr Ser Val  
                                     275                                    280                                    285  
 Ser Pro Ala Ala Gln Lys His Trp Leu Leu Arg Ser Ser Leu Leu Ile  
                                     290                                    295                                    300  
 Gly Lys Tyr Ala Leu Met Ala Thr Val Val Val Ser Leu Gly Ser Val  
                                     305                                    310                                    315                                    320  
 Leu Lys Leu Lys Ser Leu Ser Ser Ser Ala Ser Asn His Phe Ala Phe  
                                     325                                    330                                    335  
 Ala Cys Pro Glu Glu Gly Val Leu Pro Arg Ser Leu Lys Ala Ala Glu  
                                     340                                    345                                    350  
 Lys Thr Val Lys Ala Ile Gly Lys Lys Asn Ser Ala Ser Asn Tyr Pro  
                                     355                                    360                                    365  
 Leu Leu Pro Thr Ile Pro Thr Ser Glu Gln Thr Leu Lys Phe Leu Leu  
                                     370                                    375                                    380  
 Ala Leu Gly Lys Ser Ser Pro Ser Ile Lys Phe Ser Tyr Phe Ser Tyr  
                                     385                                    390                                    395                                    400  
 Thr Met Thr Ser Tyr Pro Ser Lys Asp Asn Pro Ser Leu Pro Tyr Ser  
                                     405                                    410                                    415  
 Ala Leu Val Glu Val Lys Gly Gln Gly Gln Pro Glu Asp Ile Pro Gln  
                                     420                                    425                                    430  
 Phe Leu Lys Lys Ile Ser Ser His Pro Lys Leu Gln His Val Ser Glu  
                                     435                                    440                                    445  
 Ser Leu Glu Asp Gln Arg Ser Phe Lys Leu Gln Phe Thr Leu Ser Ser  
                                     450                                    455                                    460  
 <210>817  
 <211>130  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>817  
 Met Ala Ala Pro Ile Phe Ile Lys Asn Ile Leu Leu Arg Ser Ser Ile  
                                     1                                    5                                    10                                    15  
 Val Tyr Ala Pro Leu Ala Gly Phe Ser Asp Tyr Pro Tyr Arg Cys Met  
                                     20                                    25                                    30  
 Ser Ala Leu Tyr Gln Pro Gly Leu Met Phe Cys Glu Met Val Lys Val  
                                     35                                    40                                    45  
 Glu Gly Ile Leu Tyr Ala Pro Glu Arg Thr Ser Lys Leu Leu Asp Tyr  
                                     50                                    55                                    60  
 Asn Glu Asn Met Arg Pro Ile Gly Ala Gln Leu Cys Gly Ser Asn Pro  
                                     65                                    70                                    75                                    80  
 Glu Thr Ser Gly Glu Ala Ala Lys Ile Leu Glu Gly Leu Gly Phe Asp



85 90 95  
 Leu Ile Asp Leu Asn Cys Gly Cys Pro Thr Asp Lys Ile Thr Lys Asp  
 100 105 110  
 Gly Ser Gly Ser Gly Leu Phe Glu Asp Ala Arg Ala Tyr Trp Glu Asp  
 115 120 125  
 Phe Arg  
 130  
 <210>818  
 <211>235  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>818  
 Ile Val Asp Val Leu Gln Ile Lys Ser Pro Lys Met Ala Val Gly Gln  
 1 5 10 15  
 Val Phe Leu Lys Thr Pro Glu Leu Ile Gly Arg Ile Leu Asp Lys Ile  
 20 25 30  
 Ile Asn Ser Val Ser Ile Pro Val Thr Val Lys Ile Arg Ser Gly Trp  
 35 40 45  
 Asp Met Glu His Ile Asn Val Glu Asp Thr Val Arg Ile Ile Arg Asp  
 50 55 60  
 Ala Gly Ala Ser Ala Val Phe Val His Gly Arg Thr Arg Ala Gln Gly  
 65 70 75 80  
 Tyr His Gly Pro Ser Lys Gln Glu Tyr Ile Ser Arg Ala Lys Ala Ala  
 85 90 95  
 Ala Gly Lys Glu Phe Pro Val Phe Gly Asn Gly Asp Ile Phe Ser Pro  
 100 105 110  
 Glu Ala Ala Gln Ala Met Leu Thr Thr Gly Cys Asp Gly Val Leu Val  
 115 120 125  
 Ala Arg Gly Thr Leu Gly Ala Pro Trp Ile Gly Lys Gln Ile Gln Asp  
 130 135 140  
 Tyr Leu Thr Thr Gly Ser Tyr Glu Lys Ile Pro Phe Ile Lys Arg Lys  
 145 150 155 160  
 Ala Ala Phe Leu Glu His Met Arg Leu Val Glu Asp Tyr Tyr Gln Ser  
 165 170 175  
 Glu Thr Lys Phe Leu Ser Glu Thr Arg Lys Leu Cys Gly His Tyr Leu  
 180 185 190  
 Ile Ser Ala Ala Lys Val Arg Phe Leu Arg Ser Ser Leu Ala Lys Ala  
 195 200 205  
 Thr Ser Tyr Gln Glu Val Tyr Gln Leu Val Asn Asp Tyr Glu Glu Ala  
 210 215 220  
 Asp Asp Ser Ser Leu Glu Thr Phe Val Lys Cys  
 225 230 235  
 <210>819  
 <211>827  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>819  
 Met Lys Lys Ser Leu Ile Ile Val Glu Ser Pro Ala Lys Ile Lys Thr  
 1 5 10 15  
 Leu Gln Lys Leu Leu Gly Ser Glu Phe Val Phe Ala Ser Ser Ile Gly  
 20 25 30  
 His Ile Val Asp Leu Pro Ala Lys Glu Phe Gly Ile Asp Val Asp His  
 35 40 45  
 Asp Phe Glu Pro Gln Tyr Gln Val Leu Pro Asp Lys Gln Glu Val Ile  
 50 55 60  
 Asn His Ile Arg Lys Leu Ala Ala Lys Cys Glu Lys Val Tyr Leu Ser  
 65 70 75 80  
 Pro Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp His Ile Ala Asn  
 85 90 95  
 Gln Leu Pro Asp Ser Pro Leu Ile Gln Arg Val Ser Phe Asn Ala Ile  
 100 105 110  
 Thr Lys Asn Ala Val Thr Glu Ala Leu Lys His Pro Arg Thr Ile Asp  
 115 120 125  
 Met Ala Leu Val Asn Ala Gln Gln Ala Arg Arg Leu Leu Asp Arg Ile

898

645 650 655  
 Val Arg His Gly Arg Tyr Gly Thr Phe Leu Gly Cys Glu Lys Tyr Pro  
 660 665 670  
 Glu Cys Arg Gly Thr Ile Ser Ile His Lys Lys Gly Glu Glu Ile Glu  
 675 680 685  
 Gln Glu Glu Pro Ile Pro Cys Pro Ala Ile Gly Cys Asn Gly Lys Ile  
 690 695 700  
 Phe Lys Lys Arg Ser Arg Tyr Asn Lys Ile Phe Tyr Ser Cys Ser Glu  
 705 710 715 720  
 Tyr Pro Glu Cys Ser Val Ile Gly Asn Ser Ile Asp Ala Val Ile Thr  
 725 730 735  
 Lys Tyr Ser Gly Thr Glu Lys Ile Pro Tyr Lys Lys Lys Thr Pro Thr  
 740 745 750  
 Lys Lys Lys Ser Ser Ala Lys Thr Thr Lys Ala Ala Lys Thr Pro Ser  
 755 760 765  
 Lys Lys Gly Lys Ala Lys Ser Ser Val Lys Lys Ser Ser Glu Lys Lys  
 770 775 780  
 Thr Gly Pro Leu Phe Leu Pro Ser Pro Asp Leu Ala Lys Met Ile Gly  
 785 790 795 800  
 Asn Glu Xaa Arg Ile Ser Gly Arg Ser Asn Gln Lys Asn Leu Gly Leu  
 805 810 815  
 His Gln Gly Thr Ser Ile Thr Gly Thr Arg Lys  
 820 825

&lt;210&gt;820

&lt;211&gt;270

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;820

Lys Pro Arg Thr Arg Asn Val Glu Lys Leu Glu Phe Val Thr Ser Leu  
 1 5 10 15  
 Ser Ser Pro Asp Asp Asp Leu Ile Thr Phe Asn Lys Gln Gly Leu Ile  
 20 25 30  
 Ala Gly Pro Glu Glu Glu Lys Val Ala Phe Leu Val Arg Ser Asn Ala  
 35 40 45  
 Met Leu Asp Ala Gly Pro Glu Thr Pro Ala Ser Phe Pro Glu Ser Leu  
 50 55 60  
 Arg Glu Gln Phe Asp Ile Phe Pro Glu Tyr Val Glu Val Leu Tyr Ser  
 65 70 75 80  
 Asn Glu Gly Leu Asp Val Trp Glu Ala Gly Cys Thr Trp Ile Leu Asn  
 85 90 95  
 Asn Glu Val Thr Ile Gln Leu Arg Lys His His Arg Lys Ala Ser Arg  
 100 105 110  
 Trp Leu Gly Met Tyr Ser Arg Asp Glu Val Leu Ala His Glu Ala Val  
 115 120 125  
 His Ala Val Arg Met Lys Phe His Glu Pro Val Phe Glu Glu Val Leu  
 130 135 140  
 Ala Tyr Gln Thr Ser Arg Trp Gly Trp Arg Arg Phe Phe Gly Pro Leu  
 145 150 155 160  
 Phe Arg Ser Pro Gly Glu Ser Tyr Leu Leu Leu Phe Phe Thr Ile Leu  
 165 170 175  
 Gly Leu Gly Ile Ser Leu Trp Tyr Pro Ala Gly Ile Leu Ile Met Leu  
 180 185 190  
 Val Leu Pro Met Tyr Phe Leu Met Arg Leu Cys Met Ala Gln Ser Tyr  
 195 200 205  
 Leu Tyr Arg Ala Met Lys Lys Ile Arg Lys Met Leu Gly Val Pro Pro  
 210 215 220  
 Leu Trp Val Leu Leu Arg Leu Thr Asp Lys Glu Ile Lys Met Phe Ala  
 225 230 235 240  
 Lys Glu Pro Ile Pro Val Leu Glu His Tyr Ala Arg Lys Arg Lys Leu  
 245 250 255  
 Glu Asn Val Arg Trp Lys Gln Ile Tyr Gln Ser Tyr Phe Val  
 260 265 270

&lt;210&gt;821

&lt;211&gt;456

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;821

```

Ile Phe Lys Gly Asn Ser Lys Arg Leu Tyr Asp Ser Ser Ala Leu Asp
 1           5           10           15
Met Phe Gln Gln Lys Gln Lys Leu Ser Leu Lys Tyr Leu Pro Ser Leu
          20           25           30
Arg Met Gln Gln Gly Leu Gln Met Leu Gln Ser Pro Leu Thr Glu Leu
          35           40           45
Ser Ser Tyr Val Val Gln Glu Ile Ile Asp Asn Pro Phe Phe Asp Leu
          50           55           60
Ser Ser Leu Glu Glu Glu Glu Trp Ser Pro Cys Tyr Arg Pro Thr Asn
          65           70           75           80
Ser Thr Phe Ser Tyr Leu Asn Gln Thr Pro Gly Pro Gln Glu Ser Leu
          85           90           95
Tyr Thr Arg Leu Leu Pro Gln Ile Glu Glu Ala Phe Ser Thr Ala Glu
          100          105          110
Glu Arg Phe Ile Ala His Gln Ile Ala Gly Asn Leu Ser Asp Glu Gly
          115          120          125
Leu Phe Leu Arg Asn Pro Glu Asp Phe Ala Gln Glu Leu Glu Leu Pro
          130          135          140
Leu Glu Lys Ile His Lys Val Trp Asp Thr Ile Gln Asn Leu Ser Pro
          145          150          155          160
Glu Gly Ile Ala Ser Pro Ser Leu Gln Ser Tyr Trp Met Lys Leu Leu
          165          170          175
Arg Asn Ser Ser His Gln Gln Ala Tyr Ser Ile Val Arg Asp Cys Tyr
          180          185          190
Pro Leu Met Thr Asn Cys Glu Phe Ala Pro Ile Met Lys Lys Phe Ser
          195          200          205
Leu Ser Leu Ser Glu Leu Arg Asn Ile Leu Lys Lys Ala Leu Gly Ser
          210          215          220
Ile Pro Trp Cys Pro Ala Ala Ala Cys Thr Val Lys Pro Met Val Ser
          225          230          235          240
Thr Pro Leu Pro Asp Ile Tyr Leu Phe Tyr Ser Ser Gly Ser Trp Lys
          245          250          255
Ile Glu Val Ser Thr Arg Gly Leu Pro Ser Ile Lys Leu Asn Lys Glu
          260          265          270
Thr Phe His Phe Tyr Glu His Leu Pro Lys Glu Glu Gln Lys Asn Leu
          275          280          285
Ser Gln Gln Ile Leu Ser Ala Lys Trp Leu Ile Lys Asn Leu Arg Lys
          290          295          300
Arg Glu Gln Thr Leu Leu Gln Val Met Glu Thr Leu Leu Pro Lys Gln
          305          310          315          320
Glu Asp Phe Leu Leu Gly Lys Ile Pro Ala Pro Tyr Pro Leu Gly Ile
          325          330          335
Lys Asp Leu Ala Glu Asp Leu Ser Phe His Glu Ser Thr Ile Phe Arg
          340          345          350
Ala Ile Glu Asn Lys Ala Val Ala Ala Pro Ile Gly Ile Phe Pro Leu
          355          360          365
Lys His Leu Phe Pro Arg Gly Ile His Gln Asp Ser Ser His Ser Lys
          370          375          380
Glu Asn Val Leu Gln Trp Ile Arg Gln Trp Ile Ala Thr Glu Gln Thr
          385          390          395          400
Pro Leu Ser Asp Ser Val Ile Ser Asp Arg Ile Thr Ala Lys Gly Ile
          405          410          415
Pro Cys Ala Arg Arg Thr Val Ala Lys Tyr Arg Ala Gln Leu Lys Ile
          420          425          430
Leu Pro Ala Asn Lys Arg Lys Lys Leu Phe Tyr Ile Arg Ser Ser Asn
          435          440          445
Ser His Phe Arg Asp Arg Gln Phe
          450          455

```

&lt;210&gt;822

&lt;211&gt;644

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;822

Lys Leu Gly Leu Ile Met Thr Cys Ile Ser Glu Leu Asn Glu Ala Gln  
 1 5 10 15  
 Arg Lys Ala Val Thr Ala Pro Leu Asn Pro Val Leu Val Leu Ala Gly  
 20 25 30  
 Ala Gly Ala Gly Lys Thr Arg Val Val Thr Tyr Arg Ile Leu His Leu  
 35 40 45  
 Ile Asn Gln Gly Ile Ala Pro Arg Glu Ile Leu Ala Val Thr Phe Thr  
 50 55 60  
 Asn Lys Ala Ala Arg Glu Leu Lys Glu Arg Ile Val Asn Gln Cys Ala  
 65 70 75 80  
 Ser Thr Asn Glu Phe Asp Val Pro Met Val Cys Thr Phe His Ser Leu  
 85 90 95  
 Gly Val Phe Ile Leu Arg Arg Ser Ile Asn Leu Leu Asn Arg Glu Asn  
 100 105 110  
 Asn Phe Thr Ile Tyr Asp Gln Ser Asp Ala Glu Lys Leu Ile Lys His  
 115 120 125  
 Ala Leu Gln Gln His Asn Leu Lys Pro Asn Leu Ala Ser Lys Ile Gln  
 130 135 140  
 Ala His Val Ser Gln Ala Lys Asn Arg Leu Leu Phe Pro Glu Asp Leu  
 145 150 155 160  
 Asp Pro Asn Asp Tyr Ile Asp Pro Val Val Ser Ile Tyr Gln Glu Tyr  
 165 170 175  
 Gln Lys Lys Leu Ile Glu Ala Asn Ala Leu Asp Phe Asp Asp Leu Leu  
 180 185 190  
 Phe Leu Thr Val Arg Leu Leu Arg Glu Ser Pro Glu Ala Gln Glu Leu  
 195 200 205  
 Tyr Asn Gln Leu Trp Lys Ala Leu Leu Ile Asp Glu Tyr Gln Asp Thr  
 210 215 220  
 Asn His Ala Gln Tyr Thr Leu Met Gln Leu Leu Ser Lys Gln His Arg  
 225 230 235 240  
 Asn Val Phe Ala Val Gly Asp Pro Asp Gln Ser Ile Tyr Ser Trp Arg  
 245 250 255  
 Gly Ala Asn Ile His Asn Ile Leu Asn Phe Glu Asn Asp Tyr Pro Asn  
 260 265 270  
 Ala Lys Val Leu Cys Leu Glu Glu Asn Tyr Arg Ser Tyr Gly Asn Ile  
 275 280 285  
 Leu Asn Ala Ala Asn Ala Leu Ile Lys Asn Asn Ala Ser Arg Leu Glu  
 290 295 300  
 Lys Glu Leu Arg Ser Val Lys Gly Pro Gly Glu Lys Ile Arg Leu Phe  
 305 310 315 320  
 Leu Gly Ser Thr Asp Arg Glu Glu Ala Asp Phe Val Ala Ala Glu Ile  
 325 330 335  
 Leu Gln Leu His Arg Val Gly Asn Ile Lys Leu Arg Asp Ile Cys Ile  
 340 345 350  
 Phe Tyr Arg Thr Asn Ser Gln Ser Arg Thr Phe Glu Asp Ala Leu Leu  
 355 360 365  
 Arg Arg Arg Ile Pro Tyr Glu Ile Ile Gly Gly Leu Ser Phe Tyr Lys  
 370 375 380  
 Arg Lys Glu Ile Gln Asp Ile Leu Ala Phe Leu Arg Ile Phe Ile Ser  
 385 390 395 400  
 Lys Ser Asp Ile Val Ala Phe Asp Arg Thr Val Asn Leu Pro Lys Arg  
 405 410 415  
 Gly Ile Gly Ser Thr Thr Ile Phe Ala Leu Thr Gln Tyr Ala Ile Ala  
 420 425 430  
 Gln Gly Leu Pro Ile Leu Lys Ala Cys Gln Gln Ala Leu Asp Thr Lys  
 435 440 445  
 Asp Val Lys Leu Ser Lys Lys Gln Gln Glu Gly Leu Gln Glu Tyr Leu  
 450 455 460  
 Ala Leu Phe Pro Gln Ile Glu His Ala Tyr Asn Thr Leu Ser Leu Arg  
 465 470 475 480  
 Asp Phe Ile Glu Ser Val Val Arg Ile Thr Gly Tyr Leu Glu Ile Leu  
 485 490 495

Lys Glu Asp Ala Asp Thr Phe Lys Asp Arg Lys Ser Asn Leu Glu Glu  
 500 505 510  
 Leu Tyr His Lys Ala Leu Glu Ser Glu Gln Gln Asn Pro Lys Thr His  
 515 520 525  
 Leu Glu Leu Phe Leu Asp Asp Leu Ala Leu Lys Gly Ser Asp Asp Asp  
 530 535 540  
 Leu Asn Leu Thr Ala Asp Arg Val Asn Leu Met Thr Leu His Asn Gly  
 545 550 555 560  
 Lys Gly Leu Glu Phe Arg Val Ser Phe Leu Val Gly Leu Glu Glu Gln  
 565 570 575  
 Leu Leu Pro His Ala Asn Ser Leu Gly Gly Thr Tyr Glu Asn Ile Glu  
 580 585 590  
 Glu Glu Arg Arg Leu Cys Tyr Val Gly Ile Thr Arg Ala Gln Asp Leu  
 595 600 605  
 Leu Tyr Leu Thr Ala Ala Gln Val Arg Ser Leu Trp Gly Thr Val Arg  
 610 615 620  
 Met Met Lys Pro Ser Arg Phe Leu Lys Glu Ile Pro Lys Asp Tyr Met  
 625 630 635 640  
 Ile Gln Val Arg

&lt;210&gt;823

&lt;211&gt;236

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;823

Met Gln Asn Ala Thr Ile Asp Gln Leu Pro Val Ser Trp Gln Glu Gln  
 1 5 10 15  
 Leu Pro Leu Cys Trp Arg Glu Gln Leu Lys Glu Glu Trp Ser Lys Pro  
 20 25 30  
 Tyr Met Gln Gln Leu Leu Ile Phe Leu Lys Gln Glu Tyr Lys Glu His  
 35 40 45  
 Thr Val Tyr Pro Glu Glu Asn Cys Val Phe Ser Ala Leu Arg Ser Thr  
 50 55 60  
 Pro Phe Asp Gln Val Arg Val Val Ile Leu Gly Gln Asp Pro Tyr Pro  
 65 70 75 80  
 Gly Lys Gly Gln Ala His Gly Leu Ser Phe Ser Val Pro Glu Gly Gln  
 85 90 95  
 Arg Leu Pro Pro Ser Leu Ile Asn Ile Phe Arg Glu Leu Lys Thr Asp  
 100 105 110  
 Leu Gly Ile Glu Asn His Lys Gly Cys Leu Gln Ser Trp Ala Asn Gln  
 115 120 125  
 Gly Ile Leu Leu Leu Asn Thr Val Leu Thr Val Arg Ala Gly Glu Pro  
 130 135 140  
 Phe Ser His Ala Gly Lys Gly Trp Glu Leu Phe Thr Asp Ala Ile Val  
 145 150 155 160  
 Thr Lys Leu Ile Gln Glu Arg Thr His Ile Ile Phe Val Leu Trp Gly  
 165 170 175  
 Ala Ala Ala Arg Lys Lys Cys Glu Leu Leu Phe Asn Ser Lys His Gln  
 180 185 190  
 His Ala Val Leu Ser Ser Pro His Pro Ser Pro Leu Ala Ala His Arg  
 195 200 205  
 Gly Phe Phe Gly Cys Ser His Phe Ser Lys Ile Asn Tyr Leu Leu Asn  
 210 215 220  
 Lys Leu Asn Lys Pro Met Ile Asn Trp Lys Leu Pro  
 225 230 235

&lt;210&gt;824

&lt;211&gt;206

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;824

Met Lys Ile Val Ile Ala Ser Ser His Gly Tyr Lys Ile Arg Glu Thr  
 1 5 10 15  
 Lys Thr Phe Leu Lys Arg Leu Gly Asp Phe Asp Ile Phe Ser Leu Ser  
 20 25 30

Asp Phe Pro Asp Tyr Lys Leu Pro Gln Glu Gln Glu Asp Ser Ile Thr  
           35                          40                          45  
 Ala Asn Ala Leu Thr Lys Gly Ile His Ala Ala Asn His Leu Gly Cys  
           50                          55                          60  
 Trp Val Ile Ala Asp Asp Thr Met Leu Arg Val Pro Ala Leu Asn Gly  
           65                          70                          75                          80  
 Leu Pro Gly Pro Leu Ser Ala Asn Phe Ala Gly Val Gly Ala Tyr Asp  
                           85                          90                          95  
 Lys Asp His Arg Lys Lys Leu Leu Asp Leu Met Ser Ser Leu Glu Ser  
                           100                          105                          110  
 Leu Val Asp Arg Ser Ala Tyr Phe Glu Cys Cys Val Val Leu Val Ser  
                           115                          120                          125  
 Pro Asn Gln Glu Ile Phe Lys Thr Tyr Gly Ile Cys Glu Gly Tyr Ile  
                           130                          135                          140  
 Ser His Gln Glu Lys Gly Ser Ser Gly Phe Gly Tyr Asp Pro Ile Phe  
                           145                          150                          155                          160  
 Val Lys Tyr Asp Tyr Lys Gln Thr Phe Ala Glu Leu Ser Glu Asp Val  
                           165                          170                          175  
 Lys Asn Gln Val Ser His Arg Ala Lys Ala Leu Gln Lys Leu Ala Pro  
                           180                          185                          190  
 His Leu Gln Ser Leu Phe Glu Lys His Leu Leu Thr Arg Asp  
                           195                          200                          205

&lt;210&gt;825

&lt;211&gt;424

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;825

Leu Met Phe Phe Gln Phe Leu Ser Phe Thr Met Lys Lys Ile Phe Tyr  
   1                          5                          10                          15  
 Ser Phe Val Leu Leu Ser Cys Ile Phe Pro Tyr Val Gly Cys Ala Gln  
                           20                          25                          30  
 Val Phe Val Gly Leu Asp Arg Ile Phe Ser Glu Gly Glu Tyr Thr Arg  
                           35                          40                          45  
 Cys Ile Gln Gly Lys Lys Ile Ala Leu Ile Ser His Ser Ala Ala Ile  
                           50                          55                          60  
 Asn Ser Arg Gly Gln Asp Ala Leu Ser Val Phe Tyr Ser Arg Lys His  
                           65                          70                          75                          80  
 Asp Cys Thr Val Glu Ile Leu Cys Thr Leu Glu His Gly Tyr Tyr Gly  
                           85                          90                          95  
 Ala Thr Pro Thr Glu Thr Val Gly Asn Gln Pro Ser Arg Tyr Pro Asn  
                           100                          105                          110  
 Leu Arg Ser Val Ser Leu Tyr Gly Val Lys Glu Val Pro Lys Glu Val  
                           115                          120                          125  
 Ala Glu His Cys Asp Val Phe Val Tyr Asp Val Gln Asp Ile Gly Val  
                           130                          135                          140  
 Arg Ser Tyr Ser Phe Val Thr Val Leu Met Gln Ile Val Lys Ala Ser  
                           145                          150                          155                          160  
 Glu Arg Tyr Gly Lys Gln Leu Ile Val Leu Asp Arg Pro Asn Pro Met  
                           165                          170                          175  
 Gly Gly Arg Ile Val Asp Gly Pro Leu Pro Asn Pro Thr Thr Ser Gly  
                           180                          185                          190  
 Ser Leu Ala Ile Pro Tyr Cys Tyr Gly Met Thr Pro Gly Glu Leu Ala  
                           195                          200                          205  
 Leu Phe Phe Lys Lys Thr Tyr Ala Pro Asn Ala Asn Val Val Val Ile  
                           210                          215                          220  
 Pro Met Lys Gly Trp Asn Arg Ser Met Thr Phe Asp Glu Thr Gly Leu  
                           225                          230                          235                          240  
 Ile Trp Met Pro Thr Ser Pro Gln Met Pro Asp Pro Gln Ser Pro Phe  
                           245                          250                          255  
 Phe Tyr Ala Ala Thr Gly Ile Leu Gly Ala Leu Ser Val Ala Ser Ile  
                           260                          265                          270  
 Gly Val Gly Tyr Thr Leu Pro Phe Lys Val Leu Gly Ala Pro Trp Met  
                           275                          280                          285  
 Asp Gly Glu Lys Val Ala Asp Glu Leu Asn Arg Met Lys Leu Pro Gly

290 295 300  
 Val Leu Phe Leu Pro Phe Phe Tyr Glu Pro Phe Phe Gly Lys Tyr Lys  
 305 310 315 320  
 Met Glu Met Cys Ser Gly Val Leu Leu Val Leu Gln Asp Pro Lys Ile  
 325 330 335  
 Phe Tyr Pro Val Glu Thr Gln Cys Thr Ile Trp Gly Val Leu Lys Ala  
 340 345 350  
 Leu Tyr Pro Lys Gln Val Glu Gln Thr Leu Lys Ser Ile Glu Arg Ile  
 355 360 365  
 Pro Ala Arg Arg Ser Ser Ile Cys Asn Leu Phe Gly Gly Asp Glu Phe  
 370 375 380  
 Leu Ser Ile Ser His Lys Glu Arg Tyr Ile Val Trp Pro Leu Arg Arg  
 385 390 395 400  
 Leu Cys Lys Glu Ser Arg Glu Ser Phe His Gln Leu Arg Ser Ser Cys  
 405 410 415  
 Leu Leu Ser Glu Tyr Ala Glu Ser  
 420  
 <210>826  
 <211>527  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>826  
 Arg Val Val Trp Val Phe Lys Ser Gln Phe Glu Gly Leu Ser Ala Leu  
 1 5 10 15  
 Lys Arg Gly Val His Ala Leu Thr Lys Ala Val Thr Pro Ala Phe Gly  
 20 25 30  
 Pro Arg Gly Tyr Asn Val Val Ile Lys Lys Gly Lys Ala Pro Ile Val  
 35 40 45  
 Leu Thr Lys Asn Gly Ile Arg Ile Ala Lys Glu Ile Ile Leu Gln Asp  
 50 55 60  
 Ala Phe Glu Ser Leu Gly Val Lys Leu Ala Lys Glu Ala Leu Leu Lys  
 65 70 75 80  
 Val Val Glu Gln Thr Gly Asp Gly Ser Thr Thr Ala Leu Val Val Ile  
 85 90 95  
 Asp Ala Leu Phe Thr Gln Gly Leu Lys Gly Ile Ala Ala Gly Leu Asp  
 100 105 110  
 Pro Gln Glu Ile Lys Ala Gly Ile Leu Leu Ser Val Glu Met Val Tyr  
 115 120 125  
 Gln Gln Leu Gln Arg Gln Ala Ile Glu Leu Gln Ser Pro Lys Asp Val  
 130 135 140  
 Leu His Val Ala Met Val Ala Ala Asn His Asp Val Thr Leu Gly Thr  
 145 150 155 160  
 Val Val Ala Thr Val Ile Ser Gln Ala Asp Leu Lys Gly Val Phe Ser  
 165 170 175  
 Ser Lys Asp Ser Gly Ile Ser Lys Thr Arg Gly Leu Gly Lys Arg Val  
 180 185 190  
 Lys Ser Gly Tyr Leu Ser Pro Tyr Phe Val Thr Arg Pro Glu Thr Xaa  
 195 200 205  
 Asp Val Val Trp Glu Glu Ala Leu Val Leu Ile Leu Ser His Ser Leu  
 210 215 220  
 Val Ser Leu Ser Glu Glu Leu Ile Arg Tyr Leu Glu Leu Ile Ser Glu  
 225 230 235 240  
 Gln Asn Thr His Pro Leu Val Ile Ile Ala Glu Asp Phe Asp Gln Asn  
 245 250 255  
 Val Leu Arg Thr Leu Ile Leu Asn Lys Leu Arg Asn Gly Leu Pro Val  
 260 265 270  
 Cys Ala Val Lys Ala Pro Gly Ser Arg Glu Leu Arg Gln Val Val Leu  
 275 280 285  
 Glu Asp Leu Ala Ile Leu Thr Gly Ala Thr Leu Ile Gly Gln Glu Ser  
 290 295 300  
 Glu Asn Cys Glu Ile Pro Val Ser Leu Asp Val Leu Gly Arg Val Lys  
 305 310 315 320  
 Gln Val Met Ile Thr Lys Glu Thr Phe Thr Phe Leu Glu Gly Gly Gly  
 325 330 335



Asp Ala Glu Ile Ile Gln Ala Arg Lys Gln Glu Leu Cys Leu Ala Ile  
 340 345 350  
 Ala Gly Ser Thr Ser Glu Ser Glu Cys Gln Glu Leu Glu Glu Arg Leu  
 355 360 365  
 Ala Ile Phe Ile Gly Ser Ile Pro Gln Val Gln Ile Thr Ala Asp Thr  
 370 375 380  
 Asp Thr Glu Gln Arg Glu Arg Gln Phe Gln Leu Glu Ser Ala Leu Arg  
 385 390 395 400  
 Ala Thr Lys Ala Ala Met Lys Gly Gly Ile Val Pro Gly Gly Gly Val  
 405 410 415  
 Ala Phe Leu Arg Ala Ala His Ala Ile Glu Val Pro Ala Asn Leu Ser  
 420 425 430  
 Ser Gly Met Thr Phe Gly Phe Glu Thr Leu Leu Gln Ala Val Arg Thr  
 435 440 445  
 Pro Leu Lys Val Leu Ala Gln Asn Cys Gly Arg Ser Ser Glu Glu Val  
 450 455 460  
 Ile His Thr Ile Leu Ser His Glu Asn Pro Arg Phe Gly Tyr Asn Gly  
 465 470 475 480  
 Met Thr Asp Thr Phe Glu Asp Leu Val Asp Ala Gly Ile Cys Asp Pro  
 485 490 495  
 Leu Ile Val Thr Thr Ser Ser Leu Lys Cys Ala Val Ser Val Ser Cys  
 500 505 510  
 Leu Leu Leu Thr Ser Ser Phe Phe Ile Ser Ser Arg Thr Lys Thr  
 515 520 525

&lt;210&gt;827

&lt;211&gt;189

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;827

Ser Leu Val Arg Asn Asn Lys Arg Val Glu Glu Glu Val Phe Met Thr  
 1 5 10 15  
 Leu Ser Leu Val Gly Lys Glu Ala Pro Asp Phe Val Ala Gln Ala Val  
 20 25 30  
 Val Asn Gly Glu Thr Cys Thr Val Ser Leu Lys Asp Tyr Leu Gly Lys  
 35 40 45  
 Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val Cys Pro  
 50 55 60  
 Thr Glu Leu His Ala Phe Gln Asp Ala Leu Gly Glu Phe His Thr Arg  
 65 70 75 80  
 Gly Ala Glu Val Ile Gly Cys Ser Val Asp Asp Ile Ala Thr His Gln  
 85 90 95  
 Gln Trp Leu Ala Thr Lys Lys Lys Gln Gly Gly Ile Glu Gly Ile Thr  
 100 105 110  
 Tyr Pro Leu Leu Ser Asp Glu Asp Lys Val Ile Ser Arg Ser Tyr His  
 115 120 125  
 Val Leu Lys Pro Glu Glu Glu Leu Ser Phe Arg Gly Val Phe Leu Ile  
 130 135 140  
 Asp Lys Gly Glu Ile Ile Arg His Leu Val Val Asn Asp Leu Pro Leu  
 145 150 155 160  
 Gly Arg Ser Ile Glu Glu Glu Leu Arg Thr Leu Asp Ala Leu Ile Phe  
 165 170 175  
 Phe Glu Thr Asn Gly Leu Val Cys Pro Ala Lys Leu Ala  
 180 185

&lt;210&gt;828

&lt;211&gt;136

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;828

Arg Phe Asp Leu Ile Phe Gln Met Lys Phe Thr Val Ala Leu Phe Gly  
 1 5 10 15  
 Glu Ala Glu Lys Gly Ser Tyr Asp Thr Ala Tyr Phe Cys Arg Ser Leu  
 20 25 30  
 Val Asp Leu His Asn Tyr Leu Gly Asp Val Ser Ser Pro Gly Ile Thr  
 35 40 45

Leu Ala Ile Lys Thr Leu Leu Ser Asp Tyr Asn Val Val Tyr Phe Arg  
 50 55 60  
 Val Arg Glu Glu Gly Tyr Cys Val Asp Ser Tyr Phe Phe Gly Leu His  
 65 70 75 80  
 Phe Leu Asn Thr Gln Thr Thr Leu Lys Asn Ile Ile Ala Ile Gly Leu  
 85 90 95  
 Pro Gly Val Gly Asn Gln His Ile Ile Glu Ala Ser Arg Ser Leu Cys  
 100 105 110  
 Gln Lys His Asn Ser Leu Leu Leu Phe Phe Asp His Asp Leu Tyr Asp  
 115 120 125  
 Leu Leu Thr Phe Asn Gln Pro Xaa  
 130 135

&lt;210&gt;829

&lt;211&gt;205

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;829

Met His Ala Lys Leu Ser Phe Phe Ile Leu Leu Ser Leu Leu Phe Ser  
 1 5 10 15  
 Gly Ile Asp Cys Ser Arg Leu His Ala Ala Gly Arg Ser Pro Ser Leu  
 20 25 30  
 Gln Gly Val Leu Ala Glu Ile Glu Asp Ile Ser Ala Lys Leu Ala Ser  
 35 40 45  
 His Glu Val Glu Ile Val Met Leu Ser Glu Arg Leu Asp Glu Gln Asp  
 50 55 60  
 Ser Lys Phe Gln Lys Trp Thr Ala Ala Lys Pro Glu Thr Leu Ala Gln  
 65 70 75 80  
 Lys Ile Arg Glu Leu Glu Ser Asp Gln Lys Ala Leu Ala Lys Thr Leu  
 85 90 95  
 Ala Val Leu Thr Thr Ser Val Lys Asp Leu Gln Thr Asn Leu Gln Ser  
 100 105 110  
 Lys Leu Gln Glu Ile Gln Lys Asp His Arg Ala Leu Ala Gln Asp Leu  
 115 120 125  
 Arg Leu Val Arg Arg Ser Leu Leu Ala Leu Val Asp Ser Ser Ser Pro  
 130 135 140  
 Gly Ala Tyr Ala Asp Phe Ser Asp Pro Val Pro Glu Asn Ile Tyr Ile  
 145 150 155 160  
 Val Arg Glu Gly Asp Ser Leu Ser Lys Ile Ala Lys Lys Tyr Lys Leu  
 165 170 175  
 Ser Val Thr Glu Leu Lys Lys Ile Asn Lys Leu Asp Ser Asp Ala Ile  
 180 185 190  
 Tyr Ala Gly Gln Arg Leu Cys Leu Gln Arg Asn Lys Gln  
 195 200 205

&lt;210&gt;830

&lt;211&gt;192

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;830

Met Asn Ile His Ser Leu Trp Lys Leu Cys Thr Leu Leu Ala Leu Leu  
 1 5 10 15  
 Ala Leu Pro Ala Cys Ser Leu Ser Pro Asn Tyr Gly Trp Glu Asp Ser  
 20 25 30  
 Cys Asn Thr Cys His His Thr Arg Arg Lys Lys Pro Ser Ser Phe Gly  
 35 40 45  
 Phe Val Pro Leu Tyr Thr Glu Glu Asp Phe Asn Pro Asn Phe Thr Phe  
 50 55 60  
 Gly Glu Tyr Asp Ser Lys Glu Glu Lys Gln Tyr Lys Ser Ser Gln Val  
 65 70 75 80  
 Ala Ala Phe Arg Asn Ile Thr Phe Ala Thr Asp Ser Tyr Thr Ile Lys  
 85 90 95  
 Gly Glu Glu Asn Leu Ala Ile Leu Thr Asn Leu Val His Tyr Met Lys  
 100 105 110  
 Lys Asn Pro Lys Ala Thr Leu Tyr Ile Glu Gly His Thr Asp Glu Arg  
 115 120 125

Gly Ala Ala Ser Tyr Asn Leu Ala Leu Gly Ala Arg Arg Ala Asn Ala  
 130 135 140  
 Ile Lys Glu His Leu Arg Lys Gln Gly Ile Ser Ala Asp Arg Leu Ser  
 145 150 155 160  
 Thr Ile Ser Tyr Gly Lys Glu His Pro Leu Asn Ser Gly His Asn Glu  
 165 170 175  
 Leu Ala Trp Gln Gln Asn Arg Arg Thr Glu Phe Lys Ile His Ala Arg  
 180 185 190  
 <210>831  
 <211>431  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>831  
 Met Leu Arg Gln Leu Cys Phe Gln Val Phe Phe Phe Cys Phe Ala Ser  
 1 5 10 15  
 Leu Val Tyr Ala Glu Glu Leu Glu Val Val Val Arg Ser Glu His Ile  
 20 25 30  
 Thr Leu Pro Ile Glu Val Ser Cys Gln Thr Asp Thr Lys Asp Pro Lys  
 35 40 45  
 Ile Gln Lys Tyr Leu Ser Ser Leu Thr Glu Ile Phe Cys Lys Asp Ile  
 50 55 60  
 Ala Leu Gly Asp Cys Leu Gln Pro Thr Ala Ala Ser Lys Glu Ser Ser  
 65 70 75 80  
 Ser Pro Leu Ala Ile Ser Leu Arg Leu His Val Pro Gln Leu Ser Val  
 85 90 95  
 Val Leu Leu Gln Ser Ser Lys Thr Pro Gln Thr Leu Cys Ser Phe Thr  
 100 105 110  
 Ile Ser Gln Asn Leu Ser Val Asp Arg Gln Lys Ile His His Ala Ala  
 115 120 125  
 Asp Thr Val His Tyr Ala Leu Thr Gly Ile Pro Gly Ile Ser Ala Gly  
 130 135 140  
 Lys Ile Val Phe Ala Leu Ser Ser Leu Gly Lys Asp Gln Lys Leu Lys  
 145 150 155 160  
 Gln Gly Glu Leu Trp Thr Thr Asp Tyr Asp Gly Lys Asn Leu Ala Pro  
 165 170 175  
 Leu Thr Thr Glu Cys Ser Leu Ser Ile Thr Pro Lys Trp Val Gly Val  
 180 185 190  
 Gly Ser Asn Phe Pro Tyr Leu Tyr Val Ser Tyr Lys Tyr Gly Val Pro  
 195 200 205  
 Lys Ile Phe Leu Gly Ser Leu Glu Asn Thr Glu Gly Lys Lys Val Leu  
 210 215 220  
 Pro Leu Lys Gly Asn Gln Leu Met Pro Thr Phe Ser Pro Arg Lys Lys  
 225 230 235 240  
 Leu Leu Ala Phe Val Ala Asp Thr Tyr Gly Asn Pro Asp Leu Phe Ile  
 245 250 255  
 Gln Pro Phe Ser Leu Thr Ser Gly Pro Met Gly Arg Pro Arg Arg Leu  
 260 265 270  
 Leu Asn Glu Asn Phe Gly Thr Gln Gly Asn Pro Ser Phe Asn Pro Glu  
 275 280 285  
 Gly Ser Gln Leu Val Phe Ile Ser Asn Lys Asp Gly Arg Pro Arg Leu  
 290 295 300  
 Tyr Ile Met Ser Leu Asp Pro Glu Pro Gln Ala Pro Arg Leu Leu Thr  
 305 310 315 320  
 Lys Lys Tyr Arg Asn Ser Ser Cys Pro Ala Trp Ser Pro Asp Gly Lys  
 325 330 335  
 Lys Ile Ala Phe Cys Ser Val Ile Lys Gly Val Arg Gln Ile Cys Ile  
 340 345 350  
 Tyr Asp Leu Ser Ser Gly Glu Asp Tyr Gln Leu Thr Thr Ser Pro Thr  
 355 360 365  
 Asn Lys Glu Ser Pro Ser Trp Ala Ile Asp Ser Arg His Leu Val Phe  
 370 375 380  
 Ser Ala Gly Asn Ala Glu Glu Ser Glu Leu Tyr Leu Ile Ser Leu Val  
 385 390 395 400  
 Thr Lys Lys Thr Asn Lys Ile Ala Ile Gly Val Gly Glu Lys Arg Phe

405 410 415  
 Pro Ser Trp Gly Ala Phe Pro Gln Gln Pro Ile Lys Arg Thr Leu  
 420 425 430  
 <210>832  
 <211>194  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>832  
 Asn Asp Thr Pro Leu Cys Thr Thr Gln Pro Gln Lys Gln Ala Lys Cys  
 1 5 10 15  
 Ser Pro Pro Gln Glu Asn Val Gln Lys Ala Leu Gln Lys Pro Ile Pro  
 20 25 30  
 Lys Val Ile Lys Thr Glu Pro Pro Lys Pro Ser Pro Ala Pro Thr Val  
 35 40 45  
 Ala Lys Lys Thr Thr Ala Thr Glu Lys Pro Pro Pro Ser Thr Thr Lys  
 50 55 60  
 Lys Asn Thr Gln Leu Ser Lys Thr Gln Leu Gln Thr Leu Ser Glu Val  
 65 70 75 80  
 Ala Gln Ala Leu Ser Leu His Val Asp Lys Ile Glu Lys Ser Glu Thr  
 85 90 95  
 Ser Leu Lys Asn Ile Ser Trp Pro Ser Thr Ala Gln Leu Thr Met His  
 100 105 110  
 Ser Glu Leu Lys Ala Thr Gln Glu Asp Glu Leu Cys Glu Leu Phe Arg  
 115 120 125  
 Thr His Ile Ala Leu Pro Ser Lys Gly Tyr Val Arg Ile Lys Leu Val  
 130 135 140  
 Leu Ser Pro Asn Gly Glu Ile Gln Glu Cys Ser Phe Leu Ser Glu Val  
 145 150 155 160  
 Ser Ala Ala Asp Lys Gln Leu Leu Thr Gln Arg Ile His Ala Leu Pro  
 165 170 175  
 Phe Gln Lys Phe Leu Glu Lys Tyr Lys Val Ser Lys Asn Ile Ile Phe  
 180 185 190  
 Ser Tyr

<210>833  
 <211>135  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>833  
 Met Lys Tyr Arg Phe Thr Glu Glu Ile Glu Glu Glu Pro Leu Val Asn  
 1 5 10 15  
 Leu Thr Pro Leu Ile Asp Ile Val Phe Val Ile Leu Met Ala Phe Ile  
 20 25 30  
 Val Ala Val Pro Leu Ile Lys Leu Asp Ser Ile Ala Leu Ala Pro Gly  
 35 40 45  
 Thr Gln Glu Gln Glu Val Leu Ser Ser Glu Asn Asp Ser Ile Ala Val  
 50 55 60  
 Ile Lys Val Phe Ala Asp His Ser Leu Thr Leu Asn Glu His Pro Ile  
 65 70 75 80  
 Thr Leu Gln Glu Leu Thr Val Arg Leu Thr Leu Leu His Lys Ala Tyr  
 85 90 95  
 Pro Glu Lys Thr Pro Leu Leu Leu Gln Asp Gly Glu Thr Ser Phe Arg  
 100 105 110  
 Thr Tyr Gln Asn Val Lys Asn Ala Ile Glu Ala Ala Gly Phe His Glu  
 115 120 125  
 Leu His Val Ala Leu Gln Asn  
 130 135

<210>834  
 <211>232  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>834  
 Met Val His Phe Ser His Asn Pro Ile Ile Gln Ala Tyr Thr Glu Ala  
 1 5 10 15

Asp Phe Phe Gly Lys Ser Ile Phe Phe Cys Leu Leu Ile Leu Ser Val  
                   20                                  25                                  30  
 Cys Thr Trp Thr Val Leu His Gln Lys Leu Ala Ile Gln Lys Asn Phe  
                   35                                  40                                  45  
 Leu Lys Ala Gly Lys Ser Leu Lys Asp Phe Leu Ile Lys Asn Arg His  
                   50                                  55                                  60  
 Ala Pro Leu Ser Leu Asp Ile His Pro Glu Leu Ser Pro Phe Ala Asp  
                   65                                  70                                  75                                  80  
 Leu Tyr Phe Thr Ile Lys Arg Gly Thr Leu Glu Leu Leu Asp Lys Asn  
                                   85                                  90                                  95  
 Arg Gln Ser Ala Pro Asp Arg Gly Pro Ile Leu Ser Ser Glu Asp Ile  
                                   100                                  105                                  110  
 Gln Ser Leu Glu Thr Leu Leu Gly Ala Ile Met Pro Lys Tyr Lys Ala  
                                   115                                  120                                  125  
 Leu Leu His Lys Asn Ser Phe Ile Pro Ala Thr Thr Ile Ser Leu Ala  
                                   130                                  135                                  140  
 Pro Phe Leu Gly Leu Leu Gly Thr Val Trp Gly Ile Leu Val Ala Phe  
                                   145                                  150                                  155                                  160  
 Thr His Ile Ser Ser Gly Ser Ser Gly Asn Ser Ala Ile Met Glu Gly  
                                   165                                  170                                  175  
 Leu Ala Thr Ala Leu Gly Thr Thr Ile Ile Gly Leu Phe Val Ala Ile  
                                   180                                  185                                  190  
 Pro Ser Leu Ile Ala Phe Asn Tyr Leu Lys Ala His Ser Ser Glu Leu  
                                   195                                  200                                  205  
 Ile Ser Glu Ile Glu Gln Thr Ala Tyr Leu Leu Leu Asn Ser Ile Glu  
                                   210                                  215                                  220  
 Val Lys Tyr Arg Asn Thr Asn Leu  
                                   225                                  230

&lt;210&gt;835

&lt;211&gt;135

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;835

Leu Lys Ala Ile Ser Glu Gly Ile Ala Thr Lys Ser Pro Ile Ile Val  
                   1                                  5                                  10                                  15  
 Val Pro Arg Ala Val Ala Ser Pro Ser Ile Met Ala Glu Phe Pro Leu  
                                   20                                  25                                  30  
 Leu Pro Glu Leu Met Trp Val Lys Ala Thr Lys Ile Pro His Thr Val  
                                   35                                  40                                  45  
 Pro Lys Ser Pro Arg Lys Gly Ala Lys Leu Ile Val Val Ala Gly Ile  
                                   50                                  55                                  60  
 Lys Leu Phe Leu Cys Lys Arg Ala Leu Tyr Phe Gly Met Met Ala Pro  
                                   65                                  70                                  75                                  80  
 Arg Ser Val Ser Lys Asp Trp Ile Ser Ser Glu Glu Arg Met Gly Pro  
                                   85                                  90                                  95  
 Arg Ser Gly Ala Asp Cys Arg Phe Leu Ser Lys Ser Ser Lys Val Pro  
                                   100                                  105                                  110  
 Arg Phe Ile Val Lys Tyr Lys Ser Ala Lys Gly Leu Ser Ser Gly Trp  
                                   115                                  120                                  125  
 Ile Ser Arg Asp Arg Gly Ala  
                                   130                                  135

&lt;210&gt;836

&lt;211&gt;676

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;836

Ile Ile Gln Val Gln Asn Ser Phe Leu Arg Val Ala Thr Ser Leu Asp  
                   1                                  5                                  10                                  15  
 Tyr Arg His Ser Asp Trp Gly Ser Arg Phe Thr Ala Ser Lys Gly Ser  
                                   20                                  25                                  30  
 His Ile Tyr Trp Lys Asn Pro Gly Glu Ile Gly Ser Pro Leu Lys Ile  
                                   35                                  40                                  45  
 Ser Trp Gln Leu Pro Lys Gly Phe Val Val Glu Glu His Trp Pro  
                                   50                                  55                                  60

Thr Pro Lys Val Phe Glu Glu Glu Gly Thr Thr Phe Phe Gly Tyr Glu  
 65 70 75 80  
 Asp Ser Ala Leu Ile Val Ala Asp Val Arg Ala Pro Glu Gly Tyr Thr  
 85 90 95  
 Pro Gly Gln Glu Val Glu Leu Arg Ala Gln Val Glu Trp Leu Ala Cys  
 100 105 110  
 Gly Asp Ser Cys Leu Pro Gly Asn Val Asp Leu Lys Leu Thr Leu Pro  
 115 120 125  
 Tyr Glu Glu Lys Glu Pro Ser Leu Tyr Pro Asp Thr His Ala Glu Phe  
 130 135 140  
 Thr Lys Thr Leu His Ala Gln Pro Arg Val Leu Glu Asn Asp His Ser  
 145 150 155 160  
 Val Gln Val Ala Gln Gly Lys Gly Asn Glu Ile Ile Leu Asn Ile Ser  
 165 170 175  
 Lys Lys Ile Asn Ala Thr Lys Ala Trp Phe Val Ser Glu Lys Ala Asp  
 180 185 190  
 Lys Leu Phe Ala Tyr Ala Glu Thr Ser Tyr Ser Gly Gly Thr Gly Thr  
 195 200 205  
 Ala Trp Arg Leu Lys Val Lys Asn Leu Ser Gly Val Gln Lys Asn Glu  
 210 215 220  
 Lys Leu His Gly Ile Leu Leu Leu Ala Asp His Thr Gly Arg Pro Val  
 225 230 235 240  
 Glu Ser Leu Thr Ile His Ser Glu Val Leu Gly Gln Thr Gly Ser Ala  
 245 250 255  
 Val Ala Gly Leu Ser Gln Tyr Ile Thr Ile Leu Ile Met Ala Phe Leu  
 260 265 270  
 Gly Gly Val Leu Leu Asn Ile Met Pro Cys Val Leu Pro Leu Val Thr  
 275 280 285  
 Leu Lys Val Tyr Gly Leu Ile Lys Ser Ala Gly Glu His Arg Ser Ser  
 290 295 300  
 Val Ile Ala Asn Gly Leu Trp Phe Thr Leu Gly Val Val Gly Cys Phe  
 305 310 315 320  
 Trp Gly Leu Ala Gly Val Ala Phe Ile Leu Lys Val Leu Gly His Asn  
 325 330 335  
 Ile Gly Trp Gly Phe Gln Leu Gln Glu Pro Met Phe Val Ala Thr Leu  
 340 345 350  
 Ile Ile Val Phe Phe Leu Phe Ala Leu Ser Ser Leu Gly Leu Phe Glu  
 355 360 365  
 Met Gly Thr Met Phe Ala Asn Leu Gly Gly Lys Leu Gln Ser Ser Glu  
 370 375 380  
 Met Lys Ser Ser Asn Asn Lys Ala Val Gly Ala Phe Phe Asn Gly Ile  
 385 390 395 400  
 Leu Ala Thr Leu Val Thr Thr Pro Cys Thr Gly Pro Phe Leu Gly Ser  
 405 410 415  
 Val Leu Gly Leu Val Met Ser Leu Ser Phe Leu Gln Gln Leu Leu Ile  
 420 425 430  
 Phe Thr Ala Ile Gly Leu Gly Met Ala Ser Pro Tyr Leu Val Phe Ser  
 435 440 445  
 Val Phe Pro Lys Met Leu Ser Val Leu Pro Lys Pro Gly Gly Trp Met  
 450 455 460  
 Ser Thr Phe Lys Gln Leu Thr Gly Phe Met Leu Leu Val Thr Val Thr  
 465 470 475 480  
 Trp Leu Val Trp Ile Phe Gly Ser Glu Thr Ser Thr Thr Ser Val Val  
 485 490 495  
 Val Leu Leu Gly Gly Leu Trp Leu Ala Gly Leu Gly Ala Trp Ile Leu  
 500 505 510  
 Gly Arg Trp Gly Thr Pro Val Ser Pro Lys Lys Gln Arg Val Cys Ala  
 515 520 525  
 Ser Leu Leu Phe Phe Ala Phe Leu Gly Gly Ala Ile Ser Val Ser Gly  
 530 535 540  
 Leu Ala Ser His Tyr Phe Ala Glu Pro Gln Gln Thr Val Ser Val Asn  
 545 550 555 560  
 Glu Asp Ser Leu Trp Gln Pro Phe Ser Leu Glu Lys Leu Ala Gln Leu  
 565 570 575

Arg Ala Gln Gly Arg Pro Val Phe Val Asn Phe Thr Ala Lys Trp Cys  
 580 585 590  
 Leu Thr Cys Gln Met Asn Lys Pro Val Leu Tyr Gly Asp Ala Val Gln  
 595 600 605  
 Lys Met Phe Glu Thr His Gly Ile Val Thr Leu Glu Ala Asp Trp Thr  
 610 615 620  
 Arg Lys Asp Pro Gly Ile Thr Glu Glu Leu Ala Arg Leu Gly Arg Ala  
 625 630 635 640  
 Ser Val Pro Ser Tyr Val Tyr Tyr Pro Gly Asp Asn Ser Ala Pro Val  
 645 650 655  
 Val Leu Pro Xaa Lys Ile Thr Gln Asn Leu Leu Glu Asp Val Val Ser  
 660 665 670  
 Arg Phe Val Arg  
 675

&lt;210&gt;837

&lt;211&gt;261

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;837

Val Asp Leu Ala Asp Ala His Val His Leu Ser Asp Asp Ala Phe Glu  
 1 5 10 15  
 Glu Asp Ile Asn Ser Val Leu Gln Arg Ala Gln Asp Ser Gly Val Ser  
 20 25 30  
 Leu Val Val Asn Val Thr Thr Thr Glu Lys Glu Leu Asn Arg Ser Phe  
 35 40 45  
 Ala Tyr Ala Glu Arg Phe Pro Lys Ile Arg Phe Cys His Val Gly Gly  
 50 55 60  
 Thr Pro Pro Gln Asp Val Asp Gln Asp Ile Glu Asp Tyr Arg Asn  
 65 70 75 80  
 Phe His Ala Ala Ala His Ser Lys Lys Leu Ala Ala Ile Gly Glu Val  
 85 90 95  
 Gly Leu Asp Tyr Cys Phe Ala Thr Glu Glu Gly Ile Ala Arg Gln Lys  
 100 105 110  
 Glu Val Leu Gln Arg Tyr Leu Ala Leu Ser Leu Glu Cys Glu Leu Pro  
 115 120 125  
 Leu Val Val His Cys Arg Gly Ala Phe Asn Asp Phe Phe Arg Met Leu  
 130 135 140  
 Asp Gln Tyr Tyr His Asn Asp Pro Arg Ser Arg Pro Gly Met Leu His  
 145 150 155 160  
 Cys Phe Thr Gly Thr Leu Glu Glu Ala Gln Glu Leu Ile Ser Arg Gly  
 165 170 175  
 Trp Phe Ile Ser Ile Ser Gly Ile Val Thr Phe Lys Asn Ala Gln Asp  
 180 185 190  
 Leu Arg Asp Leu Val Val Glu Leu Pro Leu Glu His Leu Leu Ile Glu  
 195 200 205  
 Thr Asp Ala Pro Phe Leu Ala Pro Val Pro Tyr Arg Gly Lys Lys Asn  
 210 215 220  
 Glu Pro Ala His Val Leu His Thr Ile Asn Ala Val Ala Asn Val Lys  
 225 230 235 240  
 Gly Met Phe Pro Gln Glu Leu Ala Ala Leu Ala Tyr Lys Asn Val Leu  
 245 250 255  
 Arg Phe Leu His Gly  
 260

&lt;210&gt;838

&lt;211&gt;297

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;838

Met Ser Arg His Glu Ile Cys Pro Glu Val Ser His Lys Lys Gly Lys  
 1 5 10 15  
 Tyr Tyr Ser Thr Phe Ile Phe Arg Cys Ile His Ser Leu Ala Gly Ile  
 20 25 30  
 Ala Phe Thr Phe Phe Leu Cys Glu His Leu Phe Thr Asn Met Leu Ala  
 35 40 45

Ser Ser Tyr Phe Ser Gln Gly Lys Gly Phe Val Ala Met Val Asn Gly  
 50 55 60  
 Phe His Lys Ile Pro Gly Leu Lys Ile Ile Glu Val Ala Gly Leu Val  
 65 70 75 80  
 Leu Pro Phe Leu Cys His Ala Ile Ile Gly Ile Val Tyr Leu Phe Gln  
 85 90 95  
 Gly Lys Ser Asn Cys Tyr Ser Gly Asp Gly Ser Arg Pro His Leu Arg  
 100 105 110  
 Tyr Ala Lys Asn Tyr Ser Tyr Thr Trp Gln Arg Trp Thr Ala Trp Ile  
 115 120 125  
 Leu Leu Phe Gly Ile Ala Phe His Val Val His Leu Arg Phe Ile Arg  
 130 135 140  
 Tyr Pro Val His Val Asp Ile His Gly Thr Thr Tyr Tyr Ala Val Asp  
 145 150 155 160  
 Ile Gln Pro Ser Arg Tyr Asp Val Ile Val Arg Gly Thr Lys Gly Phe  
 165 170 175  
 Leu Thr Leu Asn Leu Pro Asn Thr Glu Ala Ser Ser Ile Glu Val Ser  
 180 185 190  
 Arg His Asp Leu Gly Gly Ala Asp Ala Ala Leu Leu Ser Glu Arg Asn  
 195 200 205  
 Ser Tyr Leu Leu Thr Pro Ser Ala Gly Thr Ala Phe Leu Tyr Val Val  
 210 215 220  
 Arg Asp Ala Leu Gly Ser Leu Phe Ile Ala Leu Leu Tyr Thr Ile Leu  
 225 230 235 240  
 Val Ile Ala Ala Ala Phe His Gly Phe Asn Gly Leu Trp Thr Phe Cys  
 245 250 255  
 Cys Arg Trp Gly Val Val Val Ser Leu Arg Met Gln Gly Val Leu Arg  
 260 265 270  
 Ile Val Cys Tyr Leu Ala Met Ile Val Val Thr Phe Met Gly Val Ser  
 275 280 285  
 Ala Val Trp Asn Leu Tyr Ser Val Ala  
 290 295  
 <210>839  
 <211>626  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>839  
 Met Asp Glu Asn Arg Lys Val Ile Val Val Gly Gly Gly Leu Ala Gly  
 1 5 10 15  
 Leu Ser Ala Ala Met Gln Leu Ala Asn Leu Gly Ile Ile Val Glu Leu  
 20 25 30  
 Val Ser Leu Thr Lys Val Lys Arg Ser His Ser Val Cys Ala Gln Gly  
 35 40 45  
 Gly Ile Asn Ala Ala Leu Asn Leu Lys Pro Glu Glu Asp Ser Pro  
 50 55 60  
 Tyr Val His Ala Tyr Asp Thr Ile Lys Gly Gly Asp Phe Leu Ala Asp  
 65 70 75 80  
 Gln Pro Pro Val Leu Glu Met Cys Leu Ala Ala Pro Arg Ile Ile Lys  
 85 90 95  
 Met Leu Asp Asn Phe Gly Cys Pro Phe Asn Arg Gly Pro Ser Gly Asn  
 100 105 110  
 Leu Asp Val Arg Arg Phe Gly Gly Thr Leu Tyr His Arg Thr Val Phe  
 115 120 125  
 Cys Gly Ala Ser Thr Gly Gln Gln Leu Met Tyr Thr Leu Asp Glu Gln  
 130 135 140  
 Val Arg Arg Arg Glu His Ala Gly Arg Val Ile Lys Arg Glu Asn His  
 145 150 155 160  
 Glu Phe Val Arg Leu Val Thr Asp His Ser Gly Arg Ala Cys Gly Ile  
 165 170 175  
 Ile Leu Met Asn Leu Phe Asn Asn Arg Leu Glu Ile Leu Arg Gly Asp  
 180 185 190  
 Ala Val Ile Ile Ala Thr Gly Gly Pro Gly Val Ile Phe Lys Met Ser  
 195 200 205  
 Thr Asn Ser Thr Phe Cys Thr Gly Ala Ala Asn Gly Arg Leu Phe Leu



210 215 220  
 Gln Gly Met Ala Tyr Ala Asn Pro Glu Phe Ile Gln Ile His Pro Thr  
 225 230 235 240  
 Ala Ile Pro Gly Arg Asp Lys Leu Arg Leu Ile Ser Glu Ser Val Arg  
 245 250 255  
 Gly Glu Gly Gly Arg Val Trp Val Pro Gly Asp Ser Ser Lys Arg Ile  
 260 265 270  
 Val Phe Pro Asp Gly Ser Glu Arg Pro Cys Gly Glu Thr Gly Ala Pro  
 275 280 285  
 Trp Tyr Phe Leu Glu Asp Met Tyr Pro Ala Tyr Gly Asn Leu Val Ser  
 290 295 300  
 Arg Asp Val Gly Ala Arg Ala Ile Leu Arg Val Cys Glu Ala Gly Leu  
 305 310 315 320  
 Gly Ile Asp Gly Arg Met Glu Ala Tyr Leu Asp Val Thr His Leu Pro  
 325 330 335  
 Glu Lys Thr Arg His Lys Leu Glu Val Val Leu Asp Ile Tyr Lys Lys  
 340 345 350  
 Phe Thr Gly Glu Asp Pro Asn Thr Val Pro Met Arg Ile Phe Pro Ala  
 355 360 365  
 Val His Tyr Ser Met Gly Gly Ala Trp Val Asp Trp Pro Ala Ala Asp  
 370 375 380  
 Asp Pro Asp Arg Asp Ser Arg Phe Arg Gln Met Thr Asn Ile Pro Gly  
 385 390 395 400  
 Cys Phe Asn Cys Gly Glu Ser Asp Phe Gln Tyr His Gly Ala Asn Arg  
 405 410 415  
 Leu Gly Ala Asn Ser Leu Leu Ser Cys Leu Phe Ala Gly Leu Val Ser  
 420 425 430  
 Gly Asp Glu Ala Ser Arg Phe Ile Glu Ala Phe Gly Ala Ser Gln Ala  
 435 440 445  
 Thr Ser Ser Asp Phe Asp Arg Ala Leu Gln Gln Glu Lys Glu Glu Asn  
 450 455 460  
 Ala Arg Leu Leu Ser Ala Ser Gly Lys Glu Asn Ile Phe Val Leu His  
 465 470 475 480  
 Glu Glu Ile Ala Lys Ile Met Val Arg Asn Val Thr Val Lys Arg Asn  
 485 490 495  
 Asn Arg Asp Leu Gln Glu Thr Met Asp Lys Leu Lys Glu Phe Arg Glu  
 500 505 510  
 Arg Leu Lys Asn Val Ser Val Leu Asp Ser Ser Pro Phe Ala Asn Lys  
 515 520 525  
 Ser Phe His Phe Val Arg Gln Met Gly Pro Met Leu Glu Leu Ala Leu  
 530 535 540  
 Ala Ile Thr Lys Gly Ala Leu Leu Arg Asn Glu Phe Arg Gly Ser His  
 545 550 555 560  
 Tyr Lys Pro Glu Phe Pro Glu Arg Asp Asp Glu His Trp Leu Lys Thr  
 565 570 575  
 Thr Val Ala Val Tyr Ala Pro Glu Glu Pro Glu Ile Ser Tyr Leu Pro  
 580 585 590  
 Val Asp Thr Arg His Val Ala Pro Thr Leu Arg Asp Tyr Thr Lys Ser  
 595 600 605  
 Ser Thr Gly Lys Ile Glu Leu Thr Asn Ile Pro Asp Asn Ile Arg Leu  
 610 615 620  
 Pro Ile  
 625  
 <210>840  
 <211>270  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>840  
 Leu Ile Ile Ser Val Tyr Pro Tyr Arg Lys Arg Glu Met Met Glu Asn  
 1 5 10 15  
 Leu Glu Thr Phe Ile Leu Lys Ile Tyr Arg Gly Val Pro Gly Lys Gln  
 20 25 30  
 Tyr Trp Glu Ser Phe Glu Leu Pro Leu His Pro Gly Glu Asn Val Ile  
 35 40 45

Ser Ala Leu Met Glu Ile Glu Lys Arg Pro Val Asn Ile Leu Gly Glu  
 50 55 60  
 Lys Val Asn Pro Val Val Trp Glu Gln Gly Cys Leu Glu Glu Val Cys  
 65 70 75 80  
 Gly Ser Cys Ser Ile Leu Val Asn Gly Val Pro Arg Gln Ala Cys Thr  
 85 90 95  
 Ala Leu Ile Gln Glu Tyr Ile Asp Ala Thr Gln Ser Arg Glu Ile Val  
 100 105 110  
 Leu Ala Pro Leu Thr Lys Phe Pro Leu Ile Arg Asp Leu Ile Val Asp  
 115 120 125  
 Arg Ser Ile Met Phe Asp Asn Leu Glu Arg Ile Gln Gly Trp Val Ala  
 130 135 140  
 Ala Asp Ile Glu Gly Glu Thr Phe Gly Pro Gln Val Thr Gln Glu Gln  
 145 150 155 160  
 Gln Glu Leu Leu Tyr Ala Leu Ser Gln Cys Met Thr Cys Gly Cys Cys  
 165 170 175  
 Thr Glu Ala Cys Pro Gln Ile Asp Asn Lys Ser Asp Phe Ile Gly Pro  
 180 185 190  
 Ala Ala Ile Ser Gln Ala Arg Tyr Phe Asn Thr Tyr Pro Gly Asp Lys  
 195 200 205  
 Gln Ser Lys Lys Arg Trp Arg Ala Leu Met Gly Lys Gly Gly Ile Glu  
 210 215 220  
 Gly Cys Gly Gln Ala His Asn Cys Val Arg Val Cys Pro Lys Lys Leu  
 225 230 235 240  
 Pro Leu Thr Glu Ser Ile Ser Ala Val Gly Arg Glu Ile Ser Lys Phe  
 245 250 255  
 Ser Leu Arg Ser Leu Phe Ser Ala Leu Phe Lys Lys Lys Lys  
 260 265 270

&lt;210&gt;841

&lt;211&gt;998

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;841

Thr Cys Leu Arg Ser Ser Arg Lys Ile Val Val Glu Asp Ile Ser Asp  
 1 5 10 15  
 Arg Asn Met Tyr Ser Cys Tyr Ser Lys Gly Ile Ser His Asn Tyr Leu  
 20 25 30  
 Leu His Pro Met Ser Arg Leu Asp Ile Phe Val Phe Asp Ser Leu Ile  
 35 40 45  
 Ala Asn Gln Asp Gln Asn Leu Leu Glu Glu Ile Phe Cys Ser Glu Asp  
 50 55 60  
 Thr Val Leu Phe Lys Ala Tyr Arg Thr Thr Ala Leu Gln Ser Pro Leu  
 65 70 75 80  
 Ala Ala Lys Asn Leu Asn Ile Ala Arg Lys Val Ala Asn Tyr Ile Leu  
 85 90 95  
 Ala Asp Asn Gly Glu Ile Asp Thr Val Lys Leu Val Glu Ala Ile His  
 100 105 110  
 His Leu Ser Gln Cys Thr Tyr Pro Leu Gly Pro His Arg His Asn Glu  
 115 120 125  
 Ala Gln Asp Arg Glu His Leu Leu Lys Met Leu Lys Ala Leu Lys Glu  
 130 135 140  
 Asn Pro Lys Leu Lys Glu Ser Ile Lys Thr Leu Phe Val Pro Ser Tyr  
 145 150 155 160  
 Ser Thr Ile Gln Asn Leu Ile Arg His Thr Leu Ala Leu Asn Pro Gln  
 165 170 175  
 Thr Ile Leu Ser Thr Ile His Val Arg Gln Ala Ala Leu Thr Ala Leu  
 180 185 190  
 Phe Thr Tyr Leu Arg Gln Asp Val Gly Ser Cys Phe Ala Thr Ala Pro  
 195 200 205  
 Ala Ile Leu Ile His Gln Glu Tyr Pro Glu Arg Phe Leu Lys Asp Leu  
 210 215 220  
 Asn Asp Leu Ile Ser Ser Gly Lys Leu Ser Arg Ile Val Asn Gln Arg  
 225 230 235 240  
 Glu Ile Ala Val Pro Ile Asn Leu Ser Gly Cys Ile Gly Glu Leu Phe

245 250 255  
 Lys Pro Leu Arg Ile Leu Asp Leu Tyr Pro Asp Pro Leu Val Lys Leu  
 260 265 270  
 Ser Ser Ser Pro Gly Leu Lys Lys Ala Phe Ser Ala Ala Asn Leu Ile  
 275 280 285  
 Glu Thr Leu Gly Asp Ser Glu Ala Gln Ile Gln Gln Leu Leu Ser His  
 290 295 300  
 Gln Tyr Leu Met Gln Lys Leu Gln Asn Val His Glu Thr Leu Thr Ala  
 305 310 315 320  
 Asn Asp Ile Ile Lys Ser Thr Leu Leu His Tyr Tyr Gln Leu Gln Glu  
 325 330 335  
 Ser Thr Val Arg Ala Ile Phe Phe Lys Glu Gly Leu Phe Ser Lys Glu  
 340 345 350  
 Gln Val Ala Phe Ser Thr Gln His Pro Arg Glu Leu Ser Glu Ile Gln  
 355 360 365  
 Arg Val Tyr His Tyr Leu His Ala Tyr Glu Glu Ala Lys Ser Ala Phe  
 370 375 380  
 Ile His Asp Thr Gln Asn Pro Leu Leu Lys Ala Trp Glu Tyr Thr Leu  
 385 390 395 400  
 Ala Thr Leu Ala Asp Ala Ser Gln Pro Thr Ile Ser Asn His Ile Arg  
 405 410 415  
 Leu Ala Leu Gly Trp Lys Ser Glu Asp Pro His Ser Leu Val Ser Leu  
 420 425 430  
 Val Thr His Phe Val Glu Glu Glu Val Glu Asn Ile Arg Ile Leu Val  
 435 440 445  
 Gln Gln Cys Glu Gln Thr Tyr His Glu Ala Arg Ser Gln Leu Glu Tyr  
 450 455 460  
 Ile Glu Gly Arg Met Arg Asn Pro Leu Asn Asn Gln Asp Ser Gln Ile  
 465 470 475 480  
 Leu Thr Met Asp His Met Arg Phe Arg Gln Glu Leu Asn Lys Ala Leu  
 485 490 495  
 Tyr Glu Trp Asp Ser Ala Gln Glu Lys Ala Lys Lys Phe Leu His Leu  
 500 505 510  
 Pro Glu Phe Leu Leu Ser Phe Tyr Thr Lys Gln Ile Pro Leu Tyr Phe  
 515 520 525  
 Arg Ser Ser Tyr Asp Ala Phe Ile Gln Glu Phe Ala His Leu Tyr Ala  
 530 535 540  
 Asn Ala Pro Ala Gly Phe Arg Ile Leu Phe Thr His Gly Arg Thr His  
 545 550 555 560  
 Pro Asn Thr Trp Ser Pro Ile Tyr Ser Ile Asn Glu Phe Ile Arg Phe  
 565 570 575  
 Leu Ser Glu Phe Phe Thr Ser Thr Glu Ser Glu Leu Leu Gly Lys His  
 580 585 590  
 Ala Val Ile Asn Leu Glu Lys Glu Thr Ser Arg Leu Val His Asn Ile  
 595 600 605  
 Thr Ala Met Leu His Thr Asp Val Phe Gln Glu Ala Leu Leu Thr Arg  
 610 615 620  
 Ile Leu Glu Ala Tyr Gln Leu Pro Val Pro Pro Ser Ile Leu Asn His  
 625 630 635 640  
 Leu Asp Gln Leu Ser Gln Thr Pro Trp Val Tyr Val Ser Gly Gly Thr  
 645 650 655  
 Val Asp Thr Leu Leu Leu Asp Tyr Phe Glu Ser Ser Glu Pro Leu Thr  
 660 665 670  
 Leu Thr Glu Lys His Pro Glu Asn Pro His Glu Leu Ala Ala Phe Tyr  
 675 680 685  
 Ala Asp Ala Leu Lys Asp Leu Pro Thr Gly Ile Lys Ser Tyr Leu Glu  
 690 695 700  
 Glu Gly Ser His Ser Leu Leu Ser Ser Ser Pro Thr His Val Phe Ser  
 705 710 715 720  
 Ile Ile Ala Gly Ser Pro Leu Phe Arg Glu Ala Trp Asp Asn Asp Trp  
 725 730 735  
 Tyr Ser Tyr Thr Trp Leu Arg Asp Val Trp Val Lys Gln His Gln Asp  
 740 745 750  
 Phe Leu Gln Asp Thr Ile Leu Pro Gln Leu Ser Ile Tyr Ala Phe Ile

755 760 765  
 Glu Asn Phe Cys Asn Lys Tyr Ala Leu Gln His Val Val His Asp Phe  
 770 775 780  
 His Asp Phe Cys Ser Asp His Ser Leu Thr Leu Pro Glu Leu Tyr Asp  
 785 790 795 800  
 Lys Gly Ser Arg Phe Leu Ser Ser Leu Phe Thr Lys Asp Lys Thr Val  
 805 810 815  
 Ala Leu Ile Tyr Ile Arg Arg Leu Leu Tyr Leu Met Val Arg Glu Val  
 820 825 830  
 Pro Tyr Val Ser Glu Gln Gln Leu Pro Glu Val Leu Asp Asn Val Ser  
 835 840 845  
 Ser Tyr Leu Gly Ile Ser Ser Arg Ile Thr Tyr Glu Lys Phe Arg Ser  
 850 855 860  
 Leu Ile Glu Glu Thr Ile Pro Lys Met Thr Leu Ser Ser Ala Asp  
 865 870 875 880  
 Leu Arg His Ile Tyr Lys Gly Leu Leu Met Gln Ser Tyr Gln Lys Ile  
 885 890 895  
 Tyr Thr Glu Glu Asp Thr Tyr Leu Arg Leu Thr Thr Ala Met Arg His  
 900 905 910  
 His Asn Leu Ala Tyr Pro Ala Pro Leu Leu Phe Ala Asp Ser Asn Trp  
 915 920 925  
 Pro Ser Ile Tyr Phe Gly Phe Ile Leu Asn Pro Gly Thr Thr Glu Ile  
 930 935 940  
 Asp Leu Trp Lys Phe Asn Tyr Ala Gly Leu Gln Gly Gln Pro Leu Asp  
 945 950 955 960  
 Asn Ile Gln Glu Leu Phe Ala Thr Ser Arg Pro Trp Thr Leu Tyr Ala  
 965 970 975  
 Asn Pro Ile Asp Tyr Gly Met Pro Pro Pro Gly Tyr Arg Ser Arg  
 980 985 990  
 Leu Pro Lys Glu Phe Phe  
 995  
 <210>842  
 <211>616  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>842  
 Arg His His Leu Ile Asn Ile Lys Gly Ile Ser Ile Met Lys His Thr  
 1 5 10 15  
 Phe Thr Lys Arg Val Leu Phe Phe Phe Leu Val Ile Pro Ile Pro  
 20 25 30  
 Leu Leu Leu Asn Leu Met Val Val Gly Phe Phe Ser Phe Ser Ala Ala  
 35 40 45  
 Lys Ala Asn Leu Val Gln Val Leu His Thr Arg Ala Thr Asn Leu Ser  
 50 55 60  
 Ile Glu Phe Glu Lys Lys Leu Thr Ile His Lys Leu Phe Leu Asp Arg  
 65 70 75 80  
 Leu Ala Asn Thr Leu Ala Leu Lys Ser Tyr Ala Ser Pro Ser Ala Glu  
 85 90 95  
 Pro Tyr Ala Gln Ala Tyr Asn Glu Met Met Ala Leu Ser Asn Thr Asp  
 100 105 110  
 Phe Ser Leu Cys Leu Ile Asp Pro Phe Asp Gly Ser Val Arg Thr Lys  
 115 120 125  
 Asn Pro Gly Asp Pro Phe Ile Arg Tyr Leu Lys Gln His Pro Glu Met  
 130 135 140  
 Lys Lys Lys Leu Ser Ala Ala Val Gly Lys Ala Phe Leu Leu Thr Ile  
 145 150 155 160  
 Pro Gly Lys Pro Leu Leu His Tyr Leu Ile Leu Val Glu Asp Val Ala  
 165 170 175  
 Ser Trp Asp Ser Thr Thr Thr Ser Gly Leu Leu Val Ser Phe Tyr Pro  
 180 185 190  
 Met Ser Phe Leu Gln Lys Asp Leu Phe Gln Ser Leu His Ile Thr Lys  
 195 200 205  
 Gly Asn Ile Cys Leu Val Asn Lys Tyr Gly Glu Val Leu Phe Cys Ala  
 210 215 220

Gln Asp Ser Glu Ser Ser Phe Val Phe Ser Leu Asp Leu Pro Asn Leu  
 225 230 235 240  
 Pro Gln Phe Gln Ala Arg Ser Pro Ser Ala Ile Glu Ile Glu Lys Ala  
 245 250 255  
 Ser Gly Ile Leu Gly Gly Glu Asn Leu Ile Thr Val Ser Ile Asn Lys  
 260 265 270  
 Lys Arg Tyr Leu Gly Leu Val Leu Asn Lys Ile Pro Ile Gln Gly Thr  
 275 280 285  
 Tyr Thr Leu Ser Leu Val Pro Val Ser Asp Leu Ile Gln Ser Ala Leu  
 290 295 300  
 Lys Val Pro Leu Asn Ile Cys Phe Phe Tyr Val Leu Ala Phe Leu Leu  
 305 310 315 320  
 Met Trp Trp Ile Phe Ser Lys Ile Asn Thr Lys Leu Asn Lys Pro Leu  
 325 330 335  
 Gln Glu Leu Thr Phe Cys Met Glu Ala Ala Trp Arg Gly Asn His Asn  
 340 345 350  
 Val Arg Phe Glu Pro Gln Pro Tyr Gly Tyr Glu Phe Asn Glu Leu Gly  
 355 360 365  
 Asn Ile Phe Asn Cys Thr Leu Leu Leu Leu Leu Asn Ser Ile Glu Lys  
 370 375 380  
 Ala Asp Ile Asp Tyr His Ser Gly Glu Lys Leu Gln Lys Glu Leu Gly  
 385 390 395 400  
 Ile Leu Ser Ser Leu Gln Ser Ala Leu Leu Ser Pro Asp Phe Pro Thr  
 405 410 415  
 Phe Pro Lys Val Thr Phe Ser Ser Gln His Leu Arg Arg Arg Gln Leu  
 420 425 430  
 Ser Gly His Phe Asn Gly Trp Thr Val Gln Asp Gly Gly Asp Thr Leu  
 435 440 445  
 Leu Gly Ile Ile Gly Leu Ala Gly Asp Ile Gly Leu Pro Ser Tyr Leu  
 450 455 460  
 Tyr Ala Leu Ser Ala Arg Ser Leu Phe Leu Ala Tyr Ala Ser Ser Asp  
 465 470 475 480  
 Val Ser Leu Gln Lys Ile Ser Lys Asp Thr Ala Asp Ser Phe Ser Lys  
 485 490 495  
 Thr Thr Glu Gly Asn Glu Ala Val Val Ala Met Thr Phe Ile Lys Tyr  
 500 505 510  
 Val Glu Lys Asp Arg Ser Leu Glu Leu Leu Ser Leu Ser Glu Gly Ala  
 515 520 525  
 Pro Thr Met Phe Leu Gln Arg Gly Glu Ser Phe Val Arg Leu Pro Leu  
 530 535 540  
 Glu Thr His Gln Ala Leu Gln Pro Gly Asp Arg Leu Ile Cys Leu Thr  
 545 550 555 560  
 Gly Gly Glu Asp Ile Leu Lys Tyr Phe Ser Gln Leu Pro Ile Glu Glu  
 565 570 575  
 Leu Leu Lys Asp Pro Leu Asn Pro Leu Asn Thr Glu Asn Leu Ile Asp  
 580 585 590  
 Ser Leu Thr Met Met Leu Asn Asn Glu Thr Glu His Ser Ala Asp Gly  
 595 600 605  
 Thr Leu Thr Ile Leu Ser Phe Ser  
 610 615  
 <210>843  
 <211>629  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>843  
 Asn Asn Arg Val Pro Phe Val Val Cys Cys Ala Val Ala Ile Ile Ala  
 1 5 10 15  
 Pro Leu Gly Ile Asn Ile Val Trp Leu Asn Leu Asp Gln Tyr Arg Thr  
 20 25 30  
 Ile Val Ser Ala Ile Ser Thr Ala Leu Lys Glu Asn Ala Ala Phe Lys  
 35 40 45  
 Ala Asn Thr Leu Thr Gln Ile Val Pro Leu Asn Val Asp Val Leu Ser  
 50 55 60  
 Leu Phe Ser Asp Val Leu Asp Leu Asp Ala Gly Ile Pro Glu Thr Pro

65	70	75	80
Asn Val Leu Leu Ser	Asn Glu Met Gln Lys	Val Phe Gln Gly Ile Tyr	
	85	90	95
Asn Glu Ile Ser Leu Ile Lys Val Phe Pro Asn Gly Asp Lys Ile Val			
	100	105	110
Val Ala Ser Ser Ile Pro Glu His Leu Gly Glu Asn Tyr Asn His Lys			
	115	120	125
Ile Asp Ile Pro Lys Asn Thr Pro Phe Leu Ala Ala Leu Lys Gln Ser			
	130	135	140
Pro Lys Asn Gln Glu Val Phe Ser Val Met Gln Ala Asn Val Phe Asp			
	145	150	155
Ala Lys Thr Gln Glu Leu Gln Gly Ile Leu Tyr Thr Thr Phe Ser Ala			
	165	170	175
Glu Ser Leu Leu Lys Asp Leu Leu Ile Asn Lys Gln Ser Tyr Leu Thr			
	180	185	190
Val Lys Thr Ala Ile Leu Ser Lys Tyr Gly Val Ile Leu Lys Ala Ser			
	195	200	205
Asp Pro Ala Leu His Leu His Thr Val Tyr Pro Asp Met Thr Lys Glu			
	210	215	220
Lys Phe Cys Gln Val Phe Leu Asn Asp Asp Pro Cys Pro Ile Asp Ser			
	225	230	235
Glu Leu Gly Pro Leu Thr Leu Ser Pro Leu Asp Ile Gly Glu Asn Phe			
	245	250	255
Tyr Ser Phe Lys Ile Lys Asp Thr Glu Ile Trp Gly Cys Ile Glu Asn			
	260	265	270
Val Pro Ser Ile Asp Ile Ala Val Leu Ser Tyr Ala Lys Lys Glu Glu			
	275	280	285
Ser Phe Ala Pro Leu Trp Arg Arg Ala Arg Met Tyr Thr Ala Tyr Phe			
	290	295	300
Phe Cys Ile Leu Leu Gly Ser Leu Ile Ala Phe Ile Val Ala Arg Arg			
	305	310	315
Leu Ser Leu Pro Ile Arg Lys Leu Ala Thr Ala Met Ile Glu Ser Arg			
	325	330	335
Lys Asn Lys Asn Cys Leu Tyr Thr Asp Asp Ser Leu Gly Phe Glu Ile			
	340	345	350
Asn Arg Leu Gly His Ile Phe Asn Ala Met Val Glu Asn Leu His Lys			
	355	360	365
Gln Gln His Leu Ala Lys Thr Asn Phe Glu Met Lys Glu Asn Ala Gln			
	370	375	380
Asn Ala Leu His Leu Gly Glu Gln Ala Gln Gln Arg Leu Leu Pro Asn			
	385	390	395
Thr Leu Pro Ser Tyr Pro His Ile Glu Leu Ala Lys Ala Tyr Ile Pro			
	405	410	415
Ala Ile Thr Val Gly Gly Asp Phe Phe Asp Val Phe Val Val Gly Glu			
	420	425	430
Gly Ser Lys Ala Arg Leu Phe Leu Ile Val Ala Asp Ala Ser Gly Lys			
	435	440	445
Gly Val Asn Ala Cys Gly Tyr Ser Leu Phe Leu Lys Asn Met Leu Arg			
	450	455	460
Thr Phe Leu Ser Arg Ser Ser Ser Leu Gln Gln Ala Ile Gln Glu Thr			
	465	470	475
Ser Arg Leu Phe Tyr Asn Asn Thr Lys Asn Ser Gly Met Phe Val Thr			
	485	490	495
Leu Cys Val Tyr Cys Tyr His Gln Thr Ser Asn Thr Met Glu Tyr Tyr			
	500	505	510
Ser Cys Gly His Pro Pro Ala Cys Tyr Leu Asp Pro Asp Gly Glu Thr			
	515	520	525
Ser Trp Leu Phe His Pro Gly Met Ala Leu Gly Phe Leu Pro Glu Val			
	530	535	540
Ala Asn Ile Thr Ser Lys Leu Phe His Pro Lys Pro Gly Ser Leu Phe			
	545	550	555
Val Leu Tyr Ser Asp Gly Ile Thr Glu Ala His Asn Asn Asn Asn Asp			
	565	570	575
Met Phe Gly Glu Glu Arg Leu Gln Ala Ala Ile Gln Gly Leu Thr Gly			

580 585 590  
 Lys Ser Ala Asp Ala Val His Arg Leu Met Leu Ser Val Lys Thr  
 595 600 605  
 Phe Val Gly Asn Ser His Gln His Asp Asp Ile Thr Leu Leu Ile Leu  
 610 615 620  
 Lys Val Leu Ala Ser  
 625  
 <210>844  
 <211>195  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>844  
 Lys Ser Ser Lys His Arg Ser Phe Leu Leu Lys Lys Ser Gly Gly Asn  
 1 5 10 15  
 Gln Val Ser Leu Tyr Gln Lys Trp Trp Asn Ser Gln Leu Lys Lys Ser  
 20 25 30  
 Leu Cys Tyr Ser Thr Val Ala Ala Leu Ile Phe Met Ile Pro Ser Gln  
 35 40 45  
 Glu Ser Phe Ala Asp Ser Leu Ile Asp Leu Asn Leu Gly Leu Asp Pro  
 50 55 60  
 Ser Val Glu Cys Leu Ser Gly Asp Gly Ala Phe Ser Val Gly Tyr Phe  
 65 70 75 80  
 Thr Lys Ala Gly Ser Thr Pro Val Glu Tyr Gln Pro Phe Lys Tyr Asp  
 85 90 95  
 Val Ser Lys Lys Thr Phe Thr Ile Leu Ser Val Glu Thr Ala Asn Gln  
 100 105 110  
 Ser Gly Tyr Ala Tyr Gly Ile Ser Tyr Asp Gly Thr Ile Thr Val Gly  
 115 120 125  
 Thr Cys Ser Leu Gly Ala Gly Lys Tyr Asn Gly Ala Lys Trp Ser Ala  
 130 135 140  
 Asp Gly Thr Leu Thr Pro Leu Thr Gly Ile Thr Gly Gly Thr Ser His  
 145 150 155 160  
 Thr Glu Ala Arg Ala Ile Ser Lys Asp Thr Gln Val Ile Glu Gly Phe  
 165 170 175  
 Ser Tyr Asp Ala Ser Gly Gln Pro Lys Ala Val Gln Trp Ala Ser Gly  
 180 185 190  
 Gly Leu Gln  
 195  
 <210>845  
 <211>115  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>845  
 Cys Phe Arg Ala Thr Gln Gly Cys Ala Val Gly Lys Arg Arg Xaa Thr  
 1 5 10 15  
 Val Thr Gln Leu Ala Asp Ile Ser Gly Gly Ser Arg Ser Ser Tyr Ala  
 20 25 30  
 Tyr Ala Ile Ser Asp Asp Gly Thr Ile Ile Val Gly Ser Met Glu Ser  
 35 40 45  
 Thr Ile Thr Arg Lys Thr Thr Ala Val Lys Trp Val Asn Asn Val Pro  
 50 55 60  
 Thr Tyr Leu Gly Thr Leu Gly Gly Asp Ala Ser Thr Gly Leu Tyr Ile  
 65 70 75 80  
 Ser Gly Asp Gly Thr Val Ile Val Gly Ala Ala Asn Thr Ala Thr Val  
 85 90 95  
 Thr Asn Gly Asn Gln Glu Ser His Ala Tyr Met Tyr Lys Asp Asn Gln  
 100 105 110  
 Met Lys Asp  
 115  
 <210>846  
 <211>182  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>846

Gly Thr Leu Gly Gly Ala Asn Ser Ser Ala Thr Gly Val Ser Ser Asp  
 1 5 10 15  
 Gly Ser Val Ile Val Gly Gln Ala Gln Thr Ala Asp Lys Ser Val His  
 20 25 30  
 Ala Phe Gln Tyr Tyr Asn Gly Glu Met Lys Asp Leu Gly Thr Leu Gly  
 35 40 45  
 Gly Thr Ser Ser Thr Ala Lys Thr Val Ser Pro Asp Gly Lys Val Ile  
 50 55 60  
 Met Gly Arg Ser Gln Ile Ala Asp Gly Ser Trp His Ala Phe Met Cys  
 65 70 75 80  
 His Thr Asp Phe Ser Ser Asn Asn Val Leu Phe Asp Leu Asp Asn Thr  
 85 90 95  
 Tyr Lys Thr Leu Arg Glu Asn Gly Arg Gln Leu Asn Ser Ile Phe Asn  
 100 105 110  
 Leu Gln Asn Met Met Leu Gln Arg Ala Ser Asp His Glu Phe Thr Glu  
 115 120 125  
 Phe Gly Arg Ser Asn Ile Ala Leu Gly Ala Gly Leu Tyr Val Asn Ala  
 130 135 140  
 Leu Gln Asn Leu Pro Ser Xaa Leu Ala Ala Gln Tyr Phe Gly Ile Ala  
 145 150 155 160  
 Tyr Lys Ile Arg Pro Lys Tyr Arg Leu Gly Val Phe Leu Asp His Asn  
 165 170 175  
 Phe Ser Ser His Val Ser  
 180

&lt;210&gt;847

&lt;211&gt;244

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;847

Gln His Asn Ile Leu Glu Ser His Thr Lys Tyr Val Leu Asn Ile Val  
 1 5 10 15  
 Trp Gly Cys Phe Trp Thr Ile Ile Ser Ala Pro Thr Phe Pro Asn Asn  
 20 25 30  
 Phe Asn Val Ser His Asn Arg Leu Trp Met Gly Ala Phe Ile Gly Trp  
 35 40 45  
 Gln Asp Ser Asp Ala Leu Gly Ser Ser Val Lys Val Ser Phe Gly Tyr  
 50 55 60  
 Gly Lys Gln Lys Ala Thr Ile Thr Arg Glu Gln Leu Glu Asn Thr Glu  
 65 70 75 80  
 Ala Gly Ser Gly Glu Ser His Phe Glu Gly Val Ala Ala Gln Ile Glu  
 85 90 95  
 Gly Arg Tyr Gly Lys Ser Leu Gly Gly His Val Arg Val Gln Pro Phe  
 100 105 110  
 Leu Gly Leu Gln Phe Val His Ile Thr Arg Lys Glu Tyr Thr Glu Asn  
 115 120 125  
 Ala Val Gln Phe Pro Val His Tyr Asp Pro Ile Asp Tyr Ser Thr Gly  
 130 135 140  
 Val Val Tyr Leu Gly Ile Gly Ser His Ile Ala Leu Val Asp Ser Leu  
 145 150 155 160  
 His Val Gly Thr Arg Met Gly Met Glu Gln Asn Phe Ala Ala His Thr  
 165 170 175  
 Asp Arg Phe Ser Gly Ser Ile Ala Ser Ile Gly Asn Phe Val Phe Glu  
 180 185 190  
 Lys Leu Asp Val Thr His Thr Arg Ala Phe Ala Glu Met Arg Val Asn  
 195 200 205  
 Tyr Glu Leu Pro Tyr Leu Gln Ser Leu Asn Leu Ile Leu Arg Val Asn  
 210 215 220  
 Gln Gln Pro Leu Gln Gly Val Met Gly Phe Ser Ser Asp Leu Arg Tyr  
 225 230 235 240  
 Ala Leu Gly Phe

&lt;210&gt;848

&lt;211&gt;687

&lt;212&gt;PRT



&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;848

Ser Glu Leu Tyr Ser Ser Tyr Leu Gln Pro Cys Leu Asn Met Ser Ile  
 1 5 10 15  
 Val Arg Asn Ser Ala Leu Pro Leu Pro Cys Leu Ser Arg Ser Glu Thr  
 20 25 30  
 Phe Lys Lys Val Arg Ser His Met Lys Phe Met Lys Val Leu Thr Pro  
 35 40 45  
 Trp Ile Tyr Arg Lys Asp Leu Trp Val Thr Ala Phe Leu Leu Thr Ala  
 50 55 60  
 Ile Pro Gly Ser Phe Ala His Thr Leu Val Asp Ile Ala Gly Glu Pro  
 65 70 75 80  
 Arg His Ala Ala Gln Ala Thr Gly Val Ser Gly Asp Gly Lys Ile Val  
 85 90 95  
 Ile Gly Met Lys Val Pro Asp Asp Pro Phe Ala Ile Thr Val Gly Phe  
 100 105 110  
 Gln Tyr Ile Asp Gly His Leu Gln Pro Leu Glu Ala Val Arg Pro Gln  
 115 120 125  
 Cys Ser Val Tyr Pro Asn Gly Ile Thr Pro Asp Gly Thr Val Ile Val  
 130 135 140  
 Gly Thr Asn Tyr Ala Ile Gly Met Gly Ser Val Ala Val Lys Trp Val  
 145 150 155 160  
 Asn Gly Lys Val Ser Glu Leu Pro Met Leu Pro Asp Thr Leu Asp Ser  
 165 170 175  
 Val Ala Ser Ala Val Ser Ala Asp Gly Arg Val Ile Gly Gly Asn Arg  
 180 185 190  
 Asn Ile Asn Leu Gly Ala Ser Val Ala Val Lys Trp Glu Asp Asp Val  
 195 200 205  
 Ile Thr Gln Leu Pro Ser Leu Pro Asp Ala Met Asn Ala Cys Val Asn  
 210 215 220  
 Gly Ile Ser Ser Asp Gly Ser Ile Ile Val Gly Thr Met Val Asp Val  
 225 230 235 240  
 Ser Trp Arg Asn Thr Ala Val Gln Trp Ile Gly Asp Gln Leu Ser Val  
 245 250 255  
 Ile Gly Thr Leu Gly Gly Thr Thr Ser Val Ala Ser Ala Ile Ser Thr  
 260 265 270  
 Asp Gly Thr Val Ile Val Gly Gly Ser Glu Asn Ala Asp Ser Gln Thr  
 275 280 285  
 His Ala Tyr Ala Tyr Lys Asn Gly Val Met Ser Asp Ile Gly Thr Leu  
 290 295 300  
 Gly Gly Phe Tyr Ser Leu Ala His Ala Val Ser Ser Asp Gly Ser Val  
 305 310 315 320  
 Ile Val Gly Val Ser Thr Asn Ser Glu His Arg Tyr His Ala Phe Gln  
 325 330 335  
 Tyr Ala Asp Gly Gln Met Val Asp Leu Gly Thr Leu Gly Gly Pro Glu  
 340 345 350  
 Ser Tyr Ala Gln Gly Val Ser Gly Asp Gly Lys Val Ile Val Gly Arg  
 355 360 365  
 Ala Gln Val Pro Ser Gly Asp Trp His Ala Phe Leu Cys Pro Phe Gln  
 370 375 380  
 Ala Pro Ser Pro Ala Pro Val His Gly Gly Ser Thr Val Val Thr Ser  
 385 390 395 400  
 Gln Asn Pro Arg Gly Met Val Asp Ile Asn Ala Thr Tyr Ser Ser Leu  
 405 410 415  
 Lys Asn Ser Gln Gln Gln Leu Gln Arg Leu Leu Ile Gln His Ser Ala  
 420 425 430  
 Lys Val Glu Ser Val Ser Ser Gly Ala Pro Ser Phe Thr Ser Val Lys  
 435 440 445  
 Gly Ala Ile Ser Lys Gln Ser Pro Ala Val Gln Asn Asp Val Gln Lys  
 450 455 460  
 Gly Thr Phe Leu Ser Tyr Arg Ser Gln Val His Gly Asn Val Gln Asn  
 465 470 475 480  
 Gln Gln Leu Leu Thr Gly Ala Phe Met Asp Trp Lys Leu Ala Ser Ala  
 485 490 495

Pro Lys Cys Gly Phe Lys Val Ala Leu His Tyr Gly Ser Gln Asp Ala  
 500 505 510  
 Leu Val Glu Arg Ala Ala Leu Pro Tyr Thr Glu Gln Gly Leu Gly Ser  
 515 520 525  
 Ser Val Leu Ser Gly Phe Gly Gly Gln Val Gln Gly Arg Tyr Asp Phe  
 530 535 540  
 Asn Leu Gly Glu Thr Val Val Leu Gln Pro Phe Met Gly Ile Gln Val  
 545 550 555 560  
 Leu His Leu Ser Arg Glu Gly Tyr Ser Glu Lys Asn Val Arg Phe Pro  
 565 570 575  
 Val Ser Tyr Asp Ser Val Ala Tyr Ser Ala Ala Thr Ser Phe Met Gly  
 580 585 590  
 Ala His Val Phe Ala Ser Leu Ser Pro Lys Met Ser Thr Ala Ala Thr  
 595 600 605  
 Leu Gly Val Glu Arg Asp Leu Asn Ser His Ile Asp Glu Phe Lys Gly  
 610 615 620  
 Ser Val Ser Ala Met Gly Asn Phe Val Leu Glu Asn Ser Thr Val Ser  
 625 630 635 640  
 Val Leu Arg Pro Phe Ala Ser Leu Ala Met Tyr Tyr Asp Val Arg Gln  
 645 650 655  
 Gln Gln Leu Val Thr Leu Ser Val Val Met Asn Gln Gln Pro Leu Thr  
 660 665 670  
 Gly Thr Leu Ser Leu Val Ser Gln Ser Ser Tyr Asn Leu Ser Phe  
 675 680 685

&lt;210&gt;849

&lt;211&gt;228

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;849

Val Leu Ile Leu Thr Trp Ile Asn Val Leu Thr Lys Leu Gly Leu Asn  
 1 5 10 15  
 Met Ser Lys Lys Ile Lys Val Leu Gly His Leu Thr Leu Cys Thr Leu  
 20 25 30  
 Phe Arg Gly Val Leu Cys Ala Ala Ala Leu Ser Asn Ile Gly Tyr Ala  
 35 40 45  
 Ser Thr Ser Gln Glu Ser Pro Tyr Gln Lys Ser Ile Glu Asp Trp Lys  
 50 55 60  
 Gly Tyr Thr Phe Thr Asp Leu Glu Leu Leu Ser Lys Glu Gly Trp Ser  
 65 70 75 80  
 Glu Ala His Ala Ile Ser Gly Asn Gly Ser Arg Ile Val Gly Ala Ser  
 85 90 95  
 Gly Ala Gly Gln Gly Ser Val Thr Ala Val Ile Trp Glu Ser His Leu  
 100 105 110  
 Ile Lys His Leu Gly Thr Leu Gly Gly Glu Ala Ser Ser Ala Glu Gly  
 115 120 125  
 Ile Ser Asn Asp Gly Glu Val Val Val Gly Trp Ser Asp Thr Arg Glu  
 130 135 140  
 Gly Tyr Thr His Ala Phe Val Phe Asp Gly Arg Asp Met Lys Asp Leu  
 145 150 155 160  
 Gly Thr Leu Gly Ala Thr Tyr Ser Val Ala Arg Gly Val Ser Gly Asp  
 165 170 175  
 Gly Ser Ile Ile Val Gly Val Ser Ala Thr Ala Arg Gly Glu Asp Tyr  
 180 185 190  
 Gly Met Ala Ser Trp Cys Gln Val Gly Lys Arg Glu Asn Gln Thr Ile  
 195 200 205  
 Glu Val Val Ala Ser Arg Ser Leu Gly Leu Arg Arg Met Gln Ser Leu  
 210 215 220  
 Arg Met Val Arg  
 225

&lt;210&gt;850

&lt;211&gt;173

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;850

Ser Cys Cys Leu Lys Val Ser Gly Ser Glu Ala Asn Ala Ile Ser Glu  
 1 5 10 15  
 Asp Gly Thr Val Ile Val Gly Arg Gly Glu Ile Ser Arg Asn His Ile  
 20 25 30  
 Val Ala Val Lys Trp Asn Lys Asn Ala Val Tyr Ser Leu Gly Thr Leu  
 35 40 45  
 Gly Gly Ser Val Ala Ser Ala Glu Ala Ile Ser Ala Asn Gly Lys Val  
 50 55 60  
 Ile Val Gly Trp Ser Thr Thr Asn Asn Gly Glu Thr His Ala Phe Met  
 65 70 75 80  
 His Lys Asp Glu Thr Met His Asp Leu Gly Thr Leu Gly Gly Gly Phe  
 85 90 95  
 Ser Val Ala Thr Gly Val Ser Ala Asp Gly Arg Ala Ile Val Gly Phe  
 100 105 110  
 Ser Ala Val Lys Thr Gly Glu Ile His Ala Phe Tyr Tyr Ala Glu Gly  
 115 120 125  
 Glu Met Glu Asp Leu Thr Thr Leu Gly Gly Glu Glu Ala Arg Val Phe  
 130 135 140  
 Asp Ile Ser Ser Glu Gly Asn Asp Ile Ile Gly Ser Ile Lys Thr Asp  
 145 150 155 160  
 Ala Gly Ala Glu Arg Ala Tyr Leu Phe His Ile His Lys  
 165 170

&lt;210&gt;851

&lt;211&gt;349

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;851

Val Val Phe Glu Ile Ile Phe Val Val Arg Val Pro Met Lys Lys Thr  
 1 5 10 15  
 Cys Cys Gln Asn Tyr Arg Ser Ile Gly Val Val Phe Ser Val Val Leu  
 20 25 30  
 Phe Val Leu Thr Thr Gln Thr Leu Phe Ala Gly His Phe Ile Asp Ile  
 35 40 45  
 Gly Thr Ser Gly Leu Tyr Ser Trp Ala Arg Gly Val Ser Gly Asp Gly  
 50 55 60  
 Arg Val Val Val Gly Tyr Glu Gly Gly Asn Ala Phe Lys Tyr Val Asp  
 65 70 75 80  
 Gly Glu Lys Phe Leu Leu Glu Gly Leu Val Pro Arg Ser Glu Ala Leu  
 85 90 95  
 Val Phe Lys Ala Ser Tyr Asp Gly Ser Val Ile Ile Gly Ile Ser Asp  
 100 105 110  
 Gln Asp Pro Ser Cys Arg Ala Val Lys Trp Val Asn Gly Ala Leu Val  
 115 120 125  
 Asp Leu Gly Ile Phe Ser Glu Gly Met Gln Ser Phe Ala Glu Gly Val  
 130 135 140  
 Ser Ser Asp Gly Lys Thr Ile Val Gly Cys Leu Tyr Ser Asp Asp Thr  
 145 150 155 160  
 Glu Thr Asn Phe Ala Val Lys Trp Asp Glu Thr Gly Met Val Val Leu  
 165 170 175  
 Pro Asn Leu Pro Glu Asp Arg His Ser Cys Ala Trp Asp Ala Ser Glu  
 180 185 190  
 Asp Gly Ser Val Ile Val Gly Asp Ala Met Gly Ser Glu Ile Ala  
 195 200 205  
 Lys Ala Val Tyr Trp Lys Asp Gly Glu Gln His Leu Leu Ser Asn Ile  
 210 215 220  
 Pro Gly Ala Lys Arg Ser Ser Ala His Ala Val Ser Lys Asp Gly Ser  
 225 230 235 240  
 Phe Ile Val Gly Glu Phe Ile Ser Glu Glu Asn Glu Val His Ala Phe  
 245 250 255  
 Val Tyr His Asn Gly Val Ile Lys Asp Ile Gly Thr Leu Gly Gly Asp  
 260 265 270  
 Tyr Ser Val Ala Thr Gly Val Ser Arg Asp Gly Lys Val Ile Val Gly  
 275 280 285  
 His Ser Thr Arg Thr Asp Gly Glu Tyr Arg Ala Phe Lys Tyr Val Asp

290                      295                      300  
 Gly Arg Met Ile Asp Leu Gly Thr Leu Gly Gly Ser Ala Ser Phe Ala  
 305                      310                      315                      320  
 Phe Gly Val Ser Asp Asp Gly Lys Thr Ile Val Gly Lys Phe Glu Thr  
                          325                      330                      335  
 Glu Leu Gly Glu Cys His Ala Phe Ile Tyr Leu Asp Asp  
                          340                      345  
 <210>852  
 <211>354  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>852  
 Lys Arg Glu Glu Asn Met Ala Ala Ile Lys Gln Ile Leu Arg Ser Met  
   1                      5                      10                      15  
 Leu Ser Gln Ser Ser Leu Trp Met Val Leu Phe Ser Leu Tyr Ser Leu  
                          20                      25                      30  
 Ser Gly Tyr Cys Tyr Val Ile Thr Asp Lys Pro Glu Asp Asp Phe His  
                          35                      40                      45  
 Ser Ser Ser Ala Val Lys Trp Asp His Trp Gly Lys Thr Thr Leu Ser  
                          50                      55                      60  
 Arg Leu Ser Asn Lys Lys Ala Ser Ala Lys Ala Val Ser Gly Thr Gly  
   65                      70                      75                      80  
 Ala Thr Thr Val Gly Phe Ile Lys Asp Thr Trp Ser Arg Thr Tyr Ala  
                          85                      90                      95  
 Val Arg Trp Asn Tyr Trp Gly Thr Lys Glu Leu Pro Thr Ser Ser Trp  
                          100                      105                      110  
 Val Lys Lys Ser Lys Ala Thr Gly Ile Ser Ser Asp Gly Ser Ile Ile  
                          115                      120                      125  
 Ala Gly Ile Val Glu Asn Glu Leu Ser Gln Ser Phe Ala Val Thr Trp  
   130                      135                      140  
 Lys Asn Asn Glu Met Tyr Leu Leu Pro Ser Thr Trp Ala Val Gln Ser  
 145                      150                      155                      160  
 Lys Ala Tyr Gly Ile Ser Ser Asp Gly Ser Val Ile Val Gly Ser Ala  
                          165                      170                      175  
 Lys Asp Ala Trp Ser Arg Thr Phe Ala Val Lys Trp Thr Gly His Glu  
                          180                      185                      190  
 Ala Gln Val Leu Pro Val Gly Trp Ala Val Lys Ser Val Ala Asn Ser  
                          195                      200                      205  
 Val Ser Ala Asn Gly Ser Ile Ile Val Gly Ser Val Gln Asp Ala Ser  
   210                      215                      220  
 Gly Ile Leu Tyr Ala Val Lys Trp Glu Gly Asn Thr Ile Thr His Leu  
 225                      230                      235                      240  
 Gly Thr Leu Gly Gly Tyr Ser Ala Ile Ala Lys Ala Val Ser Asn Asn  
                          245                      250                      255  
 Gly Lys Val Ile Val Gly Arg Ser Glu Thr Tyr Tyr Gly Glu Val His  
                          260                      265                      270  
 Ala Phe Cys His Lys Asn Gly Val Met Ser Asp Leu Gly Thr Leu Gly  
                          275                      280                      285  
 Gly Ser Tyr Ser Ala Ala Lys Gly Val Ser Ala Thr Gly Lys Val Ile  
   290                      295                      300  
 Val Gly Met Ser Thr Thr Ala Asn Gly Lys Leu His Ala Phe Lys Tyr  
 305                      310                      315                      320  
 Val Gly Gly Arg Met Ile Asp Leu Gly Glu Tyr Ser Trp Lys Glu Ala  
                          325                      330                      335  
 Cys Ala Asn Ala Val Ser Ile Asp Gly Glu Ile Ile Val Gly Val Gln  
                          340                      345                      350  
 Ser Glu

&lt;210&gt;853

&lt;211&gt;452

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;853

Met Phe Glu Ala Val Ile Ala Asp Ile Gln Ala Arg Glu Ile Leu Asp

1 5 10 15  
 Ser Arg Gly Tyr Pro Thr Leu His Val Lys Val Thr Thr Ser Thr Gly  
 20 25 30  
 Ser Val Gly Glu Ala Arg Val Pro Ser Gly Ala Ser Thr Gly Lys Lys  
 35 40 45  
 Glu Ala Leu Glu Phe Arg Asp Thr Asp Ser Pro Arg Tyr Gln Gly Lys  
 50 55 60  
 Gly Val Leu Gln Ala Val Lys Asn Val Lys Glu Ile Leu Phe Pro Leu  
 65 70 75 80  
 Val Lys Gly Cys Ser Val Tyr Glu Gln Ser Leu Ile Asp Ser Leu Met  
 85 90 95  
 Met Asp Ser Asp Gly Ser Pro Asn Lys Glu Thr Leu Gly Ala Asn Ala  
 100 105 110  
 Ile Leu Gly Val Ser Leu Ala Thr Ala His Ala Ala Ala Thr Leu  
 115 120 125  
 Arg Arg Pro Leu Tyr Arg Tyr Leu Gly Gly Cys Phe Ala Cys Ser Leu  
 130 135 140  
 Pro Cys Pro Met Met Asn Leu Ile Asn Gly Gly Met His Ala Asp Asn  
 145 150 155 160  
 Gly Leu Gly Phe Gln Glu Phe Met Ile Arg Pro Ile Gly Ala Ser Ser  
 165 170 175  
 Ile Lys Glu Ala Val Asn Met Gly Ala Asp Val Phe His Thr Leu Lys  
 180 185 190  
 Lys Leu Leu His Glu Arg Gly Leu Ser Thr Gly Val Gly Asp Glu Gly  
 195 200 205  
 Gly Phe Ala Pro Asn Leu Ala Ser Asn Glu Glu Ala Leu Glu Leu Leu  
 210 215 220  
 Leu Leu Ala Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ser  
 225 230 235 240  
 Leu Ala Leu Asp Cys Ala Ala Ser Ser Phe Tyr Asn Val Lys Thr Gly  
 245 250 255  
 Thr Tyr Asp Gly Arg His Tyr Glu Glu Gln Ile Ala Ile Leu Ser Asn  
 260 265 270  
 Leu Cys Asp Arg Tyr Pro Ile Asp Ser Ile Glu Asp Gly Leu Ala Glu  
 275 280 285  
 Glu Asp Tyr Asp Gly Trp Ala Leu Leu Thr Glu Val Leu Gly Glu Lys  
 290 295 300  
 Val Gln Ile Val Gly Asp Asp Leu Phe Val Thr Asn Pro Glu Leu Ile  
 305 310 315 320  
 Leu Glu Gly Ile Ser Asn Gly Leu Ala Asn Ser Val Leu Ile Lys Pro  
 325 330 335  
 Asn Gln Ile Gly Thr Leu Thr Glu Thr Val Tyr Ala Ile Lys Leu Arg  
 340 345 350  
 Lys Trp Leu Ala Ile Leu Gln Leu Phe Leu Ile Ala Gln Glu Lys Leu  
 355 360 365  
 Arg Thr Leu Arg Leu Gln Ile Leu Leu Leu Pro Ser Thr Leu Val Lys  
 370 375 380  
 Ser Lys Gln Ala Leu Tyr His Val Leu Ser Val Leu Gln Asn Thr Ile  
 385 390 395 400  
 Asp Ser Trp Lys Leu Lys Lys Ser Leu Asp Pro Lys Gln Phe Ser Gln  
 405 410 415  
 Ile Leu Met Tyr Phe Leu Thr Arg Ile Leu Arg Asn Arg Gly Ile Phe  
 420 425 430  
 Ser Ile Ser Ile Leu Ser Pro Asn Gln Glu Tyr Ile Ala Asp Leu Trp  
 435 440 445  
 Ala Leu Ser Phe  
 450  
 <210>854  
 <211>84  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>854  
 Asn Ser Val Cys Tyr Gln Val Ala Gln Met Ala Gly Tyr Thr Thr Ile  
 1 5 10 15

Ile Ser His Arg Ser Gly Glu Thr Thr Asp Thr Thr Ile Ala Asp Leu  
                   20                  25                  30  
 Ala Val Ala Phe Asn Ala Gly Gln Ile Lys Thr Gly Ser Leu Ser Arg  
                   35                  40                  45  
 Ser Glu Arg Val Ala Lys Tyr Asn Arg Leu Met Glu Ile Glu Glu Glu  
                   50                  55                  60  
 Leu Gly Ser Glu Ala Ile Phe Thr Asp Ser Asn Val Phe Ser Tyr Glu  
                   65                  70                  75                  80  
 Asp Ser Glu Glu

&lt;210&gt;855

&lt;211&gt;285

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;855

Pro Phe Glu Glu Ala Gln Lys Tyr Phe Arg Lys Val Ile Tyr Val Ser  
   1                  5                  10                  15  
 Ala Thr Pro Gly Asp Thr Glu Val Gln Glu Ser Ser Gly His Ile Val  
                   20                  25                  30  
 Gln Gln Ile Ile Arg Pro Thr Gly Ile Pro Asp Pro Met Pro Glu Ile  
                   35                  40                  45  
 Arg Pro Ala Thr Gly Gln Val Asp Asp Leu Leu Glu Glu Ile Arg Leu  
                   50                  55                  60  
 Arg Leu Ser Gln Lys His Glu Lys Ile Leu Val Ile Ser Ile Thr Lys  
                   65                  70                  75                  80  
 Lys Leu Ala Glu Asp Met Ala Gly Phe Leu Ser Glu Leu Glu Ile Pro  
                   85                  90                  95  
 Ala Ala Tyr Leu His Ser Gly Ile Glu Thr Ala Glu Arg Thr Gln Ile  
                   100                  105                  110  
 Leu Thr Asp Leu Arg Ser Gly Val Ile Asp Val Leu Ile Gly Val Asn  
                   115                  120                  125  
 Leu Leu Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val Ala Ile  
                   130                  135                  140  
 Leu Asp Ala Asp Lys Glu Gly Phe Leu Arg Ser Thr Ser Ser Leu Ile  
                   145                  150                  155                  160  
 Gln Phe Cys Gly Arg Ala Ala Arg Asn Ile Asn Gly Lys Val Ile Phe  
                   165                  170                  175  
 Tyr Ala Asp Gln Lys Thr Arg Ser Ile Glu Glu Thr Leu Arg Glu Thr  
                   180                  185                  190  
 Glu Arg Arg Arg Gln Ile Gln Leu Asp Tyr Asn Lys Glu His Asn Ile  
                   195                  200                  205  
 Val Pro Lys Pro Ile Ile Lys Ala Ile Phe Ala Asn Pro Ile Leu Gln  
                   210                  215                  220  
 Thr Ser Lys Asp Ser Glu Ser Pro Lys Glu Ser Gln Arg Pro Leu Ser  
                   225                  230                  235                  240  
 Lys Glu Asp Leu Glu Glu Gln Ile Lys Lys Tyr Glu Ala Leu Met Gln  
                   245                  250                  255  
 Arg Ala Ala Lys Glu Phe Arg Phe Asn Glu Ala Ala Lys Tyr Arg Asp  
                   260                  265                  270  
 Ala Met Gln Ala Cys Lys Glu Gln Leu Leu Tyr Leu Phe  
                   275                  280                  285

&lt;210&gt;856

&lt;211&gt;372

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;856

Ile Ile Phe Thr Met Thr Phe Gln Leu His Ala Pro Phe Ala Pro Cys  
   1                  5                  10                  15  
 Gly Asp Gln Pro Glu Ala Ile Ala Arg Leu Ser Ala Gly Val Arg Asn  
                   20                  25                  30  
 Gln Val Lys Ser Gln Val Leu Leu Gly Thr Thr Gly Ser Gly Lys Thr  
                   35                  40                  45  
 Phe Thr Ile Ala Asn Val Val Ala Asn Val Asn Leu Pro Thr Leu Val  
                   50                  55                  60

Leu Ala His Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gln Glu Phe Arg  
 65 70 75 80  
 Glu Phe Phe Pro Asn Asn Ala Val Glu Tyr Phe Ile Ser Tyr Tyr Asp  
 85 90 95  
 Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Arg Ser Asp Thr Tyr Ile Glu  
 100 105 110  
 Lys Ser Leu Leu Ile Asn Asp Glu Ile Asp Lys Leu Arg Leu Ser Ala  
 115 120 125  
 Thr Arg Ser Ile Leu Glu Arg Arg Asp Thr Leu Ile Val Ser Ser Val  
 130 135 140  
 Ser Cys Ile Tyr Gly Ile Gly Ser Pro Glu Asn Tyr Thr Ser Met Ala  
 145 150 155 160  
 Leu Val Leu Glu Val Gly Lys Glu Tyr Pro Arg Asn Ile Leu Thr Ala  
 165 170 175  
 Gln Leu Val Lys Met His Tyr Gln Ala Ser Pro Ile Pro Gln Arg Ser  
 180 185 190  
 Ala Phe Arg Glu Arg Gly Ser Val Ile Asp Ile Phe Pro Ala Tyr Glu  
 195 200 205  
 Ser Glu Leu Ala Leu Arg Leu Glu Phe Leu Asn Asp Thr Leu Thr Ser  
 210 215 220  
 Ile Glu Tyr Ser Asp Pro Leu Thr Met Ile Pro Lys Glu Ser Val Pro  
 225 230 235 240  
 Ser Ala Thr Leu Tyr Pro Gly Ser His Tyr Val Ile Pro Glu Ala Ile  
 245 250 255  
 Arg Glu Gln Ala Ile Arg Thr Ile Gln Glu Glu Leu Glu Glu Arg Met  
 260 265 270  
 Ala Phe Phe Asp Asp Arg Pro Ile Glu Lys Asp Arg Ile Phe His Arg  
 275 280 285  
 Thr Thr His Asp Ile Glu Met Ile Lys Glu Ile Gly Phe Cys Lys Gly  
 290 295 300  
 Ile Glu Asn Tyr Ser Arg His Phe Thr Gly Ala Pro Pro Gly Ala Pro  
 305 310 315 320  
 Pro Thr Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu Leu Ile Ile  
 325 330 335  
 Asp Glu Ser His Gln Thr Leu Pro Gln Ile Arg Ala Met Tyr Arg Gly  
 340 345 350  
 Asp Gln Ser Arg Lys Gln Ser Leu Val Glu Tyr Gly Phe Arg Phe Pro  
 355 360 365  
 Ser Gly Leu Arg  
 370  
 <210>857  
 <211>344  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>857  
 Met Asn Lys Lys Lys Arg Val Leu Thr Gly Asp Arg Pro Thr Gly Lys  
 1 5 10 15  
 Leu His Leu Gly His Trp Val Gly Ser Ile Lys Asn Arg Leu Glu Leu  
 20 25 30  
 Gln Asn Ser Pro Glu Tyr Asp Cys Phe Phe Ile Ile Ala Asp Leu His  
 35 40 45  
 Thr Leu Thr Thr Lys Ile Arg Lys Glu Glu Val Leu Asp Val Asp Asn  
 50 55 60  
 His Ile Tyr Glu Val Leu Ala Asp Trp Leu Ser Val Gly Ile Asp Pro  
 65 70 75 80  
 Thr Lys Ser Ile Ile Tyr Leu Gln Ser Ala Ile Pro Glu Ile Tyr Glu  
 85 90 95  
 Leu His Leu Leu Phe Ser Met Leu Ile Ser Ile Asn Arg Val Met Gly  
 100 105 110  
 Ile Pro Ser Leu Lys Asp Met Ala Arg Asn Ala Ser Ile Glu Glu Gly  
 115 120 125  
 Ser Leu Ser Tyr Gly Leu Ile Gly Tyr Pro Ile Leu Gln Ser Ala Asp  
 130 135 140  
 Ile Leu Leu Ala Lys Ala Gln Phe Val Pro Val Gly Lys Asp Asn Glu

```

145          150          155          160
Ala His Val Glu Leu Thr Arg Asp Ile Ala Arg Asn Phe Asn Arg Leu
          165          170          175
Tyr Gly Gln Val Phe Pro Glu Pro Glu Val Leu Gln Gly Glu Leu Thr
          180          185          190
Ser Leu Val Gly Ile Asp Gly Gln Gly Lys Met Ser Lys Ser Ala Asn
          195          200          205
Asn Ala Ile Tyr Leu Ser Asp Ser Asp Ala Thr Ile Thr Glu Lys Val
          210          215          220
Arg Lys Met Tyr Thr Asp Pro Asn Arg Ile Arg Ala Thr Thr Pro Gly
225          230          235          240
Arg Val Glu Gly Asn Pro Leu Phe Ile Tyr His Asp Ile Phe Asn Pro
          245          250          255
His Lys Asp Glu Val Glu Glu Phe Lys Ala Arg Tyr Arg Gln Gly Cys
          260          265          270
Ile Lys Asp Ile Glu Val Lys Ala Arg Leu Ala Glu Glu Leu Ile His
          275          280          285
Phe Leu Lys Pro Ile Lys Glu Arg Arg Ser Glu Phe Leu Ser Lys Pro
          290          295          300
Leu Ala Leu Gln Asn Val Leu Glu Asp Gly Thr His Lys Met Arg Glu
305          310          315          320
Val Ala Lys Val Thr Met Glu Glu Val His Asp Lys Phe Gly Phe Ser
          325          330          335
His Lys Trp Arg Ser Leu Leu Lys
          340

```

&lt;210&gt;858

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;858

```

Phe Met Ala Ala Lys Thr Lys Thr Leu Glu Leu Glu Asp Asn Val Phe
 1          5          10          15
Leu Leu Leu Glu Gly Asn Leu Lys Arg Ile Phe Ala Thr Pro Ile Gly
          20          25          30
Tyr Thr Thr Phe Arg Glu Phe Gln Asn Val Val Phe Asn Cys Ala Asn
          35          40          45
Gly Gln Gln Glu Ile Ala Asn Phe Phe Phe Glu Met Leu Ile Asn Gly
          50          55          60
Lys Leu Thr Gln Glu Leu Ala Pro Gln Gln Lys Gln Ala Ala His Ser
          65          70          75          80
Leu Ile Ala Glu Phe Met Met Pro Ile Arg Val Ala Lys Asp Ile His
          85          90          95
Glu Arg Gly Glu Phe Ile Asn Phe Ile Thr Ser Asp Met Leu Thr Gln
          100          105          110
Gln Glu Arg Cys Ile Phe Leu Asn Arg Leu Ala Arg Val Asp Gly Gln
          115          120          125
Glu Phe Leu Leu Met Thr Asp Val Gln Asn Thr Cys His Leu Ile Arg
          130          135          140
His Leu Leu Ala Arg Leu Leu Glu Ala Gln Lys Asn Pro Val Gly Glu
145          150          155          160
Lys Asn Leu Gln Glu Ile Gln Glu Glu Ile Thr Ser Leu Lys Asn His
          165          170          175
Phe Asp Glu Leu Thr Lys Ala Leu Gln
          180          185

```

&lt;210&gt;859

&lt;211&gt;250

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;859

```

Met Gly Asn Leu Lys Thr Leu Leu Glu Ser Arg Phe Lys Lys Asn Thr
 1          5          10          15
Pro Thr Lys Met Glu Ala Leu Ala Arg Lys Arg Met Glu Gly Asp Pro
          20          25          30
Ser Pro Leu Ala Val Arg Leu Ser Asn Pro Thr Leu Ser Ser Lys Glu

```



35 40 45  
 Lys Glu Gln Leu Arg His Leu Leu Gln His Tyr Asn Phe Arg Glu Gln  
 50 55 60  
 Ile Glu Glu Pro Asp Leu Thr Gln Leu Cys Thr Leu Ser Ala Glu Val  
 65 70 75 80  
 Lys Gln Ile His His Gln Ser Val Leu Leu His Gly Glu Arg Ile Thr  
 85 90 95  
 Lys Val Arg Asp Leu Leu Lys Ser Tyr Arg Glu Gly Ala Phe Ser Ser  
 100 105 110  
 Trp Leu Leu Leu Thr Tyr Gly Asn Arg Gln Thr Pro Tyr Asn Phe Leu  
 115 120 125  
 Val Tyr Tyr Glu Leu Phe Thr Leu Leu Pro Glu Pro Leu Lys Ile Glu  
 130 135 140  
 Met Glu Lys Met Pro Arg Gln Ala Val Tyr Thr Leu Ala Ser Arg Gln  
 145 150 155 160  
 Gly Pro Gln Glu Lys Lys Glu Glu Ile Ile Arg Asn Tyr Arg Gly Glu  
 165 170 175  
 Arg Lys Ser Glu Leu Leu Asp Arg Ile Arg Lys Glu Phe Pro Leu Val  
 180 185 190  
 Glu Thr Asp Cys Arg Lys Thr Ser Pro Val Lys Gln Ala Leu Ala Met  
 195 200 205  
 Leu Thr Lys Gly Ser Gln Ile Leu Thr Lys Cys Thr Ser Leu Ser Ser  
 210 215 220  
 Asp Glu Gln Ile Ile Leu Glu Lys Leu Ile Lys Lys Leu Glu Lys Val  
 225 230 235 240  
 Lys Ser Asn Leu Phe Pro Asp Thr Lys Val  
 245 250  
 <210>860  
 <211>255  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>860  
 Met Lys Thr Ile Ala Val Asn Ser Phe Lys Gly Gly Thr Ala Lys Thr  
 1 5 10 15  
 Ser Thr Thr Leu His Leu Gly Ala Ala Leu Ala Gln Tyr His Gln Ala  
 20 25 30  
 Arg Val Leu Leu Ile Asp Phe Asp Ala Gln Ala Asn Leu Thr Ser Gly  
 35 40 45  
 Leu Gly Leu Asp Pro Asp Cys Tyr Asp Ser Leu Ala Val Val Leu Gln  
 50 55 60  
 Gly Glu Lys Glu Ile Gln Glu Val Ile Arg Pro Ile Gln Asp Thr Gln  
 65 70 75 80  
 Leu Asp Leu Ile Pro Ala Asp Thr Trp Leu Glu Arg Ile Glu Val Ser  
 85 90 95  
 Gly Asn Leu Ala Ala Asp Arg Tyr Ser His Glu Arg Leu Lys Tyr Val  
 100 105 110  
 Leu Gly Ser Val Gln Asp Lys Tyr Asp Tyr Val Ile Ile Asp Thr Pro  
 115 120 125  
 Pro Ser Leu Cys Trp Leu Thr Glu Ser Ala Leu Ile Ala Ala Asp Tyr  
 130 135 140  
 Ala Leu Ile Cys Ala Thr Pro Glu Phe Tyr Ser Val Lys Gly Leu Glu  
 145 150 155 160  
 Arg Leu Ala Gly Phe Ile Gln Gly Ile Ser Ala Arg His Pro Leu Thr  
 165 170 175  
 Ile Leu Gly Val Ala Leu Ser Phe Trp Asn Cys Arg Gly Lys Asn Asn  
 180 185 190  
 Ser Ala Phe Ala Glu Leu Ile His Lys Thr Phe Pro Gly Lys Leu Leu  
 195 200 205  
 Asn Thr Lys Ile Arg Arg Asp Ile Thr Val Ser Glu Ala Ala Ile His  
 210 215 220  
 Gly Lys Pro Val Phe Ala Thr Ser Pro Ser Ala Arg Ala Ser Glu Asp  
 225 230 235 240  
 Tyr Phe Asn Leu Thr Lys Glu Leu Leu Ile Leu Leu Arg Asp Ile  
 245 250 255

&lt;210&gt;861

&lt;211&gt;593

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;861

```

Arg Ser Phe His Pro Pro Lys Arg Arg Arg His Leu Ser Ile Ser Asp
 1          5          10          15
Phe Arg Arg Ser Arg Arg Arg Glu Ile Phe Leu His Thr Ser Ala His
 20          25          30
Leu Leu Ala Gln Ala Val Leu Arg Leu Trp Pro Asp Ala Ile Pro Thr
 35          40          45
Ile Gly Pro Val Ile Asp His Gly Phe Tyr Tyr Asp Phe Ala Asn Leu
 50          55          60
Ser Ile Ser Glu Ser Asp Phe Pro Leu Ile Glu Asp Thr Val Lys Gln
 65          70          75          80
Ile Val Asp Glu Lys Leu Ala Ile Ser Arg Phe Thr Tyr Gly Asp Lys
 85          90          95
Gln Gln Ala Leu Ala Gln Phe Pro Gln Asn Pro Phe Lys Thr Glu Leu
 100          105          110
Ile Arg Glu Leu Pro Glu Asn Glu Glu Ile Ser Ala Tyr Ser Gln Gly
 115          120          125
Glu Phe Phe Asp Leu Cys Arg Gly Pro His Leu Pro Ser Thr Ala His
 130          135          140
Val Lys Ala Phe Lys Val Leu Arg Thr Ser Ala Ala Tyr Trp Arg Gly
 145          150          155          160
Asp Pro Ser Arg Glu Ser Leu Val Arg Ile Tyr Gly Thr Ser Phe Pro
 165          170          175
Thr Ser Lys Glu Leu Arg Ala His Leu Glu Gln Ile Glu Glu Ala Lys
 180          185          190
Lys Arg Asp His Arg Val Leu Gly Ala Lys Leu Asp Leu Phe Ser Gln
 195          200          205
Gln Glu Ser Ser Pro Gly Met Pro Phe Phe His Pro Arg Gly Met Ile
 210          215          220
Val Trp Asp Ala Leu Ile Arg Tyr Trp Lys Gln Leu His Thr Ala Ala
 225          230          235          240
Gly Tyr Lys Glu Ile Leu Thr Pro Gln Leu Met Asn Arg Gln Leu Trp
 245          250          255
Glu Val Ser Gly His Trp Asp Asn Tyr Lys Ala Asn Met Tyr Thr Leu
 260          265          270
Gln Ile Asp Asp Glu Asp Tyr Ala Ile Lys Pro Met Asn Cys Pro Gly
 275          280          285
Cys Met Leu Tyr Tyr Lys Thr Arg Leu His Ser Tyr Lys Glu Phe Pro
 290          295          300
Leu Arg Val Ala Glu Val Gly His Val His Arg Gln Glu Ala Ser Gly
 305          310          315          320
Ala Leu Ser Gly Leu Met Arg Val Arg Ala Phe His Gln Asp Asp Ala
 325          330          335
His Val Phe Leu Thr Pro Glu Gln Val Glu Glu Glu Thr Leu Asn Ile
 340          345          350
Leu Gln Leu Val Ser Thr Leu Tyr Gly Thr Phe Gly Leu Glu Tyr His
 355          360          365
Leu Glu Leu Ser Thr Arg Pro Glu Lys Asp Thr Ile Gly Asp Asp Ser
 370          375          380
Leu Trp Glu Leu Ala Thr Asp Ala Leu Asn Arg Ala Leu Val Gln Ser
 385          390          395          400
Gly Thr Pro Phe Ile Val Arg Pro Gly Glu Gly Ala Phe Tyr Gly Pro
 405          410          415
Lys Ile Asp Ile His Val Lys Asp Ala Ile Gln Arg Thr Trp Gln Cys
 420          425          430
Gly Thr Ile Gln Leu Asp Met Phe Leu Pro Glu Arg Phe Glu Leu Glu
 435          440          445
Tyr Thr Thr Ala Gln Gly Thr Lys Ser Val Pro Val Met Leu His Arg
 450          455          460
Ala Leu Phe Gly Ser Ile Glu Arg Phe Leu Gly Ile Leu Ile Glu Asn

```



Ser Lys Lys Ile Phe Leu Tyr Ile Val Leu Leu Ala Leu Thr Gly Phe  
 65 70 75 80  
 Tyr Leu Thr Asn Ile Phe Glu Phe Ile Gly Leu Gln Ser Leu Ser Ser  
 85 90 95  
 Ser Lys Thr Cys Phe Ile Tyr Gly Leu Ser Pro Leu Met Ser Ala Leu  
 100 105 110  
 Phe Ser Tyr Ile Gln Leu Lys Glu Lys Val Thr Leu Lys Lys Val Leu  
 115 120 125  
 Gly Leu Ser Leu Gly Leu Val Ser Tyr Ile Cys Tyr Leu Thr Phe Gly  
 130 135 140  
 Gly Gly Gly Asp Asp Ser Gln Pro Trp Thr Trp Gln Ile Gly Leu Pro  
 145 150 155 160  
 Glu Leu Leu Ile Leu Gly Ala Ala Ser Leu Ala Ser Phe Gly Trp Thr  
 165 170 175  
 Leu Leu Arg Gln Ile Glu Lys Gln Ser Thr Leu Ser Val Thr Ala Ile  
 180 185 190  
 Asn Ala Tyr Ala Met Leu Ile Ala Gly Met Leu Ser Ile Met His Ser  
 195 200 205  
 Ala Val Val Glu Pro Trp Arg Pro Leu Pro Val Gln Asp Ile Ser Gln  
 210 215 220  
 Phe Leu Tyr Ala Thr Leu Ala Leu Val Val Ile Ser Asn Leu Ile Cys  
 225 230 235 240  
 Tyr Asn Leu Tyr Ala Lys Leu Leu Arg Lys Tyr Ser Ser Thr Phe Leu  
 245 250 255  
 Ser Phe Cys Asn Leu Val Met Pro Leu Tyr Ser Gly Phe Tyr Gly Trp  
 260 265 270  
 Ile Leu Leu Gly Glu Lys Gly Val Ser Leu Gly Leu Val Leu Ala Val  
 275 280 285  
 Ala Phe Met Val Ala Gly Cys Arg Leu Ile Tyr His Glu Glu Phe Arg  
 290 295 300  
 Gln Gly Tyr Ile Val Ser  
 305 310

&lt;210&gt;865

&lt;211&gt;118

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;865

Lys Ser Leu Gln Arg Tyr Glu Arg Ser Glu Thr Gln Gly Ala Arg Val  
 1 5 10 15  
 Ala Ser Phe Ala Gly Asn Ala Leu Ser Ser Ser Met Gln Met Ser Gln  
 20 25 30  
 Leu Met His Gly Leu Thr Ala Ala Val Glu Gly Leu Ser Ala Gly Gln  
 35 40 45  
 Thr Gly Ile Glu Val Ala His His Gln Arg Leu Ala Gly Gln Ala Glu  
 50 55 60  
 Ala Gln Ala Glu Val Leu Lys Gln Met Ser Ser Val Tyr Gly Gln Gln  
 65 70 75 80  
 Ala Gly Gln Ala Gly Gln Leu Gln Glu Gln Ala Met Gln Ser Phe Asn  
 85 90 95  
 Thr Ala Leu Gln Thr Leu Gln Asn Ile Ala Asp Ser Gln Thr Gln Thr  
 100 105 110  
 Thr Ser Ala Ile Phe Asn  
 115

&lt;210&gt;866

&lt;211&gt;392

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;866

Leu Lys Lys Leu Pro Ser Trp Ala Leu Lys Ser Leu Lys Arg Met Pro  
 1 5 10 15  
 Gln Ser Ala Glu Pro Ser Trp Arg Ser Ile Lys Pro Ile Ile Phe Lys  
 20 25 30  
 Gly Ala Cys Ile Ala Met Thr Ser Gly Val Ser Gly Ser Ser Ser Gln  
 35 40 45

Asp Pro Thr Leu Ala Ala Gln Leu Ala Gln Ser Ser Gln Lys Ala Gly  
 50 55 60  
 Asn Ala Gln Ser Gly His Asp Thr Lys Asn Val Thr Lys Gln Gly Ala  
 65 70 75 80  
 Gln Ala Glu Val Ala Ala Gly Gly Phe Glu Asp Leu Ile Gln Asp Ala  
 85 90 95  
 Ser Ala Gln Ser Thr Gly Lys Lys Glu Ala Thr Ser Ser Thr Lys  
 100 105 110  
 Ser Ser Lys Gly Glu Lys Ser Glu Lys Ser Gly Lys Ser Lys Ser Ser  
 115 120 125  
 Thr Ser Val Ala Ser Ala Ser Lys Thr Ala Thr Ala Gln Ala Val Gln  
 130 135 140  
 Gly Pro Lys Gly Leu Arg Gln Asn Asn Tyr Asp Ser Pro Ser Leu Pro  
 145 150 155 160  
 Thr Pro Glu Ala Gln Thr Ile Asn Gly Ile Val Leu Lys Lys Gly Met  
 165 170 175  
 Gly Thr Leu Ala Leu Leu Gly Leu Val Met Thr Leu Met Ala Asn Ala  
 180 185 190  
 Ala Gly Glu Ser Trp Lys Ala Ser Phe Gln Ser Gln Asn Gln Ala Ile  
 195 200 205  
 Arg Ser Gln Val Glu Ser Ala Pro Ala Ile Gly Glu Ala Ile Lys Arg  
 210 215 220  
 Gln Ala Asn His Gln Ala Ser Ala Thr Glu Ala Gln Ala Lys Gln Ser  
 225 230 235 240  
 Leu Ile Ser Gly Ile Val Asn Ile Val Gly Phe Thr Val Ser Val Gly  
 245 250 255  
 Ala Gly Ile Phe Ser Ala Ala Lys Gly Ala Thr Ser Ala Leu Lys Ser  
 260 265 270  
 Ala Ser Phe Ala Lys Glu Thr Gly Ala Ser Ala Ala Gly Gly Ala Ala  
 275 280 285  
 Ser Lys Ala Leu Thr Ser Ala Ser Ser Ser Val Gln Gln Thr Met Ala  
 290 295 300  
 Ser Thr Ala Lys Ala Ala Thr Thr Ala Ala Ser Ser Ala Gly Ser Ala  
 305 310 315 320  
 Ala Thr Lys Ala Ala Ala Asn Leu Thr Asp Asp Met Ala Ala Ala Ala  
 325 330 335  
 Ser Lys Met Ala Ser Asp Gly Ala Ser Lys Ala Ser Gly Gly Leu Phe  
 340 345 350  
 Gly Glu Val Leu Asn Lys Pro Asn Trp Ser Glu Lys Val Ser Arg Gly  
 355 360 365  
 Met Asn Val Val Lys Leu Arg Glu Arg Val Leu His His Leu Gln Glu  
 370 375 380  
 Met Leu Phe Leu Pro Leu Cys Lys  
 385 390

&lt;210&gt;867

&lt;211&gt;496

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;867

Asp Thr Asn Met Ser Ile Ser Ser Ser Gly Pro Asp Asn Gln Lys  
 1 5 10 15  
 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln  
 20 25 30  
 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg  
 35 40 45  
 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala  
 50 55 60  
 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro  
 65 70 75 80  
 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala  
 85 90 95  
 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn  
 100 105 110  
 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys

```

      115      120      125
Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
      130      135      140
Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
145      150      155      160
Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
      165      170      175
Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
      180      185      190
Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
      195      200      205
Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
      210      215      220
Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
225      230      235      240
Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
      245      250      255
Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
      260      265      270
Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
      275      280      285
Gly Ala Ala Val Gly Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
      290      295      300
Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
305      310      315      320
Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
      325      330      335
Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
      340      345      350
Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
      355      360      365
Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
      370      375      380
Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
385      390      395      400
Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
      405      410      415
Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
      420      425      430
Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
      435      440      445
Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
      450      455      460
Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
465      470      475      480
Ala Ala Ile Ser Gly Ala Ile Val Ala Gln His Lys Thr Asn Asn Phe
      485      490      495

```

&lt;210&gt;868

&lt;211&gt;123

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;868

```

Gly Glu Ile Met Asn Lys Lys Pro Lys Lys Thr Lys Lys Ala Val Gln
 1      5      10      15
Ser Lys Ala Ala Pro Val Lys Arg Val Pro Glu Glu Ser Gln Glu Ala
      20      25      30
Ala Ile Gln Gln Leu Glu Leu Ala Val Ser Asp Leu Tyr Lys Glu Leu
      35      40      45
Pro Leu Ala Gln Thr Phe Ala Ser Leu Thr Asp Lys Asn Gln Ile Asn
      50      55      60
Ser Ile Ile Ala Ala Leu Ser Gly Thr Leu Glu Ser Leu His Leu Glu
      65      70      75      80
Glu Leu Thr Gln Gly Leu Phe Pro Ser Ala Gln Glu Asp Ala Asn Phe
      85      90      95

```

Ala Lys Glu Leu Ser Ser Val Val His Gly Leu Lys Asn Leu Thr Thr  
 100 105 110  
 Val Val Asn Lys Gln Met Val Lys Gly Ala Glu  
 115 120

&lt;210&gt;869

&lt;211&gt;210

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;869

Lys Asn Ala Asn Arg Leu Ala Glu Leu Ala Ala Gln Lys Lys Ala Lys  
 1 5 10 15  
 Ala Asp Asp Leu Glu Gln Val His Pro Val Pro Thr Glu Glu Glu Ile  
 20 25 30  
 Lys Lys Ala Leu Gly Asn Ile Phe Glu Gly Leu Ser Asn Gly Leu Asp  
 35 40 45  
 Leu Gln Gln Ile Leu Gly Leu Ser Asp Tyr Leu Leu Glu Glu Ile Tyr  
 50 55 60  
 Thr Val Ala Tyr Thr Phe Tyr Ser Gln Gly Lys Tyr Asn Glu Ala Val  
 65 70 75 80  
 Gly Leu Phe Gln Leu Leu Ala Ala Ala Gln Pro Gln Asn Tyr Lys Tyr  
 85 90 95  
 Met Leu Gly Leu Ser Ser Cys Tyr His Gln Leu His Leu Tyr Asn Glu  
 100 105 110  
 Ala Ala Phe Gly Phe Phe Leu Ala Phe Asp Ala Gln Pro Asp Asn Pro  
 115 120 125  
 Ile Pro Pro Tyr Tyr Ile Ala Asp Ser Leu Leu Lys Leu Gln Gln Pro  
 130 135 140  
 Glu Glu Ser Asn Asn Phe Leu Asp Val Thr Met Asp Ile Cys Gly Asn  
 145 150 155 160  
 Asn Pro Glu Phe Lys Ile Leu Lys Glu Arg Cys Gln Ile Met Lys Gln  
 165 170 175  
 Ser Ile Glu Lys Gln Met Ala Gly Glu Thr Lys Lys Ala Pro Thr Lys  
 180 185 190  
 Lys Pro Ala Gly Lys Ser Lys Thr Thr Thr Asn Lys Lys Ser Gly Lys  
 195 200 205

Lys Arg

210

&lt;210&gt;870

&lt;211&gt;580

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;870

Met Ser Thr Arg Arg Pro Ile Gln Leu Leu Asp Pro Leu Thr Ile Asn  
 1 5 10 15  
 Gln Ile Ala Ala Gly Glu Val Ile Glu Asn Ser Val Ser Val Val Lys  
 20 25 30  
 Glu Leu Ile Glu Asn Ser Leu Asp Ala Gly Ala Asp Glu Ile Glu Ile  
 35 40 45  
 Glu Thr Leu Gly Gly Gly Gln Gly Ala Ile Ile Ile Arg Asp Asn Gly  
 50 55 60  
 Cys Gly Phe Arg Ala Glu Asp Ile Pro Ile Ala Leu Gln Arg His Ala  
 65 70 75 80  
 Thr Ser Lys Ile Arg Glu Phe Ser Asp Ile Phe Ser Leu Asn Ser Phe  
 85 90 95  
 Gly Phe Arg Gly Glu Ala Leu Pro Ser Ile Ala Ser Ile Ser Lys Met  
 100 105 110  
 Glu Ile Gln Ser Ser Ile Glu Gly Asp Glu Gly Val Arg Thr Val Ile  
 115 120 125  
 His Gly Gly Asp Ile Val Ser Cys Glu Pro Cys Ala Arg Gln Leu Gly  
 130 135 140  
 Thr Thr Val Ile Val Asn Ser Leu Phe Tyr Asn Val Pro Val Arg Arg  
 145 150 155 160  
 Gly Phe Gln Lys Ser Met Gln Ser Asp Arg Leu Gly Ile Arg Lys Leu  
 165 170 175

Ile Glu Asn Arg Ile Leu Ser Thr Ala Asn Ile Gly Trp Ser Trp Ile  
 180 185 190  
 Ser Glu Gly His His Glu Ile Gln Ile Ala Lys Gln Gln Gly Phe Gln  
 195 200 205  
 Glu Arg Val Ala Tyr Val Met Gly Asp His Phe Met Gln Asp Ala Leu  
 210 215 220  
 Thr Ile Asp Lys Glu Ala Asn Gly Val Arg Ile Val Gly Val Leu Gly  
 225 230 235 240  
 Ser Pro Ser Phe His Arg Pro Thr Arg Gln Gly Gln Lys Ile Phe Ile  
 245 250 255  
 Asn Asp Arg Pro Ile Glu Ser Leu Phe Ile Ser Lys Lys Val Gly Asp  
 260 265 270  
 Ala Tyr Ala Leu Leu Leu Pro Leu His Arg Tyr Pro Val Phe Val Leu  
 275 280 285  
 Lys Leu Tyr Leu Pro Ser Ser Trp Cys Asp Phe Asn Val His Pro Gln  
 290 295 300  
 Lys Ile Glu Ala Arg Ile Leu Lys Glu Glu Leu Val Gly Asp Cys Ile  
 305 310 315 320  
 Lys Glu Ala Ile Val Glu Thr Leu Ala Cys Pro Pro Gly Ile Leu Cys  
 325 330 335  
 Arg Thr His Gln Glu Ile Glu Glu Ser Asp Ser Val Pro Leu Pro Met  
 340 345 350  
 Phe Arg Met Leu Glu Thr Ser Asp Val Gln Glu Glu Glu Ser Val Glu  
 355 360 365  
 Phe Asp Gln Asn Leu Phe Ala Tyr Ser Ser Glu Asp Val Ser Leu Glu  
 370 375 380  
 Lys Gln Glu Tyr Thr Ser Arg Gly Pro Lys Ser Gln Met Asp Trp Ile  
 385 390 395 400  
 Tyr Ser Ser Asp Val Arg Phe Leu Thr Ser Leu Gly Arg Val Val Leu  
 405 410 415  
 Ala Glu Asp Leu Glu Gly Val His Ile Phe Thr Ala Ala Ala Arg  
 420 425 430  
 Lys His Leu Phe Phe Leu Ser Leu Met Gln Glu Asn Ser Arg Met Tyr  
 435 440 445  
 Gln Ser Gln Ala Leu Leu Ile Pro Leu Arg Leu Gln Val Thr Pro Glu  
 450 455 460  
 Glu Ala Phe Phe Phe Ser His His Gly Arg Thr Leu Cys Asp Leu Gly  
 465 470 475 480  
 Ile Glu Ile Ser Gln Val Gly Pro Cys Val Phe Ser Ile Glu Ser Thr  
 485 490 495  
 Pro Thr Val Ile Gly Glu Glu Glu Leu Lys Glu Trp Leu Leu Leu Leu  
 500 505 510  
 Ala Ala Arg Gly Ser Thr Asp Ile Asn Ser Glu Ala Leu Thr Ala Leu  
 515 520 525  
 Met Lys Glu Thr Leu Thr Gln Ala Thr Phe Ser Lys His Gln His Val  
 530 535 540  
 Phe Asp Val Ser Trp Leu Lys Leu Leu Trp Ser Val Gly Lys Pro Glu  
 545 550 555 560  
 Lys Gly Phe Asp Gly Ala Arg Ile Arg Arg Leu Ile Leu Asp Ser Asp  
 565 570 575  
 Phe Met Glu Gly  
 580

&lt;210&gt;871

&lt;211&gt;355

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;871

Met Ser His Asp Arg Ile Leu Arg Ala Gln Arg Ala Leu Ser Glu His  
 1 5 10 15  
 Asn Leu Asp Ala Ile Leu Val Glu Lys Ser Glu Asp Leu Ala Tyr Phe  
 20 25 30  
 Leu His Asp Glu Ala Ile Ala Gly Ile Leu Leu Ile Gly Gln Gln Glu  
 35 40 45  
 Val Met Phe Phe Val Tyr Arg Met Asp Lys Asp Leu Tyr Ser His Ile



50 55 60  
 Gln Arg Val Pro Leu Thr Phe Leu Thr Gln Asp Val Val Ala Asp Leu  
 65 70 75 80  
 Ser Leu Tyr Val Gln Lys Gln Arg Tyr Gln Lys Ile Gly Phe Asp Ser  
 85 90 95  
 Ala Ser Thr Val Tyr His Lys Phe Ala Gln Arg Gln Val Leu Pro Cys  
 100 105 110  
 Leu Trp Glu Pro Leu Glu Cys Phe Thr Glu Lys Ile Arg Ser Ile Lys  
 115 120 125  
 Ser Glu Glu Glu Ile Arg Arg Met Gln Glu Ala Ala Ala Leu Gly Ser  
 130 135 140  
 Ala Gly Tyr Asp Tyr Val Leu Thr Leu Leu Arg Glu Gly Ile Thr Glu  
 145 150 155 160  
 Lys Glu Val Val Arg Gln Leu Arg Ala Phe Trp Ala Glu Ala Gly Ala  
 165 170 175  
 Glu Gly Pro Ser Phe Pro Pro Ile Ile Ala Phe Gly Glu His Ser Ala  
 180 185 190  
 Phe Pro His Ser Ile Pro Thr Asp Arg Pro Leu Lys Lys Gly Asp Ile  
 195 200 205  
 Val Leu Ile Asp Ile Gly Val Leu Leu Asn Gly Tyr Cys Ser Asp Met  
 210 215 220  
 Thr Arg Met Thr Ala Leu Gly Thr Pro His Pro Lys Leu Leu Glu Ser  
 225 230 235 240  
 Tyr Pro Val Val Val Glu Ala Gln Lys Arg Ala Met Ala Leu Cys Lys  
 245 250 255  
 Glu Gly Val Leu Trp Gly Asp Ile Asp Ala Glu Ala Val Arg Val Leu  
 260 265 270  
 Arg Glu His His Leu Asp Thr Tyr Phe Ile His Gly Ile Gly His Gly  
 275 280 285  
 Val Gly Arg His Ile His Glu Tyr Pro Cys Ser Pro Arg Gly Ser Gln  
 290 295 300  
 Val Lys Leu Glu Ser Gly Met Thr Ile Thr Val Glu Pro Gly Val Tyr  
 305 310 315 320  
 Phe Pro Gly Ile Gly Gly Ile Arg Ile Glu Asp Thr Leu Cys Ile Asp  
 325 330 335  
 Lys Asn Lys Asn Phe Ser Leu Thr Ala Arg Pro Val Ile Ser Glu Leu  
 340 345 350  
 Val Cys Leu  
 355

&lt;210&gt;872

&lt;211&gt;465

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;872

Phe Phe Leu Phe Phe Lys Leu Ser Tyr Asn Phe Ile Phe Asn Leu Pro  
 1 5 10 15  
 Leu Thr Met Tyr Gln Leu Leu Ser Ile Gly Tyr Ser Phe Val Ser Phe  
 20 25 30  
 Ile Ala Leu Leu Trp Met Leu Cys Tyr Ser Pro Asn Tyr Val Thr Asp  
 35 40 45  
 Leu Tyr Arg Ile Ser Leu Ser Ala Glu Glu Ser Leu Gly Gly Ile Arg  
 50 55 60  
 Ala Phe Pro Gln Ala Glu Ser Leu Leu Gly Gly Ala Cys Ala Leu Asn  
 65 70 75 80  
 Phe Pro Asp Leu Glu Glu Arg Leu Pro Asp Leu Arg Lys Glu Leu Leu  
 85 90 95  
 Phe Leu Gly Ser Asn Asp Arg Pro Asp Ala Cys Gly Gly Lys Phe Ser  
 100 105 110  
 Leu Gln Leu Ala Ser Ser Lys Glu Cys Tyr Ile Ala Ala Leu Lys Glu  
 115 120 125  
 Arg Val Tyr Leu Asn Val Thr Asn Ser Ser Arg Gly Pro Val Tyr Ser  
 130 135 140  
 Phe Ser Pro Lys Gly Val Pro Thr Glu Leu Trp Ile Glu Cys Phe Ser  
 145 150 155 160

Val Ser Val Asp Gly Arg Val Glu Val Lys Val Arg Leu Gln Gly Leu  
 165 170 175  
 His Lys Glu Leu Ile Ser Lys Pro Arg Asp Cys Glu Thr Leu Phe Leu  
 180 185 190  
 Asn Pro Pro Ala Asn Lys Leu Asp Cys Trp Glu Ile Ala Gly Phe Arg  
 195 200 205  
 Val Asp Ala Ser Phe Pro Val Lys Gln Lys Ile Arg Arg Ile Gly Val  
 210 215 220  
 Asp Lys Phe Leu Leu Met His Gly Gly Ala Glu Tyr Ala Asp Lys Ala  
 225 230 235 240  
 Thr Lys Glu Arg Val Asp Phe Val Ser Ser Asp Glu Glu Asn Tyr Ser  
 245 250 255  
 Arg Tyr Leu Ala Val Gly Asp Val Leu Leu Trp Asp Gly Asn Cys Trp  
 260 265 270  
 Gln Thr Cys Gly Glu Phe Gln Gly Ala Ser Ser Arg Ala Pro Leu Phe  
 275 280 285  
 Glu Val Lys Arg Ile Asp Asp Lys Val Met Ile Ala Asp Leu Trp Asn  
 290 295 300  
 Val Gly Gly Thr Gln Arg Gln Thr Ile Ser Leu Val Lys Gly Val Pro  
 305 310 315 320  
 Ser Pro Ile Glu Ile Asn Glu Val Ile Arg Glu Ile Glu Phe Thr Gly  
 325 330 335  
 Met Arg Ser Trp Ser Lys Pro Ile Val Leu Val Gly Gly Gln Arg Leu  
 340 345 350  
 Ile Leu Ser Pro Asp Asp Trp Ile Leu Arg Thr Ala Lys Gly Trp Glu  
 355 360 365  
 Lys Leu Ser Arg Ala Asp Gln Ile Gln Asp Tyr Val Thr Gly Lys Val  
 370 375 380  
 Thr Gly Pro Leu Leu Val Phe Glu Lys Leu Glu Lys Asp Leu Arg Gly  
 385 390 395 400  
 Phe Val Leu Arg Gly His Met Phe Asn Ala Gln Arg Thr Leu Val Glu  
 405 410 415  
 Thr Ile Ser Leu Pro Leu Lys Gln Gly Phe Glu Pro Ala Val Ala Ser  
 420 425 430  
 Gln Glu Val Ser Ser Asn Thr Arg Ser Ala Gln His Ile Gln Gly Arg  
 435 440 445  
 Pro Ile Val Gly Asp His Arg Trp Phe Phe Ser Val Ile Leu Tyr Cys  
 450 455 460

Ile

465

&lt;210&gt;873

&lt;211&gt;123

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;873

Phe Ser Ser Ser Glu Glu Thr Lys Ser Thr Arg Ser Phe Val Ala Leu  
 1 5 10 15  
 Ser Ala Tyr Ser Ala Pro Pro Cys Ile Lys Arg Asn Leu Ser Thr Pro  
 20 25 30  
 Ile Arg Arg Ile Phe Cys Phe Thr Gly Lys Leu Ala Ser Thr Leu Asn  
 35 40 45  
 Pro Ala Ile Ser Gln Gln Ser Ser Leu Leu Ala Gly Gly Phe Lys Asn  
 50 55 60  
 Lys Val Ser Gln Ser Arg Gly Phe Glu Ile Asn Ser Leu Cys Lys Pro  
 65 70 75 80  
 Trp Arg Arg Thr Leu Thr Ser Thr Leu Pro Ser Thr Leu Thr Glu Lys  
 85 90 95  
 His Ser Ile His Asn Ser Val Gly Thr Pro Leu Gly Leu Asn Glu Tyr  
 100 105 110  
 Thr Gly Pro Arg Glu Glu Leu Val Thr Phe Lys  
 115 120

&lt;210&gt;874

&lt;211&gt;754

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;874

Met Val Phe Phe Arg Asn Ser Leu Leu His Leu Val Ala Leu Ser Gly  
 1 5 10 15  
 Met Leu Cys Cys Ser Ser Gly Val Ala Leu Thr Ile Ala Glu Lys Met  
 20 25 30  
 Ala Ser Leu Glu His Ser Gly Arg Gly Ala Asp Asp Tyr Glu Gly Met  
 35 40 45  
 Ala Ser Phe Asn Ala Asn Met Arg Glu Tyr Ser Leu Gln Leu Ser Lys  
 50 55 60  
 Leu Tyr Glu Glu Ala Arg Lys Leu Arg Ala Ser Gly Thr Glu Asp Glu  
 65 70 75 80  
 Ala Leu Trp Lys Asp Leu Ile Arg Arg Ile Gly Glu Val Arg Gly Tyr  
 85 90 95  
 Leu Arg Glu Ile Glu Glu Leu Trp Ala Ala Glu Ile Arg Glu Lys Gly  
 100 105 110  
 Gly Asn Leu Glu Asp Tyr Ala Leu Trp Asn His Pro Glu Thr Thr Ile  
 115 120 125  
 Tyr Asn Leu Val Thr Asp Tyr Gly Thr Glu Asp Ser Ile Tyr Leu Ile  
 130 135 140  
 Pro Gln Glu Ile Gly Ala Ile Lys Ile Ala Thr Leu Ser Lys Phe Val  
 145 150 155 160  
 Val Pro Lys Glu Ser Phe Glu Asp Cys Leu Thr Gln Ile Leu Ser Arg  
 165 170 175  
 Leu Gly Ile Gly Val Arg Gln Val Asn Ser Trp Ile Lys Glu Leu Tyr  
 180 185 190  
 Met Met Arg Lys Glu Gly Cys Ser Val Ala Gly Val Phe Ser Ser Arg  
 195 200 205  
 Lys Asp Leu Glu Ala Leu Pro Glu Thr Ala Tyr Ile Gly Phe Val Leu  
 210 215 220  
 Asn Ser Asn Val Asp Ala His Thr Asn Gln His Val Leu Lys Lys Phe  
 225 230 235 240  
 Ile Asn Pro Glu Thr Thr His Val Asp Val Ile Ala Gly Arg Val Trp  
 245 250 255  
 Ile Phe Gly Ser Ala Gly Glu Val Gly Glu Leu Leu Lys Ile Tyr Asn  
 260 265 270  
 Phe Val Gln Ser Glu Ser Ile Arg Gln Glu Tyr Arg Val Ile Pro Leu  
 275 280 285  
 Thr Lys Ile Asp Pro Gly Glu Met Ile Ser Ile Leu Asn Ala Ala Phe  
 290 295 300  
 Arg Glu Asp Leu Thr Lys Asp Val Ser Glu Glu Ser Leu Gly Leu Arg  
 305 310 315 320  
 Val Val Pro Leu Gln Tyr Gln Gly Arg Ser Leu Phe Leu Ser Gly Thr  
 325 330 335  
 Ala Ala Leu Val Gln Gln Ala Leu Thr Leu Ile Arg Glu Leu Glu Glu  
 340 345 350  
 Gly Ile Glu Asn Pro Thr Asp Lys Thr Val Phe Trp Tyr Asn Val Lys  
 355 360 365  
 His Ser Asp Pro Gln Glu Leu Ala Ala Leu Leu Ser Gln Val His Asp  
 370 375 380  
 Val Phe Ser Gly Glu Asn Lys Ala Ser Val Gly Ala Ala Asp Gly Cys  
 385 390 395 400  
 Gly Ser Gln Leu Asn Ala Ser Ile Gln Ile Asp Thr Thr Val Ser Ser  
 405 410 415  
 Ser Ala Lys Asp Gly Ser Val Lys Tyr Gly Asn Phe Ile Ala Asp Ser  
 420 425 430  
 Lys Thr Gly Thr Leu Ile Met Val Val Glu Lys Glu Val Leu Pro Arg  
 435 440 445  
 Ile Gln Met Leu Leu Lys Lys Leu Asp Val Pro Lys Lys Met Val Arg  
 450 455 460  
 Ile Glu Val Leu Leu Phe Glu Arg Lys Leu Ala His Glu Gln Lys Ser  
 465 470 475 480  
 Gly Leu Asn Leu Leu Arg Leu Gly Glu Glu Val Cys Lys Lys Gly Cys  
 485 490 495

Ser Pro Ser Val Ser Trp Ala Gly Gly Thr Gly Ile Leu Glu Phe Leu  
 500 505 510  
 Phe Lys Gly Ser Thr Gly Ser Ser Ile Val Pro Gly Tyr Asp Leu Ala  
 515 520 525  
 Tyr Gln Phe Leu Met Ala Gln Glu Asp Val Arg Ile Asn Ala Ser Pro  
 530 535 540  
 Ser Val Val Thr Met Asn Gln Thr Pro Ala Arg Ile Ala Val Val Asp  
 545 550 555 560  
 Glu Met Ser Ile Ala Val Ser Ser Asp Lys Asp Lys Ala Gln Tyr Asn  
 565 570 575  
 Arg Ala Gln Tyr Gly Ile Met Ile Lys Met Leu Pro Val Ile Asn Val  
 580 585 590  
 Gly Glu Glu Asp Gly Lys Ser Tyr Ile Thr Leu Glu Thr Asp Ile Thr  
 595 600 605  
 Phe Asp Thr Thr Gly Lys Asn His Asp Asp Arg Pro Asp Val Thr Arg  
 610 615 620  
 Arg Asn Ile Thr Asn Lys Val Arg Ile Ala Asp Gly Glu Thr Val Ile  
 625 630 635 640  
 Ile Gly Gly Leu Arg Cys Lys Gln Met Ser Asp Ser His Asp Gly Ile  
 645 650 655  
 Pro Phe Leu Gly Asp Ile Pro Gly Ile Gly Lys Leu Phe Gly Met Ser  
 660 665 670  
 Ser Thr Ser Asp Ser Leu Thr Glu Met Phe Val Phe Ile Thr Pro Lys  
 675 680 685  
 Ile Leu Glu Asn Pro Val Glu Gln Gln Glu Arg Lys Glu Glu Ala Leu  
 690 695 700  
 Leu Ser Ser Arg Pro Gly Glu Arg Glu Glu Tyr Tyr Gln Ala Leu Ala  
 705 710 715 720  
 Ala Ser Glu Ala Ala Arg Ala Ala His Lys Lys Leu Glu Met Phe  
 725 730 735  
 Pro Ala Ser Gly Val Ser Leu Ser Gln Val Glu Arg Gln Glu Tyr Asp  
 740 745 750  
 Gly Cys

&lt;210&gt;875

&lt;211&gt;453

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;875

Arg Gly Lys Asn Thr Met Ala Ala Ser Ile Leu Ser Gln Glu Leu Leu  
 1 5 10 15  
 Asp Ile Leu Pro Tyr Thr Phe Leu Lys Lys His Cys Leu Leu Pro Ile  
 20 25 30  
 Glu Glu Ser Ser Glu Ala Ile Thr Ile Ala His Ala Thr Ala Thr Ser  
 35 40 45  
 Val Ile Ala Gln Asp Glu Val Lys Leu Leu Ile Lys Lys Pro Val Arg  
 50 55 60  
 Phe Val Leu Lys Glu Glu Ser Glu Ile Leu Gln Arg Leu Gln Gln Leu  
 65 70 75 80  
 Tyr Ser Asn Arg Glu Gly Asn Val Ser Asp Met Leu Leu Thr Met Lys  
 85 90 95  
 Glu Glu Asp Gly Thr Thr Ile Ser Glu Glu Asp Leu Leu Glu Thr  
 100 105 110  
 Thr Asp Thr Ile Pro Val Val Arg Leu Leu Asn Trp Ile Leu Lys Glu  
 115 120 125  
 Ala Ile Glu Glu Arg Ala Ser Asp Ile His Phe Glu Pro Cys Glu Asp  
 130 135 140  
 Ser Met Arg Ile Arg Tyr Arg Ile Asp Gly Val Leu His Asp Arg His  
 145 150 155 160  
 Ser Pro Pro Ser His Leu Arg Ser Ala Leu Thr Thr Arg Leu Lys Val  
 165 170 175  
 Leu Ala Lys Met Asp Ile Ala Glu His Arg Leu Pro Gln Asp Gly Arg  
 180 185 190  
 Ile Lys Ile His Ile Gly Gly Gln Glu Val Asp Met Arg Val Ser Thr

195 200 205  
 Val Pro Val Ile Tyr Gly Glu Arg Val Val Leu Arg Ile Leu Asp Lys  
 210 215 220  
 Arg Asn Val Ile Leu Asp Ile Ala Gly Leu His Met Pro Lys Gly Thr  
 225 230 235 240  
 Glu Ile Leu Phe Lys Asp Thr Ile Thr Ala Pro Glu Gly Ile Leu Leu  
 245 250 255  
 Val Thr Gly Pro Thr Gly Ser Gly Lys Thr Thr Thr Leu Tyr Ser Val  
 260 265 270  
 Leu Gln Glu Leu Lys Gly Pro Leu Thr Asn Ile Met Thr Ile Glu Asp  
 275 280 285  
 Pro Pro Glu Tyr Lys Leu Pro Gly Ile Ala Gln Ile Ala Val Lys Pro  
 290 295 300  
 Lys Ile Gly Leu Thr Phe Ala Arg Gly Leu Arg His Leu Leu Arg Gln  
 305 310 315 320  
 Asp Pro Asp Ile Leu Met Val Gly Glu Ile Arg Asp Gln Glu Thr Ala  
 325 330 335  
 Glu Ile Ala Ile Gln Ala Ala Leu Thr Gly His Leu Val Val Ser Thr  
 340 345 350  
 Leu His Thr Asn Asp Ala Ile Ser Ala Ile Pro Arg Leu Leu Asp Met  
 355 360 365  
 Gly Ile Glu Ser Tyr Leu Leu Ser Ala Thr Leu Val Gly Val Val Ala  
 370 375 380  
 Gln Arg Leu Val Arg Thr Ile Cys Pro Tyr Cys Lys Val Ala Tyr Thr  
 385 390 395 400  
 Pro Glu Asn Gln Glu Lys Ser Phe Leu Ala Ser Leu Gly Lys Asp Thr  
 405 410 415  
 Glu Met Pro Leu Tyr Arg Gly Gln Gly Cys Val His Cys Phe Val Pro  
 420 425 430  
 Asp Ile Lys Glu Asp Arg Glu Phe Thr Asn Phe Tyr Ala Arg Ile His  
 435 440 445  
 Tyr Phe Val Gln Lys  
 450  
 <210>876  
 <211>394  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>876  
 Gly Gly Arg Met Pro Arg Tyr Arg Tyr Thr Tyr Leu Asp Pro Lys Glu  
 1 5 10 15  
 Arg Arg Lys Arg Gly Tyr Leu Glu Ala Leu His Ile Gln Glu Ala Arg  
 20 25 30  
 Glu Lys Leu Ala Gln Glu Asn Ile Gln Val Leu Asp Ile Arg Glu Val  
 35 40 45  
 Ala Leu Arg Arg Met Ser Ile Lys Ser Thr Glu Leu Ile Val Phe Thr  
 50 55 60  
 Lys Gln Leu Leu Leu Leu Leu Arg Ser Gly Leu Pro Leu Tyr Glu Ser  
 65 70 75 80  
 Leu Val Ser Leu Arg Asp Gln Tyr His Glu Gln Lys Met Gly Leu Leu  
 85 90 95  
 Leu Thr Ser Phe Met Glu Thr Leu Arg Ser Gly Gly Ser Leu Ser Gln  
 100 105 110  
 Ala Met Ala Ala His Pro Asn Ile Phe Asp His Phe Tyr Cys Ser Gly  
 115 120 125  
 Val Ala Ala Gly Glu Ser Val Gly Asn Leu Glu Gly Cys Leu Gln Asn  
 130 135 140  
 Ile Ile Val Val Leu Glu Glu Arg Ala Gln Ile Thr Lys Lys Met Val  
 145 150 155 160  
 Gly Ala Leu Ser Tyr Pro Cys Val Leu Leu Val Phe Ser Phe Ala Val  
 165 170 175  
 Met Leu Phe Phe Leu Leu Gly Val Ile Pro Ser Leu Lys Glu Thr Phe  
 180 185 190  
 Glu Asn Met Glu Val Lys Gly Leu Thr Lys Ile Val Phe Gly Val Ser  
 195 200 205

Asp Cys Leu Ser Ala Tyr Arg Tyr Leu Phe Leu Gly Phe Ala Ser Ala  
 210 215 220  
 Leu Ile Thr Val Gly Ile Leu Met Arg His Arg Ile Pro Trp Lys Lys  
 225 230 235 240  
 Ile Leu Glu Lys Leu Leu Phe Ala Leu Pro Gly Thr Lys Lys Phe Val  
 245 250 255  
 Val Lys Val Ala Val Asn Arg Phe Cys Ser Val Ala Ser Ala Ile Leu  
 260 265 270  
 Lys Gly Gly Gly Thr Leu Ile Glu Gly Leu Asp Leu Gly Cys Asp Ala  
 275 280 285  
 Ile Pro Tyr Asp Arg Leu Lys Thr Asp Met Arg Asp Ile Val Gln Ala  
 290 295 300  
 Val Ile Gly Gly Gly Ser Leu Ser Gln Glu Leu Ala Gln Arg Ser Trp  
 305 310 315 320  
 Val Pro Lys Leu Ala Ile Gly Met Ile Ala Leu Gly Glu Glu Ser Gly  
 325 330 335  
 Asp Leu Ala Asp Val Leu Gly Tyr Val Ala His Ile Tyr Asn Glu Asp  
 340 345 350  
 Thr Gln Lys Thr Leu Ala Ser Ile Thr Ser Trp Cys Gln Pro Val Ile  
 355 360 365  
 Leu Ile Phe Leu Gly Gly Leu Ile Gly Val Ile Met Leu Ala Ile Leu  
 370 375 380  
 Ile Pro Leu Thr Ser Asn Ile Gln Thr Leu  
 385 390

&lt;210&gt;877

&lt;211&gt;175

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;877

Gly Tyr Thr Lys Asn Val Gly Phe Asp Asn Val Val Val Ser Thr Arg  
 1 5 10 15  
 Asp Ser Asp Phe Ser Trp Trp Pro Asp Arg Cys Asp His Val Gly Asn  
 20 25 30  
 Ile Asp Pro Thr His Lys Gln Tyr Pro Asn Ile Ile Lys Cys Val Leu  
 35 40 45  
 Arg Gly Val Gly Met Lys Arg Gln Lys Arg Lys Gln Ser Ile Thr Leu  
 50 55 60  
 Ile Glu Met Met Val Val Ile Thr Leu Ile Gly Ile Ile Gly Gly Ala  
 65 70 75 80  
 Leu Ala Phe Asn Met Arg Gly Ser Ile His Lys Gly Lys Val Phe Gln  
 85 90 95  
 Ser Glu Gln Asn Cys Ala Lys Val Tyr Asp Ile Leu Met Met Glu Tyr  
 100 105 110  
 Ala Thr Gly Gly Ser Ser Leu Lys Glu Ile Ile Ala His Lys Glu Thr  
 115 120 125  
 Val Val Glu Glu Ala Ser Trp Cys Lys Glu Gly Arg Lys Leu Leu Lys  
 130 135 140  
 Asp Ala Trp Gly Glu Asp Leu Ile Val Gln Leu Asn Asp Lys Gly Asp  
 145 150 155 160  
 Asp Leu Val Ile Phe Ser Lys Arg Val Gln Ser Ser Asn Lys Lys  
 165 170 175

&lt;210&gt;878

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;878

Leu Leu Ser Asn Ile Met Gly Ser Arg Arg Lys Leu Lys Arg Ser Phe  
 1 5 10 15  
 Leu Leu Ile Glu Val Leu Met Ala Leu Ser Leu Val Cys Ala Val Leu  
 20 25 30  
 Leu Pro Cys Ile Arg Phe Tyr Tyr Ala Ile His Arg Ser Phe Glu Glu  
 35 40 45  
 Asp Ile Phe Asn Leu Gln Leu Pro Ala Leu Ile Asp His Cys Phe Leu  
 50 55 60

Ser Val Glu Glu Lys Met Arg Gln Gln Met Ala Glu Gly Thr Val Leu  
 65 70 75 80  
 Thr Ser Gly Lys Gly Gln Thr Val Ser Leu Ala Tyr Thr Ser Gln Gly  
 85 90 95  
 Ile Gly Tyr Arg Ile Pro Tyr Gly Tyr Asn Val Asp Ile Arg Gln Glu  
 100 105 110  
 Val Arg Gly Asp Asn Leu Lys Met Lys Val Cys Leu Ala Asp Val Val  
 115 120 125  
 Val Glu Leu Phe Pro Asp Gln Lys Gln Ala Val Ser Val Gln Arg Cys  
 130 135 140  
 Leu Cys Val Thr Leu  
 145

&lt;210&gt;879

&lt;211&gt;206

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;879

Asp Glu Ser Leu Pro Cys Arg Cys Cys Cys Gly Thr Phe Pro Arg Ser  
 1 5 10 15  
 Glu Thr Ser Ser Ile Arg Thr Glu Met Pro Met Cys Asn Ser Ile Ala  
 20 25 30  
 Met Lys Lys Gln Lys Arg Gly Phe Val Leu Met Glu Leu Leu Met Ser  
 35 40 45  
 Phe Thr Leu Ile Ala Leu Leu Leu Gly Thr Leu Gly Phe Trp Tyr Arg  
 50 55 60  
 Lys Ile Tyr Thr Val Gln Lys Gln Lys Glu Arg Ile Tyr Asn Phe Tyr  
 65 70 75 80  
 Ile Glu Glu Ser Arg Ala Tyr Lys Gln Leu Arg Thr Leu Phe Ser Met  
 85 90 95  
 Ser Leu Ser Ser Ser Tyr Glu Glu Pro Gly Ser Leu Phe Ser Leu Ile  
 100 105 110  
 Phe Asp Arg Gly Val Tyr Arg Asp Pro Lys Leu Ala Gly Ala Val Arg  
 115 120 125  
 Ala Ser Leu His His Asp Thr Lys Asp Gln Arg Leu Glu Leu Arg Ile  
 130 135 140  
 Cys Asn Ile Lys Asp Gln Ser Tyr Phe Glu Thr Gln Arg Leu Leu Ser  
 145 150 155 160  
 His Val Thr His Val Val Leu Ser Phe Gln Arg Asn Pro Asp Pro Glu  
 165 170 175  
 Lys Leu Pro Glu Thr Ile Ala Leu Thr Ile Thr Arg Glu Pro Lys Ala  
 180 185 190  
 Tyr Pro Pro Arg Thr Leu Thr Tyr Gln Phe Ala Val Gly Lys  
 195 200 205

&lt;210&gt;880

&lt;211&gt;344

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;880

His Thr Asn Leu Arg Leu Gly Asn Lys Pro Met Gln Pro Phe Ile Phe  
 1 5 10 15  
 Thr Leu Leu Cys Leu Thr Ser Leu Val Ser Leu Val Ala Phe Asp Ala  
 20 25 30  
 Ala Asn Ala Arg Lys Arg Cys Ala Cys Ala Gln Thr Ile Glu Arg Gly  
 35 40 45  
 Glu Asn Phe Phe Ser Ile Lys Arg Ser Ala Cys Ala Glu Ile Glu Tyr  
 50 55 60  
 Gln Glu Lys Ser Arg His Ala Ser Ala Ile Glu Arg Ile Ser Lys Asp  
 65 70 75 80  
 Lys Gly Lys Val Thr Pro Lys Gln Ile Ala Lys Val Ala Thr Lys Lys  
 85 90 95  
 Lys Gln Arg Tyr Arg Leu Leu Gln Val Pro Phe Ser Arg Pro Pro Asn  
 100 105 110  
 Asn Ser Arg Tyr Asn Leu Tyr Ala Leu Leu Ser Glu Pro Pro Glu Cys  
 115 120 125

Tyr Ser Asp Thr Ala Ser Trp Tyr Ala Ile Phe Ile Arg Leu Leu Arg  
 130 135 140  
 Arg Ala Tyr Val Asp Thr Gly Asn Val Pro Pro Gly Ser Glu Tyr Ala  
 145 150 155 160  
 Ile Ala Asn Ala Leu Ile Ser Asn Lys Gln Glu Ile Leu Glu Arg Gly  
 165 170 175  
 Ala Gln Leu Gly Pro Asp Val Ile Glu Thr Leu Thr Leu Pro Glu Glu  
 180 185 190  
 Gln Ala Glu Ile Phe Tyr Lys Met Leu Lys Gly Ser Ser Asn Ser Gln  
 195 200 205  
 Ser Leu Leu Asn Phe Leu His Tyr Glu Glu Lys Ser Leu Gly His Cys  
 210 215 220  
 Lys Leu Asn Leu Ile Phe Met Asp Pro Leu Leu Leu Glu Ala Val Leu  
 225 230 235 240  
 Asp His Pro Asp Ala Tyr Arg Glu Thr Ser Leu Leu Arg Asp Gly Ile  
 245 250 255  
 Trp Glu Ala Val Lys Arg Gln Glu His Ala Ile Gln Glu His Gly Gln  
 260 265 270  
 Ala Ala Ala Leu Glu Leu Phe Lys Thr Arg Thr Asp Phe Arg Leu Glu  
 275 280 285  
 Leu Arg Asp Lys Met Gln Leu Leu Leu Ser Arg Tyr Asp Leu Leu Pro  
 290 295 300  
 Leu Leu Asn Lys Lys Met Phe Asp Tyr Thr Leu Gly Ser Ala Gly Asp  
 305 310 315 320  
 Tyr Leu Phe Leu Val Asp Pro Asp Thr Lys Ala Ile Ser Arg Cys Arg  
 325 330 335  
 Cys Pro Ser Lys Ser Ile Lys Leu  
 340

&lt;210&gt;881

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;881

Phe Phe Leu Ile Ile Val Leu Ile Ser Thr Ile Lys Asn Ile Ser Ile  
 1 5 10 15  
 Gly Arg Thr Met Ala Asp Glu Thr Pro Lys Glu Asn Ser Ser Lys Glu  
 20 25 30  
 Ser Ser Ser Gln Phe Asp Ser Leu Lys Arg Lys Val Lys Asp Leu His  
 35 40 45  
 Ser Asn Pro Lys Val Gly Lys Trp Lys Lys Phe Leu Ser His Arg Ala  
 50 55 60  
 Cys Glu Xaa Ser Val Val Ala Trp Cys Trp Leu Val Ser Ser Leu Ile  
 65 70 75 80  
 Leu Phe His Gly Leu Glu Asp Cys Leu Leu Val Val Trp Ser  
 85 90 95

&lt;210&gt;882

&lt;211&gt;125

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;882

Ser Arg Glu Met Glu Glu Val Ser Phe Ser Ser Ser Leu Arg Xaa Ile  
 1 5 10 15  
 Gly Gly Cys Leu Val Leu Val Gly Ile Ala Asp Phe Ile Ser Trp  
 20 25 30  
 Ala Gly Gly Leu Phe Ile Ala Cys Gly Val Val Leu Gly Phe His Val  
 35 40 45  
 Glu Ile Arg Lys Met Leu Ser Asn Leu Gln Ser Tyr Ser Ile Ala Asn  
 50 55 60  
 Gly Pro Ile Lys Asn Ala Ile Leu Cys Gly Leu Ile Leu Phe Phe Val  
 65 70 75 80  
 Leu Asn Ile Pro Ser Phe Ala Val Ser Phe Ile Val Leu Cys Val Ile  
 85 90 95  
 Leu Ser Phe Ile Thr Thr Ala Pro Ser Cys Ser Thr Cys Ser Lys Asp  
 100 105 110



His Cys Asp Lys His Gln Asp Thr Ser Asn Lys Pro Ser  
 115 120 125

&lt;210&gt;883

&lt;211&gt;305

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;883

Leu Gln Val Arg Phe Ser Lys Thr Ser Ile Asn Gly Asn Lys Glu Leu  
 1 5 10 15  
 Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr  
 20 25 30  
 Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe  
 35 40 45  
 Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe  
 50 55 60  
 Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu  
 65 70 75 80  
 Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile  
 85 90 95  
 Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu  
 100 105 110  
 Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr  
 115 120 125  
 Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln  
 130 135 140  
 Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro  
 145 150 155 160  
 His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val  
 165 170 175  
 Gly Gly His Arg Ile Val Ile Ser Leu Leu Gln Thr Leu Glu Val  
 180 185 190  
 Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala  
 195 200 205  
 Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met  
 210 215 220  
 Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp  
 225 230 235 240  
 Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile  
 245 250 255  
 Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr  
 260 265 270  
 Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala  
 275 280 285  
 Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val  
 290 295 300

Leu

305

&lt;210&gt;884

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;884

Val Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr  
 1 5 10 15  
 Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile  
 20 25 30  
 Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala  
 35 40 45  
 Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val  
 50 55 60  
 Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile  
 65 70 75 80  
 Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
 85 90 95

&lt;210&gt;885

&lt;211&gt;117

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;885

```

Arg Thr Phe Ala Leu Phe Leu Asn Ser Gln His Ser Lys Ser Thr Asn
 1           5           10           15
Ser Lys Leu Leu Gln Asp Leu Thr Glu Asn Leu Pro Ser Glu Ile Arg
           20           25           30
Ala His Leu Thr Ala Ser Asp Phe Val Ile Ile Ile Pro Ala Phe Ile
           35           40           45
Met Gly Gln Ile Lys Asn Ala Phe Glu Ile Gly Val Leu Ile Tyr Leu
           50           55           60
Pro Phe Phe Val Ile Asp Leu Val Thr Ala Asn Val Leu Val Ala Met
           65           70           75           80
Gln Met Met Met Leu Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu
           85           90           95
Leu Leu Ile Val Met Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu
           100          105          110
Met Ile Ser Phe Lys
           115

```

&lt;210&gt;886

&lt;211&gt;257

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;886

```

Thr Ser His Leu Arg Leu His His Pro Arg Ile Leu Leu Leu Tyr Leu
 1           5           10           15
Met Ile Arg Ile Arg Lys Asn Lys Gly Ile His Tyr Tyr Ala Ile His
           20           25           30
Phe Ser Ile Phe Pro Leu Phe Phe Tyr Ala Glu Arg Leu Met Leu Phe
           35           40           45
Ser Asp Ala Ser Leu Tyr Glu Asn Ser Cys Pro Ser Arg Cys Gln Pro
           50           55           60
Thr Pro Pro Pro Ser Asn Ser Asn Pro Leu Asn Val Val Gln Gln Pro
           65           70           75           80
Val Ala Ala Ser Ser Val Pro Ser Tyr Met Pro Pro Leu Asn Ala Asp
           85           90           95
Asp Val Leu Pro Arg Asp His Leu Ser Asp Gly Ser Phe Ser Asp Thr
           100          105          110
Tyr Pro Asp Ile Thr Thr Gln Ala Ile Ile Leu Ile Phe Leu Ala Leu
           115          120          125
Ser Pro Phe Leu Val Met Leu Leu Thr Ser Tyr Leu Lys Ile Ile Ile
           130          135          140
Thr Leu Val Leu Leu Arg Asn Ala Leu Gly Val Gln Gln Thr Pro Pro
           145          150          155          160
Ser Gln Val Leu Asn Gly Ile Ala Leu Ile Leu Ser Ile Tyr Val Met
           165          170          175
Phe Pro Thr Gly Val Ala Met Tyr Lys Asp Ala Arg Lys Glu Ile Glu
           180          185          190
Ala Asn Thr Ile Pro Gln Ser Leu Phe Thr Ala Glu Gly Ala Glu Thr
           195          200          205
Val Phe Val Ala Leu Asn Lys Ser Lys Glu Pro Leu Arg Ser Phe Leu
           210          215          220
Ile Arg Asn Thr Pro Lys Ala Gln Ile Gln Ser Phe Tyr Lys Ile Ser
           225          230          235          240
Gln Lys Thr Phe Leu Arg Lys Phe Glu Arg Thr Ser Leu Pro Pro Thr
           245          250          255
Leu

```

&lt;210&gt;887

&lt;211&gt;108

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;887

Lys Ser Ser His Lys Ile Asn Ile Ser Leu Leu Ser Val Asn Pro Lys  
 1 5 10 15  
 Asp Leu Pro Leu Val Glu Lys Ser Arg Pro Glu Leu Lys Asn Ile Val  
 20 25 30  
 Glu Tyr Ala Asp Ser Leu Ile Leu Thr Ala Lys Pro Asp Val Thr Pro  
 35 40 45  
 Gly Gly Cys Ile Ile Glu Thr Glu Ala Gly Ile Ile Asn Ala Gln Leu  
 50 55 60  
 Asp Val Gln Leu Asp Ala Leu Glu Lys Ala Phe Ser Thr Ile Leu Lys  
 65 70 75 80  
 Ala Lys Asn Pro Val Asp Glu Pro Ser Glu Thr Ser Ser Ser Thr Asp  
 85 90 95  
 Ser Ser Ser Leu Ser Asn Asp Gln Asp Lys Lys Glu  
 100 105

&lt;210&gt;888

&lt;211&gt;140

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;888

Phe Leu Lys Met Met Met Ser Pro Gln Ile Arg Arg Phe Tyr Leu Leu  
 1 5 10 15  
 Lys Leu Ser Ser Ala Phe Leu Asp Ala Lys Glu Leu Leu Glu Lys Thr  
 20 25 30  
 Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu Thr Glu Gln Lys Cys Ala  
 35 40 45  
 Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly Phe Lys Glu Gly Ser Glu  
 50 55 60  
 Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu Glu Thr Lys Asn Leu  
 65 70 75 80  
 Arg Ile Arg Val Arg Glu Ala Leu Val Pro Leu Ala Ile Ala Ser Val  
 85 90 95  
 Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu His Pro Glu Thr Ile Val  
 100 105 110  
 Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu Thr Gln Asn Lys His Ile  
 115 120 125  
 Ile Thr Leu Cys Gln Ser Gln Arg Phe Thr Ser Cys  
 130 135 140

&lt;210&gt;889

&lt;211&gt;280

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;889

Gly Cys Leu Val Thr Ala Asn Thr Phe Gly Thr Leu Asp Ile Leu Met  
 1 5 10 15  
 Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu  
 20 25 30  
 Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser  
 35 40 45  
 Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile  
 50 55 60  
 Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp  
 65 70 75 80  
 Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile  
 85 90 95  
 Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu  
 100 105 110  
 Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile  
 115 120 125  
 Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro  
 130 135 140  
 Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys  
 145 150 155 160  
 Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn

165 170 175  
 Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His  
 180 185 190  
 Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr  
 195 200 205  
 Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu  
 210 215 220  
 Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu  
 225 230 235 240  
 Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys  
 245 250 255  
 Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu  
 260 265 270  
 Gln Cys Met Lys Val Leu Val Lys  
 275 280

&lt;210&gt;890

&lt;211&gt;155

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;890

Ala Pro Tyr Cys Lys Cys Cys Ser Arg Thr Cys Ala Arg Glu Arg Leu  
 1 5 10 15  
 Cys Ser Glu Arg Ser Arg Xaa Tyr Ser Asp Ile Thr Ile Asn Gly Pro  
 20 25 30  
 Trp Gly Leu Thr Glu Glu Ile Asp Tyr Val Ser Val Trp Gly Ile Ile  
 35 40 45  
 Leu Ala Lys Ser Ser Leu Thr Lys Phe Arg Leu Ile Phe Tyr Val Leu  
 50 55 60  
 Ile Leu Ile Leu Phe Val Ile Ser Cys Gly Leu Leu Trp Val Ile Trp  
 65 70 75 80  
 Lys Thr His Thr Leu Ile Met Thr Met Gly Gly Thr Lys Gly Phe Phe  
 85 90 95  
 Asn Pro Thr Pro Tyr Thr Lys Asn Ala Leu Glu Ala Lys Lys Ala Glu  
 100 105 110  
 Gly Ala Ala Ala Asp Lys Glu Lys Lys Glu Asp Ala Asp Ser Gln Gly  
 115 120 125  
 Glu Ser Lys Asn Ala Glu Thr Ser Asp Lys Asp Ser Ser Asp Lys Asp  
 130 135 140  
 Ala Pro Glu Gly Ser Asn Glu Ile Glu Gly Ala  
 145 150 155

&lt;210&gt;891

&lt;211&gt;214

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;891

Met Val Arg Arg Ser Ile Ser Phe Cys Leu Phe Phe Leu Met Thr Leu  
 1 5 10 15  
 Leu Cys Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val His Gly Leu  
 20 25 30  
 Pro Gly Arg Glu Ala Asn Glu Ile Val Val Leu Leu Val Ser Lys Gly  
 35 40 45  
 Val Ala Ala Gln Lys Leu Pro Gln Ala Ala Ala Thr Ala Gly Ala  
 50 55 60  
 Ala Thr Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala Gln Ile Thr  
 65 70 75 80  
 Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg Met Lys Gly  
 85 90 95  
 Thr Ser Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val Pro Ser Glu  
 100 105 110  
 Leu Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu Gln Met Ala  
 115 120 125  
 Ser Thr Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser Val Gln Ile  
 130 135 140  
 Ser Phe Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr Ala Ser Val

145 150 155 160  
 Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser Ile Met Val  
 165 170 175  
 Ser Lys Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly Leu Val Pro  
 180 185 190  
 Glu Asn Val Ser Val Val Ser Asp Arg Ala Xaa Ile Val Ile Leu Gln  
 195 200 205  
 Leu Met Val Leu Gly Asp  
 210  
 <210>892  
 <211>224  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>892  
 Val Leu Phe Leu Ala Tyr Lys Met Ala Gly Leu Gln Ile Ile Ala Thr  
 1 5 10 15  
 Arg Ile Leu Asp Ser Phe Leu Leu Pro Cys Phe Glu Val Glu Ala Gln  
 20 25 30  
 Thr Phe Pro Gln Val Phe Ser Lys Val Val Val Tyr Lys Tyr Lys Ser  
 35 40 45  
 Ser Arg Ile Leu Leu Ile Ala Leu Leu Tyr Asn Ile Thr Leu Val Leu  
 50 55 60  
 Gly Leu Ile Phe Ile His Lys Lys Tyr Leu Gly Gln Lys Gly Arg Val  
 65 70 75 80  
 Ile Leu Lys Ile Tyr Gln Asn Glu Glu Glu Phe Phe Arg Ala Thr Glu  
 85 90 95  
 Arg Phe Pro Ser Ile Gly Ala Gly Tyr Leu Arg Val Arg Asn Lys Asn  
 100 105 110  
 Ser Val Leu Phe Pro Phe Glu Asp Leu Met Leu Val Cys Pro Ser Val  
 115 120 125  
 Pro Lys Asp Phe Pro Leu Ser Ala Phe Lys Val Thr Thr Lys Leu Ile  
 130 135 140  
 Tyr Trp Ser Val Leu Glu Ser Ile Pro Val Val Gly Ala Phe Phe Phe  
 145 150 155 160  
 Ser Ile Gly Arg Leu Phe Ala Met Trp Cys Ile Glu Asp Phe Pro Gly  
 165 170 175  
 Ser Ile Phe Ser Arg Ile Tyr His Thr Thr Val Gly Val Leu Gly Ile  
 180 185 190  
 Leu Gly Leu Gly Ile Ile Met Phe Ile Leu Arg Ile Ile Phe Thr Leu  
 195 200 205  
 Leu Thr Leu Pro Phe Trp Leu Ile Ser Cys Leu Lys Ser Ser Ala Ala  
 210 215 220  
 <210>893  
 <211>319  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>893  
 Val Met Lys Cys Arg Pro Thr Leu Asn Thr Asp Gln Pro Arg Val Arg  
 1 5 10 15  
 Lys Lys Leu Pro Glu Arg Phe Pro Lys Trp Leu Gln Arg Pro Leu Pro  
 20 25 30  
 Gln Gly Ser Ala Phe His Ala Thr Asp Ala Thr Ile Lys Arg Ser Gly  
 35 40 45  
 Met Pro Thr Val Cys Glu Glu Ala Leu Cys Pro Asn Arg Ala Glu Cys  
 50 55 60  
 Trp Ser Arg Lys Thr Ala Thr Tyr Leu Ala Leu Gly Asp Val Cys Thr  
 65 70 75 80  
 Arg Ser Cys Gly Phe Cys Asn Ile Gly His Ser Lys Thr Pro Pro Ala  
 85 90 95  
 Leu Asp Pro Thr Glu Pro Glu Arg Ile Ala Leu Ser Ala Lys Glu Leu  
 100 105 110  
 Gly Leu Lys His Val Val Ile Thr Met Val Ala Arg Asp Asp Leu Glu  
 115 120 125  
 Asp Gly Gly Ala Gln Gly Leu Val Asp Ile Ile Gln Lys Leu Arg Glu

130 135 140  
 Glu Leu Pro Gln Ala Thr Thr Glu Val Leu Ala Ser Asp Phe Gln Gly  
 145 150 155 160  
 Asn Val Ser Ala Leu His Thr Leu Leu Asp Ser Gly Ile Thr Ile Tyr  
 165 170 175  
 Asn His Asn Val Glu Thr Val Ala Arg Leu Ser Pro Leu Val Arg His  
 180 185 190  
 Lys Ala Thr Tyr Ala Arg Ser Met Phe Met Leu Glu Gln Ala Ala Asn  
 195 200 205  
 Tyr Leu Pro Asp Leu Lys Ile Lys Ser Gly Ile Met Val Gly Leu Gly  
 210 215 220  
 Glu Met Glu Gly Glu Val Lys Gln Thr Leu Gln Asp Leu Ala Ser Ile  
 225 230 235 240  
 Gly Val Arg Ile Val Thr Ile Gly Gln Tyr Leu Arg Pro Ser Arg Lys  
 245 250 255  
 His Leu Gln Val Lys Ser Tyr Val Thr Pro Glu Thr Phe Asp Tyr Tyr  
 260 265 270  
 Arg Arg Val Gly Glu Ala Met Gly Leu Phe Val Tyr Ala Gly Pro Phe  
 275 280 285  
 Val Arg Ser Ser Phe Asn Ala Asp Met Ile Leu Ala Ser Val Gln Asp  
 290 295 300  
 Lys Ala Ser Val Asn Lys His Ser Thr Ile His Leu Ile Glu Ser  
 305 310 315  
 <210>894  
 <211>397  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>894  
 Ala Cys Gly Glu Phe Gly Ile His Val Asp Gly Tyr Thr Ile Asp Tyr  
 1 5 10 15  
 Pro Ala Met Ala Lys Arg Lys Asn Thr Val Val Gln Gly Ile Arg Gln  
 20 25 30  
 Gly Leu Glu Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Leu Lys Gly  
 35 40 45  
 Thr Gly Ser Leu Val Ser Ser Thr Glu Val Lys Val Ile Gly Gln Asp  
 50 55 60  
 Thr Thr Ile Ile Lys Ala Asn His Ile Ile Leu Ala Thr Gly Ser Glu  
 65 70 75 80  
 Pro Arg Pro Phe Pro Gly Val Pro Phe Ser Ser Arg Ile Leu Ser Ser  
 85 90 95  
 Thr Gly Ile Leu Glu Leu Glu Val Leu Pro Lys Lys Leu Ala Ile Ile  
 100 105 110  
 Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu  
 115 120 125  
 Gly Val Glu Ile Thr Val Ile Glu Ala Leu Asp His Ile Leu Ala Val  
 130 135 140  
 Asn Asn Lys Glu Val Ser Gln Thr Val Thr Asn Lys Phe Thr Lys Gln  
 145 150 155 160  
 Gly Ile Arg Ile Leu Thr Lys Ala Ser Ile Ser Ala Ile Glu Glu Ser  
 165 170 175  
 Gln Asn Gln Val Arg Ile Thr Val Asn Asp Gln Val Glu Glu Phe Asp  
 180 185 190  
 Tyr Val Leu Val Ala Ile Gly Arg Gln Phe Asn Thr Ala Ser Ile Gly  
 195 200 205  
 Leu Asp Asn Ala Gly Val Ile Arg Asp Asp Arg Gly Val Ile Pro Val  
 210 215 220  
 Asp Glu Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp  
 225 230 235 240  
 Ile Thr Gly Lys Trp Leu Leu Ala His Val Ala Ser His Gln Gly Val  
 245 250 255  
 Ile Ala Ala Lys Asn Ile Ser Gly His His Glu Val Met Asp Tyr Ser  
 260 265 270  
 Ala Ile Pro Ser Val Ile Phe Thr His Pro Glu Ile Ala Met Val Gly  
 275 280 285

Leu Ser Leu Gln Glu Ala Glu Gln Gln Asn Leu Pro Ala Lys Leu Thr  
 290 295 300  
 Lys Phe Pro Phe Lys Ala Ile Gly Lys Ala Val Ala Leu Gly Ala Ser  
 305 310 315 320  
 Asp Gly Phe Ala Ala Ile Val Ser His Glu Ile Thr Gln Gln Ile Leu  
 325 330 335  
 Gly Ala Tyr Val Ile Gly Pro His Ala Ser Ser Leu Ile Gly Glu Met  
 340 345 350  
 Thr Leu Ala Ile Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr  
 355 360 365  
 Val His Ala His Pro Thr Leu Ser Glu Val Trp Ala Glu Gly Ala Leu  
 370 375 380  
 Leu Ala Thr Asn His Pro Leu His Phe Pro Pro Lys Ser  
 385 390 395

&lt;210&gt;895

&lt;211&gt;97

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;895

Met Thr Gln Glu Phe Asp Cys Val Val Ile Gly Ala Gly Pro Ser Gly  
 1 5 10 15  
 Tyr Val Ala Ala Ile Thr Ala Ala Gln Ser Lys Leu Arg Thr Ala Leu  
 20 25 30  
 Ile Glu Glu Asp Gln Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile  
 35 40 45  
 Pro Ser Lys Ala Leu Ile Ala Gly Ala Asn Val Val Ser His Ile Lys  
 50 55 60  
 His Ala Glu Ser Ser Ala Ser Met Leu Met Val Ile Gln Ser Ile Thr  
 65 70 75 80  
 Leu Arg Trp Gln Lys Glu Lys Ile Gln Ser Ser Arg Gly Ser Val Lys  
 85 90 95

Asp

&lt;210&gt;896

&lt;211&gt;157

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;896

Lys Ile Pro Met Pro Phe Ala Lys Glu Thr Glu Met Gln Arg Thr Cys  
 1 5 10 15  
 Trp Lys Cys Glu Gly Ser Val Ser Met His Val Pro Gln Cys Pro Tyr  
 20 25 30  
 Cys Ser Ala Phe Leu Gln Asp Pro Val Ala Ser Gly Gly Phe Ser  
 35 40 45  
 Ser Cys His Ile Ser Phe Pro Glu Gly Ala Ser Lys Glu Glu Ala Glu  
 50 55 60  
 Asp Leu Phe Ala Val Ser Ser Glu Asp Trp Glu Ala Val Leu Gly Asp  
 65 70 75 80  
 Gln Asn Pro Thr Gln Glu Thr Asn Lys Gln Val Ile Pro Glu Trp Thr  
 85 90 95  
 Trp Leu Gln Ser Trp Pro Leu Ala Ala Leu Phe Leu Gly Ile Gly Leu  
 100 105 110  
 Leu Ala Phe Ala Phe Leu Ile Leu Leu Phe Ser Thr Asp Ser Gly Leu  
 115 120 125  
 Val Leu Thr Trp Pro Lys Asn Arg Ala Tyr Phe Tyr Gly Ile Ile Gly  
 130 135 140  
 Ala Ala Val Ala Tyr Arg Gly Tyr Arg Lys Leu Pro Leu  
 145 150 155

&lt;210&gt;897

&lt;211&gt;170

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;897

Phe Gly Ser Leu Leu Ser Ile Leu Arg Lys Leu Gly Ser Ser Met Leu

```

      1           5           10           15
Arg Phe Gln Gly Lys Ser Leu Asn Arg Lys Glu Glu Ile Glu Thr Phe
      20           25           30
Thr Thr Asp Pro Asn Cys Gln Val Phe Val Gly Ser Leu Leu Ala Ala
      35           40           45
Gly Thr Gly Ile Asn Leu Thr Ala Gly Asn Val Val Ile Met Tyr Asp
      50           55           60
Arg Trp Trp Asn Pro Ala Lys Glu Asn Gln Ala Leu Asp Arg Val His
      65           70           75           80
Arg Ile Gly Gln Lys Asn Thr Val Phe Ile Tyr Lys Leu Ile Thr Glu
      85           90           95
Asp Thr Leu Glu Glu Arg Ile His Tyr Leu Ile Glu Lys Lys Ile Arg
      100          105          110
Leu Leu Asp Lys Val Ile Ala Ser Gln Asp Ser Asn Ile Leu His Met
      115          120          125
Leu Asn Arg Glu Asp Leu Leu Thr Ile Leu Ser Tyr Lys Asp Glu His
      130          135          140
Gly Thr Ser Asp Ser Glu Glu Ser Pro Val Asp Ala Pro Val Glu Asp
      145          150          155          160
Asp Thr Gly Val Leu Pro Pro Glu Asp Ser
      165          170
<210>898
<211>301
<212>PRT
<213>Chlamydia pneumoniae
<400>898
Leu Tyr Val Gln Gln Ser Val Leu Pro His Trp Glu His Ile Leu Ser
      1           5           10           15
Asn His Leu Pro Gly Val Ser Ile Phe Ser Phe His Gly Pro Asn Lys
      20           25           30
Pro Ser Glu Leu Pro Pro Ala Asp Ile Leu Leu Thr Ser Tyr Gly Thr
      35           40           45
Leu Arg Gln Asn Tyr Asp Lys Phe Tyr Lys Ile Ala Phe Thr Ile Val
      50           55           60
Val Phe Asp Glu Ile His Met Ala Lys Asn Lys Ser Ser Gln Ile His
      65           70           75           80
Lys Ile Leu Cys Arg Ile Asp Ala Gln Met Lys Leu Gly Leu Thr Gly
      85           90           95
Thr Pro Ile Glu Asn Asn Leu Leu Glu Phe Lys Gly Leu Leu Asp Ile
      100          105          110
Ile Leu Pro Asn Tyr Leu Pro Ser Asp Ala Leu Phe Lys Lys Leu Phe
      115          120          125
Thr Lys Arg Cys Ser Ser Glu Glu Leu Glu Glu Ile Ile Pro Ser Gln
      130          135          140
Asp Leu Leu Leu Lys Leu Thr Arg Pro Phe Ile Leu Arg Arg Thr Lys
      145          150          155          160
Lys Leu Val Leu Pro Glu Leu Pro Asp Lys Val Glu Ser Ile Ile Ala
      165          170          175
Cys Ser Leu Ser Pro Asp Gln Glu Lys Leu Tyr Met Ala Thr Leu Gln
      180          185          190
Arg Glu Lys Ser His Ile Gln Lys Leu Glu Thr Pro Glu Glu Pro Ala
      195          200          205
Thr Asn Phe Leu His Ile Phe Ala Leu Leu Asn His Leu Lys Gln Ile
      210          215          220
Cys Asp His Pro Ala Val Phe Phe Lys Asp Pro Asp Gln Tyr Lys Asn
      225          230          235          240
Tyr Glu Ser Gly Lys Trp Asn Ala Phe Val Lys Leu Leu Lys Glu Ser
      245          250          255
Leu Asn Ala Gly Tyr Lys Val Val Val Phe Ser Gln Tyr Ile His Met
      260          265          270
Ile Arg Ile Ile Thr Leu Tyr Leu Glu Glu Ile Gly Ile Lys Tyr Ala
      275          280          285
Ser Ile Ser Arg Lys Ile Ser Glu Ser Glu Gly Arg Asn
      290          295          300

```



&lt;210&gt;899

&lt;211&gt;610

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;899

Xaa Pro Leu Ser Ile Ala Leu Leu Lys Lys Phe Phe Phe Leu Asn Glu  
 1 5 10 15  
 Glu Gly Ala Glu Leu Thr Ile Gly Glu Asn Ser Gln Gly Phe Pro Ser  
 20 25 30  
 His Phe Ser Leu Gln Trp Gln Gly Leu Val Phe Lys Ala Glu Ile Leu  
 35 40 45  
 Asp Phe Pro Thr Leu Glu Asp Ile Phe Pro Lys Leu Glu Leu Ala His  
 50 55 60  
 Thr Ser Leu Glu Asn Val Ser His Asp Ile Ser Ile Thr Asn Val Thr  
 65 70 75 80  
 Val Cys Ala Glu Glu Ala Lys Val Asn Phe Thr Leu Ser Pro Val Ile  
 85 90 95  
 His Lys Lys Asp Arg Glu Asn His Pro Lys Thr Arg Ile Gly Ser Val  
 100 105 110  
 Glu Tyr Val Ala Lys Thr His Glu Met Ile Thr Gly Pro Lys Ala Ile  
 115 120 125  
 Ala Leu Pro Ile Tyr Ala Ile Pro Leu Leu Ala Asp Lys Phe Lys Asp  
 130 135 140  
 Gln Leu Leu Ser Leu Leu Cys Tyr Asp Ser Leu Glu Tyr Arg Leu Arg  
 145 150 155 160  
 Tyr Asp Ile Arg Leu Leu Arg Asp Ala Ser Phe Ser Phe Ser Ala Tyr  
 165 170 175  
 Leu Val Thr Pro Gly Asp Leu Asp Asn Gly Ser Leu Ile Tyr Pro Asn  
 180 185 190  
 Tyr Cys Tyr Ser Pro Thr Lys Gly Leu Met Gln Val Val Gly Met Leu  
 195 200 205  
 Ser Pro Lys Gln Ala Phe Ile Val Lys Ser Glu Gln Val Glu Asp Phe  
 210 215 220  
 Leu Asn Glu Arg Gly His Leu Ile Gln Glu Pro Gly Phe Gln Thr Phe  
 225 230 235 240  
 Ile Asn Glu Arg Pro Glu Gly His Leu Thr Tyr Asn Val Thr Glu Gln  
 245 250 255  
 Gly Val Leu Leu Phe His Tyr Asp Val Gly Asp Pro Ser Ser Thr Glu  
 260 265 270  
 Ile Arg Phe Gly Thr Trp Thr Tyr Tyr Thr Asn Gln Gly Phe Phe Leu  
 275 280 285  
 Glu Lys Lys Asn Asp Leu Pro Ile Gln Asp Gly Leu Ile Val Glu Pro  
 290 295 300  
 Gln Asp Ile Pro Ala Phe Ile Val Lys Asn Asp Ala Ala Leu Arg Arg  
 305 310 315 320  
 Leu Pro Asn Phe Phe Ser Ser Pro Pro Asn Leu Lys Asp Leu Leu Ile  
 325 330 335  
 Glu Val His Arg Gln Ser Arg Gly Lys Gly Leu Asp Leu Lys Pro Ile  
 340 345 350  
 Leu Val Gly Leu Gly Glu Ser Arg Cys Trp Leu Phe Gly Val Phe Leu  
 355 360 365  
 Tyr Arg Glu Asp Ile Gly Phe Ser Leu Ile Pro Thr Pro Leu Gln Gly  
 370 375 380  
 Leu Cys Phe Leu Pro Arg Val Ile Pro Pro Glu Asn Val Pro Gln Phe  
 385 390 395 400  
 Leu Thr Gln Tyr Ala Gln His Glu Arg Ile Leu Phe Pro Asn Pro Gln  
 405 410 415  
 Thr Arg Pro Pro Glu Ser Tyr Glu Leu Val Ile Gln Ser Ile His Arg  
 420 425 430  
 Pro His Pro Ala Ser Pro Leu His Leu Gln Leu Glu Leu Lys Thr Asn  
 435 440 445  
 Leu Gly Ser Val Pro Ile Gly Ile Ala Leu Gln Gly Leu Lys Ser Lys  
 450 455 460  
 His Thr Phe Leu Phe Thr Gln Ala Gly Phe Leu Asp Leu Lys Gln Asn

465                                      470                                      475                                      480  
 Leu Phe Gln Phe Leu Lys Gln Phe Leu Ser Thr Gln Lys Cys Val Ile  
    485                                      490                                      495  
 Ala Glu Asn Thr Val Ile Ala Asn Ile Thr Asp Val Phe Lys Leu Asp  
    500                                      505                                      510  
 Ala Leu Ala Pro Leu Ser Val Thr Asp Asp Thr Ile Ala Asn Pro Glu  
    515                                      520                                      525  
 Asp Leu Gln Phe Phe Ser Gln Leu Lys Ala Ala Cys Leu Pro Pro Ile  
    530                                      535                                      540  
 Pro Gln Asn Leu Phe Ser Ser Asp His Gln Leu Arg Pro Tyr Gln Asn  
 545                                      550                                      555                                      560  
 Ser Gly Leu Leu Trp Met Trp Phe Leu Tyr Asn His Arg Leu Ser Gly  
    565                                      570                                      575  
 Leu Leu Cys Asp Glu Met Gly Leu Gly Lys Thr His Gln Ala Thr Ala  
    580                                      585                                      590  
 Leu Thr Arg Tyr Cys Ile Ser Val Phe Thr Ala Leu Ser Ala Pro Glu  
    595                                      600                                      605

Ile Pro

610

&lt;210&gt;900

&lt;211&gt;181

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;900

His Asn Ile Met Val Leu Glu Ala Leu Ala Ile Phe Arg Gln Asp Ala  
 1                                      5                                      10                                      15  
 Met Gln His Leu Leu Lys His Arg Lys Glu Ile Val Val Asp Phe Cys  
    20                                      25                                      30  
 Glu Asp Ser Tyr Thr Ile Arg Ile Pro Asp Glu Glu Ala Pro Glu Gly  
    35                                      40                                      45  
 Tyr Trp Leu Ser Thr Leu Lys Leu Gln Asp Ile Asp Arg Leu Thr Phe  
    50                                      55                                      60  
 Ala Ser Cys Ser Cys Pro Asp Gly Glu Cys Cys Leu His Leu Met Thr  
    65                                      70                                      75                                      80  
 Ala Tyr Phe Ala Val Tyr Asp Ala Leu Gly Leu His Pro Leu His Asp  
    85                                      90                                      95  
 Lys Phe Arg His Ser Phe Trp Tyr Ala Val Phe Ser His Phe Phe Leu  
    100                                      105                                      110  
 Asp Ser Ile Pro Leu Gln Ala Gln Gly Glu Met Val Tyr Thr Leu Glu  
    115                                      120                                      125  
 Ser Pro His Ile Thr Leu Thr Ile Glu Cys Leu Ser Glu Glu Val Phe  
    130                                      135                                      140  
 Gln Asp Trp Leu Arg Thr Ile His Ala Ser Glu Glu Pro Thr Val Phe  
 145                                      150                                      155                                      160  
 Thr Asn Lys Thr Phe Leu Xaa Ser Ala Leu Tyr Arg Thr Ala Lys Lys  
    165                                      170                                      175  
 Ile Leu Phe Leu Lys  
    180

&lt;210&gt;901

&lt;211&gt;412

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;901

Met Lys Lys Asn Ala Ser His Lys Thr Asn Asp Lys Lys Ser Leu Ser  
 1                                      5                                      10                                      15  
 Ile Trp Ser Ile Gly Gly Ser Ile Phe Ala Met Phe Phe Gly Ala Gly  
    20                                      25                                      30  
 Asn Ile Val Phe Pro Leu Ala Leu Gly Tyr His Tyr Asn Ala His Pro  
    35                                      40                                      45  
 Trp Ser Ala Tyr Phe Gly Met Met Leu Thr Ala Val Cys Val Pro Leu  
    50                                      55                                      60  
 Leu Gly Leu Val Ser Met Leu Phe Tyr Ser Gly Asp Tyr Gln Lys Phe  
    65                                      70                                      75                                      80  
 Phe Phe Ser Ile Gly Arg Ile Pro Gly Met Ile Phe Ile Thr Ala Ile

85 90 95  
 Ile Leu Leu Ile Gly Pro Phe Gly Gly Ile Pro Arg Ala Ile Ala Val  
 100 105 110  
 Ser His Ala Thr Leu Ile Ser Leu Ser Glu His Lys Ser Ala Phe Ile  
 115 120 125  
 Pro Ser Leu Pro Ile Phe Ser Ala Ile Cys Cys Val Leu Ile Tyr Ile  
 130 135 140  
 Phe Ser Cys Lys Leu Ser Arg Leu Ile Gln Trp Leu Gly Ser Val Phe  
 145 150 155 160  
 Phe Pro Ile Met Leu Val Thr Leu Leu Trp Val Ile Ile Arg Ser Phe  
 165 170 175  
 Met Ile Pro Thr His Pro Met Val Gln Glu Phe Ile Pro Asn Ala Arg  
 180 185 190  
 Gln Ala Trp Leu Ala Gly Phe Ile Glu Gly Phe Asn Thr Met Asp Leu  
 195 200 205  
 Leu Ala Ala Phe Phe Phe Cys Ser Ile Val Leu Ile Ser Leu Arg Gln  
 210 215 220  
 Leu Val Ala Glu Glu Lys His Pro Thr Glu Glu Glu Ile Pro Leu Ser  
 225 230 235 240  
 Phe Gln Gly Ile Ser Lys Lys Asn Lys Arg Ser Leu Ala Leu Gly Phe  
 245 250 255  
 Phe Leu Ala Ala Ile Leu Leu Gly Met Thr Tyr Leu Gly Phe Val Leu  
 260 265 270  
 Ser Ala Ala Arg His Ala Gly Leu Leu Val Asn Val Ser Lys Gly His  
 275 280 285  
 Ile Leu Gly Arg Ile Ser Ala Ile Ala Leu Gly Pro Asn Ser Ile Leu  
 290 295 300  
 Ala Gly Val Ser Val Phe Ile Ala Cys Leu Thr Thr Glu Ile Ala Leu  
 305 310 315 320  
 Val Gly Ile Val Ala Asp Phe Leu Ala Arg Val Val Ser Phe Lys Lys  
 325 330 335  
 Leu Asn Tyr Ala Ser Ala Val Ile Cys Thr Leu Ile Pro Thr Tyr Leu  
 340 345 350  
 Ile Ser Ile Leu Asn Phe Glu Thr Ile Ser His Leu Leu Leu Pro Leu  
 355 360 365  
 Leu Gln Leu Ser Tyr Pro Ala Leu Ile Val Leu Ala Cys Gly Asn Ile  
 370 375 380  
 Ala Tyr Lys Leu Trp Asn Phe Arg Tyr Ser Pro Val Leu Phe Tyr Leu  
 385 390 395 400  
 Thr Leu Ser Leu Thr Ile Val Leu Lys Leu Val Asn  
 405 410

&lt;210&gt;902

&lt;211&gt;211

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;902

Leu Thr Met Lys Gln Phe Ile Leu Arg Thr Leu Asn Ala Leu Phe Pro  
 1 5 10 15  
 Asn Pro Lys Pro Ser Leu Glu Gly Trp Ser Ser Pro Phe Gln Leu Leu  
 20 25 30  
 Ile Ala Ile Leu Leu Ser Gly Asn Ser Thr Asp Lys Ala Val Asn Ser  
 35 40 45  
 Val Thr Pro Gln Leu Phe Ala Lys Ala Pro Asp Ala Gln Ser Ile Leu  
 50 55 60  
 Asp Leu Pro Pro Gly Lys Leu Tyr Gln Leu Ile Ala Pro Cys Gly Leu  
 65 70 75 80  
 Gly Glu Arg Lys Ser Ala Tyr Ile Tyr Gln Leu Ser Gln Ile Leu Val  
 85 90 95  
 Arg Asp Phe His Gly Glu Pro Pro Asn Asp Met Ala Leu Leu Thr Gln  
 100 105 110  
 Leu Pro Gly Val Gly Arg Lys Thr Ala Ser Val Phe Leu Gly Ile Ala  
 115 120 125  
 Tyr Gly Lys Pro Thr Phe Pro Val Asp Thr His Ile Leu Arg Leu Ala  
 130 135 140

Gln Arg Trp Lys Ile Ser Glu Lys Lys Ser Pro Ser Ala Ala Glu Lys  
 145 150 155 160  
 Asp Leu Ala Arg Phe Phe Gly His Glu Asn Thr Pro Lys Leu His Leu  
 165 170 175  
 Gln Leu Ile Tyr Tyr Ala Arg Gln Tyr Cys Pro Ala Leu His His Lys  
 180 185 190  
 Ile Asp Asn Cys Pro Ile Cys Ser Tyr Leu Ala Lys Glu Ala Asn Ser  
 195 200 205  
 Thr Arg Thr  
 210  
 <210>903  
 <211>442  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>903  
 Met Leu Lys His Asp Thr Ile Ala Ala Ile Ala Thr Pro Pro Gly Glu  
 1 5 10 15  
 Gly Ser Ile Ala Val Val Arg Leu Ser Gly Pro Gln Ala Ile Val Ile  
 20 25 30  
 Ala Asp Arg Ile Phe Ser Gly Ser Val Ala Ser Phe Ala Ser His Thr  
 35 40 45  
 Ile His Leu Gly Gln Val Ile Phe Glu Glu Thr Leu Ile Asp Gln Ala  
 50 55 60  
 Leu Leu Leu Leu Met Arg Ser Pro Arg Ser Phe Thr Gly Glu Asp Val  
 65 70 75 80  
 Val Glu Phe Gln Cys His Gly Gly Phe Phe Ala Cys Ser Gln Ile Leu  
 85 90 95  
 Asp Ala Leu Ile Ala Leu Gly Ala Arg Pro Ala Leu Pro Gly Glu Phe  
 100 105 110  
 Ser Gln Arg Ala Phe Leu Asn Gly Lys Ile Asp Leu Val Gln Ala Glu  
 115 120 125  
 Ala Ile Gln Asn Leu Ile Val Ala Glu Asn Ile Asp Ala Phe Arg Ile  
 130 135 140  
 Ala Gln Thr His Phe Gln Gly Asn Phe Ser Lys Lys Ile Gln Glu Ile  
 145 150 155 160  
 His Thr Leu Ile Ile Glu Ala Leu Ala Phe Leu Glu Val Leu Ala Asp  
 165 170 175  
 Phe Pro Glu Glu Glu Gln Pro Asp Leu Leu Val Pro Gln Glu Lys Ile  
 180 185 190  
 Gln Asn Ala Leu His Ile Val Glu Asp Phe Ile Ser Ser Phe Asp Glu  
 195 200 205  
 Gly Gln Arg Leu Ala Gln Gly Thr Ser Leu Ile Leu Ala Gly Lys Pro  
 210 215 220  
 Asn Val Gly Lys Ser Ser Leu Leu Asn Ala Leu Leu Gln Lys Asn Arg  
 225 230 235 240  
 Ala Ile Val Thr His Ile Pro Gly Thr Thr Arg Asp Ile Leu Glu Glu  
 245 250 255  
 Gln Trp Leu Leu Gln Gly Lys Arg Ile Arg Leu Leu Asp Thr Ala Gly  
 260 265 270  
 Gln Arg Thr Thr Asp Asn Asp Ile Glu Lys Glu Gly Ile Glu Arg Ala  
 275 280 285  
 Leu Ser Ala Met Glu Glu Ala Asp Gly Ile Leu Trp Val Ile Asp Ala  
 290 295 300  
 Thr Gln Pro Leu Glu Asp Leu Pro Lys Ile Leu Phe Thr Lys Pro Ser  
 305 310 315 320  
 Phe Leu Leu Trp Asn Lys Ala Asp Leu Thr Pro Pro Pro Phe Leu Asp  
 325 330 335  
 Thr Ser Leu Pro Gln Phe Ala Ile Ser Ala Lys Thr Gly Glu Gly Leu  
 340 345 350  
 Thr Gln Val Lys Gln Ala Leu Ile Gln Trp Met Gln Lys Gln Glu Ala  
 355 360 365  
 Gly Lys Thr Ser Lys Val Phe Leu Val Ser Ser Arg His His Met Ile  
 370 375 380  
 Leu Gln Glu Val Ala Arg Cys Leu Lys Glu Ala Gln Lys Asn Leu Tyr

385 390 395 400  
 Leu Gln Pro Pro Glu Ile Ile Ala Leu Glu Leu Arg Glu Ala Leu His  
 405 410 415  
 Ser Ile Gly Met Leu Ser Gly Lys Glu Val Thr Glu Ser Ile Leu Gly  
 420 425 430  
 Glu Ile Phe Ser Lys Phe Cys Ile Gly Lys  
 435 440  
 <210>904  
 <211>303  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>904  
 Gly Leu Val Gln Lys Pro Gln Tyr Ile Asp Arg Ile Thr Lys Lys Lys  
 1 5 10 15  
 Val Ile Glu Pro Ile Phe Tyr Glu Lys Thr Met Leu Phe Leu Tyr Asn  
 20 25 30  
 Ser Lys Leu Gly Lys Lys Leu Ser Val Phe Leu Ser Thr His Pro Ile  
 35 40 45  
 Phe Ser Arg Ile Tyr Gly Trp Leu Gln Arg Cys Ser Trp Thr Arg Arg  
 50 55 60  
 Gln Ile Arg Pro Phe Met Asn Arg Tyr Lys Ile Ser Glu Lys Glu Leu  
 65 70 75 80  
 Thr Lys Pro Val Ala Asp Phe Thr Ser Phe Asn Asp Phe Phe Thr Arg  
 85 90 95  
 Lys Leu Lys Pro Glu Ala Arg Pro Ile Val Gly Gly Lys Glu Val Phe  
 100 105 110  
 Ile Thr Pro Val Asp Gly Arg Tyr Leu Val Tyr Pro Asn Val Ser Glu  
 115 120 125  
 Phe Asp Lys Phe Ile Val Lys Ser Lys Ala Phe Ser Leu Pro Lys Leu  
 130 135 140  
 Leu Gly Asp His Glu Leu Thr Lys Leu Tyr Ala His Gly Ser Ile Val  
 145 150 155 160  
 Phe Ala Arg Leu Ala Pro Phe Asp Tyr His Arg Phe His Phe Pro Cys  
 165 170 175  
 Asp Cys Leu Pro Gln Lys Thr Arg Cys Val Asn Gly Ala Leu Phe Ser  
 180 185 190  
 Val His Pro Leu Ala Val Lys Asp Asn Phe Ile Leu Phe Cys Glu Asn  
 195 200 205  
 Lys Arg Thr Val Thr Val Leu Glu Thr Glu Gln Phe Gly Asn Val Leu  
 210 215 220  
 Tyr Leu Glu Val Gly Ala Met Asn Val Gly Ser Ile Val Gln Thr Phe  
 225 230 235 240  
 Ser Pro Asn Gln Thr Tyr Ala Lys Gly Asp Glu Lys Gly Phe Phe Ala  
 245 250 255  
 Phe Gly Gly Ser Thr Val Ile Leu Leu Phe Leu Pro Asn Ala Ile Arg  
 260 265 270  
 Phe Asp Asn Asp Leu Leu Lys Asn Ser Arg Met Gly Phe Glu Thr Arg  
 275 280 285  
 Cys Leu Met Gly Gln Ser Leu Gly Arg Ser Gln Arg Glu Glu Ile  
 290 295 300  
 <210>905  
 <211>468  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>905  
 Ile Ser Glu Arg Arg Asn Leu Lys Thr Leu Lys Thr Phe Phe Gly Ile  
 1 5 10 15  
 Ala Lys Arg Asp Lys Ser Gln Lys Trp Arg Ile Met Trp Leu Val Ile  
 20 25 30  
 Leu Trp Ala Leu Ala Ala Ser Leu Ala Ile Ala Leu Val Ala Lys Gly  
 35 40 45  
 Tyr Tyr Arg Phe Val Tyr Phe Arg Arg Tyr Ala Val Gln Val Ile Arg  
 50 55 60  
 Glu Val Arg Leu Ser Met Glu Leu Lys Glu Trp Ala Leu Ala Glu Gln

65 70 75 80  
 Gln Leu Leu Pro Ile Leu Lys Lys Arg Ser Tyr Arg Arg Gln Cys Leu  
 85 90 95  
 Phe Glu Tyr Met Arg Ile Leu Arg Lys Met Gln Arg Phe Glu Glu Ser  
 100 105 110  
 Glu Lys Leu Leu Ala Glu Ala Lys Lys Leu Gly Leu Arg Gly Pro Tyr  
 115 120 125  
 Phe Phe Leu Glu Ile Ala Tyr Lys Ala Tyr Arg Phe Gly Ala Phe Lys  
 130 135 140  
 Glu Cys Ala Gln Ala Phe Ala Ser Val Pro Gln Asp Leu Phe Glu Glu  
 145 150 155 160  
 Glu Asp Ala Ala Lys Tyr Ala Ser Ala Leu Val Arg Leu Gly Asp Leu  
 165 170 175  
 Asp Ala Ala Cys Ser Leu Ile Glu Pro Trp Ile Ser Pro Leu Ser His  
 180 185 190  
 Gln Glu Thr Phe Val Thr Met Gly His Ile Tyr Phe Thr Ser Lys Arg  
 195 200 205  
 Tyr Lys Asp Ala Ile Asp Phe Tyr Asn Arg Ala Asn Ala Leu Gly Val  
 210 215 220  
 Cys Pro Val Glu Val Thr Tyr Asn Leu Ala Gln Ala Tyr Arg Ile Thr  
 225 230 235 240  
 Ser Ser Tyr Ala Lys Ala Gly Lys Leu Phe Arg Lys Leu Leu Ser Asn  
 245 250 255  
 Pro Val Tyr Lys Glu Glu Ala Leu Phe Asn Ile Gly Leu Cys Glu Gln  
 260 265 270  
 Lys Leu Gly Arg Pro Gly Lys Ala Leu Leu Ile Tyr Gln Ser Ser Asp  
 275 280 285  
 Leu Trp Ser Arg Gly Asp Ala Leu Leu Met Lys Tyr Ala Ala Met Ala  
 290 295 300  
 Ala Met Asp Gln Arg Asp Tyr Val Leu Ala Glu Pro Cys Trp Glu Leu  
 305 310 315 320  
 Ala Leu Arg Cys Ser Thr Phe Ala Lys Asp Tyr Lys Cys Gly Leu Gly  
 325 330 335  
 Tyr Gly Phe Ser Leu Cys Arg Leu Arg Lys Tyr Gly Asp Ala Glu Arg  
 340 345 350  
 Val Tyr Cys Asn Leu Ile Gln Asn Phe Pro Glu Cys Leu Thr Ala Cys  
 355 360 365  
 Lys Ala Leu Ala Trp Leu Cys Gly Val Gly Tyr Ala Thr Leu Leu Gly  
 370 375 380  
 Ser Glu Glu Gly Leu Met Tyr Ala Lys Lys Ala Val Glu Leu Asp His  
 385 390 395 400  
 Ser Cys Glu Thr Leu Glu Leu Leu Ser Ala Cys Glu Ala Arg Cys Gly  
 405 410 415  
 Asn Phe Asp Ala Ala Tyr Glu Ile Gln Ser Phe Leu Ser Ser Arg Asp  
 420 425 430  
 Thr Ser Leu Gln Glu Lys Gln Arg Arg Ser Gln Ile Leu Arg Ile Leu  
 435 440 445  
 Arg Lys Lys Leu Pro Leu Asn Asp His His Ile Val Glu Val Asp Ala  
 450 455 460  
 Leu Leu Ala Ala  
 465  
 <210>906  
 <211>970  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>906  
 Met Leu Gly Phe Leu Lys Arg Phe Phe Gly Ser Ser Gln Glu Arg Ile  
 1 5 10 15  
 Leu Lys Lys Phe Gln Lys Leu Val Asp Lys Val Asn Ile Tyr Asp Glu  
 20 25 30  
 Met Leu Thr Pro Leu Ser Asp Asp Glu Leu Arg Asn Lys Thr Ala Glu  
 35 40 45  
 Leu Lys Gln Arg Tyr Gln Asn Gly Glu Ser Leu Asp Ser Met Leu Pro  
 50 55 60

Glu Ala Tyr Gly Val Val Lys Asn Val Cys Arg Arg Leu Ala Gly Thr  
 65 70 75 80  
 Pro Val Glu Val Ser Gly Tyr His Gln Arg Trp Asp Met Val Pro Tyr  
 85 90 95  
 Asp Val Gln Ile Leu Gly Ala Ile Ala Met His Lys Gly Phe Ile Thr  
 100 105 110  
 Glu Met Gln Thr Gly Glu Gly Lys Thr Leu Thr Ala Val Met Pro Leu  
 115 120 125  
 Tyr Leu Asn Ala Leu Thr Gly Lys Pro Val His Leu Val Thr Val Asn  
 130 135 140  
 Asp Tyr Leu Ala Gln Arg Asp Cys Glu Trp Val Gly Ser Val Leu Arg  
 145 150 155 160  
 Trp Leu Gly Leu Thr Thr Gly Val Leu Val Ser Gly Thr Leu Leu Glu  
 165 170 175  
 Lys Arg Lys Lys Ile Tyr Gln Cys Asp Val Val Tyr Gly Thr Ala Ser  
 180 185 190  
 Glu Phe Gly Phe Asp Tyr Leu Arg Asp Asn Ser Ile Ala Thr Arg Leu  
 195 200 205  
 Glu Glu Gln Val Gly Arg Gly Tyr Tyr Phe Ala Ile Ile Asp Glu Val  
 210 215 220  
 Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly  
 225 230 235 240  
 Pro Gly Glu Lys His Asn Pro Val Tyr Phe Glu Leu Lys Glu Lys Val  
 245 250 255  
 Ala Ser Leu Val Tyr Leu Gln Lys Glu Leu Cys Ser Arg Ile Ala Leu  
 260 265 270  
 Glu Ala Arg Arg Gly Leu Asp Ser Phe Leu Asp Val Asp Ile Leu Pro  
 275 280 285  
 Lys Asp Lys Lys Val Leu Glu Gly Ile Ser Glu Phe Cys Arg Ser Leu  
 290 295 300  
 Trp Leu Val Ser Lys Gly Met Pro Leu Asn Arg Val Leu Arg Arg Val  
 305 310 315 320  
 Arg Glu His Pro Asp Leu Arg Ala Met Ile Asp Lys Trp Asp Val Tyr  
 325 330 335  
 Tyr His Ala Glu Gln Asn Lys Glu Glu Ser Leu Glu Arg Leu Ser Glu  
 340 345 350  
 Leu Tyr Ile Ile Val Asp Glu His Asn Asn Asp Phe Glu Leu Thr Asp  
 355 360 365  
 Lys Gly Met Gln Gln Trp Val Glu Tyr Ala Gly Gly Ser Thr Glu Glu  
 370 375 380  
 Phe Val Met Met Asp Met Gly His Glu Tyr Ala Leu Ile Glu Asn Asp  
 385 390 395 400  
 Glu Thr Leu Ser Pro Ala Asp Lys Ile Asn Lys Lys Ile Ala Ile Ser  
 405 410 415  
 Glu Glu Asp Thr Leu Arg Lys Ala Arg Ala His Gly Leu Arg Gln Leu  
 420 425 430  
 Leu Arg Ala Gln Leu Leu Met Glu Arg Asp Val Asp Tyr Ile Val Arg  
 435 440 445  
 Asp Asp Gln Ile Val Ile Ile Asp Glu His Thr Gly Arg Pro Gln Pro  
 450 455 460  
 Gly Arg Arg Phe Ser Glu Gly Leu His Gln Ala Ile Glu Ala Lys Glu  
 465 470 475 480  
 His Val Thr Ile Arg Lys Glu Ser Gln Thr Leu Ala Thr Val Thr Leu  
 485 490 495  
 Gln Asn Phe Phe Arg Leu Tyr Glu Lys Leu Ala Gly Met Thr Gly Thr  
 500 505 510  
 Ala Ile Thr Glu Ser Arg Glu Phe Lys Glu Ile Tyr Asn Leu Tyr Val  
 515 520 525  
 Leu Gln Val Pro Thr Phe Lys Pro Cys Leu Arg Ile Asp His Asn Asp  
 530 535 540  
 Glu Phe Tyr Met Thr Glu Arg Glu Lys Tyr His Ala Ile Val Asn Glu  
 545 550 555 560  
 Ile Ala Thr Ile His Gly Lys Gly Asn Pro Ile Leu Val Gly Thr Glu  
 565 570 575

Ser Val Glu Val Ser Glu Lys Leu Ser Arg Ile Leu Arg Gln Asn Arg  
 580 585 590  
 Ile Glu His Thr Val Leu Asn Ala Lys Asn His Ala Gln Glu Ala Glu  
 595 600 605  
 Ile Ile Ala Gly Ala Gly Lys Leu Gly Ala Val Thr Val Ala Thr Asn  
 610 615 620  
 Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Asp Asn Glu Ala Val Ile  
 625 630 635 640  
 Val Gly Gly Leu His Val Ile Gly Thr Thr Arg His Gln Ser Arg Arg  
 645 650 655  
 Ile Asp Arg Gln Leu Arg Gly Arg Cys Ala Arg Leu Gly Asp Pro Gly  
 660 665 670  
 Ala Ala Lys Phe Phe Leu Ser Phe Glu Asp Arg Leu Met Arg Leu Phe  
 675 680 685  
 Ala Ser Pro Lys Leu Asn Thr Leu Ile Arg His Phe Arg Pro Pro Glu  
 690 695 700  
 Gly Glu Ala Met Ser Asp Pro Met Phe Asn Arg Leu Ile Glu Thr Ala  
 705 710 715 720  
 Gln Lys Arg Val Glu Gly Arg Asn Tyr Thr Ile Arg Lys His Thr Leu  
 725 730 735  
 Glu Tyr Asp Asp Val Met Asn Lys Gln Arg Gln Ala Ile Tyr Ala Phe  
 740 745 750  
 Arg His Asp Val Leu His Ala Glu Ser Val Phe Asp Leu Ala Lys Glu  
 755 760 765  
 Ile Leu Cys His Val Ser Leu Met Val Ala Ser Leu Val Met Ser Asp  
 770 775 780  
 Arg Gln Phe Lys Gly Trp Thr Leu Pro Asn Leu Glu Glu Trp Ile Thr  
 785 790 795 800  
 Ser Ser Phe Pro Ile Ala Leu Asn Ile Glu Glu Leu Arg Gln Leu Lys  
 805 810 815  
 Asp Thr Asp Ser Ile Ala Glu Lys Ile Ala Ala Glu Leu Ile Gln Glu  
 820 825 830  
 Phe Gln Val Arg Phe Asp His Met Val Glu Gly Leu Ser Lys Ala Gly  
 835 840 845  
 Gly Glu Glu Leu Asp Ala Ser Ala Ile Cys Arg Asp Val Val Arg Ser  
 850 855 860  
 Val Met Val Met His Ile Asp Glu Gln Trp Arg Ile His Leu Val Asp  
 865 870 875 880  
 Met Asp Leu Leu Arg Ser Glu Val Gly Leu Arg Thr Val Gly Gln Lys  
 885 890 895  
 Asp Pro Leu Leu Glu Phe Lys His Glu Ser Phe Leu Leu Phe Glu Ser  
 900 905 910  
 Leu Ile Arg Asp Ile Arg Ile Thr Ile Ala Arg His Leu Phe Arg Leu  
 915 920 925  
 Glu Leu Thr Val Glu Pro Asn Pro Arg Val Asn Asn Val Ile Pro Thr  
 930 935 940  
 Val Ala Thr Ser Phe His Asn Asn Val Asn Tyr Gly Pro Leu Glu Leu  
 945 950 955 960  
 Thr Val Val Thr Asp Ser Glu Asp Gln Asp  
 965 970

&lt;210&gt;907

&lt;211&gt;487

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;907

Met Leu Lys Ile Ala Ile Leu Gly Arg Pro Asn Val Gly Lys Ser Ser  
 1 5 10 15  
 Leu Phe Asn Arg Leu Cys Lys Arg Ser Leu Ala Ile Val Asn Ser Gln  
 20 25 30  
 Glu Gly Thr Thr Arg Asp Arg Leu Tyr Gly Glu Leu His Ala Phe Gly  
 35 40 45  
 Val Pro Ala Gln Val Ile Asp Thr Gly Gly Val Asp His Asn Ser Glu  
 50 55 60  
 Asp Tyr Phe Gln Lys His Ile Tyr Asn Gln Ala Leu Thr Gly Ala Lys



65 70 75 80  
 Glu Ala Asp Val Leu Leu Leu Val Ile Asp Ile Arg Cys Gly Ile Thr  
 85 90 95  
 Glu Glu Asp Ala His Leu Ala Lys Leu Leu Leu Pro Leu Lys Lys Pro  
 100 105 110  
 Leu Ile Leu Val Ala Asn Lys Ala Asp Ser Arg Gln Glu Glu Leu Gln  
 115 120 125  
 Ile His Glu Thr Tyr Lys Leu Gly Ile Arg Asp Ile Val Val Thr Ser  
 130 135 140  
 Thr Ala His Asp Lys His Ile Asp Thr Leu Leu Gln Arg Ile Lys Leu  
 145 150 155 160  
 Val Ala Asn Leu Pro Glu Pro Arg Glu Glu Glu Glu Gly Leu Glu  
 165 170 175  
 Glu Leu Ser Val Asp Glu His Glu Glu Ser Glu Ala Ala Leu Pro Ser  
 180 185 190  
 Asn Thr Phe Pro Asp Phe Ser Glu Val Phe Thr Glu Gly Phe Ser Pro  
 195 200 205  
 Glu Glu Pro Cys Thr Ile Pro Glu Ser Pro Gln Gln Ala Pro Lys Thr  
 210 215 220  
 Leu Lys Ile Ala Leu Ile Gly Arg Pro Asn Val Gly Lys Ser Ser Ile  
 225 230 235 240  
 Ile Asn Gly Leu Leu Asn Glu Glu Arg Cys Ile Ile Asp Asn Thr Pro  
 245 250 255  
 Gly Thr Thr Arg Asp Asn Ile Asp Ile Leu Tyr Ser His Lys Asp Arg  
 260 265 270  
 Gln Tyr Leu Phe Ile Asp Thr Ala Gly Leu Arg Lys Met Lys Ser Val  
 275 280 285  
 Lys Asn Ser Ile Glu Trp Ile Ser Ser Ser Arg Thr Glu Lys Ala Ile  
 290 295 300  
 Ser Arg Ala Asp Ile Cys Leu Leu Val Ile Asp Ala Thr Gln Lys Leu  
 305 310 315 320  
 Ser Ser Tyr Glu Lys Arg Ile Leu Ser Leu Ile Ser Lys Arg Lys Lys  
 325 330 335  
 Pro His Ile Ile Leu Ile Asn Lys Trp Asp Leu Leu Glu Glu Val Arg  
 340 345 350  
 Met Glu His Tyr Cys Lys Asp Leu Arg Ala Thr Asp Pro Tyr Leu Gly  
 355 360 365  
 Gln Ala Lys Met Leu Cys Ile Ser Ala Thr Thr Lys Arg Asn Leu Lys  
 370 375 380  
 Lys Ile Phe Ser Ala Ile Asp Glu Leu His His Val Val Ser Asn Lys  
 385 390 395 400  
 Val Pro Thr Pro Ile Val Asn Lys Thr Leu Ala Ser Ala Leu His Arg  
 405 410 415  
 Asn His Pro Gln Val Ile Gln Gly Arg Arg Leu Arg Ile Tyr Tyr Ala  
 420 425 430  
 Ile Gln Lys Thr Thr Thr Pro Leu Gln Phe Leu Leu Phe Ile Asn Ala  
 435 440 445  
 Lys Ser Leu Leu Thr Lys His Tyr Glu Tyr Tyr Leu Lys Asn Thr Leu  
 450 455 460  
 Lys Ser Ser Phe Asn Leu Tyr Gly Ile Pro Phe Asp Leu Glu Phe Lys  
 465 470 475 480  
 Glu Lys Pro Lys Arg His Asn  
 485

&lt;210&gt;908

&lt;211&gt;410

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;908

Met Thr Thr Ile Ala Ile Glu Ala Ala Lys Lys Val Leu Ile Lys Leu  
 1 5 10 15  
 Arg Asn Ala Gly Tyr Gln Ala Tyr Phe Val Gly Gly Cys Val Arg Asp  
 20 25 30  
 Met Leu Met Asn Arg Pro Leu Glu Asp Ile Asp Ile Ala Thr Asn Ala  
 35 40 45

Ser Pro Thr Ile Val Ser Thr Ile Phe Pro Asp Val Ile Ser Ile Gly  
 50 55 60  
 Val Ala Phe Gly Ile Ile Val Val Lys Gln Asp Gly Arg Leu Phe Glu  
 65 70 75 80  
 Val Ala Thr Phe Arg Ser Asp Gly Glu Tyr Lys Asp Gly Arg His Pro  
 85 90 95  
 Asp Arg Ile Ile Phe Ser Ser Met Arg Glu Asp Ala Leu Arg Arg Asp  
 100 105 110  
 Phe Thr Val Asn Gly Met Tyr Tyr Asp Pro Phe Glu Asp Lys Val Phe  
 115 120 125  
 Asp Phe Val Glu Gly Thr Arg Asp Ile Glu Lys Lys Val Ile Arg Ala  
 130 135 140  
 Ile Gly His Pro Arg Leu Arg Phe Ser Glu Asp Lys Leu Arg Ile Leu  
 145 150 155 160  
 Arg Ala Ile Arg Phe Ser Ser Ser Leu Gly Phe Thr Leu Asp Pro Thr  
 165 170 175  
 Thr Glu Arg Ala Ile Ile Lys Glu Ala Pro Ala Leu Val Asn Ser Val  
 180 185 190  
 Ser Pro Glu Arg Ile Trp Gln Glu Leu Lys Lys Met Leu Lys Arg Gln  
 195 200 205  
 Pro Tyr Gly Ala Leu Ser Leu Leu Leu Lys Leu Lys Val Leu Ile Phe  
 210 215 220  
 Ile Phe Pro Glu Leu Arg Asp Ile Pro Tyr Ser Leu Leu Arg Thr Thr  
 225 230 235 240  
 Ile Glu Phe Ala Arg Lys Phe Asn Pro Thr His Phe Pro Glu Ile Leu  
 245 250 255  
 Phe Leu Leu Pro Leu Phe Gln Gly Val Ser Glu Glu Ala Ala Thr Val  
 260 265 270  
 Ala Phe Gly Arg Leu Arg Ile Ser Asn Lys Glu Leu Lys Leu Ile Glu  
 275 280 285  
 Ser Trp Tyr Glu Ala Leu Pro His Phe Gln Asn Gln Ser Gly Asn Arg  
 290 295 300  
 Val Phe Trp Ala His Phe Leu Ala Ser Pro Thr Ala Pro Leu Phe Leu  
 305 310 315 320  
 Glu Leu Phe Ser Ala Leu Gln Lys Asp Pro Ser Arg Gln Gln His Phe  
 325 330 335  
 Ile Ser Arg Val Gln Glu Leu Glu Ser Arg Leu Glu Gln Phe Ile Leu  
 340 345 350  
 Arg Ile Lys Thr Ser Ser Pro Val Ser Ala Pro Asp Leu Ile Ala  
 355 360 365  
 Lys Gly Ile Ser Pro Gly Arg Leu Leu Gly Asp Leu Leu Arg Glu Ala  
 370 375 380  
 Glu Ile Leu Ser Ile Glu Asn Glu Cys Leu Asp Lys Glu Lys Ile Leu  
 385 390 395 400  
 Leu Leu Leu Gln Glu Lys Gly Phe Trp Lys  
 405 410

&lt;210&gt;909

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;909

Arg Val Tyr Pro Ser Gln Tyr Gly Lys Tyr Leu Ile Tyr Arg Arg Arg  
 1 5 10 15  
 Thr Phe Val Asn Leu Asp Lys Ile Ile Ala Lys Arg Leu Gly Lys Thr  
 20 25 30  
 Thr Ile Gly Phe Ser Asp Asp Gln Ala Asp Leu Ser Gln Lys Thr Arg  
 35 40 45  
 Asp His Leu Leu Ala Lys Val Glu Thr Glu Asp Leu Ile Ala Phe Gly  
 50 55 60  
 Met Ile Pro Glu Phe Val Gly Arg Phe Asn Cys Ile Val Asn Cys Glu  
 65 70 75 80  
 Glu Leu Ser Leu Asp Glu Leu Val Ala Ile Leu Thr Glu Pro Thr Asn  
 85 90 95  
 Ala Ile Val Lys Gln Tyr Met Glu Leu Phe Ala Glu Glu Asn Val Lys

100 105 110  
 Leu Val Phe Lys Lys Glu Ala Leu Tyr Ala Ile Ala Lys Lys Ala Lys  
 115 120 125  
 Gln Ala Lys Thr Gly Ala Arg Ala Leu Gly Met Ile Leu Glu Asn Leu  
 130 135 140  
 Leu Arg Asp Leu Met Phe Glu Ile Pro Ser Asp Pro Thr Val Glu Ala  
 145 150 155 160  
 Ile His Ile Gln Glu Asp Thr Ile Ala Glu Asn Lys Ala Pro Ile Ile  
 165 170 175  
 Ile Arg Arg Thr Pro Glu Ala Ile Ala  
 180 185

&lt;210&gt;910

&lt;211&gt;256

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;910

Met Asn Lys Lys Asn Leu Thr Ile Cys Ser Phe Cys Gly Arg Ser Glu  
 1 5 10 15  
 Lys Asp Val Glu Lys Leu Ile Ala Gly Pro Ser Val Tyr Ile Cys Asp  
 20 25 30  
 Tyr Cys Ile Lys Leu Cys Ser Gly Ile Leu Asp Lys Lys Pro Ser Ser  
 35 40 45  
 Thr Ile Ser Ser Ala Pro Val Ser Glu Thr Pro Ser Gln Pro Ser Asp  
 50 55 60  
 Leu Arg Val Leu Thr Pro Lys Glu Ile Lys Lys His Ile Asp Glu Tyr  
 65 70 75 80  
 Val Ile Gly Gln Glu Arg Ala Lys Lys Thr Ile Ala Val Ala Val Tyr  
 85 90 95  
 Asn His Tyr Lys Arg Ile Arg Ala Leu Leu His Asn Lys Gln Val Ser  
 100 105 110  
 Tyr Gly Lys Ser Asn Val Leu Leu Leu Gly Pro Thr Gly Ser Gly Lys  
 115 120 125  
 Thr Leu Ile Ala Lys Thr Leu Ala Lys Ile Leu Asp Val Pro Phe Thr  
 130 135 140  
 Ile Ala Asp Ala Thr Thr Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp  
 145 150 155 160  
 Val Glu Asn Ile Val Leu Arg Leu Leu Gln Ala Ala Asp Tyr Asp Val  
 165 170 175  
 Ala Arg Ala Glu Arg Gly Ile Ile Tyr Ile Asp Glu Ile Asp Lys Ile  
 180 185 190  
 Gly Arg Thr Thr Ala Asn Val Ser Ile Thr Arg Asp Val Ser Gly Glu  
 195 200 205  
 Gly Val Gln Gln Ala Leu Leu Lys Ile Val Glu Gly Thr Thr Ala Asn  
 210 215 220  
 Val Pro Pro Lys Gly Gly Arg Lys His Pro Asn Gln Glu Tyr Ile Arg  
 225 230 235 240  
 Val Asn Thr Glu Asn Ile Leu Phe Ile Val Gly Gly Leu Ser Ser Thr  
 245 250 255

&lt;210&gt;911

&lt;211&gt;116

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;911

Cys Lys Tyr Leu Leu His Arg Ser Ser Cys Ile His Gly Ser Pro Leu  
 1 5 10 15  
 Ile Ile Arg Arg Thr Lys Gly Lys Arg His Ala Leu Pro His Ser Arg  
 20 25 30  
 Met Met Ile His Gln Pro Ser Gly Gly Ile Ile Gly Thr Ser Ala Asp  
 35 40 45  
 Ile Gln Leu Gln Ala Ala Glu Ile Leu Thr Leu Lys Lys His Leu Ala  
 50 55 60  
 Asn Ile Leu Ser Glu Cys Thr Gly Gln Pro Val Glu Lys Ile Ile Glu  
 65 70 75 80  
 Asp Ser Glu Arg Asp Phe Phe Met Gly Ala Glu Glu Ala Ile Ser Tyr

85 90 95  
 Gly Leu Ile Asp Lys Val Val Thr Ser Ala Lys Glu Thr Asn Lys Asp  
 100 105 110  
 Thr Ser Ser Thr  
 115

&lt;210&gt;912

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;912

Met Thr Leu Val Pro Tyr Val Val Glu Asp Thr Gly Arg Gly Glu Arg  
 1 5 10 15  
 Ala Met Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Met Ile  
 20 25 30  
 Gly Gln Glu Ile Thr Glu Pro Leu Ala Asn Thr Val Ile Ala Gln Leu  
 35 40 45  
 Leu Phe Leu Met Ser Glu Asp Pro Lys Lys Asp Ile Gln Ile Phe Ile  
 50 55 60  
 Asn Ser Pro Gly Gly Tyr Ile Thr Ala Gly Leu Ala Ile Tyr Asp Thr  
 65 70 75 80  
 Ile Arg Phe Leu Gly Cys Asp Val Asn Thr Tyr Cys Ile Gly Gln Ala  
 85 90 95  
 Ala Ser Met Gly Ala Leu Leu Leu Ser Ala Glu Leu Lys Glu Ser Val  
 100 105 110  
 Thr Leu Phe Pro Ile Ala Val  
 115

&lt;210&gt;913

&lt;211&gt;98

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;913

Lys Lys Lys Ser Glu Leu Ile Lys Glu Ala Glu Glu Asp Ala Thr Lys  
 1 5 10 15  
 Ala Leu Lys Leu Leu Phe Leu Thr His Lys Ile Phe Ser Asp Glu Lys  
 20 25 30  
 Leu Thr Ile Ser Arg Glu Glu Leu Gln Tyr Met Met Asp Val Cys Ser  
 35 40 45  
 Arg Glu Arg Phe Gly Gln Gln Pro Pro Lys Asp Ile Ser Asn Asp Thr  
 50 55 60  
 Leu Gln Glu Leu Val Met Ser Ala Arg Asp Arg Leu Thr Tyr Ser Lys  
 65 70 75 80  
 Ala Ile Glu His Val Leu Arg Lys Ala Glu Leu Leu Ala Ser Thr Pro  
 85 90 95  
 Ser Ala

&lt;210&gt;914

&lt;211&gt;240

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;914

Lys Ala Phe Pro Ala Ile Ser Asp Leu Pro Trp Glu Asn Leu Ser Leu  
 1 5 10 15  
 Pro Gln Glu Glu Ala Ala Ser Glu Ile Ser Asp Ser Asp Ile Glu Lys  
 20 25 30  
 Gly Leu Thr Asn Ile Gly Met Phe Ala Thr Lys Thr Pro Val Glu  
 35 40 45  
 Arg Pro Ser Gln Glu Gly Asp Phe Ile Ser Ile Ser Leu His Val Ser  
 50 55 60  
 Lys Ser Asn Asp Glu Asn Ala Ser Ser Ala Ala Ile Phe Glu Asn Lys  
 65 70 75 80  
 Tyr Phe Lys Leu Ser Glu Glu Glu Met Thr Asp Ala Phe Lys Glu Lys  
 85 90 95  
 Phe Leu Gly Ile Ser Thr Gly His Arg Val Val Glu Thr Ile Thr Ser  
 100 105 110

Pro Glu Ile Gln Ser Phe Leu Arg Gly Asp Thr Leu Thr Phe Thr Val  
 115 120 125  
 Asn Ala Val Ile Glu Val Ser Ile Pro Glu Ile Asp Asp Glu Lys Ala  
 130 135 140  
 Arg Gln Leu Gln Ala Glu Ser Leu Asp Asp Leu Lys Ala Lys Leu Arg  
 145 150 155 160  
 Ile Gln Leu Glu Lys Gln Ala Lys Asp Lys Gln Leu Gln Lys Arg Phe  
 165 170 175  
 Ser Glu Ala Glu Asp Ala Leu Ala Met Leu Val Asp Phe Glu Leu Pro  
 180 185 190  
 Thr Ser Leu Leu Glu Glu Arg Ile Ser Leu Ile Thr Arg Glu Lys Leu  
 195 200 205  
 Leu Asn Ala Arg Leu Ile Gln Tyr Cys Ser Asp Glu Glu Leu Glu Lys  
 210 215 220  
 Arg Asn Gln Asn Leu Ser Arg Lys Gln Lys Lys Met Leu Gln Lys His  
 225 230 235 240

&lt;210&gt;915

&lt;211&gt;186

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;915

Val Gln Ala Ser Ser Pro Ala Phe Pro Phe Lys Ser Asn Lys Lys Gly  
 1 5 10 15  
 Cys Leu Val Pro Arg Ser Leu Ser Asn Glu Gln Phe Ser Val Asp Leu  
 20 25 30  
 Glu Glu Ser Pro Gly Cys Ile Val Ser Ala Leu Val Lys Val Ser Pro  
 35 40 45  
 Glu Val Leu Asn Lys Leu Asn Lys Gln Ala Leu Lys Lys Ile Lys Lys  
 50 55 60  
 Glu Ile Thr Leu Pro Gly Phe Arg Lys Gly Lys Ala Pro Asp Asp Val  
 65 70 75 80  
 Ile Ala Ser Arg Tyr Pro Thr Asn Val Arg Lys Glu Leu Gly Glu Leu  
 85 90 95  
 Val Thr Gln Asp Ala Tyr His Ala Leu Ser Thr Val Gly Asp Arg Arg  
 100 105 110  
 Pro Leu Ser Pro Lys Ala Val Arg Ser Asn Ser Ile Thr Gln Phe Asp  
 115 120 125  
 Leu Gln Glu Gly Ala Lys Val Glu Phe Ser Tyr Glu Lys Leu Ser Leu  
 130 135 140  
 Gln Phe Leu Ile Phe Leu Gly Lys Thr Phe Leu Tyr Leu Arg Lys Lys  
 145 150 155 160  
 Leu Leu Val Arg Phe Gln Ile Val Ile Ser Arg Arg Asp Ser Gln Thr  
 165 170 175  
 Leu Val Cys Ser Leu Gln Gln Lys Leu Leu  
 180 185

&lt;210&gt;916

&lt;211&gt;1075

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;916

Ala Asp Tyr Ile Ile His Ser Tyr Ser Arg Gly Glu Met Leu Asn Phe  
 1 5 10 15  
 Arg Lys Leu Arg Arg Asp Phe Ser Ala Asn Ile Leu Gln Asp Gly Lys  
 20 25 30  
 Lys Leu Phe Glu Gln Gly Ala Val Ile Asp Ala Lys Ile Leu Ser Met  
 35 40 45  
 Asn Gly Glu Thr Val Cys Ile Ser Ala Gln Val Arg Gly Leu Tyr Asp  
 50 55 60  
 Asn Ile Tyr Glu Cys Glu Ile Glu Val Asp Arg Ser Glu Ser Asp Thr  
 65 70 75 80  
 Val Asp Ser Asn Cys Asp Cys Ser Tyr Asn Tyr Asp Cys Gln His Ile  
 85 90 95  
 Val Ala Leu Leu Phe Tyr Leu Glu Gln Tyr Phe Asn Glu Met Val Val  
 100 105 110

Ala Tyr Ala Arg Ser Ala Asp Leu Glu Thr Asp His Glu Ile Asn Glu  
 115 120 125  
 Glu Val Lys Lys Glu Leu Lys Glu Thr Phe Val Ala Ala Ala Thr Lys  
 130 135 140  
 Glu Glu Glu Arg Lys Asp Arg Glu His Gln Lys Glu Ile Leu Arg Glu  
 145 150 155 160  
 Tyr Val His Ala Ala Asn Ala Leu Ser Ala Asn Pro Phe Phe Leu Pro  
 165 170 175  
 Leu Glu Tyr Leu Glu Lys Asp Ser Ala Glu Leu Ala Val Leu Phe Val  
 180 185 190  
 Ser Val Asn Glu Asp Thr Phe Ala Pro Ala Asn Gln Pro Ile Glu Phe  
 195 200 205  
 Gln Leu Val Leu Arg Leu Pro Cys Arg Ser Lys Pro Phe Tyr Ile Ser  
 210 215 220  
 Asn Ile Arg Thr Phe Leu Glu Gly Val Leu Tyr Gln Glu Pro Ile Val  
 225 230 235 240  
 Leu Asn Gly Arg Arg Phe Phe Thr Met Gln Ser Phe Asn Ala Ser  
 245 250 255  
 Asp Arg Lys Leu Ile Asp Leu Leu Ile Arg Tyr Val Arg Tyr Pro Asn  
 260 265 270  
 His Thr Thr Glu Glu Lys Leu Leu Lys Ser Ala Tyr Leu Met Pro Pro  
 275 280 285  
 Ala Leu Gly Val Ile Leu Ala Lys Met Phe Glu His Gln Leu Ala Asp  
 290 295 300  
 Arg Gly Gly Gly Ser Leu Gly Glu Lys Glu Ser Phe Ser Gly Leu Phe  
 305 310 315 320  
 Cys Gly Asn Leu Glu Glu Pro Leu Cys Trp Ser Leu Thr Pro Ala Lys  
 325 330 335  
 Met Lys Phe Asn Leu Asp Phe Phe Asp Met Pro Tyr Lys Ala Leu Leu  
 340 345 350  
 Met Thr Pro Val Ile Leu Val Asp Asp Glu Val Gln Pro Glu Gln  
 355 360 365  
 Thr Met Leu Leu Glu Ser Asp Ala Pro Gly Ile Ile His His Phe Val  
 370 375 380  
 Tyr His Arg Phe Ser Pro Gln Ile Lys Arg Ala His Leu Arg Ser Phe  
 385 390 395 400  
 Ser Arg Leu Arg Asp Ile Ala Ile Pro Glu Ala Leu Phe Gly Ser Phe  
 405 410 415  
 Arg Glu Asn Ala Leu Pro Val Phe Gln Glu Tyr Ala Glu Ile Ala Asn  
 420 425 430  
 Val His Leu Leu Asn Ser Phe Val Thr Leu Pro Tyr Val Asp Glu Val  
 435 440 445  
 Arg Ala Ile Cys Asp Met Ser Tyr Leu Asp Gly Glu Leu Glu Ala Lys  
 450 455 460  
 Leu His Phe Leu Tyr Gly Ser Leu Arg Val Pro Ala Ala Ser Leu Ala  
 465 470 475 480  
 Leu Gln Tyr Gln Asp Val Arg Ala Phe Ile Ser Asp Glu Gly Ile Leu  
 485 490 495  
 Ala Arg Asn Leu Val Glu Glu Arg Lys Met Leu Glu Glu Val Phe Ser  
 500 505 510  
 Gly Phe Ile Tyr Asp Glu Arg Asp Gly Ala Phe Arg Val Lys Ser Glu  
 515 520 525  
 Lys Lys Ile Val Glu Phe Met Thr Glu Thr Ile Pro Ala Asn Gln His  
 530 535 540  
 Arg Ile Thr Phe Asn Cys Pro Glu Asn Leu Ser Gly Gln Phe Ile Tyr  
 545 550 555 560  
 Asp Glu Thr Ile Phe Glu Leu Ser Phe Arg Glu Gly Ser Asp Ile Asn  
 565 570 575  
 Tyr Tyr Glu Ala Asp Leu Lys Val His Gly Leu Leu Lys Gly Val Pro  
 580 585 590  
 Leu Asp Leu Leu Trp Asp Cys Ile Ser Ala Lys Lys Arg Phe Leu Glu  
 595 600 605  
 Leu Pro Lys Ala Gly Gln Gln Ser Lys Gly Thr Arg Gly Lys Val  
 610 615 620

Asn Ser Gly Lys Leu Pro Cys Ile Leu Val Leu Asp Leu Glu Lys Ile  
 625 630 635 640  
 Ala Pro Val Val Gln Ile Phe Asn Glu Ile Gly Phe Lys Val Leu Asp  
 645 650 655  
 Asp Leu Val Gln Lys Cys Pro Leu Trp Ser Leu Thr Gly Ile Ser Leu  
 660 665 670  
 Asp Gln Phe Glu Ala Leu Pro Val Asn Phe Ser Met Ser Glu Arg Leu  
 675 680 685  
 Ile Glu Ile Gln Lys Gln Ile Arg Gly Glu Ile Glu Phe Asp Phe Gln  
 690 695 700  
 Asp Val Pro Gln Gln Ile Gln Ala Thr Leu Arg Ser Tyr Gln Thr Glu  
 705 710 715 720  
 Gly Val His Trp Leu Glu Arg Leu Arg Lys Met His Leu Asn Gly Ile  
 725 730 735  
 Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Ala Ile Ile Ala  
 740 745 750  
 Val Thr Gln Ser Lys Leu Glu Lys Gly Ser Gly Cys Ser Leu Ile Val  
 755 760 765  
 Cys Pro Thr Ser Leu Val Tyr Asn Trp Lys Glu Glu Phe Arg Lys Phe  
 770 775 780  
 Asn Pro Glu Phe Arg Thr Leu Val Ile Asp Gly Val Pro Ser Gln Arg  
 785 790 795 800  
 Arg Lys Gln Leu Thr Ala Leu Ala Asp Arg Asp Val Ala Ile Thr Ser  
 805 810 815  
 Tyr Asn Leu Leu Gln Lys Asp Val Glu Leu Tyr Lys Ser Phe Arg Phe  
 820 825 830  
 Asp Tyr Val Val Leu Asp Glu Ala His His Ile Lys Asn Arg Thr Thr  
 835 840 845  
 Arg Asn Ala Lys Ser Val Lys Met Ile Gln Ser Asp His Arg Leu Ile  
 850 855 860  
 Leu Thr Gly Thr Pro Ile Glu Asn Ser Leu Glu Glu Leu Trp Ser Leu  
 865 870 875 880  
 Phe Asp Phe Leu Met Pro Gly Leu Leu Ser Ser Tyr Asp Arg Phe Val  
 885 890 895  
 Gly Lys Tyr Ile Arg Thr Gly Asn Tyr Met Gly Asn Lys Ala Asp Asn  
 900 905 910  
 Met Val Ala Leu Lys Lys Lys Val Ser Pro Phe Ile Leu Pro Arg Met  
 915 920 925  
 Lys Glu Asp Val Leu Lys Asp Leu Pro Pro Val Ser Glu Ile Leu Tyr  
 930 935 940  
 His Cys His Leu Thr Glu Ser Gln Lys Glu Leu Tyr Gln Ser Tyr Ala  
 945 950 955 960  
 Ala Ser Ala Lys Lys Glu Leu Ser Arg Leu Val Lys Gln Glu Gly Phe  
 965 970 975  
 Glu Arg Ile His Ile His Val Leu Ala Thr Leu Thr Arg Leu Lys Gln  
 980 985 990  
 Ile Cys Cys His Pro Ala Ile Phe Ala Lys Asp Ala Pro Glu Pro Gly  
 995 1000 1005  
 Asp Ser Ala Lys Tyr Asp Met Leu Met Asp Leu Leu Ser Ser Leu Val  
 1010 1015 1020  
 Asp Ser Gly His Lys Thr Val Val Phe Ser Gln Tyr Thr Lys Met Leu  
 1025 1030 1035 1040  
 Gly Ile Ile Lys Lys Asp Leu Glu Ser Arg Gly Ile Pro Phe Val Tyr  
 1045 1050 1055  
 Leu Asp Gly Ser Thr Lys Asn Arg Leu Asp Leu Val Asn Gln Phe Asn  
 1060 1065 1070  
 Glu Asp Thr  
 1075  
 <210>917  
 <211>366  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>917  
 Met Ser Pro His Arg Asn Leu Phe Lys Leu Lys Asn Phe Ser Asn Arg

```

      1           5           10           15
Leu Tyr Asn Arg Ala Leu Gly Arg Phe Asp Lys Val Phe Asn Phe Phe
      20           25           30
Ser Gly Asn Val Gly Ile Asp Leu Gly Thr Ala Asn Thr Leu Val Tyr
      35           40           45
Val Arg Gly Arg Gly Ile Val Leu Ser Glu Pro Ser Val Val Ala Val
      50           55           60
Asp Ala Gln Thr His Ala Val Leu Ala Val Gly His Lys Ala Lys Ala
      65           70           75           80
Met Leu Gly Lys Thr Pro Arg Lys Ile Met Ala Val Arg Pro Met Lys
      85           90           95
Asp Gly Val Ile Ala Asp Phe Glu Ile Ala Glu Gly Met Leu Lys Ala
      100          105          110
Leu Ile Lys Arg Val Thr Pro Ser Arg Ser Val Phe Arg Pro Arg Ile
      115          120          125
Leu Ile Ala Val Pro Ser Gly Ile Thr Gly Val Glu Lys Arg Ala Val
      130          135          140
Glu Asp Ser Ala Leu His Ala Gly Ala Gln Glu Val Ile Leu Ile Glu
      145          150          155          160
Glu Pro Met Ala Ala Ala Ile Gly Val Asp Leu Pro Val His Glu Pro
      165          170          175
Ala Ala Ser Met Ile Ile Asp Ile Gly Gly Thr Thr Glu Ile Ala
      180          185          190
Ile Ile Ser Leu Gly Gly Ile Val Glu Ser Arg Ser Leu Arg Ile Ala
      195          200          205
Gly Asp Glu Phe Asp Glu Cys Ile Ile Asn Tyr Met Arg Arg Thr Tyr
      210          215          220
Asn Leu Met Ile Gly Pro Arg Thr Ala Glu Glu Ile Lys Ile Thr Ile
      225          230          235          240
Gly Ser Ala Tyr Pro Leu Gly Asp Gln Glu Leu Glu Met Glu Val Arg
      245          250          255
Gly Arg Asp Gln Val Ala Gly Leu Pro Ile Thr Lys Arg Ile Asn Ser
      260          265          270
Val Glu Ile Arg Glu Cys Leu Ala Glu Pro Ile Gln Gln Ile Ile Glu
      275          280          285
Cys Val Arg Leu Thr Leu Glu Lys Cys Pro Pro Glu Leu Ser Ala Asp
      290          295          300
Leu Val Glu Arg Gly Met Val Leu Ala Gly Gly Ala Leu Ile Lys
      305          310          315          320
Gly Leu Asp Lys Ala Leu Ser Lys Asn Thr Gly Leu Ser Val Ile Thr
      325          330          335
Ala Pro His Pro Leu Leu Ala Val Cys Leu Gly Thr Gly Lys Ala Leu
      340          345          350
Glu His Leu Asp Gln Phe Lys Lys Arg Lys Gly Asn Leu Val
      355          360          365

```

&lt;210&gt;918

&lt;211&gt;579

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;918

```

Ile Asn Asp Ser Glu Asp Ile Arg Leu Cys Asp Gly Ser Asp Thr Glu
      1           5           10           15
Tyr Asp Glu Leu Cys Thr Leu Met Glu Ser Thr Gly Thr Met Ile Arg
      20           25           30
Leu Asn Pro Glu Phe His Pro Asn Cys Phe Leu Val Arg Ser Ser Ala
      35           40           45
Asp Asp Val Ala Arg Val Glu Gln Phe Thr Phe Ile Cys Thr Ser Thr
      50           55           60
Glu Ala Glu Ala Gly Pro Thr Asn Asn Trp Arg Asp Pro Gln Glu Met
      65           70           75           80
Arg Arg Glu Leu His Gln Leu Phe Arg Gly Cys Met Gln Gly Arg Thr
      85           90           95
Leu Tyr Ile Val Pro Phe Cys Met Gly Pro Leu Asp Ser Pro Phe Ser
      100          105          110

```



```

Ile Val Gly Val Glu Leu Thr Asp Ser Pro Tyr Val Val Cys Ser Met
115 120 125
Lys Ile Met Thr Arg Met Gly Asp Asp Val Leu Arg Ser Leu Gly Thr
130 135 140
Ser Gly Lys Phe Leu Lys Cys Leu His Ser Val Gly Lys Pro Leu Ser
145 150 155 160
Pro Gly Glu Ala Asp Val Ser Trp Pro Cys Asn Pro Lys Ser Met Arg
165 170 175
Ile Val His Phe Gln Asp Asp Ser Ser Val Met Ser Phe Gly Ser Gly
180 185 190
Tyr Gly Gly Asn Ala Leu Leu Gly Lys Lys Cys Val Ala Leu Arg Leu
195 200 205
Ala Ser Tyr Met Ala Lys Ser Gln Gly Trp Leu Ala Glu His Met Leu
210 215 220
Ile Ile Gly Ile Thr Asn Pro Glu Gly Lys Lys Tyr Phe Ser Ala
225 230 235 240
Ser Phe Pro Ser Ala Cys Gly Lys Thr Asn Leu Ala Met Leu Met Pro
245 250 255
Lys Leu Pro Gly Trp Lys Ile Glu Cys Ile Gly Asp Asp Ile Ala Trp
260 265 270
Ile Arg Pro Gly Arg Asp Gly Arg Leu Tyr Ala Val Asn Pro Glu Tyr
275 280 285
Gly Phe Phe Gly Val Ala Pro Gly Thr Ser Glu Arg Thr Asn Pro Asn
290 295 300
Ala Leu Ala Thr Cys Arg Ser Asn Ser Ile Phe Thr Asn Val Ala Leu
305 310 315 320
Thr Ala Asp Gly Asp Val Trp Trp Glu Gly Leu Thr Glu Gln Pro Pro
325 330 335
Glu Pro Leu Thr Asp Trp Leu Gly Lys Pro Trp Lys Pro Gly Gly Ser
340 345 350
Pro Ala Ala His Pro Asn Ser Arg Phe Thr Ala Pro Leu Arg Gln Cys
355 360 365
Pro Ser Leu Asp Pro Glu Trp Asn Ser Pro Gln Gly Val Pro Leu Asp
370 375 380
Ala Ile Ile Phe Gly Gly Arg Arg Ser Glu Thr Ile Pro Leu Val Tyr
385 390 395 400
Glu Ala Leu Ser Trp Glu His Gly Val Thr Ile Gly Ala Gly Met Ser
405 410 415
Ser Thr Thr Thr Ala Ala Ile Val Gly Gln Leu Gly Lys Leu Arg His
420 425 430
Asp Pro Phe Ala Met Leu Pro Phe Cys Gly Tyr Asn Met Ala Tyr Tyr
435 440 445
Phe Gln His Trp Leu Ser Phe Ala Glu Asn Arg Ser Leu Lys Leu Pro
450 455 460
Lys Ile Phe Gly Val Asn Trp Phe Arg Lys Asn Asn Gln Gly Glu Phe
465 470 475 480
Leu Trp Pro Gly Phe Ser Glu Asn Leu Arg Val Leu Glu Trp Ile Phe
485 490 495
Gln Arg Thr Asp Gly Leu Glu Asp Ile Ala Glu Arg Thr Pro Ile Gly
500 505 510
Tyr Leu Pro Asn Ile Gln Lys Phe Asn Leu Asn Gly Leu Asn Leu Asp
515 520 525
Leu Gln Thr Val Gln Glu Leu Phe Ser Val Asp Ala Glu Gly Trp Leu
530 535 540
Ala Glu Val Glu Asn Ile Gly Glu Tyr Leu Lys Ile Phe Gly Ser Asp
545 550 555 560
Cys Pro Gln Gln Ile Thr Asp Glu Leu Leu Arg Ile Lys Ser Glu Leu
565 570 575
Lys Glu Lys

```

&lt;210&gt;919

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;919

Arg Lys Gly Ala Val Asn Arg Glu Phe Gly Trp Ala Ala Gly Leu Pro  
 1 5 10 15  
 Pro Gly Phe Gln Gly Phe Pro Ser Gln Ser Val Lys Gly Ser Gly Gly  
 20 25 30  
 Cys Ser Val Asn Pro Ser His Gln Thr Ser Pro Ser Ala Val Lys Ala  
 35 40 45  
 Thr Phe Val Lys Ile Glu Phe Asp Leu Gln Val Ala Lys Ala Leu Gly  
 50 55 60  
 Phe Val Arg Ser Glu Val Pro Gly Ala Thr Pro Lys Asn Pro Tyr Ser  
 65 70 75 80  
 Gly Phe Thr Ala Tyr Asn Leu Pro Ser Arg Pro Gly Arg Ile Gln Ala  
 85 90 95  
 Ile Ser Ser Pro Ile His Ser Ile Phe Gln Pro Gly Ser Leu Gly Ile  
 100 105 110  
 Asn Ile Ala Lys Phe Val Leu Pro Gln Ala Leu Gly Asn Glu Ala Glu  
 115 120 125  
 Lys Tyr Phe Phe Phe Pro Ser Gly Leu Val Ile Pro Ile Ile Asn Met  
 130 135 140  
 Cys Ser Ala Ser Gln Pro  
 145 150

&lt;210&gt;920

&lt;211&gt;780

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;920

Ile Lys Leu Arg Ile Ile Asp Tyr Tyr Tyr Leu Ile Asn Thr Val Thr  
 1 5 10 15  
 Leu Gln Pro Ser Tyr Ile Asn Phe Thr Pro Asn Val Thr Thr Ala Leu  
 20 25 30  
 Ser Gly Gly Lys Ile Asp Thr Ser Ala Ile Glu Leu Ser Cys Ser Ala  
 35 40 45  
 Leu Phe Phe Gln Glu Leu Gln Asp Lys Ala Gln Gly Leu Lys His Ala  
 50 55 60  
 Leu Gly Leu Val Gln Glu Leu Ser Ala Glu Ala Leu Arg Pro Ala Gln  
 65 70 75 80  
 Val Gln Thr Ser Ile Ser Tyr Leu Pro Thr Glu Glu Ser Ser Arg Pro  
 85 90 95  
 Gly Ile Ser Ala Gly Ile Ile Asp Arg Thr Met Pro Thr Phe Thr Asp  
 100 105 110  
 Asp Glu Val Lys Ala Ile Leu Gln Asn Pro Asn Phe Glu Thr Ser Lys  
 115 120 125  
 Ile Phe Val Glu Gly Leu Asp Lys Val Phe Lys Ser Tyr Leu Asp Ser  
 130 135 140  
 Val Thr Pro Pro Glu Gly Ile Asp Pro Ser Asn Pro Glu Ser Ala Ile  
 145 150 155 160  
 Ile Leu Asn Tyr Ile Thr Leu Leu Asn Asn Leu Lys Pro Lys Phe Ala  
 165 170 175  
 Ala Gly Ser Thr Pro Thr Asp Ala Asp Tyr Asn Ala Leu Tyr Ala Leu  
 180 185 190  
 Pro Gly Asp Phe Val Lys Glu Ile Glu Ala Leu Lys Ala Ala Asp Ala  
 195 200 205  
 Pro Pro Lys Ser Lys Val His Ala Phe Trp Gln Glu Ile Met Thr Ile  
 210 215 220  
 Tyr Asn Asn Met Gln Val Leu Ser Tyr Pro Val Thr Asp Tyr Leu Asn  
 225 230 235 240  
 Val Gln Ile Ala Asp Leu Ser Leu Asn Ile Thr Ala Ala Gln Glu Val  
 245 250 255  
 Gln Gln Tyr Leu Lys Asn Phe Tyr Ser Ile Leu Lys Asp Ile Leu Asn  
 260 265 270  
 Pro Gly Trp Thr Asp Pro Gln Ala Thr His Tyr Pro Ala Asp Ala Glu  
 275 280 285  
 Tyr Asn Ala Arg Asp Ala Gly Val Ile Gln Ser Leu Leu Asn Leu Ser  
 290 295 300

Gly Asn Tyr Arg Gln Leu Thr Glu Asn Met Leu Pro Asn Thr Asp Thr  
 305 310 315 320  
 Ser Leu Pro Gln Glu Ile Ile Ala Gln Ile Arg Ser Phe Gln Asn Gly  
 325 330 335  
 Val Asn Gly Thr Ile Ile Ala Ser Asn Thr Leu Leu Pro Thr Thr Met  
 340 345 350  
 Arg Leu Asp Thr Leu Leu Gly Val Ile Tyr Thr Tyr Gln Cys Cys Ala  
 355 360 365  
 Thr Ile Phe Gly Met Ser Tyr Gly Thr Ser Thr Pro Ala Lys Gln Asn  
 370 375 380  
 Tyr Ile Asp Ala Ile Asn Gln Glu Lys Ser Tyr Trp Gln Ala Arg Ala  
 385 390 395 400  
 Asn Gly Phe Asp Val Thr Ser Asp Gln Val Phe Asp Gln Phe Ala Thr  
 405 410 415  
 Asn Ile Gln Ser Gly Thr Ser Tyr Arg Gly Ile Asp Leu Phe Lys Asn  
 420 425 430  
 Asn Lys Val Asn Glu Ile Asn Pro Ile Phe Leu Ser Gln Ala Ala Ser  
 435 440 445  
 Phe Leu Arg Tyr Pro Tyr Asn Leu Met Ser Arg Ser Met Tyr Gln Thr  
 450 455 460  
 Ile Glu Asp Ala Ala Asn Arg Ser Ile Thr Ala Leu Asp Gly Leu Ile  
 465 470 475 480  
 Ser Gly Trp Ser Thr Gln Ile Ala Thr Phe Gln Thr Gln Lys Asn Ser  
 485 490 495  
 Leu Asp Pro Ser Leu Leu Lys Tyr Phe Asp Thr Met Lys Ala Asn Lys  
 500 505 510  
 Glu Ser Phe Val Thr Thr Ala Pro Leu Gln Met Val Tyr Ser Ser Leu  
 515 520 525  
 Met Leu Asp Lys Tyr Leu Pro Thr Gln Gln Asn Val Ile Ala Ser Leu  
 530 535 540  
 Gly Ile Gln Met Thr Tyr Ser Asn Lys Ala Ala Lys Tyr Leu Asn Glu  
 545 550 555 560  
 Leu Ile Lys Glu Ile Thr Thr Phe Gln Ser Ala Asp Ile Tyr Tyr Ser  
 565 570 575  
 Leu Ser Ile Tyr Leu Lys Gln Met Asn Leu Gln Ala Val Ala Asp Pro  
 580 585 590  
 Ile Gly Lys Ala Val Gly Val Leu Asn Asp Glu Lys Thr Arg Ala Met  
 595 600 605  
 Ala Asp Ile Thr Arg Cys Asn Lys Ile Lys Ala Ala Ile Asp Lys Met  
 610 615 620  
 Leu Val Glu Ile Lys Ala Asp Ala Glu Leu Ser Lys Ser Gln Ile Arg  
 625 630 635 640  
 Glu Leu Val Asp Thr Leu Thr Asn Phe Lys Ser Gln Ser Asp Asp Leu  
 645 650 655  
 Ile Arg Asn Leu Ser Cys Leu Leu Gly Phe Leu Ser Gly Leu Thr Leu  
 660 665 670  
 Lys Ala Val Asn Asp Pro Asn Ala Thr Tyr Glu Ala Phe Thr Ala Glu  
 675 680 685  
 Ile Phe Thr Glu Pro Phe Asn Asn Trp Lys Arg Gln Leu Ala Thr Phe  
 690 695 700  
 Glu Ser Phe Val Ile Gln Gly Gly Gln Asn Gly Ile Thr Pro Gly Gly  
 705 710 715 720  
 Gln Gln Gln Leu Leu Gln Ala Met Glu Ser Ser Gln Gln Asp Phe Ser  
 725 730 735  
 Thr Phe Asn Gln Asn Gln Gln Leu Ala Leu Gln Leu Glu Ser Ser Ala  
 740 745 750  
 Met Gln Gln Glu Trp Thr Leu Val Ser Ala Ala Leu Ala Leu Leu Asn  
 755 760 765  
 Gln Met Val Ser Lys Ile Ala Arg Arg Ile Lys Ser  
 770 775 780  
 <210>921  
 <211>391  
 <212>PRT  
 <213>Chlamydia pneumoniae

&lt;400&gt;921

```

Asn Ile Met His Pro Lys Ile Glu Lys Arg Asn Ser Leu Pro Leu Thr
 1           5           10           15
Ala Val Ala Pro Val Phe Glu Glu Ser Tyr His Pro Ser Val Ala Thr
          20           25           30
Thr Val Asp Tyr Val Asp Ala Thr Thr Leu Ser Arg His Leu Thr Val
          35           40           45
Leu Lys Asp Val Ile Lys Glu Ala Arg Asn Leu Asp Leu Gly Lys Ala
          50           55           60
Phe Leu Thr Ser Met Lys Gln Gly Phe Ile Asn Thr Gly Thr Glu Leu
          65           70           75           80
Ala Ile Ile Gln Ala Ser Leu Ala Asp Gln Ser Ser Arg Glu Ser Arg
          85           90           95
Lys Lys Glu Glu Lys Ile Phe His Gln His Leu Gly Lys Ala Ala Pro
          100          105          110
Gln Ala Ala Thr Ala Thr Ser Gly Val Gln Pro Thr Ala Asp Pro Val
          115          120          125
Ala Asp Lys Met Pro Leu Gln Ser Ala Phe Ala Tyr Val Leu Leu Asp
          130          135          140
Lys Tyr Ile Pro Ala Gln Glu Glu Ala Leu Tyr Ala Leu Gly Arg Glu
          145          150          155          160
Leu Asn Leu Ser Gly Tyr Ala Gln Asn Leu Phe Ser Pro Leu Leu Asp
          165          170          175
Met Ile Lys Ser Phe Asn Ser Ala Pro Ile Asn Tyr Asn Leu Gly Ser
          180          185          190
Tyr Ile Ser Gln Thr Ser Gly Thr Ala Asn Phe Ala Tyr Gly Tyr Glu
          195          200          205
Met Ile Leu Ser Arg Tyr Asn Asn Glu Val Ser Gln Cys Arg Leu Asp
          210          215          220
Ile Ala Ser Thr Val Lys Ala Lys Ala Ala Leu Ala Asn Met Ser Ala
          225          230          235          240
Ser Val Lys Ala Asn Val Ser Leu Thr Asp Ala Gln Lys Lys Gln Ile
          245          250          255
Glu Asp Ile Ile Ala Ser Tyr Thr Lys Ser Leu Asp Val Ile His Thr
          260          265          270
Gln Leu Thr Asp Val Met Thr Asn Leu Ala Ser Ile Thr Phe Val Pro
          275          280          285
Gly Leu Asn Lys Tyr Asp Pro Ser Tyr Arg Ile Val Gly Gly Asp Leu
          290          295          300
Ser Ile Ile Ala Leu Gln Asn Asp Glu Lys Val Leu Val Asp Gly Lys
          305          310          315          320
Val Asp Ile Thr Thr Ala Val Asn Glu Gly Gly Leu Leu Asn Phe Phe
          325          330          335
Thr Thr Val Leu Thr Asp Val Gln Asn Tyr Gly Asp Leu Ala Gln Thr
          340          345          350
Gln Gln Leu Met Leu Asp Leu Glu Leu Lys Ala Met Gln Gln Gln Trp
          355          360          365
Ser Leu Val Ser Ala Ser Leu Lys Leu Leu Asn Gly Met Tyr Thr Thr
          370          375          380
Val Ile Ser Gly Phe Lys Asn
          385          390

```

&lt;210&gt;922

&lt;211&gt;348

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;922

```

Gly Pro Phe Asp Met Asn Ser Lys Met Leu Lys His Leu Arg Leu Ala
 1           5           10           15
Thr Leu Ser Phe Ser Met Phe Phe Gly Ile Val Ser Ser Pro Ala Val
          20           25           30
Tyr Ala Leu Gly Ala Gly Asn Pro Ala Ala Pro Val Leu Pro Gly Val
          35           40           45
Asn Pro Glu Gln Thr Gly Trp Cys Ala Phe Gln Leu Cys Asn Ser Tyr
          50           55           60

```

Asp Leu Phe Ala Ala Leu Ala Gly Ser Leu Lys Phe Gly Phe Tyr Gly  
 65 70 75 80  
 Asp Tyr Val Phe Ser Glu Ser Ala His Ile Thr Asn Val Pro Val Ile  
 85 90 95  
 Thr Ser Val Thr Thr Ser Gly Thr Gly Thr Thr Pro Thr Ile Thr Ser  
 100 105 110  
 Thr Thr Lys Asn Val Asp Phe Asp Leu Asn Asn Ser Ser Ile Ser Ser  
 115 120 125  
 Ser Cys Val Phe Ala Thr Ile Ala Leu Gln Glu Thr Ser Pro Ala Ala  
 130 135 140  
 Ile Pro Leu Leu Asp Ile Ala Phe Thr Ala Arg Val Gly Gly Leu Lys  
 145 150 155 160  
 Gln Tyr Tyr Arg Leu Pro Leu Asn Ala Tyr Arg Asp Phe Thr Ser Asn  
 165 170 175  
 Pro Leu Asn Ala Glu Ser Glu Val Thr Asp Gly Leu Ile Glu Val Gln  
 180 185 190  
 Ser Asp Tyr Gly Ile Val Trp Gly Leu Ser Leu Gln Lys Val Leu Trp  
 195 200 205  
 Lys Asp Gly Val Ser Phe Val Gly Val Ser Ala Asp Tyr Arg His Gly  
 210 215 220  
 Ser Ser Pro Ile Asn Tyr Ile Ile Val Tyr Asn Lys Ala Asn Pro Glu  
 225 230 235 240  
 Ile Tyr Phe Asp Ala Thr Asp Gly Asn Leu Ser Tyr Lys Glu Trp Ser  
 245 250 255  
 Ala Ser Ile Gly Ile Ser Thr Tyr Leu Asn Asp Tyr Val Leu Pro Tyr  
 260 265 270  
 Ala Ser Val Ser Ile Gly Asn Thr Ser Arg Lys Ala Pro Ser Asp Ser  
 275 280 285  
 Phe Thr Glu Leu Glu Lys Gln Phe Thr Asn Phe Lys Phe Lys Ile Arg  
 290 295 300  
 Lys Ile Thr Asn Phe Asp Arg Val Asn Phe Cys Phe Gly Thr Thr Cys  
 305 310 315 320  
 Cys Ile Ser Asn Asn Phe Tyr Tyr Ser Val Glu Gly Arg Trp Gly Tyr  
 325 330 335  
 Gln Arg Ala Ile Asn Ile Thr Ser Gly Leu Gln Phe  
 340 345

&lt;210&gt;923

&lt;211&gt;334

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;923

Met Lys Gln His Ile Gly Tyr Leu Gly Met Gly Ile Trp Gly Phe Cys  
 1 5 10 15  
 Leu Ala Ser Leu Leu Ala Asn Lys Gly Tyr Pro Val Val Ala Trp Ser  
 20 25 30  
 Arg Asn Pro Asp Leu Ile Lys Gln Leu Gln Glu Glu Arg Arg His Pro  
 35 40 45  
 Leu Ala Pro Asn Val Val Ile Ser Pro Asn Leu Ser Phe Thr Thr Asp  
 50 55 60  
 Met Lys Glu Ala Ile His Asn Ala Phe Met Ile Val Glu Gly Val Thr  
 65 70 75 80  
 Ser Ala Gly Ile Arg Pro Val Ala Glu Gln Leu Lys Gln Ile Thr Asp  
 85 90 95  
 Leu Ser Val Pro Phe Val Ile Thr Ser Lys Gly Ile Glu Gln Asn Thr  
 100 105 110  
 Gly Leu Leu Leu Ser Glu Ile Met Leu Glu Val Leu Gly Asp Ser Val  
 115 120 125  
 Thr Pro Tyr Leu Gly Tyr Leu Ser Gly Pro Ser Ile Ala Lys Glu Val  
 130 135 140  
 Leu Asn Gly Ser Pro Cys Ser Val Val Val Ser Ala Tyr Asp Ser Gln  
 145 150 155 160  
 Thr Leu Lys Gln Ile His Glu Ala Phe Ser Leu Pro Thr Phe Arg Val  
 165 170 175  
 Tyr Pro Asn Thr Asp Ile Lys Gly Ala Ala Leu Gly Gly Ala Leu Lys

```

      180      185      190
Asn Val Ile Ala Ile Ala Cys Gly Ile Ala Glu Gly Leu Ser Phe Gly
      195      200      205
Asn Asn Ala Lys Ala Gly Leu Val Thr Arg Gly Leu His Glu Met Arg
      210      215      220
Lys Leu Ala Ala Ile Met Asp Cys Lys Pro Glu Thr Leu Asn Gly Leu
      225      230      235
Ala Gly Leu Gly Asp Leu Cys Val Thr Cys Phe Ser Glu Ser Ser Arg
      245      250      255
Asn Leu Arg Phe Gly His Leu Leu Ala Gln Gly Leu Thr Phe Glu Gln
      260      265      270
Ala Lys Ala Lys Ile Gly Met Val Val Glu Gly Ala Tyr Thr Ala Leu
      275      280      285
Ser Ala Tyr Gln Val Ala Lys His His Lys Ile Asp Met Pro Ile Thr
      290      295      300
Thr Gly Ile Tyr Arg Val Leu Tyr Glu Asn Leu Asp Leu Lys Glu Gly
      305      310      315      320
Ile Ala Leu Leu Leu Gln Arg Asn Thr Lys Glu Glu Phe Leu
      325      330

<210>924
<211>461
<212>PRT
<213>Chlamydia pneumoniae
<400>924
Met Thr Glu Ser Val Tyr Ser Pro Ser Ala Met His Val Asn Ser Leu
  1      5      10      15
Ala Asp Lys Leu Lys Ala Ile Asn Gln Glu His Ile Leu Asp Ile Trp
      20      25      30
Pro Ser Leu Ser Pro Lys Gln Gln Gln Arg Leu Phe Gln Gln Leu Thr
      35      40      45
Ser Val Asp Ile Asp Phe Phe Arg Lys Gln Gln Gln Leu Leu Ser Ser
      50      55      60
Pro Thr Ala Ile Leu Lys Asp Phe His Pro Ile Thr Ser Phe Ala Ser
      65      70      75      80
Ser Gly Glu Asp Pro Glu Arg Ala His Ala Gly Thr Thr Leu Leu Lys
      85      90      95
Glu Lys Lys Val Ala Cys Val Val Leu Ala Gly Gly Gln Gly Ser Arg
      100      105      110
Leu Lys Cys Asp Gly Pro Lys Gly Leu Phe Pro Val Ser Pro Ile Lys
      115      120      125
Lys Lys Pro Leu Phe Gln Leu Val Ala Glu Lys Val Arg Ala Ala Ser
      130      135      140
Lys Leu Ala Gly Gln Pro Leu Pro Leu Ala Phe Met Thr Ser Pro Leu
      145      150      155      160
Asn Thr Arg Gln Thr Arg Ser Phe Phe Glu Ser Asn Asp Tyr Phe His
      165      170      175
Leu Asp Pro Asn Gln Val Asp Phe Phe Cys Gln Pro Leu Trp Pro Leu
      180      185      190
Leu Thr Leu Ser Gly Asp Leu Phe Leu Glu Asp Met Asp Thr Leu Ala
      195      200      205
Leu Gly Pro Asn Gly Asn Gly Cys Ile Ala Thr Leu Leu Tyr Thr Ser
      210      215      220
Gly Val Trp Glu Lys Trp Lys Asn Ala Gly Ile Glu Met Val Ser Val
      225      230      235      240
Ile Pro Ile Asp Asn Pro Leu Ala Leu Pro Phe Asp Val Glu Leu Cys
      245      250      255
Gly Phe His Ala Met Ser Asn Asn Glu Val Thr Ile Lys Ala Ala Leu
      260      265      270
Arg Gln Thr Ala Ile Glu Asp Val Gly Ile Leu Val Lys Ser His Asp
      275      280      285
Ser Gly Lys Thr Ser Val Ile Glu Tyr Ser Glu Ile Pro Gln Asn Glu
      290      295      300
Arg Phe Ala Leu Asn Glu Asp Gly Lys Leu Lys Tyr Cys Leu Ala Asn
      305      310      315      320

```

Ile Gly Leu Tyr Cys Leu Ser Met Asp Phe Ile Arg His Ala Ala Tyr  
 325 330 335  
 Gln Gln Leu Pro Leu Tyr Lys Val His Lys His Ala Lys Gln Leu Gly  
 340 345 350  
 His Thr Ser Leu Asn Glu Lys Asn Ala Trp Lys Phe Glu Glu Phe Ile  
 355 360 365  
 Phe Asp Leu Phe Cys Tyr Ser Asp His Cys Gln Thr Leu Val Tyr Pro  
 370 375 380  
 Arg Gln Glu Cys Phe Ala Pro Leu Lys Asn Leu Glu Gly Asn His Ser  
 385 390 395 400  
 Pro Asp Thr Val Arg Gln Ala Leu Ser Asp Arg Glu Arg Gln Leu Phe  
 405 410 415  
 His Lys Val Thr Gly Lys Lys Leu Ser Pro Asn Thr Thr Phe Glu Leu  
 420 425 430  
 Glu Ala Asp Phe Tyr Tyr Pro Ser Thr Ser Thr Ser Leu His Trp Glu  
 435 440 445  
 Asn Lys Ala Phe Phe Glu Glu Pro Phe Phe Glu Ala Ser  
 450 455 460  
 <210>925  
 <211>433  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>925  
 Met Asn His Leu Asn Lys Glu Lys Leu His Ile His Asn Trp Gln Pro  
 1 5 10 15  
 Tyr Arg Ala Cys Gly Leu Leu Ser Lys Val Ser Gly Asn Leu Ile Glu  
 20 25 30  
 Val Asp Gly Leu Ser Ala Cys Leu Gly Glu Leu Cys Lys Ile Ser Ser  
 35 40 45  
 Thr Lys Asp Pro Asn Leu Leu Ala Glu Val Ile Gly Phe His Asn His  
 50 55 60  
 Thr Thr Leu Leu Met Ser Leu Ser Pro Leu His Ser Val Ala Leu Gly  
 65 70 75 80  
 Thr Glu Val Leu Pro Leu Arg Arg Pro Pro Ser Leu His Leu Ser Asp  
 85 90 95  
 His Leu Leu Gly Arg Val Leu Asp Ala Phe Gly Asn Pro Ile Asp Lys  
 100 105 110  
 Lys Glu Asp Leu Pro Lys Thr His Arg Lys Pro Leu Leu Ser Leu Pro  
 115 120 125  
 Pro Ser Pro Met Met Arg Gln Pro Ile Asp Gln Ile Phe Pro Thr Gly  
 130 135 140  
 Ile Lys Ala Ile Asp Ala Phe Leu Thr Leu Gly Lys Gly Gln Arg Ile  
 145 150 155 160  
 Gly Val Phe Ser Glu Pro Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala  
 165 170 175  
 Ile Ala Leu Gly Ser Lys Ser Thr Ile Asn Val Ile Ala Leu Ile Gly  
 180 185 190  
 Glu Arg Gly Arg Glu Val Arg Glu His Ile Glu Lys His Ser Asn Ala  
 195 200 205  
 Leu Lys Gln Gln Arg Thr Ile Ile Ile Ala Ala Pro Ala His Glu Thr  
 210 215 220  
 Ala Pro Thr Lys Val Ile Ala Gly Arg Ala Ala Met Thr Ile Ala Glu  
 225 230 235 240  
 Tyr Phe Arg Glu Gln Gly His Glu Val Leu Phe Ile Met Asp Ser Leu  
 245 250 255  
 Ser Arg Trp Ile Ala Ala Leu Gln Glu Val Ala Leu Ala Arg Gly Glu  
 260 265 270  
 Thr Leu Ser Ala His Gln Tyr Ala Ala Ser Val Phe His His Val Ser  
 275 280 285  
 Glu Phe Thr Glu Arg Ala Gly Asn Asn Asp Lys Gly Ser Ile Thr Ala  
 290 295 300  
 Leu Tyr Ala Ile Leu Tyr Tyr Pro Lys His Pro Asp Ile Phe Thr Asp  
 305 310 315 320  
 Tyr Leu Lys Ser Leu Leu Asp Gly His Phe Phe Leu Thr Ser Gln Gly

325 330 335  
 Lys Ala Leu Ala Ser Pro Pro Ile Asp Ile Leu Ser Ser Leu Ser Arg  
 340 345 350  
 Ser Ala Gln Ala Leu Ala Leu Pro His His Tyr Ala Ala Ala Glu Arg  
 355 360 365  
 Leu Arg Ser Leu Leu Lys Val Tyr Asn Glu Ala Leu Asp Ile Ile His  
 370 375 380  
 Leu Gly Ala Tyr Thr Pro Gly Gln Asp Glu Glu Leu Asp Lys Ala Val  
 385 390 395 400  
 Lys Leu Leu Pro Ser Ile Lys Ala Phe Leu Ala Gln Pro Leu Ser Ser  
 405 410 415  
 Tyr Cys Tyr Leu Asp Asn Thr Leu Lys Gln Leu Glu Ala Leu Ala Asp  
 420 425 430  
 Ser

&lt;210&gt;926

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;926

Met Ile His Ala Val Lys Thr Glu Ser Arg Trp Ser Ser Ser Ser Leu  
 1 5 10 15  
 Ile Ser Cys Leu Arg Ile Pro Leu Gly Val Ser Ile Leu Asn Pro Asp  
 20 25 30  
 Arg Leu Gln Glu Val Ser Gly Lys Asn Ser Ala Cys Leu Ile Met Gly  
 35 40 45  
 Ser Ser Trp Val Glu Ile Gln Ser Val Ser Val Leu Arg Ser Ser Gly  
 50 55 60  
 Trp Arg Asn Thr Leu Met Gly Val Arg Asp Leu Asn Val Val Cys Leu  
 65 70 75 80  
 Trp Ser Ala Val Glu Arg Ser Arg Ala Ser Ser  
 85 90

&lt;210&gt;927

&lt;211&gt;266

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;927

Met Thr Leu Pro Leu Glu Pro Met Ile Phe Trp Ser Ser Leu Ser Ala  
 1 5 10 15  
 Lys Val Met Lys Lys Phe Leu Thr Pro His Cys Ala Gly Thr Phe Ser  
 20 25 30  
 Glu Glu Asp Ala Glu Ala Lys Glu Ala His Leu Val Thr Gly Lys Gln  
 35 40 45  
 Gly His Arg Leu Met Gly Asn Cys Val Thr Phe Tyr Trp Leu Val Asp  
 50 55 60  
 Lys Lys Asn Gly Val Ile Leu Asp Ala Lys Phe Gln Tyr Phe Gly His  
 65 70 75 80  
 Pro Tyr Leu Ile Pro Leu Ala Glu Ala Val Cys Asn Leu Val Cys Gly  
 85 90 95  
 Lys Ser Tyr Ser Glu Ala Tyr Lys Met Thr Leu Asp Asp Ile Asp Lys  
 100 105 110  
 Ser Leu Arg Val His Ala His Gln Pro Ala Leu Pro Glu Asp Ser Ile  
 115 120 125  
 Ser Leu Tyr His Phe Val Ile Asp Ala Leu Asp Thr Ala Val Glu Gln  
 130 135 140  
 Cys Leu Glu Ile Pro Leu Glu Asp Gly Ser Leu Pro Leu Gln Asn Ser  
 145 150 155 160  
 Pro Met Asn Leu Asp Phe Glu Asp Ala Asn Pro Tyr Ser Gln Ser Asp  
 165 170 175  
 Trp Glu Ala Leu Thr His Glu Gln Lys Leu Tyr Ala Leu Arg Ala Thr  
 180 185 190  
 Ile Ala Glu Lys Ile Gly Pro Tyr Ile Ala Met Asp Gly Gly Glu Val  
 195 200 205  
 Thr Val Glu Ser Leu Glu Asn Phe Ile Val Thr Ile Ala Tyr Ser Gly



210 215 220  
 Asn Cys Ser Gly Cys Pro Ser Ser Leu Gly Ser Thr Leu Asn Ser Ile  
 225 230 235 240  
 Gly Gln Leu Leu Arg Ala Tyr Ile Tyr Pro Glu Leu Gln Val Lys Val  
 245 250 255  
 Asp Glu Ser Ser Leu Asn Leu Ser His Pro  
 260 265  
 <210>928  
 <211>401  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>928  
 Gly Arg Gly Thr Ile Phe Arg Ile Thr Asp Gly Lys Thr Ser Cys Ile  
 1 5 10 15  
 Ser Met Glu Lys Pro Gln Asn Arg Lys Ala Pro Arg Ile Phe Trp Leu  
 20 25 30  
 Asn Asn Gln Val Ala Ile Pro Pro Ser Glu Arg Val Lys Glu Ser Tyr  
 35 40 45  
 Ala Leu His Ser Asp Ile Phe Ser Leu Pro Pro Gly Ser Ala Leu Lys  
 50 55 60  
 Leu Ala Glu Lys Thr Glu Glu Ser Ile Arg Gln Leu Val Gly Leu Lys  
 65 70 75 80  
 Asp Ser His Ile Phe Arg Phe Val Pro His Phe Pro His Val Val His  
 85 90 95  
 Ile Val Leu Ala Ala Leu Val Glu Asn Leu Ser Met Phe Gln Gly Arg  
 100 105 110  
 Asn His Ile Ile Leu Pro Ala His Asp Gln Gln Leu Leu Ile Asn Ser  
 115 120 125  
 Leu Cys Arg His Gln Gly Leu Gly Thr Thr Tyr Asp Trp Val Thr Val  
 130 135 140  
 Asn His Glu Gly Arg Ile Val Glu Glu Gln Leu Ile Glu Thr Leu Ser  
 145 150 155 160  
 Pro Arg Ser Leu Leu Phe Ser Leu Ser Ala Ala His Gly Leu Thr Gly  
 165 170 175  
 Val Ile Gln Pro Leu Asp Pro Leu Leu Ser Leu Cys Lys Asp Arg Arg  
 180 185 190  
 Ile Leu Leu His Leu Asp Ile Ser Asp Ile Leu Gly Arg Ala Pro Leu  
 195 200 205  
 Thr Pro Glu Ile Leu Asn Ala Asp Ile Ile Thr Phe Ser Ser Ala Ala  
 210 215 220  
 Leu Gly Gly Met Gly Ser Ile Gly Gly Ile Phe Ile Arg Lys Ser Leu  
 225 230 235 240  
 Glu Arg Val Phe Ser Ser Trp Phe Pro Pro His Thr Ser Ala Ser Leu  
 245 250 255  
 Cys Phe Ser Ala Val Ala Ala Met Gln Thr Ala Cys Glu Glu Arg Ile  
 260 265 270  
 Ser Ala Leu Pro Leu Phe Thr Phe His Thr Ser Asn Leu Cys Lys Lys  
 275 280 285  
 Leu Ile Gln Glu Leu Gln Ser Val Leu Pro Ser Ile Gln Leu Ala Phe  
 290 295 300  
 Ser Glu Val Gln Asn Arg Leu Pro Asn Ile Val Val Ala Ala Ile Pro  
 305 310 315 320  
 Asp Ile Pro Ala Glu Ser Leu Ala Phe His Leu His Gln Gln Gly Ile  
 325 330 335  
 Tyr Pro Ser Leu Gly Tyr Glu Arg Phe Gln Pro Leu Ala Gln Val Leu  
 340 345 350  
 Gln Asn Cys Gly Ile Ser Pro Phe Leu Cys His Ser Ala Leu His Phe  
 355 360 365  
 Ser Leu Thr Glu Arg Ser Lys Asp Leu Glu Phe Ser Lys Leu Ala Arg  
 370 375 380  
 Ala Met His Asp Ala Ile Lys His Leu Thr Pro Leu Leu Gly Ser Ser  
 385 390 395 400  
 Ser

&lt;210&gt;929

&lt;211&gt;228

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;929

```

Met Ala Leu Leu Ile Leu Leu Arg His Gly Gln Ser Val Trp Asn Glu
 1          5          10          15
Lys Asn Leu Phe Ser Gly Trp Val Asp Ile Pro Leu Ser Gln Gln Gly
          20          25          30
Ile Glu Glu Ala Phe Ser Ala Gly Arg Ala Ile Gln Asn Leu Pro Ile
          35          40          45
Asp Cys Ile Phe Thr Ser Thr Leu Val Arg Ser Leu Met Thr Ala Leu
          50          55          60
Leu Ala Met Thr Asn His Ser Lys Lys Ile Pro Tyr Ile Val His
65          70          75          80
Glu Asp Pro Lys Ala Lys Glu Met Ser Arg Ile Tyr Ser Ala Glu Glu
          85          90          95
Glu Asn Asn Met Ile Pro Leu Tyr Gln Ser Ser Ala Leu Asn Glu Arg
          100          105          110
Met Tyr Gly Glu Leu Gln Gly Lys Asn Lys Lys Gln Thr Ala Glu Gln
          115          120          125
Phe Gly Glu Glu Arg Val Lys Leu Trp Arg Arg Ser Tyr Lys Thr Ala
130          135          140
Pro Pro Gln Gly Glu Ser Leu Tyr Asp Thr Lys Gln Arg Thr Leu Pro
145          150          155          160
Tyr Phe Glu Lys Asn Ile Leu Pro Gln Leu Gln Asn Gly Lys Asn Val
          165          170          175
Phe Val Ser Ala His Gly Asn Ser Leu Arg Ser Leu Ile Met Asp Leu
          180          185          190
Glu Lys Leu Ser Glu Glu Glu Val Leu Ser Leu Glu Leu Pro Thr Gly
          195          200          205
Lys Pro Val Val Tyr Gln Trp Lys Asn His Lys Ile Glu Lys His Pro
210          215          220
Glu Phe Phe Gly
225

```

&lt;210&gt;930

&lt;211&gt;235

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;930

```

Val Thr Lys Val Arg Leu Asn Lys Phe Leu Ala Ser Ala Gly Val Ala
 1          5          10          15
Ser Arg Arg Lys Cys Asp Glu Ile Ile Phe Ser Gly Ser Val Thr Val
          20          25          30
Asn Gly Arg Val Ala Glu Gly Pro Phe Val Leu Val Asp Pro Glu Asp
          35          40          45
Lys Val Gln Val Gly Gly Thr Ser Val His Leu Thr Lys Lys Val Tyr
          50          55          60
Phe Met Val His Lys Ala Ile Gly Tyr Leu Cys Ser Ser Glu Lys Lys
65          70          75          80
Phe Pro Gly Thr Lys Leu Val Ile Asp Leu Phe Ala His Leu Pro Tyr
          85          90          95
Arg Val Phe Thr Val Gly Arg Leu Asp Lys Glu Thr Ser Gly Leu Ile
          100          105          110
Leu Val Thr Asn Asp Gly Glu Phe Ala Asn Lys Ile Ile His Pro Ser
          115          120          125
Ser Gly Ile Thr Lys Glu Tyr Leu Leu Lys Val Ser Arg Asp Val Ser
130          135          140
Ala Lys Asp Leu Gly Lys Leu Met Glu Gly Thr Phe Ile Asp Gly Lys
145          150          155          160
His Val Arg Pro Val Ser Val Thr Lys Ile Arg Arg Gly Thr Val Lys
          165          170          175
Ile Val Val Ser Glu Gly Lys Lys His Glu Ile Arg Leu Phe Ala Asp
180          185          190

```

Ala Ala Gly Leu Pro Ile Leu Glu Leu Lys Arg Ile Arg Ile Gly Ser  
 195 200 205  
 Leu Val Leu Gly Gly Leu Arg Tyr Gly Glu Tyr Arg Glu Leu Thr Asp  
 210 215 220  
 Ala Glu Leu Gly Thr Tyr Met Lys Leu Ser Asp  
 225 230 235  
 <210>931  
 <211>193  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>931  
 Asn Met Lys Val Ile Tyr Tyr Glu Ile Glu Glu Ile Pro Ser Thr Asn  
 1 5 10 15  
 Thr Met Ala Lys Ser Tyr Met His Leu Trp Asp Pro Tyr Ala Leu Thr  
 20 25 30  
 Val Ile Ser Thr Lys Cys Gln Thr Ala Gly Thr Gly Lys Phe Gly Lys  
 35 40 45  
 Ser Trp Lys Ser Ser Lys Gly Asp Leu Leu Asn Thr Phe Cys Phe Phe  
 50 55 60  
 Ile Thr Asp Leu His Ile Asp Val Ser Arg Leu Phe Arg Leu Gly Thr  
 65 70 75 80  
 Glu Ala Val Val Ala Leu Cys Lys Asp Leu Gly Ile Thr Glu Ala Lys  
 85 90 95  
 Ile Lys Trp Pro Asn Asp Val Leu Val His Gly Glu Lys Leu Cys Gly  
 100 105 110  
 Val Leu Pro Glu Thr Leu Pro Val Glu Gly Leu Leu Gly Val Val Leu  
 115 120 125  
 Gly Ile Gly Leu Asn Gly Asn Thr Thr Lys Gln Ala Leu Lys Asp Val  
 130 135 140  
 Gly Gln Pro Ala Thr Ser Leu Gln Glu Ile Leu Gly His Pro Ile Asp  
 145 150 155 160  
 Leu Glu Thr Thr Arg Glu Leu Leu Ile His His Leu Leu Gly Val Leu  
 165 170 175  
 Gln Glu Asn Leu Pro Asp Ser Leu Ala Thr Lys Ser Asn Arg Gly Asn  
 180 185 190  
 Ile

&lt;210&gt;932

&lt;211&gt;421

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;932

Cys Ile Arg Ile Pro Gln Met His Ile Gly Phe Cys His Cys Val Arg  
 1 5 10 15  
 Gly Gly Asn Phe Phe Tyr Phe Val Ile Asn Asn Phe His Ile Leu Glu  
 20 25 30  
 Ile Tyr Ser Leu Leu Asn Ser Asn Thr Ile Met Arg Tyr His Lys Tyr  
 35 40 45  
 Phe Arg Tyr Val Asn Ser Trp Val Phe Leu Val Val Leu Thr Leu Met  
 50 55 60  
 Leu Leu Ser Val Val Val Ile Ser Ser Met Asp Pro Thr Ala Met Leu  
 65 70 75 80  
 Val Thr Ser Ser Lys Gly Leu Leu Thr Asn Lys Ser Ile Met Gln Leu  
 85 90 95  
 Arg His Phe Ala Leu Gly Trp Val Val Phe Phe Ile Cys Ala Tyr Phe  
 100 105 110  
 Asp Tyr His Leu Phe Lys Arg Trp Ala Trp Val Leu Tyr Phe Phe Met  
 115 120 125  
 Ile Cys Ala Leu Val Gly Leu Phe Phe Val Pro Ser Val Gln Asn Val  
 130 135 140  
 His Arg Trp Tyr Arg Ile Pro Phe Ile His Met Ser Val Gln Pro Ser  
 145 150 155 160  
 Glu Tyr Gly Lys Leu Val Ile Val Ile Met Leu Ser Tyr Ile Leu Glu  
 165 170 175

Ser Arg Lys Ala Asp Ile Thr Ser Lys Thr Thr Ala Phe Leu Ala Cys  
 180 185 190  
 Leu Val Val Ala Leu Pro Phe Phe Leu Ile Leu Lys Glu Pro Asp Leu  
 195 200 205  
 Gly Thr Ala Leu Val Leu Cys Pro Val Thr Leu Thr Ile Phe Tyr Leu  
 210 215 220  
 Ser Asn Val His Ser Leu Leu Val Lys Phe Cys Thr Val Val Ala Thr  
 225 230 235 240  
 Ile Gly Ile Ile Gly Ser Leu Leu Ile Phe Ser Gly Ile Val Ser His  
 245 250 255  
 Gln Lys Val Lys Pro Tyr Ala Leu Lys Val Ile Lys Glu Tyr Gln Tyr  
 260 265 270  
 Glu Arg Leu Ser Pro Ser Asn His His Gln Arg Ala Ser Leu Ile Ser  
 275 280 285  
 Ile Gly Leu Gly Gly Ile Arg Gly Arg Gly Trp Lys Thr Gly Glu Phe  
 290 295 300  
 Ala Gly Arg Gly Trp Leu Pro Tyr Gly Tyr Thr Asp Ser Val Phe Ser  
 305 310 315 320  
 Ala Leu Gly Glu Glu Phe Gly Leu Leu Gly Leu Leu Phe Thr Leu Gly  
 325 330 335  
 Leu Phe Tyr Cys Leu Ile Cys Phe Gly Cys Arg Thr Val Ala Val Ala  
 340 345 350  
 Thr Asp Asp Phe Gly Lys Leu Leu Ala Ala Gly Ile Thr Val Tyr Leu  
 355 360 365  
 Ala Met His Val Leu Ile Asn Ile Ser Met Met Cys Gly Leu Leu Pro  
 370 375 380  
 Ile Thr Gly Val Pro Leu Ile Leu Ile Ser Tyr Gly Gly Ser Ser Val  
 385 390 395 400  
 Ile Ser Thr Met Ala Ser Leu Gly Val Leu Gln Ser Ile Tyr Ser His  
 405 410 415  
 Arg Phe Ala Lys Tyr  
 420  
 <210>933  
 <211>392  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>933  
 Ile Phe Phe Ser Ile Cys Ser Leu Tyr Phe Cys Asn Cys Leu Trp Asn  
 1 5 10 15  
 Cys Pro Phe Gly Ser Phe Ile Tyr Phe His Ser Ile Val Arg Thr Ser  
 20 25 30  
 Glu Cys Ile Leu Pro Cys Pro Ser Val Ser Tyr Cys Ser Val Ser Val  
 35 40 45  
 Cys Phe Asp His Cys Asp Ser Tyr Cys Leu Phe Lys Cys Tyr Gln Cys  
 50 55 60  
 Leu Cys Glu Thr Trp Gly Ser Xaa Glu Arg Arg Cys Val Leu Asp Arg  
 65 70 75 80  
 Leu Val Ser Cys Asn Ser Val Val Met Asp Lys Thr Gly Thr Leu Thr  
 85 90 95  
 Thr Gly Glu Leu Thr Cys Ile Gly Cys Asp Tyr Phe Gly Ser Lys Asn  
 100 105 110  
 Glu Thr Phe Phe Pro Ser Val Leu Ala Leu Glu Gln Ser Ser Ser His  
 115 120 125  
 Pro Ile Ala Glu Ala Ile Val Ser Tyr Leu Met Glu Gln Lys Val Ser  
 130 135 140  
 Ser Leu Pro Ala Asp Arg Tyr Leu Thr Val Pro Gly Glu Gly Val Arg  
 145 150 155 160  
 Gly Tyr Phe Asn Glu Gln Glu Ala Phe Val Gly Arg Val Glu Thr Gly  
 165 170 175  
 Leu Gly Lys Val Pro Ser Glu Tyr Leu Glu Asp Ile Glu Gln Lys Ile  
 180 185 190  
 Tyr Gln Ala Lys Gln His Gly Glu Ile Cys Ser Leu Ala Tyr Val Gly  
 195 200 205  
 Asn Ser Phe Ala Leu Phe Tyr Phe Arg Asp Ile Pro Arg Pro Gln Ala

210 215 220  
 Lys Glu Ile Ile Gln Asp Leu Lys Asp Leu Gly Tyr Pro Val Ser Met  
 225 230 235 240  
 Leu Thr Gly Asp His Lys Val Ser Ala Glu Asn Thr Ala Glu Ile Leu  
 245 250 255  
 Gly Ile Ser Glu Val Phe Phe Asp Leu Thr Pro Glu Asp Lys Leu Ala  
 260 265 270  
 Lys Ile Arg Glu Leu Ala Thr Gln Arg Gln Ile Met Met Val Gly Asp  
 275 280 285  
 Gly Ile Asn Asp Ala Pro Ala Leu Ala Gln Ala Thr Val Gly Ile Ala  
 290 295 300  
 Met Gly Glu Ala Gly Ser Ala Thr Ala Ile Glu Ala Ala Asp Ile Val  
 305 310 315 320  
 Leu Leu His Asp Ser Leu Ser Ser Leu Pro Trp Ile Ile Gln Lys Ala  
 325 330 335  
 Lys Gln Thr Lys Lys Val Val Ser Gln Asn Leu Ala Leu Ala Leu Ala  
 340 345 350  
 Ile Ile Leu Leu Val Ser Trp Pro Ala Ser Leu Gly Ile Ile Pro Leu  
 355 360 365  
 Trp Leu Ala Val Ile Leu His Glu Gly Ser Thr Val Ile Val Gly Leu  
 370 375 380  
 Asn Ala Leu Arg Leu Leu Lys Ser  
 385 390  
 <210>934  
 <211>373  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>934  
 Asn Phe Arg Asn Gly Leu Gly Val Arg Asp Leu His His Phe Arg Glu  
 1 5 10 15  
 Tyr Tyr Leu Ile Ile Asn Glu Ile Ile Ile Thr Gly Arg Tyr Val Phe  
 20 25 30  
 Ser Arg Leu Phe Phe Thr Ser Phe Ser Ala Glu Val Val Asn Thr Phe  
 35 40 45  
 Phe Glu Ser Gly Met Ser Glu Asp Thr Ser Pro Leu Leu Ser Lys Gln  
 50 55 60  
 Asn Arg Lys Leu Ser His Asn Leu Pro Leu Lys Ser Ala Tyr Leu Ser  
 65 70 75 80  
 Leu Gly Thr Tyr Leu Ile Ala Leu Leu Ser Phe Trp Leu His Ala Lys  
 85 90 95  
 Asn Leu Ser Asn Leu Phe Val Val Phe Thr Phe Phe Leu Ala Gly Thr  
 100 105 110  
 Pro Ala Leu Ile Lys Ser Leu Val Asn Ile Cys Gln Lys Val Val Asn  
 115 120 125  
 Ile Asp Ile Leu Met Thr Ser Ala Pro Phe Gly Ser Ile Phe Ile Gly  
 130 135 140  
 Gly Ala Leu Glu Gly Ala Leu Leu Leu Val Leu Phe Ala Ile Ser Glu  
 145 150 155 160  
 Ala Leu Gly Gln Met Val Ser Gly Lys Ala Lys Ser Thr Leu Val Ser  
 165 170 175  
 Leu Lys Gln Leu Ala Pro Thr Thr Gly Trp Leu Val Leu Glu Asp Gly  
 180 185 190  
 Asn Leu Gln Lys Val Ala Ile Asn Lys Ile Glu Val Gly Asn Ile Leu  
 195 200 205  
 Arg Ile Lys Ser Gly Glu Val Val Pro Leu Asp Gly Glu Ile Leu His  
 210 215 220  
 Gly Ser Ser Ser Ile Asn Leu Met His Leu Thr Gly Glu Lys Val Pro  
 225 230 235 240  
 Lys Ser Cys His Pro Gly Ser Ile Val Pro Ala Gly Ala His Asn Met  
 245 250 255  
 Glu Gly Ser Phe Asp Leu Arg Val Leu Arg Thr Gly Ser Asp Ser Thr  
 260 265 270  
 Ile Ala His Ile Ile Asn Leu Val Ile Gln Ala Gln Asn Ser Lys Pro  
 275 280 285

Arg Leu Gln Gln Arg Leu Asp Lys Tyr Ser Ser Val Tyr Ala Leu Ser  
 290 295 300  
 Ile Phe Ala Ile Ala Cys Gly Ile Ala Leu Leu Val Pro Leu Phe Thr  
 305 310 315 320  
 Ser Ile Pro Leu Leu Gly Pro Gln Ser Ala Phe Tyr Arg Ala Leu Ala  
 325 330 335  
 Phe Leu Ile Ala Ala Ser Pro Cys Ala Leu Ile Ile Ala Ile Pro Ile  
 340 345 350  
 Ala Tyr Leu Ser Ala Ile Asn Ala Cys Ala Lys His Gly Val Leu Xaa  
 355 360 365  
 Lys Gly Gly Val Phe  
 370  
 <210>935  
 <211>274  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>935  
 Glu Gly Trp Arg Phe Phe Phe Pro Lys Thr Ser Glu Asn Thr Ser Asp  
 1 5 10 15  
 Cys Arg Gln His Gln Ile Leu Arg Lys Ile Met Thr Gln Asp Pro His  
 20 25 30  
 Asp His Phe Lys Ser Arg Thr Pro Glu Asp His Ile Lys His Val Arg  
 35 40 45  
 Asp Lys His Arg Val Cys Lys Gly Glu Pro His Thr Thr Phe Lys Gly  
 50 55 60  
 Phe Phe Tyr His Leu Ala Asn Asn Ala Leu Ser Thr Gly Val Phe Ile  
 65 70 75 80  
 Phe Phe Ile Arg Thr Leu Phe Phe Leu Ile Pro Thr Asn Arg Ala Leu  
 85 90 95  
 Gln Val Lys Ser Leu Ile Ser Leu Gly Val Gly Trp Thr Phe Tyr His  
 100 105 110  
 Gly Cys Leu Lys Ala Arg Lys Ala Trp Ala Tyr Met Glu Leu Ser His  
 115 120 125  
 Arg Ser Met Leu Glu Glu Lys Asn Glu Ile Glu Glu Asn Phe Glu Gln  
 130 135 140  
 Glu Lys Ile Glu Leu Arg Ile Leu Phe Glu Asn Gln Gly Phe Lys Asp  
 145 150 155 160  
 Pro Leu Leu Gln Glu Met Val Glu Tyr Val Cys Ser Asp Ser Thr Leu  
 165 170 175  
 Leu Leu Asp Thr Met Ile Arg Glu Glu Leu Tyr Ile Arg Lys Glu Asp  
 180 185 190  
 Leu Pro His Pro Leu Ile Gln Gly Gly Ser Arg Ile Leu Gly Gly Leu  
 195 200 205  
 Cys Gly Leu Ala Ile Phe Leu Pro Leu Val Leu Cys Ile Ser Tyr Thr  
 210 215 220  
 Leu Ala Gly Val Phe Ser Ala Leu Met Val Leu Val Leu Ser Phe Leu  
 225 230 235 240  
 Lys Ala Lys Ile Leu Lys Asn Asp Lys Ile Ser Glu Met Val Trp Val  
 245 250 255  
 Leu Gly Ile Phe Ile Thr Ser Ala Ser Ile Ile Ser Ser Leu Met Lys  
 260 265 270  
 Leu Leu

&lt;210&gt;936

&lt;211&gt;466

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;936

Val Ile Leu Pro Phe Ser Pro Ile Ser Ile Ala Arg Arg Ile Lys Lys  
 1 5 10 15  
 Ser Cys Cys Ser Glu Lys Ser Ser Ile Tyr Ser His Phe Cys Thr Leu  
 20 25 30  
 Leu Leu Asn Asn Glu Thr Ser Met Leu Asp Ile Lys Ile Ile Arg Lys  
 35 40 45

Thr Pro Glu Glu Cys Glu Thr Arg Leu Arg Lys Lys Asp Pro Lys Ile  
 50 55 60  
 Ser Leu Glu Pro Val Leu Ser Leu Asp Lys Glu Val Arg Gln Leu Lys  
 65 70 75 80  
 Thr Asp Ser Glu Thr Leu Gln Ala Gln Arg Arg Leu Leu Ser Gln Asp  
 85 90 95  
 Ile His Lys Ala Lys Thr Gln Gly Val Asp Ala Thr Asn Leu Ile Gln  
 100 105 110  
 Glu Val Glu Thr Leu Ala Ala Asp Leu Glu Lys Ile Glu Gln His Leu  
 115 120 125  
 Asp Gln Lys Asn Ala Gln Leu His Glu Leu Leu Ser His Leu Pro Asn  
 130 135 140  
 Tyr Pro Ala Asp Asp Ile Pro Val Ser Glu Asp Lys Ala Gly Asn Gln  
 145 150 155 160  
 Val Ile Lys Ser Val Gly Asp Leu Pro Ile Phe Ser Phe Pro Pro Lys  
 165 170 175  
 His His Leu Glu Leu Asn Gln Glu Leu Asp Ile Leu Asp Phe Gln Ala  
 180 185 190  
 Ala Ala Lys Thr Thr Gly Ser Gly Trp Pro Ala Tyr Lys Asn Arg Gly  
 195 200 205  
 Val Leu Leu Glu Trp Ala Leu Leu Thr Tyr Met Leu Gln Lys Gln Ala  
 210 215 220  
 Ala His Gly Phe Gln Leu Trp Leu Pro Pro Leu Leu Val Lys Lys Glu  
 225 230 235 240  
 Ile Leu Phe Gly Ser Gly Gln Ile Pro Lys Phe Asp Gly Gln Tyr Tyr  
 245 250 255  
 Arg Val Glu Asp Gly Glu Gln Tyr Leu Tyr Leu Ile Pro Thr Ala Glu  
 260 265 270  
 Val Val Leu Asn Gly Phe Arg Ser Gln Asp Ile Leu Thr Glu Lys Glu  
 275 280 285  
 Leu Pro Leu Tyr Tyr Ala Ala Cys Thr Pro Cys Phe Arg Arg Glu Ala  
 290 295 300  
 Gly Ala Ala Gly Ala Gln Glu Arg Gly Leu Val Arg Val His Gln Phe  
 305 310 315 320  
 His Lys Val Glu Met Phe Ala Phe Thr Thr Pro Asn Gln Asp Asp Ile  
 325 330 335  
 Ala Tyr Glu Lys Met Leu Ser Ile Val Glu Glu Met Leu Thr Glu Leu  
 340 345 350  
 Lys Leu Pro Tyr Arg Leu Ser Leu Leu Ser Thr Gly Asp Met Ser Phe  
 355 360 365  
 Thr Xaa Ser Lys Thr Ile Asp Ala Glu Val Trp Leu Pro Gly Gln Lys  
 370 375 380  
 Ala Phe Tyr Glu Val Ser Ser Ile Ser Gln Cys Thr Asp Phe Gln Ser  
 385 390 395 400  
 Arg Arg Ser Gly Thr Arg Tyr Lys Asp Ser Gln Gly Lys Leu Gln Phe  
 405 410 415  
 Val His Thr Leu Asn Gly Ser Gly Leu Ala Thr Pro Arg Leu Leu Val  
 420 425 430  
 Ala Ile Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val Val Ile Pro  
 435 440 445  
 Glu Val Leu Arg Pro Tyr Leu Gly Gly Leu Glu Ile Leu Leu Pro Lys  
 450 455 460  
 Asp Gln  
 465  
 <210>937  
 <211>376  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>937  
 Met Glu Asp Phe Ser Glu Gln Gln Leu Phe Phe Met Arg Arg Ala Ile  
 1 5 10 15  
 Glu Ile Gly Glu Lys Gly Arg Ile Thr Ala Pro Pro Asn Pro Trp Val  
 20 25 30  
 Gly Cys Val Val Val Gln Glu Asn Arg Ile Ile Gly Glu Gly Phe His

35 40 45  
 Ala Tyr Ala Gly Gly Pro His Ala Glu Glu Leu Ala Ile Gln Asn Ala  
 50 55 60  
 Ser Met Pro Ile Ser Gly Ser Asp Val Tyr Val Ser Leu Glu Pro Cys  
 65 70 75 80  
 Ser His Phe Gly Ser Cys Pro Pro Cys Ala Asn Leu Leu Ile Lys His  
 85 90 95  
 Lys Val Ser Arg Val Phe Val Ala Leu Val Asp Pro Asp Pro Lys Val  
 100 105 110  
 Ala Gly Gln Gly Ile Ala Met Leu Arg Gln Ala Gly Ile Gln Val Tyr  
 115 120 125  
 Val Gly Ile Gly Glu Ser Glu Ala Gln Ala Ser Leu Gln Pro Tyr Leu  
 130 135 140  
 Tyr Gln Arg Thr His Asn Phe Pro Trp Thr Ile Leu Lys Ser Ala Ala  
 145 150 155 160  
 Ser Val Asp Gly Gln Val Ala Asp Ser Gln Gly Lys Ser Gln Trp Ile  
 165 170 175  
 Thr Cys Pro Glu Ala Arg His Asp Val Gly Lys Leu Arg Ala Glu Ser  
 180 185 190  
 Gln Ala Ile Leu Val Gly Ser Arg Thr Val Leu Ser Asp Asp Pro Trp  
 195 200 205  
 Leu Thr Ala Arg Gln Pro Gln Gly Met Leu Tyr Pro Lys Gln Pro Leu  
 210 215 220  
 Arg Val Val Leu Asp Ser Arg Gly Ser Val Pro Pro Thr Ser Lys Val  
 225 230 235 240  
 Phe Asp Lys Thr Ser Pro Thr Leu Tyr Val Thr Thr Glu Arg Cys Pro  
 245 250 255  
 Glu Asn Tyr Ile Lys Val Leu Asp Ser Leu Asp Val Pro Val Leu Leu  
 260 265 270  
 Thr Glu Ser Thr Pro Ser Gly Val Asp Leu His Lys Val Tyr Glu Tyr  
 275 280 285  
 Leu Ala Gln Lys Lys Ile Leu Gln Val Leu Val Glu Gly Gly Thr Thr  
 290 295 300  
 Leu His Thr Ser Leu Leu Lys Glu Arg Phe Val Asn Ser Leu Val Leu  
 305 310 315 320  
 Tyr Ser Gly Pro Met Ile Leu Gly Asp Gln Lys Arg Pro Leu Val Gly  
 325 330 335  
 Val Leu Gly Asn Leu Leu Glu Ser Ala Ser Pro Leu Thr Leu Lys Ser  
 340 345 350  
 Ser Gln Ile Leu Gly Asn Ser Leu Lys Val Val Trp Glu Ile Ser Pro  
 355 360 365  
 Gln Val Phe Glu Pro Ile Arg Asn  
 370 375  
 <210>938  
 <211>418  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>938  
 Met Ile Glu Thr Arg Glu Glu Val Gly Ser Ala Asn Phe Val Ser Leu  
 1 5 10 15  
 Glu Arg Ala Ile Glu Asp Leu Arg Ala Gly Lys Phe Val Ile Val Val  
 20 25 30  
 Asp Glu Ala Ser Arg Glu Asp Glu Gly Asp Leu Ile Ile Ala Gly Glu  
 35 40 45  
 Lys Ile Thr Val Glu Lys Met Thr Phe Leu Leu Gln His Thr Thr Gly  
 50 55 60  
 Val Val Cys Ala Ala Leu Ser Gln Glu Arg Leu Leu Ser Leu Asp Leu  
 65 70 75 80  
 Pro Pro Met Val Lys Asp Asn Arg Cys Arg Phe Lys Thr Pro Phe Thr  
 85 90 95  
 Val Ser Val Asp Ala Ala His Gly Val Thr Thr Gly Val Ser Ala Ala  
 100 105 110  
 Asp Arg Thr Lys Val Val Gln Leu Leu Ala Asp Pro Lys Ser Lys Pro  
 115 120 125



Glu Asp Phe Ile Ser Pro Gly His Phe Phe Pro Leu Ala Ser Ser Pro  
 130 135 140  
 Gly Gly Val Leu Lys Arg Ala Gly His Thr Glu Ser Thr Val Asp Leu  
 145 150 155 160  
 Met Glu Leu Ala Gly Leu Gln Pro Cys Gly Val Leu Ala Glu Leu Val  
 165 170 175  
 Asn Glu Asp Tyr Ser Met Met Arg Leu Pro Gln Ile Leu Glu Phe Ala  
 180 185 190  
 Arg Lys His Asn Ile Ala Val Ile Pro Val Thr Ser Ile Ile Ala His  
 195 200 205  
 Arg Met Leu Ser Asp Arg Leu Val Ser Lys Ile Ser Ser Ala Arg Leu  
 210 215 220  
 Pro Thr Ile Tyr Gly Asp Phe Thr Ile His Val Tyr Glu Ser Leu Leu  
 225 230 235 240  
 Glu Gly Met Gln His Leu Ala Leu Val Lys Gly Asn Val Ala Gly Lys  
 245 250 255  
 Ser Asn Val Leu Val Arg Val His Ser Glu Cys Val Thr Gly Asp Ile  
 260 265 270  
 Leu Gly Ser Lys Arg Cys Asp Cys Gly Glu Gln Leu Ser Ser Ala Met  
 275 280 285  
 Ser Tyr Ile Ala Glu Lys Gly Thr Gly Val Leu Val Tyr Leu Arg Gly  
 290 295 300  
 Gln Glu Gly Arg Gly Ile Gly Leu Gly His Lys Val Arg Ala Tyr Ala  
 305 310 315 320  
 Leu Gln Asp Asn Gly Tyr Asp Thr Val Asp Ala Asn Leu Ala Met Gly  
 325 330 335  
 Phe Pro Val Asp Ser Arg Glu Tyr Gly Ile Gly Ala Gln Ile Xaa Ile  
 340 345 350  
 Asp Leu Xaa Leu Thr Thr Ile Lys Leu Ile Thr His Asn Pro Gln Lys  
 355 360 365  
 Tyr Phe Gly Leu Gln Gly Phe Gly Leu Ser Ile Thr Glu Arg Val Pro  
 370 375 380  
 Leu Pro Val Arg Ile Ser Glu Asp Asn Glu Gln Tyr Leu Arg Thr Lys  
 385 390 395 400  
 Gln Glu Arg Met Gly His Trp Leu Asp Leu Pro Cys Cys Asn Asn Arg  
 405 410 415  
 Val Gln

&lt;210&gt;939

&lt;211&gt;154

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;939

Met Lys Thr Leu Lys Gly His Leu Ser Ala Lys Asn Leu Arg Ile Ala  
 1 5 10 15  
 Ile Val Gly Ser Cys Phe Asn Gln Ala Met Ala Asp Ala Leu Val Ser  
 20 25 30  
 Gly Thr Gln Glu Thr Phe Leu Lys Phe Gly Gly Ser Glu Asp Gly Leu  
 35 40 45  
 Met Thr Ile Arg Val Pro Gly Ala Phe Glu Ile Pro Cys Thr Ile Lys  
 50 55 60  
 Lys Leu Leu Ser Ser Glu Arg Lys Phe Asp Ala Ile Val Ala Cys Gly  
 65 70 75 80  
 Val Leu Ile Gln Gly Glu Thr Asp His Tyr Asn Gln Ile Val Asn Gln  
 85 90 95  
 Val Ala Ala Gly Ile Gly Ala Leu Ser Leu Glu Phe Cys Leu Pro Ile  
 100 105 110  
 Thr Leu Ser Ile Val Ala Ala Pro Ser Ala Glu Ile Ala Trp Gln Arg  
 115 120 125  
 Ser Gly Ile Lys Gly Arg His Leu Gly Val Ser Gly Met Thr Thr Ala  
 130 135 140  
 Ile Glu Met Ala Thr Leu Phe Thr Gln Ile  
 145 150  
 <210>940

&lt;211&gt;472

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;940

```

Leu Ile Ser Leu Asn Leu Lys Ile Leu Thr Lys Gln Arg Asp Arg Glu
 1           5           10           15
Glu Ala Ser Met Leu Lys Ile Leu Lys Ile Lys Val Leu Val Phe Pro
          20           25           30
Leu Ala Leu Leu Met Gly Cys Asn Ser Ile Gly Tyr Ala Gly Pro Gln
          35           40           45
Gly Ser Leu Gln Thr Asn Ser Gln Thr Lys Val Lys Ile Gly Ser Glu
          50           55           60
Val Trp Ile Glu Gln Lys Leu Arg Gln Tyr Pro Glu Leu Leu Trp Leu
          65           70           75           80
Thr Glu Ser Gly Gly Ala Pro Leu Leu Thr Ser Thr Pro Ile Asp Met
          85           90           95
Ala Tyr Ser Glu Lys Leu Phe Asn Lys Lys Val Pro Ala Leu Asp Ile
          100          105          110
Ala Ile Arg Ser Met Ile His Leu His Leu Leu Ile Gln Gly Ser Arg
          115          120          125
Gln Ser Tyr Met Gln Leu Ser Gln Ile Leu Pro Ser Glu Glu Gly Gly
          130          135          140
Met Thr Phe Lys Gln Phe Gln Thr Ala His Lys Gln Leu Leu Phe Phe
          145          150          155          160
Leu Asn Ser Pro Lys Ser Phe Asp Asn Thr Leu Arg Ile Leu Glu Thr
          165          170          175
Ala Ile Val Leu Arg His Val Gly Cys Ser Ala Lys Ala Val Thr Thr
          180          185          190
Phe Lys Pro Tyr Phe Thr Asp Ser Cys Pro Gln Ser Phe Tyr Ala Lys
          195          200          205
Ala Leu His Val Leu Arg Thr Phe Pro Glu Leu Cys Pro Ser Tyr Ala
          210          215          220
Arg Leu Ser Pro Glu Gln Gln Glu Val Leu Leu Ser Leu Arg Arg Leu
          225          230          235          240
Gly Asn Tyr Asp Ser Leu Leu Asn Leu Thr Glu Val Pro Ser Ala Gln
          245          250          255
Leu Leu Ser Ala Trp Arg Thr Arg Arg Ser Leu Ala Ile Leu Asp Leu
          260          265          270
Tyr Leu Tyr Cys Leu Asp Thr Cys Gly Asp Lys Asn Cys Ser Gln Glu
          275          280          285
Phe Tyr Ile Asn Phe Ala Pro Leu Leu Ser Met Leu Gln Gln His Ala
          290          295          300
Thr Ile Glu Glu Ala Phe Ser Arg Tyr Phe Thr Tyr Arg Ala Asn Arg
          305          310          315          320
Leu Gly Phe Glu Gly Thr Ser Arg Thr Asp Met Thr Leu Val Arg Leu
          325          330          335
Ala Thr Leu Met Asn Leu Ser Pro Ser Glu Ala Ser Thr Leu Ala Trp
          340          345          350
Ser Phe Lys Asn Leu Pro Ser Asp Glu Ala Glu Asn Leu Val Asn Ser
          355          360          365
Phe Tyr Thr Val Gln Gly Glu His Ile Pro Leu Thr Phe Arg Gly Leu
          370          375          380
Pro Ser Leu Val Ala Gly Leu Ser Val Ala Thr His Gly Ser Thr Val
          385          390          395          400
Ser Pro Glu Asn Arg Leu Arg Gln Leu Tyr Ser Thr Met Leu Ser Leu
          405          410          415
Leu Val Lys Ser Leu Arg Ser His Arg Glu Met Leu Asn Lys Gln Leu
          420          425          430
Leu Pro Gln Gly Thr Val Leu Asp Phe Ser Glu Thr Thr Leu Ser Ser
          435          440          445
Gly Gly Leu Asp Val Phe Ala Glu Ser Ile Ala Val Arg Ile His Leu
          450          455          460
Asn Gly Ala Val Ser Ile Asn Leu
          465          470

```

&lt;210&gt;941

&lt;211&gt;220

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;941

```

Leu Lys Ile Met Lys Arg Val Ile Tyr Lys Thr Ile Phe Cys Gly Leu
 1           5           10           15
Thr Leu Leu Thr Ser Leu Ser Ser Cys Ser Leu Asp Pro Lys Gly Tyr
          20           25           30
Asn Leu Glu Thr Lys Asn Ser Arg Asp Leu Asn Gln Glu Ser Val Ile
          35           40           45
Leu Lys Glu Asn Arg Glu Thr Pro Ser Leu Val Lys Arg Leu Ser Arg
          50           55           60
Arg Ser Arg Arg Leu Phe Ala Arg Arg Asp Gln Thr Gln Lys Asp Thr
          65           70           75           80
Leu Gln Val Gln Ala Asn Phe Lys Thr Tyr Ala Glu Lys Ile Ser Glu
          85           90           95
Gln Asp Glu Arg Asp Leu Ser Phe Val Val Ser Ser Ala Ala Glu Lys
          100          105          110
Ser Ser Ile Ser Leu Ala Leu Ser Gln Gly Glu Ile Lys Asp Ala Leu
          115          120          125
Tyr Arg Ile Arg Glu Val His Pro Leu Ala Leu Ile Glu Ala Leu Ala
          130          135          140
Glu Asn Pro Ala Leu Ile Glu Gly Met Lys Lys Met Gln Gly Arg Asp
          145          150          155          160
Trp Ile Trp Asn Leu Phe Leu Thr Gln Leu Ser Glu Val Phe Ser Gln
          165          170          175
Ala Trp Ser Gln Gly Val Ile Ser Glu Glu Asp Ile Ala Ala Phe Ala
          180          185          190
Ser Thr Leu Gly Leu Asp Ser Gly Thr Val Ala Ser Ile Val Gln Gly
          195          200          205
Glu Arg Trp Pro Glu Leu Val Asp Ile Val Ile Thr
          210          215          220

```

&lt;210&gt;942

&lt;211&gt;385

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;942

```

Gln Glu Ile Leu Ala Arg Glu Ile Ser Pro Glu Cys Cys Arg Leu Ser
 1           5           10           15
Leu Trp Arg Ser Arg Arg Pro Gly Leu Gly Leu Leu Ala Ala Leu Leu
          20           25           30
Gly Ala Ile Val Gln Tyr Ala Gly Ser Tyr Leu Gly Ser Lys Tyr Arg
          35           40           45
Lys Pro Glu Gly Asn Thr Gly Glu Phe Ile Gly Gly Pro Ile Ala Cys
          50           55           60
Leu Ala Phe Gly Met Arg Lys Lys Ile Leu Ala Gly Phe Phe Ala Leu
          65           70           75           80
Phe Thr Ile Met Thr Ala Phe Cys Ala Gly Asn Cys Val Gln Val Ser
          85           90           95
Cys Ile Val Pro Leu Cys Ala Glu Gly Thr Pro Gly Lys Leu Leu Val
          100          105          110
Gly Ile Leu Leu Ala Leu Val Val Ile Pro Val Leu Ala Gly Gly Asn
          115          120          125
Asn Arg Ile Leu Arg Phe Ser Ala Arg Val Ile Pro Phe Ile Ala Gly
          130          135          140
Phe Tyr Cys Ile Ser Cys Gly Ile Ile Leu Phe Gln His Ala Ser Ala
          145          150          155          160
Ile Leu Pro Ala Ile Lys Leu Ile Cys Ser Ser Ala Phe Gly Ile Lys
          165          170          175
Ala Gly Leu Ala Gly Ile Gly Gly Tyr Thr Leu Ser Gln Val Ile Ser
          180          185          190
Thr Gly Ile Asn Arg Ala Val Met Ala Thr Asp Cys Gly Ser Gly Met
          195          200          205

```

Val Ser Ile Leu Gln Ala Asn Thr Lys Ser Lys Asn Pro Val Val Asp  
 210 215 220  
 Gly Leu Val Thr Leu Val Pro Pro Val Ile Val Met Val Val Cys Ser  
 225 230 235 240  
 Ile Thr Met Leu Val Leu Ile Val Ser Gly Ala Tyr Ser Ser Gly Ala  
 245 250 255  
 Gln Gly Thr Leu Met Val Met Ser Ala Phe Lys Asn Ser Leu Gly Ser  
 260 265 270  
 Leu Gly Ser Val Ile Val Ile Leu Ala Met Ala Leu Phe Gly Tyr Thr  
 275 280 285  
 Thr Ile Leu Thr Trp Phe Ala Cys Ala Glu Lys Ser Leu Gln Tyr Met  
 290 295 300  
 Ile Pro Gly Arg Arg Ala Asn Leu Trp Leu Lys Ala Ile Tyr Val Leu  
 305 310 315 320  
 Ile Ile Pro Leu Gly Gly Val Ile Asp Met Arg Met Ile Trp Ala Leu  
 325 330 335  
 Ser Asp Thr Gly Phe Ser Gly Met Val Ile Leu Asn Cys Ile Ala Leu  
 340 345 350  
 Ile Ala Leu Leu Lys Asp Val Leu Ser Thr Asn Arg Asp Val Ala Leu  
 355 360 365  
 Leu Lys Glu Arg Glu Cys Ser Val Ala Asp Pro Val Arg Asn Leu Asp  
 370 375 380

Ala

385

&lt;210&gt;943

&lt;211&gt;110

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;943

Arg Arg Arg Ile Met Gln Leu Leu Ser Pro Ala Phe Ala Tyr Gly Ala  
 1 5 10 15  
 Pro Ile Pro Lys Lys Tyr Thr Cys Gln Gly Ala Gly Ile Ser Pro Pro  
 20 25 30  
 Leu Thr Phe Val Asp Val Pro Gly Ala Ala Gln Ser Leu Ala Leu Ile  
 35 40 45  
 Val Glu Asp Pro Asp Val Pro Lys Glu Ile Arg Ser Asp Gly Leu Trp  
 50 55 60  
 Ile His Trp Ile Val Tyr Asn Leu Ser Thr Thr Ile Thr Asn Leu Ala  
 65 70 75 80  
 Glu Gly Ala Glu Ile Phe Ala Val Gln Gly Leu Asn Thr Ser Gly Lys  
 85 90 95  
 Pro Val Tyr Glu Gly Pro Cys Pro Pro Asp Lys Gln His Arg  
 100 105 110

&lt;210&gt;944

&lt;211&gt;223

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;944

Gly Cys Met Ser Thr Val Thr Thr Glu Pro Cys Ser Ser Ile His Ile  
 1 5 10 15  
 Ser Leu Asn Asn Asp Trp Arg Asp Ser Gln Pro Tyr Ser Leu Asp Arg  
 20 25 30  
 Ala Ser Glu Leu Leu His Phe Arg Phe Leu Pro Ser Leu Val Phe Ser  
 35 40 45  
 Asn Trp Lys Val Glu Gln Gln Ile Glu Thr Leu Cys His Lys Ser Glu  
 50 55 60  
 Lys Arg Arg Leu Ile Ser Pro Leu Ala Lys Trp Leu Gly Lys Leu His  
 65 70 75 80  
 Lys Gln Asp Leu Leu Cys Pro Pro Ala Pro Pro Val Ser Val Cys Trp  
 85 90 95  
 Ile Asn Ala His Val Gly Tyr Gly Val Phe Ala Arg Asp Glu Ile Ala  
 100 105 110  
 Pro Trp Thr Tyr Ile Gly Glu Tyr Thr Gly Ile Leu Arg His Arg Gln  
 115 120 125

Ala Ile Trp Met Asp Glu Asn Asp Tyr Cys Phe Arg Tyr Pro Met Pro  
 130 135 140  
 Leu Phe Thr Leu Arg Tyr Phe Thr Ile Asp Ser Gly Lys Gln Gly Asn  
 145 150 155 160  
 Val Thr Arg Phe Ile Asn His Ser Glu Gln Pro Asn Ala Glu Ala Ile  
 165 170 175  
 Gly Val Phe Ser Glu Gly Leu Phe His Val Ile Ile Arg Thr Ile Ala  
 180 185 190  
 Pro Ile Tyr Ala Gly Gln Glu Ile Cys Tyr His Tyr Gly Pro Leu Tyr  
 195 200 205  
 Trp Lys His Arg Lys Lys Arg Glu Glu Phe Ile Pro Glu Glu Glu  
 210 215 220

&lt;210&gt;945

&lt;211&gt;265

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;945

Met Gln Gly Phe Phe Pro Leu Ala Ser Gly Ser Lys Gly Asn Ser Ala  
 1 5 10 15  
 Tyr Leu Gly Thr Asp Ser Cys Lys Ile Leu Ile Asp Leu Gly Val Ser  
 20 25 30  
 Lys Gln Val Val Thr Arg Glu Leu Ser Met Asn Ile Asp Pro Glu  
 35 40 45  
 Asp Ile Gln Ala Ile Phe Val Thr His Glu His Ser Asp His Ile Ser  
 50 55 60  
 Gly Ile Lys Ser Phe Val Lys Ala Tyr Asn Thr Pro Ile Val Cys Asn  
 65 70 75 80  
 Leu Glu Thr Ala Arg Ala Leu Cys His Leu Leu Asp Ser His Pro Glu  
 85 90 95  
 Phe Lys Ile Phe Ser Thr Gly Ser Ser Phe Cys Phe Gln Asp Leu Glu  
 100 105 110  
 Val Gln Thr Phe Asn Val Pro His Asp Ala Val Asp Pro Val Ala Phe  
 115 120 125  
 Ile Phe His Tyr Arg Glu Glu Lys Leu Gly Phe Cys Thr Asp Leu Gly  
 130 135 140  
 Trp Val Thr Ser Trp Ile Thr His Glu Leu Tyr Asp Cys Asp Tyr Leu  
 145 150 155 160  
 Leu Ile Glu Ser Asn His Ser Pro Glu Leu Val Arg Gln Ser Gln Arg  
 165 170 175  
 Pro Asp Val Tyr Lys Lys Arg Val Leu Ser Lys Leu Gly His Ile Ser  
 180 185 190  
 Asn Gln Glu Cys Gly Gln Leu Leu Gln Lys Ile Ile Thr Pro Lys Leu  
 195 200 205  
 Lys Lys Leu Tyr Leu Ala His Leu Ser Thr Glu Cys Asn Thr Ala Glu  
 210 215 220  
 Leu Ala Leu Ser Thr Val Ser Glu Ser Ile Ala Ser Ile Thr Ser Ile  
 225 230 235 240  
 Ala Pro Glu Ile Ala Leu Ala Gln Gly Ile Thr Ser Pro Ile Tyr Phe  
 245 250 255  
 Ser Arg Leu Glu Val Ala Cys Pro Arg  
 260 265

&lt;210&gt;946

&lt;211&gt;553

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;946

Asp Gly Ser Ile Ser Pro Leu Pro Gln Glu Glu Ile Pro Gly Ser Lys  
 1 5 10 15  
 Lys Glu Ser Phe Phe Leu Thr Pro His Pro Cys Lys Arg Phe Leu Thr  
 20 25 30  
 Lys Phe Val Glu Pro Gln Glu Asn Lys Ala Lys Glu Gly Lys Thr Ile  
 35 40 45  
 Ala Leu Ser Ser Thr Pro Thr Val Val Arg Glu Ser Lys Gly Lys Glu  
 50 55 60

Arg Ala Ala Leu Pro Lys Leu Lys Ser Leu Ala Val Pro Glu Asn Asp  
 65 70 75 80  
 Leu Pro Gln Tyr His Leu Leu Ser Lys Asn Arg Glu Ala Arg Pro Glu  
 85 90 95  
 Ser Leu Gln Ala Glu Leu Glu Arg Lys Ala Leu Ile Leu Lys Gln Thr  
 100 105 110  
 Leu Thr Ser Phe Gly Ile Asp Ala Asp Leu Gly Asn Ile Cys Ser Gly  
 115 120 125  
 Pro Thr Leu Ala Ala Phe Glu Val Leu Pro His Ser Gly Val Lys Val  
 130 135 140  
 Gln Lys Ile Lys Ser Leu Glu Asn Asp Ile Ala Leu Lys Leu Gln Ala  
 145 150 155 160  
 Ser Ser Ile Arg Ile Ile Ala Pro Ile Pro Gly Lys Ala Ala Val Gly  
 165 170 175  
 Ile Glu Ile Pro Thr Pro Phe Pro Gln Ala Val Asn Phe Arg Asp Leu  
 180 185 190  
 Leu Glu Asp Tyr Gln Lys Thr Asn Arg Lys Leu Gln Ile Pro Leu Leu  
 195 200 205  
 Leu Gly Lys Lys Ala Asn Gly Asp Asn Leu Trp Ala Asp Leu Ala Thr  
 210 215 220  
 Met Pro His Leu Ile Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser Val  
 225 230 235 240  
 Cys Ile Asn Thr Ile Val Met Ser Met Ile Met Thr Thr Leu Pro Ser  
 245 250 255  
 Glu Ile Lys Leu Val Ile Ile Asp Pro Lys Lys Val Glu Leu Thr Gly  
 260 265 270  
 Tyr Ser Gln Leu Pro His Met Leu Ser Pro Val Ile Thr Glu Ser Arg  
 275 280 285  
 Glu Val Tyr Asn Ala Leu Val Trp Leu Val Lys Glu Met Glu Ser Arg  
 290 295 300  
 Tyr Glu Ile Leu Arg Tyr Leu Gly Leu Arg Asn Ile Gln Ala Phe Asn  
 305 310 315 320  
 Ser Arg Thr Arg Asn Lys Thr Ile Glu Ala Ser Tyr Asp Arg Glu Ile  
 325 330 335  
 Arg Glu Thr Met Pro Phe Met Val Gly Ile Ile Asp Glu Leu Ser Asp  
 340 345 350  
 Leu Leu Leu Ser Ser Ser Gln Asp Ile Glu Thr Pro Ile Ile Arg Leu  
 355 360 365  
 Ala Gln Met Ala Arg Ala Val Gly Ile His Leu Ile Leu Ala Thr Gln  
 370 375 380  
 Arg Pro Ser Arg Glu Val Ile Thr Gly Leu Ile Lys Ala Asn Phe Pro  
 385 390 395 400  
 Ser Arg Ile Ser Phe Lys Val Ser Asn Lys Val Asn Ser Gln Ile Ile  
 405 410 415  
 Ile Asp Glu Pro Gly Ala Glu Asn Leu Met Gly Asn Gly Asp Met Leu  
 420 425 430  
 Val Leu Leu Pro Ser Val Phe Gly Thr Ile Arg Ala Gln Gly Ala Tyr  
 435 440 445  
 Ile Cys Asp Glu Asp Ile Asn Lys Val Ile Gln Asp Leu Cys Ser Arg  
 450 455 460  
 Phe Pro Thr Gln Tyr Val Ile Pro Ser Phe His Ala Phe Asp Asp Ser  
 465 470 475 480  
 Asp Ser Asp Asn Ser Gly Glu Lys Asp Pro Leu Phe Ala Gln Ala Lys  
 485 490 495  
 Thr Leu Ile Leu Gln Thr Gly Asn Ala Ser Thr Thr Phe Leu Gln Arg  
 500 505 510  
 Lys Leu Lys Ile Gly Tyr Ala Arg Ala Ala Ser Leu Ile Asp Gln Leu  
 515 520 525  
 Glu Glu Ala Arg Ile Ile Gly Pro Ser Glu Gly Ala Lys Pro Arg Gln  
 530 535 540  
 Ile Leu Ile Gln Asn Pro Leu Glu Gly  
 545 550  
 <210>947  
 <211>218

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;947

Pro Met Ile Arg Glu Arg Lys Lys Ser Arg His Pro Arg Leu Pro Thr  
 1 5 10 15  
 Leu Pro Leu Ala Ala Lys Ala Ser Leu Tyr Leu Phe Phe Ala Cys Phe  
 20 25 30  
 Ser Gly Leu Ser Leu Trp Ser Phe His Arg Asp Gln Pro Cys Thr Gln  
 35 40 45  
 Asn Trp Ile Gly Leu Leu Gly Trp Ser Phe Ser Ser Phe Leu Leu Tyr  
 50 55 60  
 Phe Phe Gly Ala Ala Ala Phe Phe Ile Pro Xaa Tyr Phe Leu Trp Leu  
 65 70 75 80  
 Ser Phe Leu Tyr Phe Arg Arg Thr Pro Arg Pro Leu Phe Phe Tyr Lys  
 85 90 95  
 Ala Ala Ala Phe Leu Ser Leu Pro Phe Cys Ser Ala Ile Leu Leu Ser  
 100 105 110  
 Met Leu Ser Pro Val Gly Thr Leu Pro Ala Leu Leu Asp Thr Arg Leu  
 115 120 125  
 Pro Lys Phe Ile Leu Gly Asn Ile Pro Pro Val Ser Tyr Val Gly Gly  
 130 135 140  
 Ile Pro Phe Tyr Leu Phe Tyr Glu Gly Gln Ser Phe Cys Leu Lys His  
 145 150 155 160  
 Leu Ile Gly Ser Val Gly Thr Ala Leu Ile Phe Gly Phe Val Met Leu  
 165 170 175  
 Phe Ser Val Leu Tyr Leu Cys Gly Arg His Cys Phe Ile Lys Lys Lys  
 180 185 190  
 Xaa Leu Ser Arg Arg Gly Gln Lys Gly Phe Leu Leu Phe Phe Pro Asn  
 195 200 205  
 Leu Phe Gln Lys Phe Lys Lys Ile Asn Lys  
 210 215

&lt;210&gt;948

&lt;211&gt;162

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;948

Lys Thr Ser Asn Asn Thr Gln Lys Asn Leu Leu Leu Ile Lys Ser Ala  
 1 5 10 15  
 Glu Ser Ser Ser Leu Gln Leu Ser Leu Ala Ser Ser Ala Ile Ser Ser  
 20 25 30  
 Arg Val Glu Gln Leu Ser Ser Leu Val Leu Gly Met Glu Asn Ser Asp  
 35 40 45  
 Phe Ser Ser Leu Arg Asp Val Pro Ile Phe Ser Ala Ile Tyr Glu Ser  
 50 55 60  
 Ser Thr His Thr Pro Val Pro Thr Pro Leu Val Gly Val Gly Tyr Ile  
 65 70 75 80  
 Asn Gly Ser Gln Ser Gly Tyr Tyr Asp Thr Gln Arg Glu Ser Leu His  
 85 90 95  
 Leu Ser Gln Leu Leu Gly Ser Arg Arg Val Glu Val Val Tyr Asn Gln  
 100 105 110  
 Gly Asn Phe Met Glu Ala Ser Leu Leu Asn Leu Cys Pro Arg Arg Pro  
 115 120 125  
 Arg Arg Asp Pro Ser Pro Ile Ser Leu Ala Leu Leu Glu Leu Trp Glu  
 130 135 140  
 Ala Phe Phe Leu Glu His Pro Pro Gly Ser Thr Phe Asn Pro Ile Phe  
 145 150 155 160  
 Phe Trp

&lt;210&gt;949

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;949

Thr Arg Ser Lys Lys Ser Gln Ser Cys Leu Lys Ser Met Ala Gly Phe

```

      1           5           10           15
Arg Leu Gln Ser Leu Gln Ile Leu Tyr Arg Arg Ile Gly Ser Leu Tyr
      20           25           30
Leu Gln Lys His Asp Asn Lys Arg Ser Glu Asp Val Leu Asp Ile Glu
      35           40           45
Lys Asp Arg Tyr Gln Arg Ala Leu Tyr Ser Val His Ala Glu Leu Gly
      50           55           60
Gly Glu Leu Arg Glu His Arg Lys Leu Arg Tyr Gln Lys Asn Ile Gly
      65           70           75           80
Leu Lys Val Leu Pro Gly Gly Cys Ser Lys Lys Asn Ala Ser Gln Ser
      85           90           95
Ser Asn Arg Ala Lys Glu Ile Gly Glu Gly Ser Leu Arg Gly Leu Leu
      100          105          110
Gly His Arg Phe Ser Lys Glu Ala Ser Met Lys Phe Pro Trp Leu
      115          120          125

<210>950
<211>412
<212>PRT
<213>Chlamydia pneumoniae
<400>950
Asn Thr Pro Gln Val Ala Leu Leu Ile Gln Tyr Phe Phe Gly Asn Gly
      1           5           10           15
Ala Phe Tyr Val Arg Glu Ala Leu Arg Leu Thr Pro His Ala Gln Asn
      20           25           30
Ile Val Leu Val Gly Ile Cys Pro Ser Leu Tyr Pro Glu His Pro Arg
      35           40           45
Ser Phe Tyr Tyr Arg Val Ser Gly Asp Ile Gly Ser Arg Phe Asp Asp
      50           55           60
Arg Gly Phe Val Asn Ser Gly Val Glu Thr Leu Pro Tyr Ser Ser Gly
      65           70           75           80
Ser Phe Gly Ile Phe Trp Ile Ser Phe Thr Asp Pro Thr Phe Asn Phe
      85           90           95
Ala Ile Val Asn Thr Phe Met Arg Thr Ala Gly Ile Asn Glu Val Ser
      100          105          110
Arg Pro Met Thr Gln Asp Thr Glu Thr Ser Leu Ile Glu Met Arg Asp
      115          120          125
Leu Ser Glu Gln Gln Glu Ala Asn Asn Thr Asp Ser Leu Glu Gln Glu
      130          135          140
Glu Ser Leu Met Gly Ile Val Gly His Thr Val Gly Gly Val Ser Met
      145          150          155          160
Thr Val Thr Ser Ser Pro Asn Ile Phe Tyr Arg Ile Gln Thr Leu Leu
      165          170          175
Gly Leu Pro Glu Thr Leu Ala Glu Ala Glu Glu Asn Pro Thr Phe Pro
      180          185          190
Asn Ser Thr Ile Asp Ser Leu Ala Glu Ile Met Met Asn Leu Val Arg
      195          200          205
Ile Ser Asp Ala Val Ser Ile Phe Trp Ile Phe Pro Ile Val Asp Thr
      210          215          220
Thr Tyr Asn Gly Val Leu Leu Ala Val Cys Ile Gly Phe Phe Gly Ile
      225          230          235          240
Asn Gly Ile Cys Ser Thr Phe Leu Met Leu Thr Asn Pro Arg Ser Arg
      245          250          255
Arg Asp Arg Trp Arg Asn Leu Arg Ile Met Val Leu Cys Tyr Arg Ser
      260          265          270
Leu Gly Ser Gly Met Asn Leu Phe Asp Leu Ser Asn Asn Val Arg Met
      275          280          285
Ala Ala Arg Arg His Val Thr Ser Cys Thr Val Ala Leu Tyr Ala Met
      290          295          300
Val Thr Leu Phe Gly Trp Thr Val Ala Ile Gln Asp Ala Leu Gln Tyr
      305          310          315          320
Gly Phe Pro Ser Val Arg Asp Ala Phe Tyr Arg Tyr Cys Leu Arg His
      325          330          335
Arg Tyr Cys Leu Thr Gln Arg Asn Glu Asp Ser Leu Gln Thr Thr Gly
      340          345          350

```



Thr Arg Phe Gln Val Thr Arg Thr His Leu Glu Asp Gln Gln Met Val  
 355 360 365  
 Ala Ser Ile Leu Asn Leu Ser Val Phe Gly Leu Phe Phe Gly Phe Val  
 370 375 380  
 Gly Leu Met Thr Thr Phe Gly Gly Leu Glu Ile Ser Pro Ser Cys Arg  
 385 390 395 400  
 Trp Asp Ala Ala Asn Asn Arg Thr Val Gly Ile Phe  
 405 410

&lt;210&gt;951

&lt;211&gt;117

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;951

Lys Ile Phe Gly Leu Glu Val Thr Val Met Glu Thr Pro Pro Thr Val  
 1 5 10 15  
 Cys Pro Thr Ile Pro Ile Lys Leu Ser Ser Cys Ser Lys Glu Ser Val  
 20 25 30  
 Leu Phe Ala Ser Cys Cys Ser Leu Arg Ser Leu Ile Ser Ile Asn Glu  
 35 40 45  
 Val Ser Val Ser Cys Val Met Gly Leu Glu Thr Ser Leu Ile Pro Ala  
 50 55 60  
 Val Arg Ile Lys Val Phe Thr Ile Ala Lys Leu Asn Val Gly Ser Val  
 65 70 75 80  
 Asn Glu Ile Gln Lys Ile Pro Lys Leu Pro Glu Glu Tyr Gly Arg Val  
 85 90 95  
 Ser Thr Pro Glu Phe Thr Asn Pro Leu Ser Ser Asn Arg Glu Pro Ile  
 100 105 110  
 Ser Pro Glu Thr Arg  
 115

&lt;210&gt;952

&lt;211&gt;431

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;952

Met Thr Trp Leu Ser Gly Leu Tyr Phe Ile Cys Ile Ala Ser Leu Ile  
 1 5 10 15  
 Phe Cys Ala Ile Gly Val Ile Leu Ala Gly Val Ile Leu Leu Ser Arg  
 20 25 30  
 Lys Leu Phe Ile Lys Val His Pro Cys Lys Leu Lys Ile Asn Asp Asn  
 35 40 45  
 Glu Glu Leu Thr Lys Thr Val Glu Ser Gly Gln Thr Leu Leu Val Ser  
 50 55 60  
 Leu Leu Ser Ser Gly Ile Pro Ile Pro Ser Pro Cys Gly Gly Lys Ala  
 65 70 75 80  
 Thr Cys Lys Gln Cys Lys Val Arg Val Val Lys Asn Ala Asp Glu Pro  
 85 90 95  
 Leu Glu Thr Asp Arg Ser Thr Phe Ser Lys Arg Gln Leu Glu Glu Gly  
 100 105 110  
 Trp Arg Leu Ser Cys Gln Cys Lys Val Gln His Asp Met Ser Leu Glu  
 115 120 125  
 Ile Glu Glu Arg Tyr Leu Asn Ala Ser Ser Trp Glu Gly Thr Val Ile  
 130 135 140  
 Ser Asn Asp Asn Val Ala Thr Phe Ile Lys Glu Leu Val Val Ala Val  
 145 150 155 160  
 Asp Pro Asn Lys Pro Ile Pro Phe Lys Pro Gly Gly Tyr Leu Gln Ile  
 165 170 175  
 Thr Val Pro Ser Tyr Lys Thr Asn Ser Ser Asp Trp Lys Gln Thr Met  
 180 185 190  
 Ala Pro Glu Tyr Tyr Ser Asp Trp Glu His Phe His Leu Phe Asp Gln  
 195 200 205  
 Val Ile Asp Asn Ser Gln Leu Pro Ala Asp Ser Ala Asn Lys Ala Tyr  
 210 215 220  
 Ser Leu Ala Ser Tyr Pro Ala Glu Leu Pro Thr Ile Lys Phe Asn Ile  
 225 230 235 240

Arg Ile Ala Thr Pro Pro Phe Ile Asn Gly Lys Pro Asn Ser Glu Ile  
 245 250 255  
 Pro Trp Gly Val Cys Ser Ser Tyr Val Phe Ser Leu Lys Pro Gly Asp  
 260 265 270  
 Lys Ile Thr Val Ser Gly Pro Tyr Gly Glu Ser Phe Met Lys Asp Asp  
 275 280 285  
 Asp Arg Pro Leu Ile Phe Leu Ile Gly Gly Ala Gly Ser Ser Phe Gly  
 290 295 300  
 Arg Ser His Ile Leu Asp Leu Leu Leu Asn Lys His Ser Lys Arg Glu  
 305 310 315 320  
 Ile Asp Leu Trp Tyr Gly Ala Arg Ser Leu Lys Glu Asn Ile Tyr Gln  
 325 330 335  
 Glu Glu Tyr Glu Asn Leu Glu Arg Gln Phe Pro Asn Phe His Tyr His  
 340 345 350  
 Leu Val Leu Ser Glu Pro Leu Pro Glu Asp Ile Ala Ala Gly Trp Asp  
 355 360 365  
 Lys Asp Asp Pro Thr Lys Thr Asn Phe Leu Phe Arg Ala Phe Asn Leu  
 370 375 380  
 Gly Gln Leu Ser Arg Leu Asp Asn Pro Glu Asp Tyr Leu Tyr Tyr Val  
 385 390 395 400  
 Cys Gly Pro Pro Leu His Asn Ser Ser Ile Leu Lys Leu Leu Gly Asp  
 405 410 415  
 Tyr Gly Val Glu Arg Ser Ser Ile Ile Leu Asp Asp Phe Gly Ser  
 420 425 430

&lt;210&gt;953

&lt;211&gt;106

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;953

Leu Leu Ser Ser Leu Pro Leu Phe Ala Glu Glu Glu Ala Ala Gln Ser  
 1 5 10 15  
 Lys Asn Thr Phe Val Gln Pro Ala Val Met Leu Ala Ile Ala Ile Leu  
 20 25 30  
 Phe Phe Tyr Phe Ile Leu Trp Arg Pro Glu Gln Lys Arg Arg Lys Ala  
 35 40 45  
 Met Glu Lys Arg Lys Asn Asp Leu Ala Lys Gly Asp Lys Val Thr Ala  
 50 55 60  
 Met Gly Ile Ile Gly Thr Val Asp Asp Ile Arg Glu His Thr Val Ile  
 65 70 75 80  
 Leu Asn Ile Ala Ser Gly Lys Val Glu Val Leu Lys Gly Ala Ile Ser  
 85 90 95  
 Glu Ile Leu Lys Pro Asn Asp Asn Lys Ser  
 100 105

&lt;210&gt;954

&lt;211&gt;401

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;954

Met Ser Thr Met Gln Asn Cys Pro His Phe Gly Val Cys Gly Gly Cys  
 1 5 10 15  
 Ser Phe Pro Gln Ser Asn Tyr Ser Asp Ser Leu Lys Lys Lys Glu Glu  
 20 25 30  
 Leu Leu His Gln Leu Phe Ala Pro Leu Val Pro Ser Asp Met Ile Ala  
 35 40 45  
 Pro Ile Ile Pro Cys Ser Pro Ser Leu Arg Gly Arg Asn Lys Met Glu  
 50 55 60  
 Phe Ser Phe Phe Gln Thr Tyr Glu Gly Glu Lys Ser Leu Gly Phe Ile  
 65 70 75 80  
 Ser Ser Thr Lys Pro Lys Lys Gly Ile Pro Val Thr Thr Cys Leu Leu  
 85 90 95  
 Ile His Glu Gln Thr Met Asp Ile Leu Lys Leu Thr Arg Glu Trp Trp  
 100 105 110  
 Asp Lys His Pro Glu Leu Met Ala Tyr Phe Pro Pro Lys Asn Lys Gly  
 115 120 125

Ser Leu Cys Thr Leu Thr Val Arg Thr Gly Ser Pro Gln Gln Asn Phe  
 130 135 140  
 Met Val Ile Leu Thr Thr Ser Gly Thr Pro Glu Tyr Arg Val Asn Glu  
 145 150 155 160  
 Ala Cys Ile Asp Glu Trp Lys Glu Ile Leu Leu Ser Ser Ser Leu Asn  
 165 170 175  
 Ile Ala Ser Ile Tyr Trp Glu Glu Lys Val Ala Ala Arg Gly Ile Ser  
 180 185 190  
 Thr Tyr Tyr Glu Thr Lys Leu Leu Tyr Gly Ala Pro Ser Ile Gln Gln  
 195 200 205  
 Lys Leu Ser Leu Pro Ser Asp Gly Asn Ser Ala Ser Phe Ser Leu Arg  
 210 215 220  
 Pro Arg Ser Phe Phe Gln Pro Gln Ile Thr Gln Ala Ala Lys Ile Ile  
 225 230 235 240  
 Glu Thr Ala Lys Glu Phe Ile Asn Pro Glu Gly Ser Glu Thr Leu Leu  
 245 250 255  
 Asp Leu Tyr Cys Gly Ala Gly Thr Ile Gly Ile Met Leu Ser Pro Tyr  
 260 265 270  
 Val Lys Asn Val Ile Gly Val Glu Ile Ile Pro Asp Ala Val Ala Ser  
 275 280 285  
 Ala Gln Glu Asn Ile Lys Ala Asn Asn Lys Glu Asp Cys Val Glu Val  
 290 295 300  
 Tyr Leu Glu Asp Ala Lys Ala Phe Cys Lys Arg Asn Glu Asn Cys Lys  
 305 310 315 320  
 Ala Pro Asp Val Ile Ile Ile Asp Pro Pro Arg Cys Gly Met Gln Ser  
 325 330 335  
 Lys Val Leu Lys Tyr Ile Leu Arg Ile Gly Ser Pro Lys Ile Val Tyr  
 340 345 350  
 Ile Ser Cys Asn Pro Lys Thr Gln Phe Gln Glu Cys Ala Asp Leu Ile  
 355 360 365  
 Ser Gly Gly Tyr Arg Ile Lys Lys Met Gln Pro Ile Asp Gln Phe Pro  
 370 375 380  
 Tyr Ser Thr His Leu Glu Asn Ile Ile Leu Leu Glu Arg Glu Ile Asp  
 385 390 395 400  
 Leu

&lt;210&gt;955

&lt;211&gt;123

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;955

Met Ala Leu Lys Asp Thr Ala Lys Lys Met Lys Asp Leu Leu Asp Ser  
 1 5 10 15  
 Ile Gln His Asp Leu Ala Lys Ala Glu Lys Gly Asn Lys Ala Ala Ala  
 20 25 30  
 Gln Arg Val Arg Thr Asp Ser Ile Lys Leu Glu Lys Val Ala Lys Leu  
 35 40 45  
 Tyr Arg Lys Glu Ser Ile Lys Ala Glu Lys Ser Gly Leu Leu Lys Arg  
 50 55 60  
 Lys Pro Ser Thr Lys Ala Pro Ala Lys Val Lys Lys Thr Ala Glu Lys  
 65 70 75 80  
 Lys Ala Pro Lys Lys Ser Ser Ala Ala Ala Lys Thr Ser Lys Ala  
 85 90 95  
 Val Lys Ala Ser Lys Pro Ala Ser Lys Lys Thr Ala Ala Lys Lys Val  
 100 105 110  
 Lys Lys Pro Ser Lys Ala Arg Gly Phe Arg Lys  
 115 120

&lt;210&gt;956

&lt;211&gt;822

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;956

Met Lys Lys Leu Tyr His Pro Thr Leu Phe Leu Arg Pro Leu Ile Arg  
 1 5 10 15

Leu Ser Leu Ile Phe Ala Leu Ser Leu Thr Leu Ile Ser Gly Asn Phe  
 20 25 30  
 Pro Gln Gln Lys Ser Phe Gly His Cys Cys Ala Asp Met His Ser Ala  
 35 40 45  
 Leu Ile Ser Gly Lys Asn Cys Glu Glu Leu Phe Ala Asp Phe Ile Glu  
 50 55 60  
 Arg Val Leu Ala Asp Arg Glu Thr Leu Thr Ala Arg Asp Trp Gly Thr  
 65 70 75 80  
 Val Val Val Leu Val Arg Glu Tyr Leu Leu Lys Cys Ile Arg Lys Gly  
 85 90 95  
 Asp Cys Asp Tyr Gly Val Lys Ile Leu Gln Lys Leu Leu Ala Leu Arg  
 100 105 110  
 Leu Pro Lys Asp Ala Arg Lys Asp Leu Gln Ile Leu Trp His Arg Leu  
 115 120 125  
 Asn Pro Glu Gln Ala Pro Leu Arg Asp Val Val Asp Gln Leu Phe Thr  
 130 135 140  
 Ile Gly Cys His Glu Ser Leu Gln Asp His Leu Leu Phe Glu Leu Tyr  
 145 150 155 160  
 Thr Val Thr Leu His Ser Gly Tyr Glu Asn Arg Lys Gln Asp Met Leu  
 165 170 175  
 Leu Ala Lys Glu Gln Gly Asp Tyr Lys Lys Ala Ile Glu Leu Ala Lys  
 180 185 190  
 Glu Leu Val Ala Ala Leu Glu Lys Gly Ser Cys Ser Pro His Pro Glu  
 195 200 205  
 Ile Val Gln Ile Glu Lys Thr Phe Leu Gln Lys Thr Leu Leu Ala Leu  
 210 215 220  
 Gln Ile Lys Val Ala Gln Glu Ala Gln Glu Ser Cys Asp Ala Leu Leu  
 225 230 235 240  
 Thr Pro Tyr Cys Leu Ser Glu Ile Ala Tyr Thr Glu Ala Met Asp Ala  
 245 250 255  
 Leu Val Leu Arg Ile Ala Arg Gly Glu Val Ser Arg Thr Asn Glu Val  
 260 265 270  
 Asp Ser Val Leu Leu Ser His Ala Leu Gln His Leu Pro Phe Ala Arg  
 275 280 285  
 Glu Lys Ala Ile Pro Glu Leu Glu Val Leu Ile Asp His Gly Ala Tyr  
 290 295 300  
 Leu Glu Ser Thr Leu Leu Tyr Tyr Ala Tyr Phe Ser Leu Leu Glu Leu  
 305 310 315 320  
 Tyr His Gln Asn Lys Asp Phe Ala Ser Leu Glu Arg Leu Leu Glu Lys  
 325 330 335  
 Gly Asp Ala Val Phe Val Pro Glu His Pro Tyr Phe Pro Glu Tyr Gly  
 340 345 350  
 Phe Phe Leu Gly Ala Tyr Phe Tyr Ala Lys Gly Lys Tyr Glu Ser Ala  
 355 360 365  
 Glu Lys Val Phe Leu Gln Ile Asp Pro Ala Val Lys Leu Gly Ala  
 370 375 380  
 Thr Phe Ala Arg Ala Tyr Glu Tyr Leu Gly Cys Ile Ala Tyr Val Gln  
 385 390 395 400  
 Asn His Tyr Glu Lys Ala Glu Glu Tyr Phe Leu Arg Ala Tyr Lys Ser  
 405 410 415  
 Trp Gly Arg Glu Glu Ser Gly Ile Gly Leu Phe Leu Ala Tyr Ala Val  
 420 425 430  
 Gln Lys Lys Lys Thr Ala Cys Glu Asp Met Leu Tyr His Pro Lys Phe  
 435 440 445  
 Ser Phe Thr Tyr Arg His Leu Leu Asp Ser Leu Cys Ser Leu Ser Tyr  
 450 455 460  
 Pro His Gly Glu Asn Lys Gly Ser Ser Ala Ile Gln Arg Val His Arg  
 465 470 475 480  
 Ala Val Pro Glu Leu Ser Glu Ile Tyr Ser Arg Cys Ile Tyr Asp Met  
 485 490 495  
 Ile Lys Tyr Arg Asn Val Thr Tyr Thr His Pro Ile Ile Glu Leu Ala  
 500 505 510  
 Tyr Asn Gln Val Arg Asn Leu Glu Lys Arg Asn Leu Glu Glu Ile Cys  
 515 520 525

Arg Asp Ala Gln Asp Pro Glu Tyr Asp Lys Ala Leu Ala Phe Trp Gly  
 530 535 540  
 Ala Leu Gln Ser Gly Ala Ser Val Pro Arg Ser Leu Ile Glu Ser Ser  
 545 550 555 560  
 Asp Val Asp Glu Ala Gly Ile Thr Ile Arg Cys Tyr Glu Ala Leu Tyr  
 565 570 575  
 Phe His Asn Pro Asp Ala Ile Ala Met Leu Pro Gln Ala Phe Ser Glu  
 580 585 590  
 Glu Cys Asn Ser Trp Gln Thr Ala Leu Arg Leu Val Trp Thr Leu Val  
 595 600 605  
 Arg Pro Lys Gly Ala Pro Asn His Ala Lys Tyr Trp Asp His Leu Val  
 610 615 620  
 Leu Arg Pro His Gly Asp Ser Leu Tyr Phe Phe Gly Tyr Asp Leu Gln  
 625 630 635 640  
 Glu Tyr Leu Ile Gly Lys Glu Asp Ala Leu Lys His Leu Ser Val Phe  
 645 650 655  
 Ala Glu Leu Phe Pro Lys Ser Ser Leu Ser Leu Val Tyr Tyr Leu  
 660 665 670  
 Gln Gly Tyr Ser Glu Ser Ser Ala Leu Arg Lys Val Gly Trp Phe Val  
 675 680 685  
 Lys Ala Leu Glu Glu Phe Thr Glu Ile Ser Trp Ser Gly Glu His Met  
 690 695 700  
 Lys Thr Trp Ala Tyr Ile Tyr Tyr Met Val Lys Leu Asp Leu Ala Asp  
 705 710 715 720  
 Thr Tyr Ile Ser Leu Gly Asn Phe Ser Gln Ala Val His Ile Leu Glu  
 725 730 735  
 Glu Val Lys Glu Asp Trp Gln Val Ala Ser His Pro Lys Leu His Phe  
 740 745 750  
 Leu Lys Gly Glu Asp Cys Tyr Leu Ala Met Glu Leu Arg Trp Val Glu  
 755 760 765  
 Gly Leu Ala Tyr Ala Tyr Phe Gln Leu His Glu Thr Ala His Leu Ser  
 770 775 780  
 Asn His Leu Leu Glu His Val Glu Lys Asn Leu Ile Ser Pro Arg Ser  
 785 790 795 800  
 Tyr Arg Asp Tyr Tyr Gly Glu Ser Leu Gln Arg Thr Leu Gly Leu Cys  
 805 810 815  
 Gln Arg Phe Leu Gly Val  
 820

&lt;210&gt;957

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;957

His Gln Leu Arg Leu Ala Ser Arg Gln Leu Phe Ala Ser Gln Arg Leu  
 1 5 10 15  
 Trp His Ala Ile Cys Arg Arg Ala Ser Pro Leu Gly Asn Arg Leu Glu  
 20 25 30  
 Phe Ser Asn Leu Pro Ala Ser Thr Pro Gly Lys Thr Val Leu Ser Leu  
 35 40 45  
 Leu Ile Glu Gly Lys Trp Arg Glu Ser Glu Ala His Ala Phe Ala Ile  
 50 55 60  
 Ala Ala Leu Ser Glu Tyr Leu Asn Ile Asn Gln Lys Pro Asp Ala Phe  
 65 70 75 80  
 Ala Leu Phe Ser Ser Gln Asp Gly Met Pro Gln His Ala Val Gly Phe  
 85 90 95  
 Leu Glu Arg Lys Glu Arg Ile Leu Pro His Leu Pro Gly Asn Leu Lys  
 100 105 110  
 Ile Val Gly Gln Asn Ile Ala Gly Pro Gly Leu Asn Arg Cys Ile Ala  
 115 120 125  
 Ser Ala Tyr His Ala Ile Cys Asp Leu His Thr Glu Glu Thr Leu Ala  
 130 135 140  
 Gln Pro Gln Ser Ser Leu  
 145 150  
 <210>958

WO 99/27105

&lt;211&gt;354

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;958

Ala Glu Arg Arg Phe Cys Val Lys Arg Ala Ile Ile Ile Gly Ala Gly  
 1 5 10 15  
 Ile Ser Gly Leu Ala Ala Gly Trp Trp Leu His Lys Lys Phe Pro Gln  
 20 25 30  
 Ala Glu Ile Leu Val Leu Asp Lys Glu Ala Tyr Ala Gly Gly Phe Val  
 35 40 45  
 Arg Thr Glu Ser Pro Gln Gly Phe Ser Phe Asp Leu Gly Pro Lys Gly  
 50 55 60  
 Phe Leu Thr Arg Gly Asp Gly Glu Tyr Thr Leu Lys Leu Ile His Glu  
 65 70 75 80  
 Leu Gly Leu Gln Asn Ser Leu Ile Phe Ser Asp Arg Ala Ala Lys Asn  
 85 90 95  
 Arg Phe Val Tyr Arg Gly Lys Ala Arg Lys Ile Ser Thr Trp Thr  
 100 105 110  
 Leu Leu Arg Lys Gly Leu Leu Pro Ser Leu Ile Lys Asp Phe Arg Ala  
 115 120 125  
 Pro Cys Tyr Thr Gln Asp Ser Ser Val Gln Asp Phe Leu Lys Arg His  
 130 135 140  
 Ser Ser Gln Asn Phe Thr Ser Tyr Ile Leu Asp Pro Leu Ile Thr Ala  
 145 150 155 160  
 Ile Arg Ala Gly His Ser Ser Ile Leu Ser Thr His Met Ala Phe Pro  
 165 170 175  
 Glu Leu Ala Lys Arg Glu Ala Ser Ser Gly Ser Leu Leu Arg Ser Tyr  
 180 185 190  
 Leu Lys Asn Arg Ser Pro Lys Lys Ser Lys Thr Asp Arg Tyr Leu Ala  
 195 200 205  
 Ser Leu Ser Pro Ser Met Gly Thr Leu Ile Thr Thr Ile Gln Glu Lys  
 210 215 220  
 Leu Pro Ala Thr Trp Lys Phe Ser Thr Ser Val Thr His Ile Asp Cys  
 225 230 235 240  
 Ser Pro Lys Glu Ala Cys Val Thr Thr Pro Ser Glu Thr Phe Phe Ala  
 245 250 255  
 Asp Met Val Ile Tyr Thr Gly Pro Leu Gln Gln Leu Pro Val Leu Leu  
 260 265 270  
 Pro Asn Tyr Gly Ile Glu Asn Leu Ser Lys Arg Val Leu Pro Trp Asn  
 275 280 285  
 Leu Ser Ser Ile Ser Leu Gly Trp His His Ala Asn Phe Ser Leu Pro  
 290 295 300  
 Lys Gly Tyr Gly Met Leu Phe Ala Asp Glu Leu Pro Leu Leu Gly Ile  
 305 310 315 320  
 Val Trp Asn Ser Gln Ile Phe Pro Gln Val Arg Gln Gly Lys Gln Cys  
 325 330 335  
 Ser Pro Phe Ser Leu Lys Ala Asn Gly Gly Asn Gln Lys Leu Met Pro  
 340 345 350  
 Leu Arg

&lt;210&gt;959

&lt;211&gt;460

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;959

Phe Leu Met Phe Asn Val Asn Phe Lys Phe Leu Glu Gly Leu His Gln  
 1 5 10 15  
 Pro Ala Pro Arg Tyr Thr Ser Tyr Pro Thr Ala Leu Glu Trp Glu Pro  
 20 25 30  
 Ser Asp Ala Ala Pro Ala Leu Leu Ala Phe Gln Arg Xaa Arg Xaa Asn  
 35 40 45  
 Xaa Gln Pro Leu Ser Leu Tyr Phe His Ile Pro Phe Cys Gln Ser Met  
 50 55 60  
 Cys Leu Tyr Cys Gly Cys Ser Val Val Leu Asn Arg Arg Glu Asp Ile

```

65          70          75          80
Val Glu Ala Tyr Ile Asn Thr Leu Ile Gln Glu Met Lys Leu Val Val
          85          90          95
Glu Thr Ile Gly Phe Arg Pro Gln Val Ser Arg Ile His Phe Gly Gly
          100          105          110
Gly Thr Pro Ser Arg Leu Ser Arg Glu Leu Phe Thr Leu Leu Phe Asp
          115          120          125
His Ile His Lys Leu Phe Asp Leu Ser His Ala Glu Glu Ile Ala Ile
          130          135          140
Glu Val Asp Pro Arg Ser Leu Arg Asn Asp Met Glu Lys Ala Asp Phe
145          150          155          160
Phe Gln Asn Val Gly Phe Asn Arg Val Ser Leu Gly Val Gln Asp Thr
          165          170          175
Gln Ala Asp Val Gln Glu Ala Val Arg Arg Arg Gln Ser His Glu Glu
          180          185          190
Ser Leu Lys Ala Tyr Glu Lys Phe Lys Glu Leu Ala Phe Gln Ser Ile
          195          200          205
Asn Ile Asp Leu Ile Tyr Gly Leu Pro Lys Gln Thr Lys Glu Ser Phe
          210          215          220
Ser Lys Thr Ile Gln Asp Ile Leu Ala Met Tyr Pro Asp Arg Leu Ala
225          230          235          240
Leu Phe Ser Phe Ala Ser Val Pro Trp Ile Lys Pro His Gln Lys Ala
          245          250          255
Met Lys Ala Ser Asp Met Pro Ser Met Glu Glu Lys Phe Ala Ile Tyr
          260          265          270
Ser Gln Ser Arg His Leu Leu Thr Lys Ala Gly Tyr Gln Ala Ile Gly
          275          280          285
Met Asp His Phe Ser Leu Pro His Asp Pro Leu Thr Leu Ala Phe Lys
          290          295          300
Asn Lys Thr Leu Ile Arg Asn Phe Gln Gly Tyr Ser Leu Pro Pro Glu
305          310          315          320
Glu Asp Leu Leu Gly Leu Gly Met Thr Ser Thr Ser Phe Ile Arg Gly
          325          330          335
Ile Tyr Leu Gln Asn Ala Lys Thr Leu Glu Glu Tyr His Asn Thr Val
          340          345          350
Leu Arg Gly Thr Phe Ala Thr Val Lys Ser Lys Ile Leu Thr Glu Asp
          355          360          365
Asp Arg Ile Arg Lys Trp Ala Ile His Lys Leu Met Cys Thr Phe Thr
          370          375          380
Ile Asn Lys Glu Glu Phe Phe Asn Leu Phe Gly Tyr Glu Phe Asp Thr
385          390          395          400
Tyr Phe Ile Glu Ser Arg Asp Arg Leu Ile Ser Met Glu Thr Thr Gly
          405          410          415
Leu Ile His Asn Ser Pro Gly Ser Leu Lys Val Thr Pro Leu Gly Glu
          420          425          430
Leu Phe Val Arg Val Ile Ala Thr Ala Phe Asp His Tyr Phe Leu Asn
          435          440          445
Lys Val Ser Lys Lys Glu Cys Phe Ser Ala Ser Ile
          450          455          460
<210>960
<211>281
<212>PRT
<213>Chlamydia pneumoniae
<400>960
Ser Tyr Cys Arg Ala Thr Leu Leu Gly Pro Ser Leu Leu His Val Asp
1          5          10          15
Ala Ala Ile Leu Phe Ala Asp Ile Leu Ser Ile Leu Asp Gly Phe Ala
          20          25          30
Val Thr Tyr Asp Phe Ala Pro Gly Pro Arg Ile Gln Phe Ser Pro Glu
          35          40          45
Gln Pro Phe Thr Phe Thr Ser Asp Pro Gln Thr Ile Phe Ser Tyr Leu
          50          55          60
Leu Asp Ala Ile Arg Thr Leu Lys Gln Lys Leu Pro Val Pro Leu Ile
          65          70          75          80

```

Val Phe Ala Ala Ser Pro Phe Thr Leu Ala Cys Tyr Leu Ile Asp Gly  
 85 90 95  
 Gly Ala Ser Lys Asp Phe Ser Lys Thr Met Ser Phe Leu Tyr Val Tyr  
 100 105 110  
 Pro Glu Lys Phe Asp Gln Leu Ile Ser Thr Ile Ile Glu Gly Thr Ala  
 115 120 125  
 Ile Tyr Leu Lys Thr Gln Met Asp Ala Gly Ala Ala Val Gln Leu  
 130 135 140  
 Phe Glu Ser Ser Ser Leu Arg Leu Pro Ser Ala Leu Phe Thr Arg Tyr  
 145 150 155 160  
 Val Thr Glu Pro Asn Arg Arg Leu Ile Ala Lys Leu Lys Glu Gln Ala  
 165 170 175  
 Ile Pro Val Ser Leu Phe Cys Arg Cys Phe Glu Glu Asn Phe Tyr Thr  
 180 185 190  
 Leu Gln Ala Thr Gln Ala Asp Thr Leu His Pro Asp Tyr His Val Asp  
 195 200 205  
 Leu His Arg Ile Gln Lys Asn Leu Met Leu Ser Leu Gln Gly Asn Leu  
 210 215 220  
 Asp Pro Ala Ile Phe Leu Leu Pro Gln Glu Lys Leu Leu His Tyr Val  
 225 230 235 240  
 Glu Ala Phe Leu Val Pro Leu Arg Thr Tyr Pro Asn Phe Ile Phe Asn  
 245 250 255  
 Ser Gly His Gly Ile Leu Pro Glu Thr Pro Leu Glu Asn Val Gln Leu  
 260 265 270  
 Val Val Ser Tyr Val Gln Arg Gln Leu  
 275 280

&lt;210&gt;961

&lt;211&gt;1085

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;961

Met Ala Met Asp Phe Asn Pro Val Asn Leu Asp Phe Ser Ile Ser Lys  
 1 5 10 15  
 Glu Phe Lys Glu Glu Thr Leu Pro Leu Leu Leu Glu Asn Ile His Pro  
 20 25 30  
 Gly Ala Thr Ala Phe Leu Ala Ala Lys Met Phe His Asp Cys Arg Ala  
 35 40 45  
 Ser Val Ile Met Ile Thr Thr Pro Ala Arg Leu Asp Asp Leu Phe Glu  
 50 55 60  
 Asn Leu Arg Thr Phe Leu Asp Gln Ala Pro Val Glu Phe Pro Ser Ser  
 65 70 75 80  
 Glu Ile Asp Leu Ser Pro Lys Leu Val Asn Ile Asp Ala Val Gly Lys  
 85 90 95  
 Arg Asp His Leu Leu Tyr Ser Leu Asn Gln His Arg Ala Pro Ile Phe  
 100 105 110  
 Cys Val Thr Thr Leu Lys Ala Leu Leu Glu Lys Thr Arg Ser Pro Gln  
 115 120 125  
 Ala Thr Ser Gln Gln His Leu Asp Leu Ala Val Gly Asp Val Leu Asp  
 130 135 140  
 Pro Glu Ala Thr Thr Glu Leu Cys Lys Ser Leu Gly Tyr Ser Gln Val  
 145 150 155 160  
 Met Leu Thr Ser Glu Lys Gly Glu Phe Ser Cys Arg Gly Gly Ile Val  
 165 170 175  
 Asp Ile Phe Pro Leu Ser Ser Pro Glu Pro Phe Arg Ile Glu Phe Trp  
 180 185 190  
 Gly Glu Lys Ile Ile Ser Ile Arg Ser Tyr Asn Pro Ser Asp Gln Leu  
 195 200 205  
 Ser Thr Gly Lys Val Ser Lys Ile Ser Ile Ser Pro Ala Tyr Thr Glu  
 210 215 220  
 Glu Ala Ser Gly Gly Asn Tyr Ser His Ser Leu Leu Asp Tyr Phe Ser  
 225 230 235 240  
 Thr Pro Pro Leu Tyr Leu Phe Asp Asn Leu Glu Ile Leu Glu Asp Asp  
 245 250 255  
 Phe Ala Asp Ile Ser Gly Thr Leu Ser Ser Leu Pro Asp Arg Phe Phe



1001

```

      770              775              780
Leu Ala Glu Thr Ile Arg Asn Leu Ile Pro Glu Ala Arg Ile Gly Val
785              790              795              800
Ala His Gly Gln Met Gly Ala Glu Asp Leu Ser Asn Ile Phe Thr Lys
      805              810              815
Phe Lys Asn Gln Lys Thr Asp Ile Leu Val Ala Thr Ala Leu Ile Glu
      820              825              830
Asn Gly Ile Asp Ile Pro Asn Ala Asn Thr Ile Leu Ile Asp His Ala
      835              840              845
Asp Lys Phe Gly Met Ala Asp Leu Tyr Gln Met Lys Gly Arg Val Gly
      850              855              860
Arg Trp Asn Lys Lys Ala Tyr Cys Tyr Phe Leu Val Pro His Leu Asp
865              870              875              880
Arg Leu Ser Gly Pro Ala Ala Lys Arg Leu Ala Ala Leu Asn Lys Gln
      885              890              895
Glu Tyr Gly Gly Gly Met Lys Ile Ala Leu His Asp Leu Glu Ile Arg
      900              905              910
Gly Ala Gly Asn Ile Leu Gly Thr Asp Gln Ser Gly His Ile Gly Thr
      915              920              925
Ile Gly Phe Asn Leu Tyr Cys Lys Leu Leu Lys Lys Ala Val Ser Ala
      930              935              940
Leu Lys Lys His Thr Ser Pro Leu Leu Phe Asn Asp Asp Val Lys Ile
945              950              955              960
Glu Phe Pro Tyr Asn Ser Arg Ile Pro Asp Thr Tyr Ile Glu Thr Gly
      965              970              975
Ser Met Arg Ile Glu Phe Tyr Gln Lys Ile Gly Asn Ala Glu Ser Ser
      980              985              990
Glu Glu Leu Thr Ala Ile Gln Glu Glu Met Arg Asp Arg Phe Gly Pro
      995              1000              1005
Leu Pro Gln Glu Ile Cys Trp Leu Phe Ala Leu Ala Glu Ile Arg Leu
1010              1015              1020
Phe Ala Leu Gln His Gly Ile Ser Ser Ile Lys Gly Thr Ala Asn Ala
1025              1030              1035              1040
Leu Tyr Val Gln Lys Cys Leu Ser Lys Ser Glu Gln Thr Lys Lys Thr
      1045              1050              1055
Leu Pro Tyr Ala Leu Ser Pro Thr Pro Glu Leu Leu Val Lys Glu Val
      1060              1065              1070
Ile Glu Ser Ile Glu Arg Gly Phe Leu Ile Asn Ala Ser
      1075              1080              1085
<210>962
<211>182
<212>PRT
<213>Chlamydia pneumoniae
<400>962
Gly Gly His Trp Arg Lys Ser Arg Ser Tyr Ser Thr Pro Thr Lys Arg
 1      5      10      15
Ser Ile Arg Arg Asp Cys Thr Leu Leu Gln Val Pro Arg Asp Gln Ile
      20      25      30
Val Ser Arg Leu Thr Ala Thr Leu Asp Glu Arg Lys Gln Gln Asp Lys
      35      40      45
Arg Leu Asn Glu Leu Glu Asn Ser Leu Ile Gln Thr Lys Leu Asp Lys
      50      55      60
Leu Ile His Asn Cys His Gln Arg Gln Gly Ile Thr Cys Leu Val His
      65      70      75      80
His Leu Ala Glu His Glu Asn His Arg Leu Gln Gln Tyr Ala Gln Cys
      85      90      95
Leu His Gln Arg Ile Pro Glu Lys Leu Ile Ser Leu Trp Thr Thr Glu
      100      105      110
Lys Asn Gly Lys Tyr Ile Val Leu Ser Arg Val Ser Asp Asp Leu Ile
      115      120      125
Thr Gln Gly Val His Ala Gln Asp Leu Leu Lys Ala Val Leu Thr Pro
      130      135      140
Cys Gly Gly Arg Trp Gly Gly Lys Asp Gln Ser Ala Gln Gly Ser Ala
145      150      155      160

```

Pro Ala Leu Pro Ala Thr Glu Val Leu Asn Glu Thr Leu Trp Gln Trp  
 165 170 175  
 Ile Ser Thr Gln Leu Ile  
 180  
 <210>963  
 <211>482  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>963  
 Ser Gly Cys Val Ala Arg Leu Ile Ala Lys Thr Glu Gln Leu Ser Gly  
 1 5 10 15  
 Lys Val Tyr His Pro Asp Asp Ser Gly Ala Ala Phe Arg Val Ile Ala  
 20 25 30  
 Asp His Val Arg Ser Leu Ser Phe Ala Ile Ala Asp Gly Leu Leu Pro  
 35 40 45  
 Gly Asn Thr Glu Arg Gly Tyr Val Leu Arg Lys Ile Leu Arg Arg Ser  
 50 55 60  
 Val Asn Tyr Gly Arg Arg Leu Gly Phe Arg Asn Pro Phe Leu Ala Glu  
 65 70 75 80  
 Ile Val Pro Ser Leu Ala Asp Ala Met Gly Glu Ala Tyr Pro Glu Leu  
 85 90 95  
 Lys Asn Ser Leu Ser Gln Ile Gln Lys Val Leu Thr Leu Glu Glu Glu  
 100 105 110  
 Ser Phe Phe Lys Thr Leu Asp Arg Gly Gly Asn Leu Leu Gln Gln Val  
 115 120 125  
 Leu Lys Ser Ser Ser Ser Ser Ser Cys Ile Ser Gly Glu Asp Ala Phe  
 130 135 140  
 Lys Leu Lys Asp Thr Tyr Gly Met Pro Ile Asp Glu Ile Ser Leu Leu  
 145 150 155 160  
 Ala Lys Asp Tyr Asp Tyr Ser Val Asp Met Asp Thr Phe His Lys Leu  
 165 170 175  
 Glu Gln Glu Ala Lys Glu Arg Ser Arg Lys Asn Val Val Gln Ser Gln  
 180 185 190  
 Gly Thr Ser Glu Ser Ile Tyr Asn Glu Leu His Leu Thr Ser Glu Phe  
 195 200 205  
 Ile Gly Tyr Asp His Leu Ser Cys Asp Thr Phe Ile Glu Ala Ile Ile  
 210 215 220  
 Ser Lys Asp His Ile Val Ser Ser Leu Gln Glu Lys Gln Glu Gly Ala  
 225 230 235 240  
 Ile Val Leu Lys Val Ser Pro Phe Tyr Ala Glu Lys Gly Gly Gln Val  
 245 250 255  
 Gly Asp Ser Gly Glu Ile Phe Cys Ser Glu Gly Thr Phe Ile Val Thr  
 260 265 270  
 His Thr Thr Ser Pro Lys Ala Gly Leu Ile Val His His Gly Arg Ile  
 275 280 285  
 Ser Gln Gly Ser Leu Thr Val Glu Ala Ala Val Thr Ala Gln Val Asn  
 290 295 300  
 Arg Tyr Arg Arg Lys Arg Ile Ala Asn Asn His Thr Ala Cys His Leu  
 305 310 315 320  
 Leu His Lys Ala Leu Glu Ile Thr Leu Gly Asp His Ile Arg Gln Ala  
 325 330 335  
 Gly Ser Tyr Val Asp Asp Thr Lys Ile Arg Leu Asp Phe Thr His Pro  
 340 345 350  
 Gln Ala Ile Ser Pro Glu Asp Leu Leu Cys Ile Glu Thr Leu Val Asn  
 355 360 365  
 Glu Ser Ile Arg Glu Asn Glu Pro Val Asp Ile Arg Glu Ala Leu Tyr  
 370 375 380  
 Ser Asp Val Met Asn Ser Ser Glu Ile Lys Gln Phe Phe Gly Asp Lys  
 385 390 395 400  
 Tyr Ser Asp Val Val Arg Val Val Ser Ala Gly His Ser His Glu Leu  
 405 410 415  
 Cys Gly Gly Thr His Ala Glu Ala Thr Gly Asp Ile Gly Phe Phe Arg  
 420 425 430  
 Ile Thr Lys Glu His Ala Val Ala Met Gly Ile Arg Arg Ile Glu Ala

435 440 445  
 Val Thr Gly Glu Lys Ala Glu Ala Thr Val His Gln Gln Ser Glu Val  
 450 455 460  
 Leu Glu Glu Ile Val Arg Tyr Tyr Lys Ser Leu Gly Ile Arg Leu Ser  
 465 470 475 480  
 Pro Gly

&lt;210&gt;964

&lt;211&gt;129

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;964

Ser Arg Arg Ile Tyr Ala Thr Val His Glu Lys Asp Asp Glu Ala Phe  
 1 5 10 15  
 Ala Leu Trp Glu Ala Tyr Leu Pro Thr Asp Arg Ile Phe Arg Leu Thr  
 20 25 30  
 Asp Lys Asp Asn Phe Trp Ser Met Ala Asn Thr Gly Pro Cys Gly Tyr  
 35 40 45  
 Cys Ser Glu Leu Leu Phe Asp Arg Gly Pro Ser Phe Gly Asn Ala Ser  
 50 55 60  
 Ser Pro Leu Asp Asp Thr Asp Gly Glu Arg Phe Leu Glu Tyr Trp Asn  
 65 70 75 80  
 Leu Val Phe Met Glu Phe Asn Arg Thr Ser Glu Gly Ser Leu Leu Ala  
 85 90 95  
 Leu Pro Asn Lys His Val Asp Thr Gly Ala Gly Leu Glu Arg Leu Val  
 100 105 110  
 Ser Leu Ile Ala Gly Thr His Thr Val Phe Glu Ala Asp Val Leu Arg  
 115 120 125  
 Asp

&lt;210&gt;965

&lt;211&gt;195

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;965

Met Leu Ser Asn Thr Ile Arg Ser Asn Phe Leu Lys Phe Tyr Ala Asn  
 1 5 10 15  
 Arg His His Thr Ile Leu Pro Ser Ser Pro Val Phe Pro His Asn Asp  
 20 25 30  
 Pro Ser Ile Leu Phe Thr Asn Ala Gly Met Asn Gln Phe Lys Asp Ile  
 35 40 45  
 Phe Leu Asn Lys Glu Lys Val Ser Tyr Ser Arg Ala Thr Thr Ser Gln  
 50 55 60  
 Lys Cys Ile Arg Ala Gly Gly Lys His Asn Asp Leu Asp Asn Val Gly  
 65 70 75 80  
 His Thr Ser Arg His Leu Thr Phe Phe Glu Met Leu Gly Asn Phe Ser  
 85 90 95  
 Phe Gly Asp Tyr Phe Lys Ala Glu Ala Ile Ala Phe Ala Trp Glu Val  
 100 105 110  
 Ser Leu Ser Val Phe Asn Phe Asn Pro Glu Gly Phe Thr Leu Pro Tyr  
 115 120 125  
 Met Lys Lys Thr Met Lys His Leu Leu Phe Gly Lys His Ile Phe Leu  
 130 135 140  
 Gln Ile Val Phe Ser Val Leu Gln Thr Lys Thr Thr Ser Gly Ala Trp  
 145 150 155 160  
 Gln Thr Gln Ala Pro Val Ala Ile Val Pro Ser Ser Ser Leu Ile Val  
 165 170 175  
 Ala Pro Val Leu Glu Thr Pro Leu Leu Pro Leu Thr Ile Leu Met Glu  
 180 185 190  
 Ser Val Ser  
 195  
 <210>966  
 <211>692  
 <212>PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;966

```

Leu Gly Ile Ser Tyr Ser Cys Cys Phe Tyr Ile Glu Gly Leu Gln Gly
 1          5          10          15
Leu Leu Met Ile Asn Lys Glu Leu Asp Ile Gly Ile Leu Gly Lys Ile
          20          25          30
Ala Gly Ala Ile Lys Gln Ile Ser Ile Glu Ser Ile Gln Lys Ala Ser
          35          40          45
Ser Gly His Pro Gly Leu Pro Leu Gly Cys Ala Glu Leu Ala Ala Tyr
          50          55          60
Leu Tyr Gly Tyr Val Leu Arg Gln Asn Pro Arg Asp Pro His Trp Ile
          65          70          75          80
Asn Arg Asp Arg Phe Val Leu Ser Ala Gly His Gly Ser Ala Leu Leu
          85          90          95
Tyr Ser Cys Leu His Leu Ala Gly Phe Asp Val Ser Leu Glu Asp Leu
          100          105          110
Gln Glu Phe Arg Gln Leu His Ser Arg Thr Pro Gly His Pro Glu Tyr
          115          120          125
Gly Glu Thr Val Gly Val Glu Ala Thr Thr Gly Pro Leu Gly Gln Gly
          130          135          140
Leu Gly Asn Ala Val Gly Met Ala Leu Ser Met Lys Met Leu Glu Ser
          145          150          155          160
Arg Phe Asn Arg Pro Gly His Glu Ile Phe Asn Gly Lys Ile Tyr Cys
          165          170          175
Leu Ala Gly Asp Gly Cys Phe Met Glu Gly Val Ser His Glu Val Cys
          180          185          190
Ser Phe Ala Gly Ser Leu Asn Leu Asn Asn Leu Val Val Ile Tyr Asp
          195          200          205
Tyr Asn Asn Val Val Leu Asp Gly Tyr Leu Asn Glu Ile Ser Val Glu
          210          215          220
Asp Thr Lys Lys Arg Phe Glu Ala Tyr Gly Trp Glu Tyr Tyr Glu Ile
          225          230          235          240
Asp Gly Tyr Asp Phe Thr His Ile His Glu Thr Phe Ser Ser Ile Lys
          245          250          255
Arg Gly Gln Glu Arg Pro Val Leu Val Ile Ala His Thr Ile Ile Gly
          260          265          270
His Gly Ser Pro Lys Glu Gly Thr Asn Lys Ala His Gly Ser Pro Leu
          275          280          285
Gly Val Glu Gly Thr His Glu Thr Lys Gln Phe Trp His Leu Pro Glu
          290          295          300
Glu Lys Phe Phe Val Pro Pro Ala Val Lys Asn Phe Phe Ala His Lys
          305          310          315          320
Ile Gln Glu Asp Arg Lys Ala Gln Glu Gln Trp Leu Asp Glu Val Arg
          325          330          335
Val Trp Ser Lys Gln Phe Pro Glu Leu His Glu Glu Phe Val Ala Leu
          340          345          350
Thr Ser His Lys Leu Pro Lys Asn Leu Glu Ser Leu Val Gln Ser Val
          355          360          365
Glu Met Pro Asp Ser Ile Ala Gly Arg Ala Ala Ser Asn Lys Leu Ile
          370          375          380
Gln Val Leu Val Gln His Ile Pro Tyr Leu Ile Gly Gly Ser Ala Asp
          385          390          395          400
Leu Ser Ser Ser Asp Gly Thr Trp Ile Ala Asn Glu Lys Val Ile His
          405          410          415
Thr Tyr Asp Phe Ser Gly Arg Asn Ile Lys Tyr Gly Val Arg Glu Phe
          420          425          430
Gly Met Ala Thr Ile Met Asn Gly Leu Ala Tyr Ser Gln Val Phe Arg
          435          440          445
Pro Phe Gly Gly Thr Phe Leu Val Phe Ser Asp Tyr Met Arg Asn Ala
          450          455          460
Ile Arg Leu Ala Ala Leu Ser Lys Leu Pro Val Ile Tyr Gln Phe Thr
          465          470          475          480
His Asp Ser Ile Phe Val Gly Glu Asp Gly Pro Thr His Gln Pro Val
          485          490          495

```

Glu Gln Leu Met Ser Leu Arg Ala Ile Pro Gly Leu Tyr Val Ile Arg  
 500 505 510  
 Pro Ala Asp Ala Asn Glu Val Arg Gly Ala Trp Ile Ala Gly Leu Lys  
 515 520 525  
 His Thr Gly Pro Thr Val Ile Val Leu Ser Arg Gln Ala Leu Pro Thr  
 530 535 540  
 Leu Pro Ala Ala His Arg Pro Phe Lys Asp Gly Val Gly Arg Gly Ala  
 545 550 555 560  
 Tyr Ile Val Leu Lys Glu Ser Gly Glu Lys Pro Asp Tyr Thr Leu Phe  
 565 570 575  
 Ala Thr Gly Ser Glu Val Ser Leu Ala Leu Ser Val Ala Lys Glu Leu  
 580 585 590  
 Glu His Leu Asp Lys Gln Val Arg Val Val Ser Phe Pro Cys Trp Glu  
 595 600 605  
 Leu Phe Glu Ala Gln Asp Val Asp Tyr Lys Gln Ser Ile Val Gly Gly  
 610 615 620  
 Asp Leu Gly Ile Arg Val Ser Ile Glu Ala Gly Ser Ala Leu Gly Trp  
 625 630 635 640  
 Tyr Lys Tyr Ile Gly Ser Glu Gly Leu Leu Ser Leu Trp Ile Asp Ser  
 645 650 655  
 Asp Thr Gln Glu Leu Leu Met Met Tyr Gln Lys Asn Val Ala Leu Leu  
 660 665 670  
 Gln Ser Lys Ser Phe Arg Gly Phe Ser Leu Asn Ser His Cys Arg Lys  
 675 680 685  
 Phe Gln Ser Arg  
 690  
 <210>967  
 <211>312  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>967  
 Pro Arg Asn Asp Lys Asn Ala Lys Asn Leu Arg Arg Lys His Tyr Lys  
 1 5 10 15  
 Gly Glu Arg Val Ser Lys His Thr Ser Glu Ser Arg Ile Ala Gln Asp  
 20 25 30  
 Met Leu Glu Arg Tyr Ser Gly Ser Ser Val Lys Gln Phe Cys Pro Tyr  
 35 40 45  
 Leu Leu Leu Thr Asn Phe Ser Tyr Tyr Ile Gln Thr Phe Ala Lys Leu  
 50 55 60  
 His Gly Val Pro Val Phe Glu Gly Ser Met Phe Ser Ala Ala His Ala  
 65 70 75 80  
 Pro His Leu Lys Thr Ser Ile Leu Asp Phe Lys Leu Gly Ser Pro Gly  
 85 90 95  
 Ala Ala Leu Thr Ile Asp Leu Cys Ser Phe Leu Pro Asp Leu Lys Ala  
 100 105 110  
 Ala Leu Met Leu Gly Met Cys Gly Glu Arg Ser His Tyr Gln Val  
 115 120 125  
 Gly Asp Tyr Phe Val Pro Val Ala Ser Ile Arg Gly Glu Gly Thr Ser  
 130 135 140  
 Asp Ala Tyr Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val Val  
 145 150 155 160  
 Gln Lys Ala Thr Thr Glu Val Leu Glu Asp Lys Lys Ala Asn Tyr His  
 165 170 175  
 Ile Gly Ile Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn Lys  
 180 185 190  
 Lys Phe Arg Lys Lys Leu Tyr Glu Thr Lys Ala Gln Ser Ala Glu Met  
 195 200 205  
 Glu Cys Ala Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro Ile  
 210 215 220  
 Gly Ala Leu Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Glu Gly Ile  
 225 230 235 240  
 Lys Thr Lys Ser Ser Gly Asn Phe Ile Phe Asn Thr Tyr Thr Glu Asp  
 245 250 255  
 His Ile Leu Thr Gly Gln Glu Val Ile Glu Asn Leu Glu Lys Val Met

260 265 270  
 Leu Lys Arg Ala Ala Ser Asp His Lys Lys Asp Gln Gln Tyr Arg Gly  
 275 280 285  
 Leu Pro His Met Glu Val Gly Glu Ala Asp Asp Thr Met Ala Ser Gly  
 290 295 300  
 Ser Glu Thr Ser Asp Ser Asp Tyr  
 305 310

&lt;210&gt;968

&lt;211&gt;190

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;968

Met Val Arg Val Ser Thr Ser Glu Phe Arg Val Gly Leu Arg Ile Glu  
 1 5 10 15  
 Ile Asp Gly Gln Pro Tyr Leu Ile Leu Gln Asn Asp Phe Val Lys Pro  
 20 25 30  
 Gly Lys Gly Gln Ala Phe Asn Arg Ile Lys Val Lys Asn Phe Leu Thr  
 35 40 45  
 Gly Arg Val Ile Glu Arg Thr Tyr Lys Ser Gly Glu Ser Val Glu Thr  
 50 55 60  
 Ala Asp Ile Val Glu Arg Ser Met Arg Leu Leu Tyr Thr Asp Gln Glu  
 65 70 75 80  
 Gly Ala Thr Phe Met Asp Asp Glu Thr Phe Glu Gln Glu Val Val Phe  
 85 90 95  
 Trp Glu Lys Leu Glu Asn Ile Arg Gln Trp Leu Leu Glu Asp Thr Ile  
 100 105 110  
 Tyr Thr Leu Val Leu Tyr Asn Gly Asp Val Val Ala Val Glu Pro Pro  
 115 120 125  
 Ile Phe Met Glu Leu Ser Ile Ala Glu Thr Ala Pro Gly Val Arg Gly  
 130 135 140  
 Asp Thr Ala Ser Gly Arg Val Leu Lys Pro Ala Val Thr Asn Thr Gly  
 145 150 155 160  
 Ala Lys Ile Met Val Pro Ile Phe Ile Asp Glu Gly Glu Leu Val Lys  
 165 170 175  
 Val Asp Thr Arg Thr Gly Ser Tyr Glu Ser Arg Val Ser Lys  
 180 185 190

&lt;210&gt;969

&lt;211&gt;83

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;969

Glu Lys Tyr Phe Phe Phe Thr Val Arg Asn Met Glu Ala Lys Lys Ile  
 1 5 10 15  
 Lys Glu Leu Ser Lys Glu Ala Gln Leu Lys Lys Leu Arg Glu Lys  
 20 25 30  
 Ser Arg Val Leu Asp Glu Lys Asn Lys Arg Lys Ala Trp Val Ala Lys  
 35 40 45  
 Leu Val Ala Met Pro Glu Ser Ile Arg Glu Ile Glu Lys Glu Glu Arg  
 50 55 60  
 Val Glu Thr Pro Gln Leu Phe Gln Ala Ile Ala Glu Lys Ile Leu Glu  
 65 70 75 80  
 Glu Gly Val

&lt;210&gt;970

&lt;211&gt;314

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;970

Asn Phe Ser Leu Asp Ser Asn Thr Val Asp Gln Lys Asn Lys Ser Asn  
 1 5 10 15  
 Pro Arg Pro Met Gln Glu Lys Pro Arg His Val His Arg Ile Ile His  
 20 25 30  
 Ile Ser Asp Val His Phe His Val Leu Pro Val Asn Pro Val His Cys  
 35 40 45

Phe Asn Lys Arg Leu Lys Gly Leu Leu Arg Lys Val Phe Gly Leu Val  
 50 55 60  
 His Phe Gln Ala Thr Thr Ile Gly Gln Arg Phe Pro Lys Val Val Arg  
 65 70 75 80  
 Ser Leu Gly Ala Asp Ser Val Cys Ile Thr Gly Asp Phe Ser Leu Thr  
 85 90 95  
 Ala Met Asp Gly Glu Phe Leu Leu Ala Lys His Phe Val Glu Thr Leu  
 100 105 110  
 Ala Lys His Ser Ser Val Tyr Leu Leu Pro Gly Asn His Asp Val Tyr  
 115 120 125  
 Thr Leu Lys Ser Leu Ala Gln Gln Thr Phe Tyr Thr His Phe Pro Asn  
 130 135 140  
 Asp Gln Leu Gln Gln Asn Lys Val Ser Phe His Lys Ile Thr Asp His  
 145 150 155 160  
 Trp Trp Leu Ile Leu Leu Asp Cys Ser Cys Leu Asn Gly Trp Phe Ser  
 165 170 175  
 Ala Asn Gly Val Val His Leu Ala Gln Ile Ser Ala Ile Glu Thr Phe  
 180 185 190  
 Leu Leu Ser Leu Ser Pro Glu Glu Asn Val Ile Ile Ala Asn His Tyr  
 195 200 205  
 Pro Leu Leu Ser Ser Gln Asn Pro Ser His Asp Leu Ile Asn Asn Thr  
 210 215 220  
 His Leu Gln Asn Val Leu Lys Lys Tyr Pro Lys Val Arg Leu Tyr Leu  
 225 230 235 240  
 His Gly His Glu His Gln Ala Ala Val Tyr Asn Cys Ala Asp Thr Ser  
 245 250 255  
 Pro Ser Tyr Ile Leu Asn Ser Gly Ser Ile Ser Leu Pro Thr Asn Ser  
 260 265 270  
 Arg Phe His Val Ile Asp Leu Tyr Pro Glu Lys Tyr Gln Val His Thr  
 275 280 285  
 Met Ile Leu Lys Asn Leu Leu Asp Phe Asp Ala Pro Leu Glu Ile Ala  
 290 295 300  
 Asn Glu Ala Thr Trp Asp Cys Gln Lys Leu  
 305 310

&lt;210&gt;971

&lt;211&gt;519

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;971

Met Ser Glu Gln Glu Lys Leu Ser Asn Tyr Asn Ala Asp Lys Lys Leu  
 1 5 10 15  
 Phe Ser Gly Ile Asp Lys Leu Phe Gln Ile Val Lys Gly Ser Tyr Gly  
 20 25 30  
 Pro Lys Gln Ser Leu Ser Pro Thr Ser Phe Phe Lys Glu Arg Gly Phe  
 35 40 45  
 Tyr Ala Ile Ser Gln Thr Glu Leu Ser Asn Ser Tyr Glu Asn Leu Gly  
 50 55 60  
 Val Asp Phe Ala Lys Ala Met Val Asn Lys Ile His Lys Glu His Ser  
 65 70 75 80  
 Asp Gly Ala Thr Thr Gly Leu Ile Leu Leu His Ala Ile Leu Gln Glu  
 85 90 95  
 Ser Tyr Ala Ala Leu Glu Lys Gly Ile Ser Thr His Lys Leu Ile Ala  
 100 105 110  
 Ser Leu Lys Leu Gln Gly Glu Lys Leu Gln Glu Ala Leu Gln Gln Gln  
 115 120 125  
 Ser Trp Pro Ile Lys Asp Ala Leu Lys Val Arg Asn Ile Ile Phe Ser  
 130 135 140  
 Ser Leu His Met Pro Thr Ile Ala Asp His Phe Tyr Asn Ala Phe Ser  
 145 150 155 160  
 Val Val Gly Pro Glu Gly Leu Ile Ser Ile Thr Lys Glu Arg Glu Asn  
 165 170 175  
 Asp Lys Thr Ser Met Asp Val Phe Gln Gly Phe Lys Ile Pro Ala Gly  
 180 185 190  
 Tyr Ala Ser Thr Tyr Phe Val Ser Asp Thr Ala Ser Arg Leu Thr Arg



195 200 205  
 Ile Ala His Pro Leu Ile Leu Ile Thr Asp Arg Lys Ile Ser Met Ile  
 210 215 220  
 His Ser Leu Leu Pro Leu Leu Gln Glu Ile Ser Glu Gln Asn Gln His  
 225 230 235 240  
 Leu Ile Ile Phe Cys Glu Asp Ile Asp Pro Asp Val Leu Ala Thr Leu  
 245 250 255  
 Val Val Asn Lys Leu Gln Gly Leu Leu Gln Val Thr Val Val Thr Ile  
 260 265 270  
 Pro Gln Leu Ser Thr Thr Asn Gln Glu Leu Ala Glu Asp Ile Ala Leu  
 275 280 285  
 Phe Thr Gly Thr His Ile Cys Pro Cys Gln Glu Ala Ser His Val Leu  
 290 295 300  
 Ala Pro Glu Met Val Thr Leu Gly Ser Cys Leu Ser Ile Glu Ile Ser  
 305 310 315 320  
 Glu Ser Gln Thr Thr Leu Ile Gly Gly Leu His Ile Pro Glu Val Leu  
 325 330 335  
 Thr Leu Lys Thr Arg Gln Leu Ala Glu Glu Ile Arg Thr Thr Ser Cys  
 340 345 350  
 Leu Glu Thr Lys Lys Arg Leu Ile Lys Ser Thr Asn Arg Leu Gln Ser  
 355 360 365  
 Ser Val Ala Ile Leu Pro Thr Asp Glu Asp Asn Glu Pro Leu Tyr Thr  
 370 375 380  
 Leu Ala Leu Lys Ile Met Glu Ser Ala Leu Ser Arg Gly Tyr Val Pro  
 385 390 395 400  
 Gly Gly Gly Val Ala Leu Phe Tyr Ala Ser Leu Thr Leu Gly Thr Pro  
 405 410 415  
 Lys Asp Asp Ala Asp Glu Asn Ser Ile Ala Ile Ser Leu Leu Gln Lys  
 420 425 430  
 Ala Cys Cys Ala Pro Leu Lys Leu Leu Ala Thr Asn Ala Asp Leu Asp  
 435 440 445  
 Gly Asp Ala Val Ile Ala Lys Leu Ser Ser Leu Gly Thr Thr Ser Leu  
 450 455 460  
 Gly Ile Ser Val Phe Ser Arg Glu Ile Glu Asp Leu Ile Ala Gly Gly  
 465 470 475 480  
 Ile Leu Asp Ser Leu Ala Thr Thr Ser Thr Ile Leu Ala Gln Ala Leu  
 485 490 495  
 Asp Thr Ala Ile Leu Val Leu Ser Ser Lys Ile Leu Ile Leu Glu Asn  
 500 505 510  
 Gln Tyr Glu Ile Ser Thr Leu  
 515

&lt;210&gt;972

&lt;211&gt;447

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;972

Met Arg Ala Met Leu Leu Glu Asp Trp Val Ser Leu Met Leu Ser Asp  
 1 5 10 15  
 Val Ser Cys Pro Lys Cys Asp Lys Lys Ile Thr Gly Phe Ala Ile Asp  
 20 25 30  
 Ser Gln Lys Val Gln Pro Gly Asp Leu Phe Phe Ala Leu Pro Gly Asn  
 35 40 45  
 Ala Thr Asp Gly His Gln Phe Leu Lys His Ala Ala Thr Ala Gly Ala  
 50 55 60  
 Val Ala Ala Val Val Ser His Asp Tyr Gln Gly Asp Ser Phe Gly Leu  
 65 70 75 80  
 Glu Leu Ile Arg Val Asp Asp Thr Lys Ser Ala Leu Gln Glu Ala Gly  
 85 90 95  
 Ser Asn Gln Cys Asn Leu Phe Gln Gly Thr Leu Val Gly Ile Thr Gly  
 100 105 110  
 Ser Val Gly Lys Thr Thr Thr Lys Glu Phe Ser Lys Thr Ile Leu Ser  
 115 120 125  
 Ser Ile Tyr Lys Thr His Ala Ser Pro Lys Ser Tyr Asn Ser Gln Leu  
 130 135 140

Thr Val Pro Leu Ser Leu Leu Met Ala Glu Gly Asp Glu Asp Val Met  
 145 150 155 160  
 Ile Leu Glu Met Gly Val Ser Glu Pro Gly Asn Met Gln Asp Leu Leu  
 165 170 175  
 Arg Ile Val Gln Pro Glu Ile Ala Val Ile Thr His Ile Asn Asp Gln  
 180 185 190  
 His Ala Met His Phe Pro Gln Gly Ile Gln Glu Ile Leu Lys Glu Lys  
 195 200 205  
 Ser Tyr Ile Leu Gln Lys Ser Lys Leu Gln Leu Leu Pro Lys Asp Ser  
 210 215 220  
 Pro Tyr Tyr Leu Asp Leu Arg Ser Cys Ser Pro Thr Ala Glu Lys Phe  
 225 230 235 240  
 Ser Phe Ser Phe Asn Asp Pro Leu Ala Asp Phe Cys Tyr Lys Ala Ile  
 245 250 255  
 Ser Gly Asp Ser Val Val Ile Gln Thr Pro Glu Glu Asn Tyr Cys Leu  
 260 265 270  
 Pro Ile Ala Phe Ser Tyr Lys Pro Ala Tyr Thr Asn Leu Leu Ile Ala  
 275 280 285  
 Val Ala Leu Ser Trp Ile Leu Glu Val Pro Glu Glu Gly Val Ile Arg  
 290 295 300  
 Ser Leu Pro Glu Leu Lys Leu Pro Pro Met Arg Phe Glu His Ser Met  
 305 310 315 320  
 Arg Asn Gly Met Gln Val Ile Asn Asp Ala Tyr Asn Ala Cys Pro Glu  
 325 330 335  
 Ala Met Ile Ala Ala Leu Asp Ala Leu Pro Leu Pro Ser Asp Gly Gly  
 340 345 350  
 Lys Ile Ile Leu Ile Leu Gly His Met Ala Glu Leu Gly Arg Tyr Ser  
 355 360 365  
 Glu Glu Gly His Ala Leu Val Ala Glu Lys Ala Ala Ser Arg Gly Asp  
 370 375 380  
 Met Ile Phe Phe Ile Gly Glu Lys Trp Ile Pro Val Gln Ser Val Leu  
 385 390 395 400  
 Lys Ser Tyr Ser Cys Glu Val Ser Phe Phe Ser Ser Ala Gln Asp Val  
 405 410 415  
 Lys Asp Ile Leu Lys Gln Val Ala Arg Tyr Gly Asp Val Ile Leu Leu  
 420 425 430  
 Lys Gly Ser Arg Ala Leu Ala Leu Glu Ser Leu Leu Ala Cys Phe  
 435 440 445

&lt;210&gt;973

&lt;211&gt;349

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;973

Met Ile Pro Leu Ile Pro Met Phe Leu Lys Gln Ser Leu Phe Phe Ser  
 1 5 10 15  
 Leu Ala Leu Thr Gly Met Thr Thr Leu Val Leu Thr Val Ser Leu Gly  
 20 25 30  
 Val Pro Val Met Lys Trp Leu Lys Arg Lys Asn Tyr Arg Asp Tyr Ile  
 35 40 45  
 His Lys Glu Tyr Cys Glu Lys Leu Glu Met Leu His Lys Asp Lys Ala  
 50 55 60  
 Glu Val Pro Thr Gly Gly Val Leu Leu Phe Ile Ser Leu Ile Ala  
 65 70 75 80  
 Ser Leu Leu Val Trp Leu Pro Trp Gly Lys Phe Ser Thr Trp Phe Phe  
 85 90 95  
 Ile Ile Leu Leu Thr Cys Tyr Ala Gly Leu Gly Trp Tyr Asp Asp Arg  
 100 105 110  
 Ile Lys Ile Lys Arg Lys Gln Gly His Gly Leu Lys Ala Lys His Lys  
 115 120 125  
 Phe Met Val Gln Ile Ala Ile Ala Ala Phe Thr Leu Ile Ala Leu Pro  
 130 135 140  
 Tyr Ile Tyr Gly Ser Thr Glu Pro Leu Trp Thr Leu Lys Ile Pro Phe  
 145 150 155 160  
 Met Glu Gly Met Leu Ser Leu Pro Phe Trp Leu Gly Lys Val Phe Cys

165 170 175  
 Leu Gly Leu Ala Leu Val Ala Ile Ile Gly Thr Ser Asn Ala Val Asn  
 180 185 190  
 Leu Thr Asp Gly Leu Asp Gly Leu Ala Ala Gly Thr Met Ser Phe Ala  
 195 200 205  
 Ala Leu Gly Phe Ile Phe Val Ala Leu Arg Ser Ser Thr Ile Pro Ile  
 210 215 220  
 Ala Gln Asp Val Ala Tyr Val Leu Ala Ala Leu Val Gly Ala Cys Ile  
 225 230 235 240  
 Gly Phe Leu Trp Tyr Asn Gly Phe Pro Ala Gln Leu Phe Met Gly Asp  
 245 250 255  
 Thr Gly Ser Leu Leu Leu Gly Gly Leu Leu Gly Ser Cys Ala Val Met  
 260 265 270  
 Leu Arg Ala Glu Cys Ile Leu Val Val Ile Gly Gly Val Phe Val Ala  
 275 280 285  
 Glu Ala Gly Ser Val Ile Leu Gln Val Leu Ser Cys Arg Leu Arg Lys  
 290 295 300  
 Lys Arg Leu Phe Leu Cys Ser Pro Leu His His His Tyr Glu Tyr Gln  
 305 310 315 320  
 Gly Leu Pro Glu Thr Lys Ile Val Met Arg Phe Trp Ile Phe Ser Phe  
 325 330 335  
 Val Cys Ala Gly Leu Gly Ile Ala Ala Val Leu Trp Arg  
 340 345

&lt;210&gt;974

&lt;211&gt;419

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;974

Met Arg Arg Ser Arg Tyr Ser Gly Cys Leu Met Glu Ile Asp Met Cys  
 1 5 10 15  
 Gln Arg Ile Leu Ile Leu Gly Thr Gly Ile Thr Gly Lys Ser Val Ala  
 20 25 30  
 Arg Phe Leu Tyr Gln Gln Gly His Tyr Leu Ile Gly Ala Asp Asn Ser  
 35 40 45  
 Leu Glu Ser Leu Ile Ser Val Asp His Leu His Asp Arg Leu Leu Met  
 50 55 60  
 Gly Ala Ser Glu Phe Pro Glu Asn Ile Asp Leu Val Ile Arg Ser Pro  
 65 70 75 80  
 Gly Ile Lys Pro Tyr His Pro Trp Val Glu Gln Ala Val Ser Leu Lys  
 85 90 95  
 Ile Pro Val Val Thr Asp Ile Gln Val Ala Leu Lys Thr Pro Glu Phe  
 100 105 110  
 Gln Arg Tyr Pro Ser Phe Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr  
 115 120 125  
 Thr Thr Leu Phe Leu Thr His Leu Leu Asn Thr Leu Gly Ile Pro Ala  
 130 135 140  
 Ile Ala Met Gly Asn Ile Gly Leu Pro Ile Leu Asp His Met Gly Gln  
 145 150 155 160  
 Pro Gly Val Arg Val Val Glu Ile Ser Ser Phe Gln Leu Ala Thr Gln  
 165 170 175  
 Glu Glu His Ile Pro Ala Leu Ser Gly Ser Val Phe Leu Asn Phe Ser  
 180 185 190  
 Arg Asn His Leu Asp Tyr His Arg Asn Leu Asp Ala Tyr Phe Asp Ala  
 195 200 205  
 Lys Leu Arg Ile Gln Lys Cys Leu Arg Gln Asp Lys Thr Phe Trp Val  
 210 215 220  
 Trp Glu Glu Cys Ser Leu Gly Asn Ser Tyr Gln Ile Tyr Ser Glu Glu  
 225 230 235 240  
 Ile Glu Glu Ile Leu Asp Lys Gly Asp Ala Leu Lys Pro Ile Tyr Leu  
 245 250 255  
 His Asp Arg Asp Asn Tyr Cys Ala Ala Tyr Ala Leu Ala Asn Glu Val  
 260 265 270  
 Gly Trp Val Ser Pro Glu Gly Phe Leu Lys Ala Ile Arg Thr Phe Glu  
 275 280 285

Lys Pro Ala His Arg Leu Glu Tyr Leu Gly Lys Lys Asp Gly Val His  
 290 295 300  
 Tyr Ile Asn Asp Ser Lys Ala Thr Thr Val Thr Ala Val Glu Lys Ala  
 305 310 315 320  
 Leu Met Ala Val Gly Lys Asp Val Ile Val Ile Leu Gly Gly Lys Asp  
 325 330 335  
 Lys Gly Gly Asp Phe Pro Ala Leu Ala Ser Val Leu Ser Gln Thr Thr  
 340 345 350  
 Lys His Val Ile Ala Met Gly Glu Cys Arg Gln Thr Ile Ala Asp Ala  
 355 360 365  
 Leu Ser Glu Lys Ile Pro Leu Thr Leu Ser Lys Asp Leu Gln Glu Ala  
 370 375 380  
 Val Ser Ile Ala Gln Thr Ile Ala Gln Glu Gly Asp Thr Val Leu Leu  
 385 390 395 400  
 Ser Pro Gly Cys Ala Xaa Leu Ile Ser Phe Lys Val Leu Lys Asn Ala  
 405 410 415  
 Xaa Leu Leu

&lt;210&gt;975

&lt;211&gt;252

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;975

Arg Thr Arg Xaa Tyr Phe Lys Leu Leu Ile Arg Arg Asn Ala Gly Ser  
 1 5 10 15  
 Glu Val Asn Met Asn Arg Arg Asp Met Val Ile Thr Ala Val Val Val  
 20 25 30  
 Asn Ala Ile Leu Leu Val Ala Leu Phe Val Thr Ser Lys Arg Ile Gly  
 35 40 45  
 Val Lys Asp Tyr Asp Glu Gly Phe Arg Asn Phe Ala Ser Ser Lys Val  
 50 55 60  
 Thr Gln Ala Val Val Ser Glu Glu Lys Val Ile Glu Lys Pro Val Val  
 65 70 75 80  
 Ala Glu Val Pro Ser Arg Pro Ile Ala Lys Glu Thr Leu Ala Ala Gln  
 85 90 95  
 Phe Ile Glu Ser Lys Pro Val Ile Val Thr Thr Pro Pro Val Pro Val  
 100 105 110  
 Val Ser Glu Thr Pro Glu Val Pro Thr Val Ala Val Pro Pro Gln Pro  
 115 120 125  
 Val Arg Glu Thr Val Lys Glu Glu Gln Ala Pro Tyr Ala Thr Val Val  
 130 135 140  
 Val Lys Lys Gly Asp Phe Leu Glu Arg Ile Ala Arg Ala Asn His Thr  
 145 150 155 160  
 Thr Val Ala Lys Leu Met Gln Ile Asn Asp Leu Thr Thr Thr Gln Leu  
 165 170 175  
 Lys Ile Gly Gln Val Ile Lys Val Pro Thr Ser Gln Asp Val Ser Asn  
 180 185 190  
 Glu Lys Thr Pro Gln Thr Gln Thr Ala Asn Pro Glu Asn Tyr Tyr Ile  
 195 200 205  
 Val Gln Glu Gly Asp Ser Pro Trp Thr Ile Ala Leu Arg Asn His Ile  
 210 215 220  
 Arg Leu Asp Asp Leu Leu Lys Met Asn Asp Leu Asp Glu Tyr Lys Ala  
 225 230 235 240  
 Arg Arg Leu Lys Pro Gly Asp Gln Leu Arg Ile Arg  
 245 250

&lt;210&gt;976

&lt;211&gt;385

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;976

Met Lys Trp Phe Val Ile Ser Cys Leu Leu Gly Ile Phe Ser Leu Gly  
 1 5 10 15  
 Leu Ile Met Val Phe Glu Thr Ser Ser Ala Glu Val Leu Asp Arg Ser  
 20 25 30

Leu Glu Cys Ser Thr His Lys Ala Leu Ile Arg Gln Val Thr Tyr Leu  
 35 40 45  
 Ile Leu Gly Leu Gly Val Ala Ser Leu Leu Tyr Met Met Glu Trp Arg  
 50 55 60  
 Asp Phe Leu Lys Ile Ser Pro Val Leu Leu Ser Gly Ala Ala Leu Ala  
 65 70 75 80  
 Leu Ile Cys Val Phe Ile Pro Gly Leu Gly Ile Cys Arg Asn Gly Ala  
 85 90 95  
 Arg Arg Trp Leu Gly Phe Gly Gln Leu Thr Ile Gln Pro Ser Glu Phe  
 100 105 110  
 Val Lys Tyr Leu Val Pro Ile Val Ala Leu Tyr Phe Leu Thr Phe Ser  
 115 120 125  
 Ser Leu Tyr Gln Lys Gln Leu Lys Met Phe Leu Lys Leu Thr Ala Ile  
 130 135 140  
 Leu Phe Ile Pro Ile Leu Leu Ile Ala Ile Glu Pro Asp Asn Gly Ser  
 145 150 155 160  
 Ala Ala Val Ile Ser Ala Ser Leu Ile Pro Val Phe Ile Met Thr Ser  
 165 170 175  
 Val Arg Leu Arg Tyr Trp Leu Leu Pro Leu Leu Cys Val Leu Ile Ala  
 180 185 190  
 Gly Gly Ala Leu Ala Tyr Arg Met Pro Tyr Val Arg Tyr Arg Leu Asn  
 195 200 205  
 Val Tyr Leu His Pro Glu Leu Asp Ile Lys Gly Arg Gly His Gln Pro  
 210 215 220  
 Tyr Gln Ala Lys Ile Ala Ala Gly Ser Gly Lys Leu Leu Gly Lys Gly  
 225 230 235 240  
 Pro Gly Ala Ser Leu Gln Lys Leu Thr Tyr Leu Pro Glu Ala Gln Asn  
 245 250 255  
 Asp Tyr Ile Ala Ala Ile Tyr Ala Glu Phe Gly Phe Leu Gly Met  
 260 265 270  
 Leu Val Leu Ile Leu Leu Tyr Met Cys Phe Val Tyr Gly Gly Tyr Ala  
 275 280 285  
 Ile Ala Ile Lys Ala Ser Ser Leu Glu Gly Ala Ala Leu Ala Met Val  
 290 295 300  
 Ile Thr Leu Ile Ile Ser Met Gln Ala Phe Met Asn Leu Gly Val Val  
 305 310 315 320  
 Ser Gly Leu Leu Pro Ser Lys Gly Val Asn Leu Pro Phe Phe Ser Gln  
 325 330 335  
 Gly Gly Ser Ser Leu Ile Ala Asn Met Cys Gly Val Thr Leu Leu Leu  
 340 345 350  
 Lys Val Tyr Asp Glu Glu Asn Ser Lys Ser Ser Leu Gly Cys Arg Arg  
 355 360 365  
 Phe Arg Arg Pro His Cys Pro Ser Ser Leu Gly Lys Gly Ser Phe Phe  
 370 375 380  
 Ser  
 385  
 <210>977  
 <211>357  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>977  
 Met Met Lys Lys Ile Arg Lys Val Ala Leu Ala Val Gly Gly Ser Gly  
 1 5 10 15  
 Gly His Ile Val Pro Ala Leu Ser Val Lys Glu Ala Phe Ser Arg Glu  
 20 25 30  
 Gly Ile Asp Val Leu Leu Leu Gly Lys Gly Leu Lys Asn His Pro Ser  
 35 40 45  
 Leu Gln Gln Gly Ile Ser Tyr Arg Glu Ile Pro Ser Gly Leu Pro Thr  
 50 55 60  
 Val Leu Asn Pro Ile Lys Ile Met Ser Arg Thr Leu Ser Leu Cys Ser  
 65 70 75 80  
 Gly Tyr Leu Lys Ala Arg Lys Glu Leu Lys Ile Phe Asp Pro Asp Leu  
 85 90 95  
 Val Ile Gly Phe Gly Ser Tyr His Ser Leu Pro Val Leu Leu Ala Gly

100 105 110  
 Leu Ser His Lys Ile Pro Leu Phe Leu His Glu Gln Asn Leu Val Pro  
 115 120 125  
 Gly Lys Val Asn Gln Leu Phe Ser Arg Tyr Ala Arg Gly Ile Gly Val  
 130 135 140  
 Asn Phe Ser Pro Val Thr Lys His Phe Arg Cys Pro Ala Glu Glu Val  
 145 150 155 160  
 Phe Leu Pro Lys Arg Ser Phe Ser Leu Gly Ser Pro Met Met Lys Arg  
 165 170 175  
 Cys Thr Asn His Thr Pro Thr Ile Cys Val Val Gly Gly Ser Gln Gly  
 180 185 190  
 Ala Gln Ile Leu Asn Thr Cys Val Pro Gln Ala Leu Val Lys Leu Val  
 195 200 205  
 Asn Lys Tyr Pro Asn Met Tyr Val His His Ile Val Gly Pro Lys Ser  
 210 215 220  
 Asp Val Met Lys Val Gln His Val Tyr Asn Arg Gly Glu Val Leu Cys  
 225 230 235 240  
 Cys Val Lys Pro Phe Glu Glu Gln Leu Leu Asp Val Leu Leu Ala Ala  
 245 250 255  
 Asp Leu Val Ile Ser Arg Ala Gly Ala Thr Ile Leu Glu Glu Ile Leu  
 260 265 270  
 Trp Ala Lys Val Pro Gly Ile Leu Ile Pro Tyr Pro Gly Ala Tyr Gly  
 275 280 285  
 His Gln Glu Val Asn Ala Lys Phe Phe Val Asp Val Leu Glu Gly Gly  
 290 295 300  
 Thr Met Ile Leu Glu Lys Glu Leu Thr Glu Lys Leu Leu Val Glu Lys  
 305 310 315 320  
 Val Thr Phe Ala Leu Asp Ser His Asn Arg Glu Lys Gln Arg Asn Ser  
 325 330 335  
 Leu Ala Ala Tyr Ser Gln Gln Arg Ser Thr Lys Thr Phe His Ala Phe  
 340 345 350  
 Ile Cys Glu Cys Leu  
 355

&lt;210&gt;978

&lt;211&gt;812

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;978

Val His Tyr Met Lys Gly Thr Pro Gln Tyr His Phe Ile Gly Ile Gly  
 1 5 10 15  
 Gly Ile Gly Met Ser Ala Leu Ala His Ile Leu Leu Asp Arg Gly Tyr  
 20 25 30  
 Glu Val Ser Gly Ser Asp Leu Tyr Glu Ser Tyr Thr Ile Glu Ser Leu  
 35 40 45  
 Lys Ala Lys Gly Ala Arg Cys Phe Ser Gly His Asp Ser Ser His Val  
 50 55 60  
 Pro His Asp Ala Val Val Val Tyr Ser Ser Ser Ile Ala Pro Asp Asn  
 65 70 75 80  
 Val Glu Tyr Leu Thr Ala Ile Gln Arg Ser Ser Arg Leu Leu His Arg  
 85 90 95  
 Ala Glu Leu Leu Ser Gln Leu Met Glu Gly Tyr Glu Ser Ile Leu Val  
 100 105 110  
 Ser Gly Ser His Gly Lys Thr Gly Thr Ser Ser Leu Ile Arg Ala Ile  
 115 120 125  
 Phe Gln Glu Ala Gln Lys Asp Pro Ser Tyr Ala Ile Gly Gly Leu Ala  
 130 135 140  
 Ala Asn Cys Leu Asn Gly Tyr Ser Gly Ser Ser Lys Ile Phe Val Ala  
 145 150 155 160  
 Glu Ala Asp Glu Ser Asp Gly Ser Leu Lys His Tyr Thr Pro Arg Ala  
 165 170 175  
 Val Val Ile Thr Asn Ile Asp Asn Glu His Leu Asn Asn Tyr Ala Gly  
 180 185 190  
 Asn Leu Asp Asn Leu Val Gln Val Ile Gln Asp Phe Ser Arg Lys Val  
 195 200 205

Thr Asp Leu Asn Lys Val Phe Tyr Asn Gly Asp Cys Pro Ile Leu Lys  
 210 215 220  
 Gly Asn Val Gln Gly Ile Ser Tyr Gly Tyr Ser Pro Glu Cys Gln Leu  
 225 230 235 240  
 His Ile Val Ser Tyr Asn Gln Lys Ala Trp Gln Ser His Phe Ser Phe  
 245 250 255  
 Thr Phe Leu Gly Gln Glu Tyr Gln Asp Ile Glu Leu Asn Leu Pro Gly  
 260 265 270  
 Gln His Asn Ala Ala Asn Ala Ala Ala Cys Gly Val Ala Leu Thr  
 275 280 285  
 Phe Gly Ile Asp Ile Asn Ile Ile Arg Lys Ala Leu Lys Lys Phe Ser  
 290 295 300  
 Gly Val His Arg Arg Leu Glu Arg Lys Asn Ile Ser Glu Ser Phe Leu  
 305 310 315 320  
 Phe Leu Glu Asp Tyr Ala His His Pro Val Glu Val Ala His Thr Leu  
 325 330 335  
 Arg Ser Val Arg Asp Ala Val Gly Leu Arg Arg Val Ile Ala Ile Phe  
 340 345 350  
 Gln Pro His Arg Phe Ser Arg Leu Glu Glu Cys Leu Gln Thr Phe Pro  
 355 360 365  
 Lys Ala Phe Gln Glu Ala Asp Glu Val Ile Leu Thr Asp Val Tyr Ser  
 370 375 380  
 Ala Gly Glu Ser Pro Arg Glu Ser Ile Ile Leu Ser Asp Leu Ala Glu  
 385 390 395 400  
 Gln Ile Arg Lys Ser Ser Tyr Val His Cys Cys Tyr Val Pro His Gly  
 405 410 415  
 Asp Ile Val Asp Tyr Leu Arg Asn Tyr Ile Arg Ile His Asp Val Cys  
 420 425 430  
 Val Ser Leu Gly Ala Gly Asn Ile Tyr Thr Ile Gly Glu Ala Leu Lys  
 435 440 445  
 Asp Phe Asn Pro Lys Lys Leu Ser Ile Gly Leu Val Cys Gly Gly Lys  
 450 455 460  
 Ser Cys Glu His Asp Ile Ser Leu Leu Ser Ala Gln His Val Ser Lys  
 465 470 475 480  
 Tyr Ile Ser Pro Glu Phe Tyr Asp Val Ser Tyr Phe Ile Ile Asn Arg  
 485 490 495  
 Gln Gly Leu Trp Arg Thr Gly Lys Asp Phe Pro His Leu Ile Glu Glu  
 500 505 510  
 Thr Gln Gly Asp Ser Pro Leu Ser Ser Glu Ile Ala Ser Ala Leu Ala  
 515 520 525  
 Lys Val Asp Cys Leu Phe Pro Val Leu His Gly Pro Phe Gly Glu Asp  
 530 535 540  
 Gly Thr Ile Gln Gly Phe Phe Glu Ile Leu Gly Lys Pro Tyr Ala Gly  
 545 550 555 560  
 Pro Ser Leu Ser Leu Ala Ala Thr Ala Met Asp Lys Leu Leu Thr Lys  
 565 570 575  
 Arg Ile Ala Ser Ala Val Gly Val Pro Val Val Pro Tyr Gln Pro Leu  
 580 585 590  
 Asn Leu Cys Phe Trp Lys Arg Asn Pro Glu Leu Cys Ile Gln Asn Leu  
 595 600 605  
 Ile Glu Thr Phe Ser Phe Pro Met Ile Val Lys Thr Ala His Leu Gly  
 610 615 620  
 Ser Ser Ile Gly Ile Phe Leu Val Arg Asp Lys Glu Glu Leu Gln Glu  
 625 630 635 640  
 Lys Ile Ser Glu Ala Phe Leu Tyr Asp Thr Asp Val Phe Val Glu Glu  
 645 650 655  
 Ser Arg Leu Gly Ser Arg Glu Ile Glu Val Ser Cys Ile Gly His Ser  
 660 665 670  
 Ser Ser Trp Tyr Cys Met Ala Gly Pro Asn Glu Arg Cys Gly Ala Ser  
 675 680 685  
 Gly Phe Ile Asp Tyr Gln Glu Lys Tyr Gly Phe Asp Gly Ile Asp Cys  
 690 695 700  
 Ala Lys Ile Ser Phe Asp Leu Gln Leu Ser Gln Glu Ser Leu Asp Cys  
 705 710 715 720

Val Arg Glu Leu Ala Glu Arg Val Tyr Arg Ala Met Gln Gly Lys Gly  
 725 730 735  
 Ser Ala Arg Ile Asp Phe Phe Leu Asp Glu Glu Gly Asn Tyr Trp Leu  
 740 745 750  
 Ser Glu Val Asn Pro Ile Pro Gly Met Thr Ala Ala Ser Pro Phe Leu  
 755 760 765  
 Gln Ala Phe Val His Ala Gly Trp Thr Gln Glu Gln Ile Val Asp His  
 770 775 780  
 Phe Ile Ile Asp Ala Leu His Lys Phe Asp Lys Gln Gln Thr Ile Glu  
 785 790 795 800  
 Gln Ala Phe Thr Lys Glu Gln Asp Leu Val Lys Arg  
 805 810

&lt;210&gt;979

&lt;211&gt;192

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;979

Leu Val Asn Asp Ser Gln Leu Ser Arg Glu Ala Ser Ala Phe Arg Leu  
 1 5 10 15  
 Asp Ile Asp Phe Phe Ile Leu Asn Ile Tyr Pro Phe Phe Arg Asn Phe  
 20 25 30  
 Lys Asn Ile Glu Leu Cys Phe Phe Leu Ser Ile Ser Gln Phe Asn Leu  
 35 40 45  
 Asp Phe Met Glu Glu Phe Val Ala Tyr Ile Val Lys Asn Leu Val Thr  
 50 55 60  
 Asn Pro Glu Ala Val Glu Ile Arg Ser Ile Glu Asp Glu Asp Asn Glu  
 65 70 75 80  
 Ser Ile Lys Leu Glu Ile Arg Val Ala Ala Glu Asp Ile Gly Lys Ile  
 85 90 95  
 Ile Gly Arg Arg Gly Asn Thr Ile His Ala Leu Arg Thr Ile Leu Arg  
 100 105 110  
 Arg Val Cys Ser Arg Leu Lys Lys Val Gln Ile Asp Leu Val Gln  
 115 120 125  
 Pro Glu Asn Gly Thr Asp Val Ile Ala Asp Gln Asp Tyr Ile Cys Asp  
 130 135 140  
 Asn Asp Ser Ser Asn Ser Thr Glu Asp Thr Phe Gly Glu Ser Asp Thr  
 145 150 155 160  
 Cys Cys Ser Gly His Cys His Tyr Asp Glu Asp Leu Asn Gln Glu Glu  
 165 170 175  
 Gln Glu Glu Gly Asn Met His His Ser Cys Glu Cys Ser Asn His His  
 180 185 190

&lt;210&gt;980

&lt;211&gt;120

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;980

Lys Phe Leu Ile Ile Lys Ser Ser Met Thr Ala Val Leu Ile Leu Thr  
 1 5 10 15  
 Ser Phe Pro Ser Glu Glu Ser Ala Arg Ser Leu Ala Arg His Leu Ile  
 20 25 30  
 Thr Glu Arg Leu Ala Ser Cys Val His Val Phe Pro Lys Gly Thr Ser  
 35 40 45  
 Thr Tyr Leu Trp Glu Gly Lys Leu Cys Glu Ser Glu Glu His His Ile  
 50 55 60  
 Gln Ile Lys Ser Ile Asp Ile Arg Phe Ser Glu Ile Cys Leu Ala Ile  
 65 70 75 80  
 Gln Glu Phe Ser Gly Tyr Glu Val Pro Glu Val Leu Leu Phe Pro Ile  
 85 90 95  
 Glu Asn Gly Asp Pro Arg Tyr Leu Asn Trp Leu Thr Ile Leu Ser Tyr  
 100 105 110  
 Pro Glu Lys Pro Pro Leu Ser Asp  
 115 120

&lt;210&gt;981

&lt;211&gt;213



&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;981

```

Ile Leu Ala Ile Leu Phe Met Ile Ile Ile Lys Asn Asn Glu Leu Met
 1           5           10           15
Ile Arg Arg Phe Phe Lys Thr Leu Phe Pro Pro Gly Pro Gln Tyr Ser
          20           25           30
Leu Cys Tyr Ala Ser Ile Leu Ile Val Leu Ser Ser Leu Val Cys Val
          35           40           45
Pro Thr Phe Cys Trp Leu Phe Leu Pro Glu Leu Ser Leu Ser Lys Phe
          50           55           60
Asn Pro Ser Pro Ile Arg Asn Leu Phe Leu Val Ser Ser Thr Leu Ser
          65           70           75           80
Lys Val Pro Pro Thr Ala Ile Ala Glu His Leu Arg Leu Ser Ala Asp
          85           90           95
Ala Pro Thr Tyr Leu His Glu Phe Ser Ile Lys Glu Ala Glu Ser Ser
          100          105          110
Leu His Ala Leu Gly Ile Phe Ser Ser Leu Val Ile Glu Lys Ser Pro
          115          120          125
Asp Asn Lys Gly Ile Thr Ile Phe Tyr Thr Leu Gln Thr Pro Ile Ala
          130          135          140
Tyr Val Gly Asn Arg Ser Asn Thr Leu Cys Asn Leu Glu Gly Ser Cys
          145          150          155          160
Phe Leu Gly Gln Pro Tyr Phe Pro Ser Leu Asn Leu Pro Gln Ile Phe
          165          170          175
Phe Ser Gln Glu Asp Leu Lys Met Gln Lys Leu Pro Lys Glu Lys Met
          180          185          190
Leu Phe Thr Lys Ile Leu Leu Lys Glu Leu Ala Met Glu Ser Pro Lys
          195          200          205
Ile Ile Asp Leu Ser
          210

```

&lt;210&gt;982

&lt;211&gt;107

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;982

```

Leu Glu Arg Leu Leu Met Asn Leu Ser Ala Lys Glu Tyr Gly Asp Ile
 1           5           10           15
Ile Val Ile Tyr Leu Gln Gly Ser Leu Asp Ala Val Ser Val Pro Ser
          20           25           30
Val Gln Glu Tyr Leu Glu Gln Phe Ile Gln Lys Lys His Leu Lys Ile
          35           40           45
Ala Leu Asn Phe Thr Asp Val Ser Tyr Ile Ser Ser Ala Gly Ile Arg
          50           55           60
Leu Leu Leu Ser Asn Phe Lys Leu Val Gln Ser Leu Gly Gly Lys Met
          65           70           75           80
Cys Leu Cys Cys Val Lys Glu Ser Val Thr Glu Val Met Arg Ile Ala
          85           90           95
Arg Phe Arg Gln Met Ile Leu Leu Cys Gln Val
          100          105

```

&lt;210&gt;983

&lt;211&gt;342

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;983

```

Met Leu Pro Phe Glu Phe Glu Phe Asn Thr Thr Ser Ser Pro Glu Cys
 1           5           10           15
Asp Val Cys Leu Asp Pro Gln Lys Leu Phe Val Lys Leu Phe Lys Arg
          20           25           30
Thr Ile Val Leu Leu Ser Gly Pro Thr Gly Ser Gly Lys Thr Asp Val
          35           40           45
Ser Leu Ala Leu Ala Pro Met Ile Asp Gly Glu Ile Val Ser Val Asp
          50           55           60
Ser Met Gln Val Tyr Gln Gly Met Asp Ile Gly Thr Ala Lys Val Ser

```

```

65              70              75              80
Leu Lys Ala Arg Gln Glu Ile Pro His His Leu Ile Asp Ile Arg His
              85              90              95
Val Gln Glu Pro Phe Asn Val Val Asp Phe Tyr Tyr Glu Ala Ile Gln
              100              105              110
Ala Cys Gln Asn Ile Leu Ser Arg Asn Lys Val Pro Ile Leu Val Gly
              115              120              125
Gly Ser Gly Phe Tyr Phe His Ala Phe Leu Ser Gly Pro Pro Lys Gly
              130              135              140
Pro Ala Ala Asp Pro Gln Ile Arg Glu Gln Leu Glu Ala Ile Ala Glu
145              150              155              160
Glu His Gly Val Ser Ala Leu Tyr Glu Asp Leu Leu Leu Lys Asp Pro
              165              170              175
Glu Tyr Ala Gln Thr Ile Thr Lys Asn Asp Lys Asn Lys Ile Ile Arg
              180              185              190
Gly Leu Glu Ile Ile Gln Leu Thr Gly Lys Lys Val Ser Asp His Glu
              195              200              205
Trp Asp Ile Val Pro Lys Ala Ser Arg Glu Tyr Cys Cys Arg Ala Trp
210              215              220
Phe Leu Ser Pro Glu Thr Glu Phe Leu Lys Asn Asn Ile Gln Met Arg
225              230              235              240
Cys Glu Ala Met Leu Gln Glu Gly Leu Leu Glu Glu Val Arg Gly Leu
              245              250              255
Leu Asn Gln Gly Ile Arg Glu Asn Pro Ser Ala Phe Lys Ala Ile Gly
              260              265              270
Tyr Arg Glu Trp Ile Glu Phe Leu Asp Asn Gly Glu Lys Leu Glu Glu
              275              280              285
Tyr Glu Glu Thr Lys Arg Lys Phe Val Ser Asn Ser Trp His Tyr Thr
290              295              300
Lys Lys Gln Lys Thr Trp Phe Lys Arg Tyr Ser Ile Phe Arg Glu Leu
305              310              315              320
Pro Thr Leu Gly Leu Ser Ser Asp Ala Ile Ala Gln Lys Ile Ala Lys
              325              330              335
Asp Tyr Leu Leu Tyr Ser
              340

```

&lt;210&gt;984

&lt;211&gt;365

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;984

```

Ser Leu Leu Leu Ala Ile Phe Asn Val Asn Tyr Phe Met Asn Leu Cys
1              5              10              15
Lys Arg Ile Ser Phe Glu Glu Gly Leu Glu Leu Phe Val Ser Ser Pro
              20              25              30
Ile Glu Arg Leu Gln Glu Arg Ala Asp Ala Ile Arg Lys Glu Arg Tyr
              35              40              45
Pro Ser Asn Glu Val Thr Tyr Val Leu Asp Ala Asn Pro Asn Tyr Thr
50              55              60
Asn Ile Cys Lys Ile Asp Cys Thr Phe Cys Ala Phe Tyr Arg Lys Pro
65              70              75              80
Lys Ser Pro Asp Ala Tyr Leu Leu Ser Phe Asp Glu Val Arg Ser Leu
              85              90              95
Leu Gln Arg Tyr Val Ser Ser Gly Val Lys Thr Val Leu Leu Gln Gly
100              105              110
Gly Val His Pro Gly Leu Gly Ile Asp Tyr Leu Glu Glu Leu Val Arg
115              120              125
Ile Thr Val Gln Glu Phe Pro Ser Ile His Pro His Phe Phe Ser Ala
130              135              140
Val Glu Ile Glu His Ala Cys Arg Val Ser Gly Ile Ser Ile Glu Gln
145              150              155              160
Gly Leu Gln Arg Leu Trp Asp Ala Gly Gln Arg Thr Ile Pro Gly Gly
              165              170              175
Gly Ala Glu Ile Leu Ser Glu Arg Val Arg Lys Ile Ile Ser Pro Lys
180              185              190

```

Lys Met Gln Pro Gly Gly Trp Ile Asn Leu His Lys Leu Ala His Leu  
 195 200 205  
 Met Gly Phe Arg Thr Thr Ala Thr Met Met Phe Gly His Val Glu Asn  
 210 215 220  
 Pro Glu Asp Ile Leu Ile His Leu Gln Thr Leu Arg Asp Ala Gln Asp  
 225 230 235 240  
 Ser Cys Pro Gly Phe Tyr Ser Phe Ile Pro Trp Ser Tyr Lys Pro Gly  
 245 250 255  
 Asn Thr Ala Leu Arg Arg Asn Val Pro Gln Gln Ala Ser Ile Glu Thr  
 260 265 270  
 Tyr Tyr Arg Ile Leu Ala Leu Gly Arg Ile Phe Leu Asp Asn Phe Asp  
 275 280 285  
 His Val Ala Ala Ser Trp Phe Gly Glu Gly Lys Ser Leu Gly Ala Lys  
 290 295 300  
 Ala Leu His Tyr Gly Ala Asp Asp Phe Gly Gly Val Ile Leu Asp Glu  
 305 310 315 320  
 Ser Val His Lys Ala Thr Gly Trp Ser Ile Gln Ser Ser Glu Glu Glu  
 325 330 335  
 Ile Cys Asn Ile Ile Arg Ser Glu Gly Phe Ile Pro Val Glu Arg Asn  
 340 345 350  
 Thr Phe Tyr Gln His Ile Ser Cys Thr Val Ser Ser Leu  
 355 360 365

&lt;210&gt;985

&lt;211&gt;438

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;985

Val Val Ile Met Asp Asn Ser Asp Asn Ser Phe His Thr Leu Glu Thr  
 1 5 10 15  
 Glu Gln Gly Ser Phe Leu Asn Asp Glu Leu Ala Val Glu Glu Val Ala  
 20 25 30  
 Ser Thr Glu Ser Thr Glu Ile Ser Asp Ala Thr Leu Cys Phe Ala Asp  
 35 40 45  
 Glu Ile Gln Glu Leu Pro Ser Pro Glu Lys Lys Val Ala Phe Ile Leu  
 50 55 60  
 Asn Lys Met Arg Glu Ala Leu Thr Gly Ser Ser Gln Gly Ser Asp Leu  
 65 70 75 80  
 Arg Leu Phe Trp Asp Leu Arg Lys Gln Cys Leu Pro Leu Phe Asn Glu  
 85 90 95  
 Ile Glu Asp Thr Ala Lys Arg Ala Asp His Trp Arg Cys Tyr Ile Glu  
 100 105 110  
 Leu Thr Lys Glu Gly Arg His Leu Lys Gly Leu Gln Asp Glu Glu Gly  
 115 120 125  
 Ser Phe Val Val Gly Gln Ile Asp Leu Ala Ile Thr Cys Leu Glu Lys  
 130 135 140  
 Asp Ile Leu Lys Phe Gln Glu Gly Thr Glu Asp Lys Ile Phe Lys Asp  
 145 150 155 160  
 Arg Glu Asp Asn Phe Leu Glu Ser Gln Ala Leu Asp Lys His Gln Ala  
 165 170 175  
 Phe Tyr Lys Gln His His Thr Ser Leu Leu Trp Leu Ser Ser Phe Ser  
 180 185 190  
 Ser Lys Ile Ile Asp Leu Arg Lys Glu Leu Ile Asn Val Gly Met Arg  
 195 200 205  
 Met Arg Leu Lys Ser Lys Phe Phe Gln Arg Leu Ser Asn Leu Gly Asn  
 210 215 220  
 Gln Val Phe Pro Lys Arg Lys Glu Leu Ile Glu Lys Val Ser Gln Thr  
 225 230 235 240  
 Phe Ala Glu Asp Val Asp Ala Phe Val Ala Lys Tyr Phe Ile Gly Ser  
 245 250 255  
 Asp Lys Glu Thr Leu Lys Lys Thr Val Phe Phe Leu Arg Lys Glu Ile  
 260 265 270  
 Lys Asn Leu Gln His Ala Ala Lys Arg Leu Phe Val Ser Ser His Val  
 275 280 285  
 Phe Ala Glu Thr Arg Leu Lys Leu Ser Lys Cys Trp Asp Gln Leu Lys

290 295 300  
 Gly Met Glu Lys Glu Ile Arg Gln Glu Gln Gly Arg Leu Arg Val Val  
 305 310 315 320  
 Ser Ala Glu Asn Ser Lys Glu Val Arg Gln Met Leu Ala Glu Val Ser  
 325 330 335  
 Ser Leu Leu Ile Glu Gly Asn Asp Leu Ser Lys Val Arg Lys Asp Leu  
 340 345 350  
 Glu Gly Ile Ser Lys Lys Ile Arg Ala Leu Asp Leu Thr His Asp Asp  
 355 360 365  
 Val Ile Ser Leu Lys Lys Glu Met Gln Gln Leu Phe Asp Gln Leu Arg  
 370 375 380  
 Glu Lys Gln Asp Ala Ala Glu His Ser Tyr Gln Glu Gln Leu Ala Lys  
 385 390 395 400  
 Asp Lys Gln Val Lys Lys Glu Ala Ala Arg Ser Leu Ala Glu Arg Ile  
 405 410 415  
 Thr Thr Phe Ser Lys Thr Cys Ser Glu Gly Thr Leu Leu Pro Asn Leu  
 420 425 430  
 Glu Lys Asn Gly Arg His  
 435

&lt;210&gt;986

&lt;211&gt;142

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;986

Ala His His Asn Ile Leu Lys Asn Leu Leu Arg Arg Asn Ile Thr Ser  
 1 5 10 15  
 Glu Ser Arg Glu Glu Trp Gln Thr Leu Lys Glu Leu Leu Gly Lys Met  
 20 25 30  
 Ser Phe Leu Pro Pro Pro Glu Lys Ile Ser Leu Asp Asn Gln Leu Asn  
 35 40 45  
 Leu Ala Leu Gln Thr Ile Val Asn Phe Phe Glu Glu Gln Leu Leu Ser  
 50 55 60  
 Ser Pro Asp Ser Arg Glu Lys Leu Val Asn Met Arg Gln Val Leu Lys  
 65 70 75 80  
 Gln Arg Arg Glu Arg Arg Gln Glu Leu Lys Asp Lys Leu Glu Gln Asp  
 85 90 95  
 Lys Lys Leu Leu Gly Ser Ser Gly Leu Asp Phe Asp Arg Ala Met Gln  
 100 105 110  
 Tyr Ser Ala Leu Val Glu Glu Asp Lys Arg Ala Leu Glu Glu Leu Asp  
 115 120 125  
 Ala Ser Ile Leu Glu Leu Lys Gln Gln Ile Gln Gln Leu Leu  
 130 135 140

&lt;210&gt;987

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;987

Met Asp Ser Phe Cys Phe Asp Leu Leu Lys Val Ala Ala Lys Ala Ile  
 1 5 10 15  
 Asp Asp Lys Lys Gly Asn Asn Leu Val Val Leu Asp Val Arg Thr Ile  
 20 25 30  
 Ser Glu Phe Thr Asp Tyr Phe Val Phe Val Glu Gly Ser Val Asn Val  
 35 40 45  
 His Val Lys Ala Leu Ala Asn Thr Ile Val Glu Glu Leu Lys Lys Gln  
 50 55 60  
 Lys Val Ser Pro Leu His Val Glu Gly Ile Thr Asp Gly Asn Trp Val  
 65 70 75 80  
 Val Ile Asp Tyr Gly Phe Ile Val Val His Val Phe Val Ser Glu Ile  
 85 90 95  
 Arg Gly Lys Tyr Arg Leu Glu Glu Leu Trp Lys Asp Gly Phe Ile Val  
 100 105 110  
 Thr Ser Lys Leu Leu Ala Ser  
 115  
 <210>988

&lt;211&gt;424

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;988

Leu Leu Asn Gly Val Arg Val Tyr Met Ser Lys Lys Arg Val Val Val  
 1 5 10 15  
 Thr Gly Phe Gly Val Val Ser Cys Leu Gly Asn Glu Val Asp Thr Phe  
 20 25 30  
 Tyr Asp Asn Leu Leu Ala Gly Val Ser Gly Val Arg Pro Ile Thr Ser  
 35 40 45  
 Phe Pro Cys Glu Asp Tyr Ala Thr Arg Phe Ala Gly Trp Ile Pro Glu  
 50 55 60  
 Phe Asn Pro Glu Pro Tyr Val Asp Lys Lys Gln Ala Arg Arg Val Asp  
 65 70 75 80  
 Pro Phe Ile Thr Tyr Ala Met Val Ala Ala Lys Lys Ala Ile Ala Met  
 85 90 95  
 Ser Arg Trp Asp Lys Asp His Leu Pro Ser Asp Pro Val Arg Cys Gly  
 100 105 110  
 Val Ile Val Gly Ser Gly Met Gly Gly Leu Ser Thr Leu Asp Gln Gly  
 115 120 125  
 Met Glu Arg Leu Leu Val Ile His Lys Lys Leu Ser Pro Phe Phe Ile  
 130 135 140  
 Pro Tyr Ile Ile Thr Asn Met Ala Pro Ala Leu Ile Ala Met Asp Phe  
 145 150 155 160  
 Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Gly  
 165 170 175  
 Asn Tyr Cys Ile Asp Ala Ala Tyr Gln His Leu Val Ser Gly Arg Ala  
 180 185 190  
 Asp Met Ile Ile Cys Gly Gly Thr Glu Ala Ala Val Asn Arg Ile Gly  
 195 200 205  
 Leu Glu Gly Phe Ile Ala Asn Arg Ala Leu Ser Glu Arg Asn Asp Ala  
 210 215 220  
 Pro Asp Gln Ala Ser Arg Pro Trp Asp Arg Asp Arg Asp Gly Phe Val  
 225 230 235 240  
 Leu Gly Glu Gly Ala Gly Ile Leu Val Leu Glu Thr Leu Glu Ser Ala  
 245 250 255  
 Leu Arg Arg Asp Ala Pro Ile Phe Ala Glu Met Leu Gly Ser Tyr Val  
 260 265 270  
 Thr Cys Asp Ala Phe His Ile Thr Ala Pro Arg Asp Asp Gly Glu Gly  
 275 280 285  
 Ile Thr Ala Cys Val Leu Gly Ala Leu Asn Ser Ala Gly Ile Pro Lys  
 290 295 300  
 Glu Arg Val Asn Tyr Val Asn Ala His Gly Thr Ser Thr Pro Leu Gly  
 305 310 315 320  
 Asp Leu Ser Glu Val Leu Ala Val Lys Lys Ala Phe Gly Ser His Val  
 325 330 335  
 Arg Asn Leu Arg Met Asn Ser Thr Lys Ser Leu Ile Gly His Cys Leu  
 340 345 350  
 Gly Ala Ala Gly Gly Val Glu Ala Val Val Ala Ile Gln Ala Ile Leu  
 355 360 365  
 Thr Gly Lys Leu His Pro Thr Ile Asn Leu Asp Asn Pro Ile Ala Glu  
 370 375 380  
 Ile Glu Asp Phe Asp Val Val Ala Asn Lys Ala Gln Asp Trp Asp Ile  
 385 390 395 400  
 Asp Val Ala Met Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Thr  
 405 410 415  
 Ile Leu Phe Ser Arg Tyr Val Pro  
 420

&lt;210&gt;989

&lt;211&gt;150

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;989

Met Met Lys Thr Lys Tyr Glu Tyr Ser Phe Gly Val Ile Pro Ile Lys

BNSDOCID: <WO\_\_9927105A2\_1\_>

Met	His	Ser	Glu	Leu	Pro	Asn	Tyr	Gln	Asn	Ile	Val	Glu	Ser	Val	Val
1				5					10					15	
Thr	Glu	Ile	Thr	Thr	Gln	Leu	Leu	Asn	Tyr	Arg	Ser	Glu	His	Arg	Leu
			20					25					30		
Val	Pro	Phe	Trp	Glu	Lys	Ser	Asp	Gly	Ser	Phe	Ile	Thr	Ala	Ala	Asp
	35						40					45			
Tyr	Gly	Ser	Gln	Tyr	Tyr	Leu	Lys	Gln	Gln	Leu	Ala	Lys	Ala	Phe	Pro
	50					55					60				
Asn	Ile	Pro	Phe	Ile	Gly	Glu	Glu	Thr	Leu	Tyr	Pro	Asp	Gln	Asp	Asn
	65				70					75				80	
Glu	Lys	Ile	Pro	Glu	Ile	Leu	Lys	Phe	Thr	Arg	Leu	Leu	Thr	Ser	Ser
				85					90					95	
Val	Ser	Arg	Asp	Asp	Leu	Ile	Ser	Thr	Leu	Val	Pro	Pro	Pro	Ser	Pro
			100					105					110		
Thr	Ser	Leu	Phe	Trp	Leu	Val	Asp	Pro	Ile	Asp	Gly	Thr	Ala	Gly	Phe
			115				120					125			
Ile	Arg	His	Arg	Ala	Phe	Ala	Val	Ala	Ile	Ser	Leu	Ile	Tyr	Glu	Tyr
	130					135					140				
Arg	Pro	Ile	Leu	Ser	Val	Met	Ala	Cys	Pro	Ala	Tyr	Asn	Gln	Thr	Phe
	145				150					155				160	
Lys	Leu	Tyr	Ser	Ala	Ala	Lys	Gly	His	Gly	Leu	Ser	Ile	Val	His	Ser
				165					170					175	

Gln Asn Leu Asp Arg Arg Phe Val Tyr Ala Asp Arg Lys Gln Thr Lys  
 180 185 190  
 Gln Phe Cys Glu Ala Ser Leu Ala Ala Leu Asn Gln Gln His His Ala  
 195 200 205  
 Thr Arg Lys Leu Ser Leu Gly Leu Pro Asn Thr Pro Ser Pro Arg Arg  
 210 215 220  
 Val Glu Ser Gln Tyr Lys Tyr Ala Leu Val Ala Glu Gly Ala Val Asp  
 225 230 235 240  
 Phe Phe Ile Arg Tyr Pro Phe Ile Asp Ser Pro Ala Arg Ala Trp Asp  
 245 250 255  
 His Val Pro Gly Ala Phe Leu Val Glu Glu Ala Gly Gly Arg Val Thr  
 260 265 270  
 Asp Ala Leu Gly Ala Pro Leu Glu Tyr Arg Lys Glu Ser Leu Val Leu  
 275 280 285  
 Asn Asn His Ala Val Ile Leu Ala Ser Gly Asp Gln Glu Thr His Glu  
 290 295 300  
 Thr Thr Leu Ala Ala Leu Gln Asn Gln Leu Asn Val Val Pro Thr Asp  
 305 310 315 320  
 Lys Leu Ile Ala Leu  
 325

&lt;210&gt;993

&lt;211&gt;246

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;993

Gly Glu Leu Met Leu Ile Lys Leu Trp Arg Ala Thr Tyr Glu Gly Met  
 1 5 10 15  
 Tyr Thr Phe Leu Val Gly Ala Leu Leu Lys Leu Arg Tyr Arg Met Gln  
 20 25 30  
 Val Glu Gly Trp Asp Thr Leu Asn Ile Asn Pro Lys Gln Gly Cys Leu  
 35 40 45  
 Phe Leu Ala Asn His Val Ala Glu Val Asp Pro Ile Ile Leu Glu Tyr  
 50 55 60  
 Leu Phe Trp Ser Arg Phe His Val Arg Pro Met Ala Val Glu Tyr Leu  
 65 70 75 80  
 Phe His Ser Arg Val Val Gln Trp Phe Leu Asn Ser Val Arg Ser Ile  
 85 90 95  
 Pro Ile Pro Gln Leu Val Pro Gly Lys Glu Ser Lys Arg Ser Leu Glu  
 100 105 110  
 Arg Met Asn Val Cys Tyr Glu Glu Ala Ser Arg Ala Leu Asn Arg Gly  
 115 120 125  
 Glu Ser Leu Leu Leu Tyr Pro Ser Gly Arg Leu Ser Arg Thr Gly Lys  
 130 135 140  
 Glu Glu Ile Val Asn Gln Tyr Ser Ala Tyr Val Leu Leu His Arg Val  
 145 150 155 160  
 Met Glu Cys Asn Val Val Leu Val Arg Val Ser Gly Leu Trp Gly Ser  
 165 170 175  
 Ala Phe Ser Arg Tyr Lys Gln Asn Ser Thr Pro Lys Leu Gly Pro Ala  
 180 185 190  
 Phe Lys Glu Ala Phe Arg Ala Leu Leu Arg Arg Gly Ile Phe Phe Met  
 195 200 205  
 Pro Lys Arg Phe Val Lys Ile Thr Leu Cys Gln Val Asp His Leu Phe  
 210 215 220  
 Leu Lys Gln Phe Pro Thr Lys Gln Asp Leu Asn Thr Phe Leu Ala Ser  
 225 230 235 240  
 Trp Phe Lys Ser Arg Arg  
 245

&lt;210&gt;994

&lt;211&gt;567

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;994

Ile Leu Phe Trp Leu Leu Gly Leu Asn Gln Gly Asp Asp Asn Leu Pro  
 1 5 10 15



```

Ile Glu Val Pro Leu Arg Ile Thr Arg Lys Leu Arg Arg Met His Asp
      20      25      30
Gln Arg Asn Arg Gly His Asn Asn His Asn Leu Arg Leu Arg Pro Gly
      35      40      45
Ser Thr Leu Leu Glu Ala Phe Leu Ile Leu Cys Ser Glu His Glu Glu
      50      55      60
Gly Ile Ala Cys Phe Asp Glu His Leu Gly Ser Leu Ser Tyr Arg Glu
      65      70      75      80
Leu Arg Asn Ala Ile Ile Ala Val Ala Ile Lys Val Ser Lys Phe Ser
      85      90      95
Glu Asp Arg Val Gly Val Met Met Pro Ala Ser Ile Gly Ala Phe Ile
      100      105      110
Ala Tyr Phe Gly Ile Leu Leu Ala Gly Lys Thr Pro Val Met Met Asn
      115      120      125
Trp Ser Gln Gly Leu Arg Glu Leu Arg Ala Cys Thr Lys Thr Val Glu
      130      135      140
Val Arg Arg Val Leu Thr Ser Gln Gln Phe Ile Lys His Leu Thr Glu
      145      150      155      160
Val Gln Gly Phe Val Glu Tyr Pro Phe Asp Leu Met Tyr Met Glu Asp
      165      170      175
Val Arg Lys Arg Leu Ser Trp Trp Glu Lys Cys Arg Ile Gly Leu Tyr
      180      185      190
Ser Lys Cys Ser Val Pro Trp Leu Leu Arg Ile Phe Gly Val Ser Gly
      195      200      205
Val Glu Ser Asp Asp Thr Ala Val Ile Leu Phe Thr Ser Gly Thr Glu
      210      215      220
Lys Leu Pro Lys Ala Val Pro Leu Thr His Lys Asn Leu Met Glu Asn
      225      230      235      240
Gln Glu Ala Cys Leu Lys Phe Phe Asp Pro Asn Thr Gln Asp Val Met
      245      250      255
Leu Ala Phe Leu Pro Pro Phe His Ala Tyr Gly Phe Asn Ser Cys Gly
      260      265      270
Leu Phe Pro Leu Leu Met Gly Val His Val Val Phe Ala Ser Asn Pro
      275      280      285
Leu Asn Pro Lys Lys Leu Val Glu Phe Ile Asp Asp Lys Lys Val Thr
      290      295      300
Phe Phe Gly Ser Thr Pro Val Phe Phe Asp Tyr Ile Leu Lys Thr Ala
      305      310      315      320
Lys Lys Gln Asn Ser Cys Leu Glu Ser Leu Arg Leu Val Val Ile Gly
      325      330      335
Gly Asp Ala Leu Lys Asp Thr Leu Tyr Glu Glu Thr Lys Lys Leu Gln
      340      345      350
Pro Gln Ile Ala Leu Tyr Gln Gly Tyr Gly Ala Thr Glu Cys Ser Pro
      355      360      365
Val Ile Ser Ile Thr Thr Lys Glu Ser Pro Arg Lys Ser Glu Cys Val
      370      375      380
Gly Met Pro Ile Glu Gly Met Asp Val Leu Ile Ile Ser Lys Glu Thr
      385      390      395      400
His Ile Pro Val Ser Ser Gly Glu Gln Gly Leu Ile Val Val Arg Gly
      405      410      415
Asn Ser Val Phe Ser Gly Tyr Leu Gly Asn His Glu His Gln Ser Phe
      420      425      430
Val Ser Leu Gly Gly Asp Gln Trp Tyr Leu Thr Gly Asp Leu Gly His
      435      440      445
Ile Gly Pro Ser Gly Asp Leu Phe Leu Glu Gly Arg Leu Ser Arg Phe
      450      455      460
Val Lys Ile Gly Gly Glu Met Val Ser Leu Glu Ala Leu Glu Ser Ile
      465      470      475      480
Leu His Glu His Phe Thr Glu Asn Gln Asn Glu Asp Ala Gly Ser Leu
      485      490      495
Val Val Cys Gly Ile Pro Gly Asp Lys Val Arg Leu Cys Leu Phe Thr
      500      505      510
Thr Leu Ala Thr Thr Ile His Glu Val Asn Asp Ile Leu Lys Ser Ala
      515      520      525

```

Glu Thr Ser Ser Ile Val Lys Ile Ser Tyr Val His Gln Val Glu Ser  
 530 535 540  
 Ile Pro Ile Leu Gly Ile Gly Lys Pro Asp Tyr Val Ser Leu Asn Ala  
 545 550 555 560  
 Leu Ala Val Ser Leu Phe Gly  
 565

&lt;210&gt;995

&lt;211&gt;376

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;995

Val Cys Lys Glu Ser Phe Leu Thr Thr Ser Asp Val Ile Asp Phe Val  
 1 5 10 15  
 Thr Asn Asp Phe Leu Gly Phe Ala Arg Ser Pro Thr Ile Tyr Cys Glu  
 20 25 30  
 Val Ser Lys Arg Phe Gln Ile His Cys Gln Gln Phe Pro His Glu Lys  
 35 40 45  
 Leu Gly Ile Arg Gly Ser Arg Leu Met Val Gly Pro Ser Ser Val Ile  
 50 55 60  
 Asp Asp Leu Glu Ser Lys Ile Ala Ser Tyr His Gly Ala Pro Asn Ala  
 65 70 75 80  
 Phe Ile Val Asn Ser Gly Tyr Met Ala Asn Leu Gly Leu Cys His His  
 85 90 95  
 Val Ser Arg Ser Thr Asp Val Leu Leu Trp Asp Glu Glu Val His Met  
 100 105 110  
 Ser Val Val His Ser Leu Ser Ala Ile Ser Gly Gln His His Thr Phe  
 115 120 125  
 His His Asn Asn Leu Glu His Leu Glu Ser Leu Leu Gln Cys Tyr Arg  
 130 135 140  
 Ile Ser Ser Lys Gly Arg Ile Phe Ile Phe Val Ser Ser Val Tyr Ser  
 145 150 155 160  
 Phe Arg Gly Thr Leu Ala Pro Leu Glu Gln Ile Ile Ala Leu Ser Lys  
 165 170 175  
 Lys Tyr His Ala His Leu Ile Val Asp Glu Ala His Ala Met Gly Ile  
 180 185 190  
 Phe Gly Asp Asp Gly Lys Gly Leu Cys His Ala Leu Gly Tyr Glu Asn  
 195 200 205  
 Phe Tyr Ala Val Leu Val Thr Tyr Gly Lys Ala Leu Gly Thr Met Gly  
 210 215 220  
 Ala Ser Leu Leu Thr Ser Ser Glu Val Lys Tyr Asp Leu Met Gln Asn  
 225 230 235 240  
 Ser Pro Pro Leu Arg Tyr Ser Thr Ser Leu Ser Pro His Thr Leu Ile  
 245 250 255  
 Ser Ile Gly Thr Ala Tyr Asp Phe Leu Ala Ser Glu Gly Glu Ile Ala  
 260 265 270  
 Arg Lys Gln Val Phe Lys Leu Lys Glu His Phe His Glu Cys Phe Asp  
 275 280 285  
 Ser His Ala Pro Gly Cys Val Gln Pro Ile Phe Leu Pro His Thr Cys  
 290 295 300  
 Leu Glu Glu Ala Ile Ser Val Leu Glu Thr Thr Gly Ile His Val Gly  
 305 310 315 320  
 Val Val Ala Phe Ala Lys His Pro Phe Leu Arg Val Asn Leu His Ala  
 325 330 335  
 Tyr Asn Thr Val Asp Glu Val Asn Leu Leu Ala Gln Val Met Lys Pro  
 340 345 350  
 Tyr Leu Glu Lys Ser Ser His Arg Val His Ile Asn His Glu Phe His  
 355 360 365  
 Leu Trp Arg Glu Leu Cys Gln His  
 370 375

&lt;210&gt;996

&lt;211&gt;758

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;996

Lys Arg Phe Thr Ala Lys Thr Lys Ser Met Gly Tyr Ile Glu Ser Ser  
 1 5 10 15  
 Thr Phe Arg Leu Tyr Ala Glu Val Ile Val Gly Ser Asn Ile Asn Lys  
 20 25 30  
 Val Leu Asp Tyr Gly Val Pro Glu Asn Leu Glu His Ile Thr Lys Gly  
 35 40 45  
 Thr Ala Val Thr Ile Ser Leu Arg Gly Gly Lys Lys Val Gly Val Ile  
 50 55 60  
 Tyr Gln Ile Lys Thr Thr Thr Gln Cys Lys Lys Ile Leu Pro Ile Leu  
 65 70 75 80  
 Gly Leu Ser Asp Ser Glu Ile Val Leu Pro Gln Asp Leu Leu Asp Leu  
 85 90 95  
 Leu Phe Trp Ile Ser Gln Tyr Tyr Phe Ala Pro Leu Gly Lys Thr Leu  
 100 105 110  
 Lys Leu Phe Leu Pro Ala Ile Ser Ser Asn Val Ile Gln Pro Lys Gln  
 115 120 125  
 His Tyr Arg Val Val Leu Lys Gln Ser Lys Ala Lys Thr Lys Glu Ile  
 130 135 140  
 Leu Ala Lys Leu Glu Val Leu His Pro Ser Gln Gly Ala Val Leu Lys  
 145 150 155 160  
 Ile Leu Leu Gln His Ala Ser Pro Pro Gly Leu Ser Ser Leu Met Glu  
 165 170 175  
 Thr Ala Lys Val Ser Gln Ser Pro Ile His Ser Leu Glu Lys Leu Gly  
 180 185 190  
 Ile Leu Asp Ile Val Asp Ala Ala Gln Leu Glu Leu Gln Glu Asp Leu  
 195 200 205  
 Leu Thr Phe Phe Pro Pro Ala Pro Lys Asp Leu His Pro Glu Gln Gln  
 210 215 220  
 Ser Ala Ile Asp Lys Ile Phe Ser Ser Leu Lys Thr Ser Gln Phe His  
 225 230 235 240  
 Thr His Leu Leu Phe Gly Ile Thr Gly Ser Gly Lys Thr Glu Ile Tyr  
 245 250 255  
 Leu Arg Ala Thr Ser Glu Ala Leu Lys Gln Gly Lys Ser Thr Ile Leu  
 260 265 270  
 Leu Val Pro Glu Ile Ala Leu Thr Val Gln Thr Val Ser Leu Phe Lys  
 275 280 285  
 Ala Arg Phe Gly Lys Asp Val Gly Val Leu His His Lys Leu Ser Asp  
 290 295 300  
 Ser Asp Gln Lys Ser His Val Ala Pro Ser Phe Arg Arg Ser Leu Arg  
 305 310 315 320  
 Ile Leu Ile Gly Pro Arg Ser Ala Leu Phe Cys Pro Met Lys Asn Leu  
 325 330 335  
 Gly Leu Ile Ile Val Asp Glu Glu His Asp Pro Ala Tyr Lys Gln Thr  
 340 345 350  
 Glu Ser Pro Pro Cys Tyr His Ala Arg Asp Val Ala Val Met Arg Gly  
 355 360 365  
 Lys Leu Ala His Ala Thr Val Val Leu Gly Ser Ala Thr Pro Ser Leu  
 370 375 380  
 Glu Ser Tyr Thr Asn Ala Leu Ser Gly Lys Tyr Val Leu Ser Arg Leu  
 385 390 395 400  
 Ser Ser Arg Ala Ala Ala Ala His Pro Ala Lys Ile Ser Leu Ile Asn  
 405 410 415  
 Met Asn Leu Glu Arg Glu Lys Ser Lys Thr Lys Ile Leu Phe Ser Gln  
 420 425 430  
 Pro Val Leu Lys Lys Ile Ala Glu Arg Leu Glu Val Gly Glu Gln Val  
 435 440 445  
 Leu Ile Phe Phe Asn Arg Arg Gly Tyr His Thr Asn Val Ser Cys Thr  
 450 455 460  
 Val Cys Lys His Thr Leu Lys Cys Pro His Cys Asp Met Val Leu Thr  
 465 470 475 480  
 Phe His Lys Tyr Ala Asn Val Leu Leu Cys His Leu Cys Asn Ser Ser  
 485 490 495  
 Pro Lys Asp Leu Pro Gln Ser Cys Pro Lys Cys Leu Gly Thr Met Thr  
 500 505 510

Leu Gln Tyr Arg Gly Ser Gly Thr Glu Lys Ile Glu Lys Ile Leu Gln  
 515 520 525  
 Gln Ile Phe Pro Gln Ile Arg Thr Ile Arg Ile Asp Ser Asp Thr Thr  
 530 535 540  
 Lys Phe Lys Gly Ser His Glu Thr Leu Leu Arg Gln Phe Ala Thr Gly  
 545 550 555 560  
 Lys Ala Asp Val Leu Ile Gly Thr Gln Met Ile Ala Lys Gly Met Asn  
 565 570 575  
 Phe Ser Ala Val Thr Leu Ala Val Ile Leu Asn Gly Asp Ser Gly Leu  
 580 585 590  
 Tyr Ile Pro Asp Phe Arg Ala Ser Glu Gln Val Phe Gln Leu Ile Thr  
 595 600 605  
 Gln Val Ala Gly Arg Ser Gly Arg Ser His Leu Pro Gly Glu Ile Leu  
 610 615 620  
 Ile Gln Ser Phe Leu Pro Asp His Pro Thr Ile His Ser Ala Met Arg  
 625 630 635 640  
 Gln Asp Tyr Ser Ala Phe Tyr Ser Gln Glu Ile Thr Gly Arg Glu Leu  
 645 650 655  
 Cys Glu Tyr Pro Pro Phe Ile Arg Leu Ile Arg Cys Ile Phe Met Gly  
 660 665 670  
 Lys Cys Pro Lys Gln Thr Trp Glu Glu Ala His Arg Val His Asn Ile  
 675 680 685  
 Leu Lys Glu Gln Leu Glu Ser Thr Asn Pro Leu Met Pro Val Thr Pro  
 690 695 700  
 Cys Gly His Phe Lys Ile Lys Asp Thr Phe Arg Tyr Gln Phe Leu Ile  
 705 710 715 720  
 Lys Ser Ala Tyr Val Ile Pro Val Asn Lys Lys Leu His His Ala Leu  
 725 730 735  
 Met Leu Ala Lys Leu Ser Pro Lys Val Lys Phe Met Ile Asp Val Asp  
 740 745 750  
 Pro Met Thr Thr Phe Phe  
 755

&lt;210&gt;997

&lt;211&gt;230

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;997

Lys His Trp Leu Phe Met Glu Asn Ser Gln Asn Phe His Asp Thr Leu  
 1 5 10 15  
 Cys Gln Leu Leu Asp Arg Tyr Ser Glu Glu Leu Tyr Pro Thr Leu Ala  
 20 25 30  
 Ser Leu Leu Asn Val Thr Leu Pro Asn Thr Ala Ile Ser Ala Ser Val  
 35 40 45  
 Ser Ser Ile Pro Glu Lys Ala Val Glu Val Pro Asn Ala Glu Pro Gln  
 50 55 60  
 Pro Ile Thr Pro Pro Pro Thr Asn Leu Ser Gln Glu Lys Thr Lys  
 65 70 75 80  
 Pro Ser Asp Trp Lys Cys Val Pro Leu His Pro Asp Leu Ser Gln Asn  
 85 90 95  
 Ala Ile Leu Lys Glu Lys Tyr Pro Ala Leu Lys Asp Cys Ser Leu Pro  
 100 105 110  
 Ala Pro Lys Ile Pro Cys Ser Ile Phe Val Tyr Glu Glu Asn Asn Glu  
 115 120 125  
 Glu Val Leu Phe Phe Asn Arg Leu Ala Lys Ile Leu Thr Gln Gln Leu  
 130 135 140  
 Phe Pro Thr Lys Leu Thr Leu Ile His Ala Lys Thr Asn Ile Phe Val  
 145 150 155 160  
 Asn Asn Pro Asn Phe Phe Leu Ala Leu Ala Pro Leu Asn Val Ile Arg  
 165 170 175  
 Tyr Lys Ile Pro Thr Thr Asp Tyr His Gln Ser Leu Thr Gln Asn Gly  
 180 185 190  
 Cys Ile Phe Leu Pro Leu Tyr Ser Ser Leu Glu Tyr Glu Lys Asp Ser  
 195 200 205  
 Gln Leu Lys Arg Asn Leu Trp Ala Ile Leu Asn Arg Leu Pro Phe Ala

210 215 220  
 Tyr Thr Pro Lys Ser Ser  
 225 230  
 <210>998  
 <211>166  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>998  
 His Glu Ile Leu Val Ala Arg Met Cys Phe Cys Arg Leu Ser Ala Ile  
 1 5 10 15  
 Asp Phe Thr Leu Leu Cys Cys Thr Lys Thr Cys Phe Trp Arg Asn Leu  
 20 25 30  
 Gln Gln Thr Arg Pro Ile Ala Ala Asn Leu Gln Trp Glu Ser Tyr  
 35 40 45  
 Ala Glu Ala Leu Glu His Ser Lys Gln Asp His Lys Pro Ile Cys Leu  
 50 55 60  
 Phe Phe Thr Gly Ser Asp Trp Cys Met Trp Cys Ile Lys Met Gln Asp  
 65 70 75 80  
 Gln Ile Leu Gln Ser Ser Glu Phe Lys His Phe Ala Gly Val His Leu  
 85 90 95  
 His Met Val Glu Val Asp Phe Pro Gln Lys Asn His Gln Pro Glu Glu  
 100 105 110  
 Gln Arg Gln Lys Asn Gln Glu Leu Lys Ala Gln Tyr Lys Val Thr Gly  
 115 120 125  
 Phe Pro Glu Leu Val Phe Ile Asp Ala Glu Gly Lys Gln Leu Ala Arg  
 130 135 140  
 Met Gly Phe Glu Pro Gly Gly Gly Ala Ala Tyr Val Ser Lys Val Lys  
 145 150 155 160  
 Ser Ala Leu Lys Leu Arg  
 165

&lt;210&gt;999

&lt;211&gt;380

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;999

Met Ile Pro Ser Pro Thr Pro Ile Asn Phe Arg Asp Asp Thr Ile Leu  
 1 5 10 15  
 Glu Thr Asp Pro Lys Pro Ser Leu Ile Met Phe Ser Ser Lys Lys Thr  
 20 25 30  
 Glu Ile Ala Ser Glu Arg Arg Lys Ala His Pro Thr Leu Phe Lys Val  
 35 40 45  
 Leu Gly Thr Ile Trp Asn Ile Val Lys Phe Ile Ile Ser Ile Ile Leu  
 50 55 60  
 Phe Leu Pro Leu Ala Leu Leu Trp Val Leu Lys Lys Thr Cys Gln Phe  
 65 70 75 80  
 Phe Ile Leu Pro Ser Ser Ile Ile Ser Gln Ser Met Ser Lys Thr Ala  
 85 90 95  
 Val Ala Ile Arg Arg Met Thr Phe Leu Ser His Ile Lys Gln Leu Leu  
 100 105 110  
 Ser Leu Lys Glu Ile Ser Ala Ala Asp Arg Val Val Ile Gln Tyr Asp  
 115 120 125  
 Asp Leu Val Val Asp Ser Leu Ala Ile Lys Ile Pro His Ala Leu Pro  
 130 135 140  
 His Arg Trp Ile Leu Tyr Ser Gln Gly Asn Ser Gly Leu Met Glu Asn  
 145 150 155 160  
 Leu Phe Asp Arg Gly Asp Ser Ser Leu His Gln Leu Ala Lys Ala Thr  
 165 170 175  
 Gly Ser Asn Leu Leu Val Phe Asn Tyr Pro Gly Ile Met Ser Ser Lys  
 180 185 190  
 Gly Glu Ala Lys Arg Glu Asn Leu Val Lys Ser Tyr Gln Ala Cys Val  
 195 200 205  
 Arg Tyr Leu Arg Asp Glu Glu Thr Gly Pro Lys Ala Asn Gln Ile Ile  
 210 215 220  
 Ala Phe Gly Tyr Ser Leu Gly Thr Ser Val Gln Ala Ala Ala Leu Asp

225 230 235 240  
 Arg Glu Val Thr Asp Gly Ser Asp Gly Thr Ser Trp Ile Val Val Lys  
 245 250 255  
 Asp Arg Gly Pro Arg Ser Leu Ala Asp Val Ala Asn Gln Ile Cys Lys  
 260 265 270  
 Pro Ile Ala Ser Ala Ile Ile Lys Leu Val Gly Trp Asn Ile Asp Ser  
 275 280 285  
 Val Lys Pro Ser Glu Arg Leu Arg Cys Pro Glu Ile Phe Ile Tyr Asn  
 290 295 300  
 Ser Asn His Asp Gln Glu Leu Ile Ser Asp Gly Leu Phe Glu Arg Glu  
 305 310 315 320  
 Asn Cys Val Xaa Thr Pro Phe Leu Glu Leu Pro Glu Val Lys Thr Ser  
 325 330 335  
 Gly Thr Lys Ile Pro Ile Pro Glu Arg Asp Leu Leu His Leu Asn Pro  
 340 345 350  
 Leu Ser Pro Asn Val Val Asp Arg Leu Ala Ala Val Ile Ser Asn Tyr  
 355 360 365  
 Leu Asp Ser Glu Asn Arg Lys Ser Gln Gln Pro Asp  
 370 375 380  
 <210>1000  
 <211>377  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1000  
 Phe Thr Leu Leu Asn Leu Ser Asn Arg Ser Asp Ile Leu Ser Gly Ile  
 1 5 10 15  
 Phe Ser Asn Pro His Pro Val Ser Tyr Phe Ser Ser Thr His Ala Lys  
 20 25 30  
 Gln Leu Ser Asp Phe Ser Lys Lys His Pro Ile Leu Thr Lys Ile Val  
 35 40 45  
 Thr Ile Ile Val Lys Ile Phe Lys Leu Leu Ile Gly Leu Ile Ile Pro  
 50 55 60  
 Pro Leu Gly Ile Tyr Trp Leu Cys Gln Leu Val Cys Ser Leu Ala Leu  
 65 70 75 80  
 Phe Pro Arg Ser Ser Met Leu Tyr Ser Val Leu Lys Thr Cys Phe Lys  
 85 90 95  
 Lys Tyr Arg Leu Glu Gln Glu Ile Gln Asp Tyr Phe Val Lys Asn Leu  
 100 105 110  
 Asp Pro Ser Phe Lys Asp Pro Ala Val Ser Glu Ser Lys Arg Ile Thr  
 115 120 125  
 Ile Gln Gln Asp His Leu Thr Ile Asp Thr Leu Ala Ile His Phe Ser  
 130 135 140  
 Thr Ala Arg Pro Lys Arg Trp Leu Leu Ile Ser Leu Gly Ser Gly Asp  
 145 150 155 160  
 Phe Leu Glu Asp Met Ile Gly Leu Lys Asp Ser Leu Phe Leu Ser Trp  
 165 170 175  
 Lys Glu Leu Ala Lys Leu Leu Gly Ala Asn Ile Leu Ile Tyr Asn Tyr  
 180 185 190  
 Pro Gly Val Lys Ser Ser Thr Gly Lys Leu Asn Leu Glu Asn Leu Ala  
 195 200 205  
 Thr Val Ile Ile Tyr Val Gln Ser Thr Tyr Lys Ile Lys Phe Arg Ala  
 210 215 220  
 Leu Gly Leu Thr Lys Ser Ser Pro Arg Ile Phe Leu Arg Arg Gly Ser  
 225 230 235 240  
 Pro Val Cys Ser Phe Ala Lys Asn Pro Phe Thr Asn Ser Glu Thr Ser  
 245 250 255  
 Trp Val Ala Val Lys Asp Arg Ala Pro His Ser Leu Pro Ala Ala Ala  
 260 265 270  
 Asn Ser Phe Phe Gly Pro Ile Gly Lys Leu Ile Ala Val Leu Ala Arg  
 275 280 285  
 Trp Lys Met Asp Ala Glu Lys Asn Ser Arg Glu Leu Pro Cys Pro Glu  
 290 295 300  
 Ile Leu Val Tyr Ser Ala Asp Arg Phe Arg Pro Ser Glu Val Gly Asp  
 305 310 315 320

Asp Thr Ala Leu Leu Pro Glu Phe Thr Leu Ala His Ala Ile Lys Arg  
 325 330 335  
 Thr Pro Phe Ala Arg Ser Lys Lys Phe Ile Gly Glu Val Asn Leu Leu  
 340 345 350  
 His Ser Ser Pro Leu Lys His Pro Thr Ile Gln Lys Leu Ala Glu Ala  
 355 360 365  
 Ile Leu Glu Ser Leu Ser Arg Lys Asn  
 370 375  
 <210>1001  
 <211>369  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1001  
 Met Ala Pro Ile His Gly Ser Asn Ala Phe Val Glu Asp Ile Leu His  
 1 5 10 15  
 Ser His Pro Ser Pro Gln Ala Thr Tyr Phe Ser Ser Thr Arg Ala Gln  
 20 25 30  
 Lys Leu His Glu Phe Lys Asp Arg His Pro Val Leu Thr Arg Ile Ala  
 35 40 45  
 Ser Val Ile Ile Lys Ile Phe Lys Val Leu Ile Gly Leu Ile Ile Leu  
 50 55 60  
 Pro Leu Gly Ile Tyr Trp Leu Cys Gln Thr Leu Cys Thr Asn Ser Ile  
 65 70 75 80  
 Leu Pro Ser Lys Asn Leu Leu Lys Ile Phe Lys Lys Gln Pro Asn Thr  
 85 90 95  
 Lys Thr Leu Lys Thr Asn Tyr Leu Arg Ala Leu Gln Asp Tyr Ser Ser  
 100 105 110  
 Lys Asn Arg Val Ala Ser Met Arg Arg Val Pro Ile Leu Gln Asp Asn  
 115 120 125  
 Val Leu Ile Asp Thr Leu Glu Ile Cys Leu Ser Gln Ala Pro Thr Asn  
 130 135 140  
 Arg Trp Met Leu Ile Ser Leu Gly Ser Asp Cys Ser Leu Glu Glu Ile  
 145 150 155 160  
 Ala Cys Lys Glu Ile Phe Asp Ser Trp Gln Arg Phe Ala Lys Leu Ile  
 165 170 175  
 Gly Ala Asn Ile Leu Val Tyr Asn Tyr Pro Gly Val Met Ser Ser Thr  
 180 185 190  
 Gly Ser Ser Ser Leu Lys Asp Leu Ala Ser Ala His Asn Ile Cys Thr  
 195 200 205  
 Arg Tyr Leu Lys Asp Lys Glu Gln Gly Pro Gly Ala Lys Glu Ile Ile  
 210 215 220  
 Thr Tyr Gly Tyr Ser Leu Gly Gly Leu Ile Gln Ala Glu Ala Leu Arg  
 225 230 235 240  
 Asp Gln Lys Ile Val Ala Asn Asp Asp Thr Thr Trp Ile Ala Val Lys  
 245 250 255  
 Asp Arg Cys Pro Leu Phe Ile Ser Pro Glu Gly Phe His Ser Cys Arg  
 260 265 270  
 Arg Ile Gly Lys Leu Val Ala Arg Leu Phe Gly Trp Gly Thr Lys Ala  
 275 280 285  
 Val Glu Arg Ser Gln Asp Leu Pro Cys Leu Glu Ile Phe Leu Tyr Pro  
 290 295 300  
 Thr Asp Ser Leu Arg Arg Ser Thr Val Arg Gln Asn Lys Leu Leu Ala  
 305 310 315 320  
 Pro Glu Leu Thr Leu Ala His Ala Ile Lys Asn Ser Pro Tyr Val Gln  
 325 330 335  
 Asn Lys Glu Phe Ile Glu Val Arg Leu Ser Ser Asp Ile Asp Pro Ile  
 340 345 350  
 Asp Ser Lys Thr Arg Val Ala Leu Ala Thr Pro Ile Leu Lys Lys Leu  
 355 360 365  
 Ser

<210>1002  
 <211>160  
 <212>PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1002

```

Asn Lys Met Ser Glu Leu Ala Pro Cys Ser Thr Gly Leu Gln Met Val
 1           5           10           15
Pro His Thr Gln Val His His Ala Leu Asp Thr Arg Arg Val Ile Leu
          20           25           30
Thr Ile Ala Ala Cys Leu Ser Leu Ile Ala Gly Ile Val Leu Val Gly
          35           40           45
Leu Gly Ala Ala Ala Ile Leu Pro Ser Leu Phe Gly Val Ile Gly Gly
          50           55           60
Met Ile Leu Ile Leu Phe Ser Ser Ile Ala Leu Ile Tyr Leu Tyr Lys
          65           70           75           80
Lys Thr Arg Glu Val Asp Gln Ile Ala Leu Glu Pro Leu Pro Glu Met
          85           90           95
Ile Ser Lys Asp Gln Ser Ile Ile Asp Phe Val Lys Thr Arg Asp Tyr
          100          105          110
Ala Ser Leu Glu Lys Lys Ala Thr Phe Ala Tyr Thr His Thr His Tyr
          115          120          125
Tyr Asp Gly Ser Met Val Phe Tyr Arg Glu Ile Pro Arg Phe Met Leu
          130          135          140
Gly Ser Tyr Leu Ala Leu Arg Lys Asp Met Asp Arg Gln Ala Leu Phe
          145          150          155          160

```

&lt;210&gt;1003

&lt;211&gt;542

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1003

```

Leu Gly Trp Lys Ser Asp Ile Tyr Thr Asn Ile Leu Glu Glu Arg Met
 1           5           10           15
Thr Ala Arg Ala Glu Tyr Leu Asp His Glu Asp Phe Leu Tyr Arg Ser
          20           25           30
His Lys Leu Gln Glu Leu Ser Glu Leu Gly Val Val Leu Tyr Pro Tyr
          35           40           45
Glu Phe Pro Gly Val Phe Ser Cys Glu Asp Ile Lys Lys Thr Phe Ala
          50           55           60
Ser Gln Glu Leu Gly Asn Ser Glu Ala Ala Met Ser Arg Ser Thr Pro
          65           70           75           80
Arg Val Arg Phe Ala Gly Arg Leu Val Leu Phe Arg Ala Met Gly Lys
          85           90           95
Asn Ala Phe Gly Gln Ile Leu Asp His Asn Gln Thr Ile Gln Val Met
          100          105          110
Phe Asn Arg Glu Phe Thr Ser Val His Gly Leu Ser Glu Asp Ala Glu
          115          120          125
Ile Thr Pro Ile Lys Phe Ile Glu Lys Lys Leu Asp Leu Gly Asp Ile
          130          135          140
Leu Gly Ile Asp Gly Tyr Leu Phe Phe Thr His Ser Gly Glu Leu Thr
          145          150          155          160
Val Leu Val Glu Thr Val Thr Leu Leu Cys Lys Ser Leu Leu Ser Leu
          165          170          175
Pro Asp Lys His Ala Gly Leu Ser Asp Lys Glu Val Arg Tyr Arg Lys
          180          185          190
Arg Trp Leu Asp Leu Ile Ser Ser Arg Glu Val Ser Asp Thr Phe Val
          195          200          205
Lys Arg Ser Tyr Ile Ile Lys Leu Ile Arg Asn Tyr Met Asp Ala His
          210          215          220
Gly Phe Leu Glu Val Glu Thr Pro Ile Leu Gln Asn Ile Tyr Gly Gly
          225          230          235          240
Ala Glu Ala Lys Pro Phe Thr Thr Thr Met Glu Ala Leu His Ser Glu
          245          250          255
Met Phe Leu Arg Ile Ser Leu Glu Ile Ala Leu Lys Lys Ile Leu Val
          260          265          270
Gly Gly Ala Pro Arg Ile Tyr Glu Leu Gly Lys Val Phe Arg Asn Glu
          275          280          285
Gly Ile Asp Arg Thr His Asn Pro Glu Phe Thr Met Ile Glu Ala Tyr

```



290 295 300  
 Ala Ala Tyr Met Asp Tyr Lys Glu Val Met Val Phe Val Glu Asn Leu  
 305 310 315 320  
 Val Glu His Leu Val Arg Ala Val Asn His Asp Asn Thr Ser Leu Val  
 325 330 335  
 Tyr Ser Tyr Trp Lys His Gly Pro Gln Glu Val Asp Phe Lys Ala Pro  
 340 345 350  
 Trp Ile Arg Met Thr Met Lys Glu Ser Ile Ala Thr Tyr Ala Gly Ile  
 355 360 365  
 Asp Val Asp Val His Ser Asp Gln Lys Leu Lys Glu Ile Leu Lys Lys  
 370 375 380  
 Lys Thr Thr Phe Pro Glu Thr Ala Phe Ala Thr Ala Ser Arg Gly Met  
 385 390 395 400  
 Leu Ile Ala Ala Leu Phe Asp Glu Leu Val Ser Asp Asn Leu Ile Ala  
 405 410 415  
 Pro His His Ile Thr Asp His Pro Val Glu Thr Thr Pro Leu Cys Lys  
 420 425 430  
 Thr Leu Arg Ser Gly Asp Thr Ala Phe Val Glu Arg Phe Glu Ser Phe  
 435 440 445  
 Cys Leu Gly Lys Glu Leu Cys Asn Ala Tyr Ser Glu Leu Asn Asp Pro  
 450 455 460  
 Ile Arg Gln Arg Glu Leu Glu Gln Gln His Thr Lys Lys Glu Leu  
 465 470 475 480  
 Leu Pro Asp Ser Glu Cys His Pro Ile Asp Glu Glu Phe Leu Glu Ala  
 485 490 495  
 Leu Cys Gln Gly Met Pro Pro Ala Gly Gly Phe Gly Ile Gly Val Asp  
 500 505 510  
 Arg Leu Val Met Ile Leu Thr Asn Ala Ala Ser Ile Arg Asp Val Leu  
 515 520 525  
 Tyr Phe Pro Val Met Arg Arg Phe Asp Ala Glu Lys Thr Asn  
 530 535 540  
 <210>1004  
 <211>308  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1004  
 Val Ala Tyr Ala Ala Ala Pro Glu Phe Leu Leu Met Ser Met Thr Lys  
 1 5 10 15  
 Lys Thr Gln Val Ile Leu Tyr Cys Gly Lys His Thr Ile Gln Asn Val  
 20 25 30  
 Met Ala Ser Phe Ile Gly Lys Val Leu Ser Gly Ile Gly Arg Pro Gly  
 35 40 45  
 Trp His Leu Glu Cys Ser Ile Met Ala Met Glu Leu Leu Gly Asp Ser  
 50 55 60  
 Leu Asp Ile His Ala Gly Gly Val Asp Asn Ile Phe Pro His His Glu  
 65 70 75 80  
 Asn Glu Ile Ala Gln Ser Glu Ala Leu Ser Gly Lys Pro Phe Ala Arg  
 85 90 95  
 Tyr Trp Leu His Ser Glu His Leu Leu Ile Asp Gly Lys Lys Met Ser  
 100 105 110  
 Lys Ser Leu Gly Asn Phe Leu Thr Leu Arg Asp Leu Leu His Gln Glu  
 115 120 125  
 Phe Thr Gly Gln Glu Val Arg Tyr Met Leu Leu Gln Ser His Tyr Arg  
 130 135 140  
 Thr Gln Leu Asn Phe Thr Glu Glu Ala Leu Leu Ala Cys Arg His Ala  
 145 150 155 160  
 Leu Arg Arg Leu Lys Asp Phe Val Ser Arg Leu Glu Gly Val Asp Leu  
 165 170 175  
 Pro Gly Glu Ser Pro Leu Pro Arg Thr Leu Asp Ser Ser Ser Gln Phe  
 180 185 190  
 Ile Glu Ala Phe Ser Arg Ala Leu Ala Asn Asp Leu Asn Val Ser Thr  
 195 200 205  
 Gly Phe Ala Ser Leu Phe Asp Phe Val His Glu Ile Asn Thr Leu Ile  
 210 215 220

Asp Gln Gly His Phe Ser Lys Ala Asp Ser Leu Tyr Ile Leu Asp Thr  
 225 230 235 240  
 Leu Lys Lys Val Asp Thr Val Leu Gly Val Leu Pro Leu Thr Thr Ser  
 245 250 255  
 Val Cys Ile Pro Glu Thr Val Met Gln Leu Val Ala Glu Arg Glu Glu  
 260 265 270  
 Ala Arg Lys Thr Lys Asn Trp Ala Met Ala Asp Thr Leu Arg Asp Glu  
 275 280 285  
 Ile Leu Ala Ala Gly Phe Leu Val Glu Asp Ser Lys Ser Gly Pro Lys  
 290 295 300  
 Val Lys Pro Leu  
 305

&lt;210&gt;1005

&lt;211&gt;232

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1005

Gly Leu Tyr Phe Tyr Asn Thr Ala Ser Gln Lys Lys Glu Leu Phe Phe  
 1 5 10 15  
 Pro Asn His Thr Pro Val Arg Leu Tyr Thr Cys Gly Pro Thr Val Tyr  
 20 25 30  
 Asp Tyr Ala His Ile Gly Asn Phe Arg Thr Tyr Val Phe Glu Asp Ile  
 35 40 45  
 Leu Lys Arg Thr Leu Val Phe Gly Tyr Ser Val Thr His Val Met  
 50 55 60  
 Asn Ile Thr Asp Val Glu Asp Lys Thr Ile Ala Gly Ala Ser Lys Lys  
 65 70 75 80  
 Asn Ile Pro Leu Gln Glu Tyr Thr Gln Pro Tyr Thr Glu Ala Phe Phe  
 85 90 95  
 Glu Asp Leu Asp Thr Leu Asn Ile Ala Arg Ala Asp Phe Tyr Pro His  
 100 105 110  
 Ala Thr His Tyr Ile Pro Gln Met Ile Gln Ala Ile Thr Lys Leu Leu  
 115 120 125  
 Glu Gln Gly Ile Ala Tyr Ile Gly Gln Asp Ala Ser Val Tyr Phe Ser  
 130 135 140  
 Leu Asn Arg Phe Pro Asn Tyr Gly Lys Leu Ser His Leu Asp Leu Ser  
 145 150 155 160  
 Ser Leu Arg Cys Cys Ser Arg Ile Ser Ala Asp Glu Tyr Asp Lys Glu  
 165 170 175  
 Asn Pro Ser Asp Phe Val Leu Trp Lys Ala Tyr Asn Pro Glu Arg Asp  
 180 185 190  
 Gly Val Ile Tyr Trp Glu Ser Pro Phe Gly Asn Arg Lys Thr Trp Met  
 195 200 205  
 Ala Phe Arg Met Phe Asp Tyr Gly Asp Gly Thr Ser Trp Arg Phe Phe  
 210 215 220  
 Gly Tyr Pro Cys Gly Arg Cys Arg  
 225 230

&lt;210&gt;1006

&lt;211&gt;242

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1006

Thr Ala Val Glu Asn Ile Arg Gln Gln Asn Leu Ala Leu Lys Ser Lys  
 1 5 10 15  
 Phe Lys Ile Asn Glu Leu Pro Cys Met Ile Leu Leu Ser His Glu Glu  
 20 25 30  
 Arg Glu Ile Tyr Arg Ile Gly Ser Phe Gly Asn Glu Thr Gly Ser Asn  
 35 40 45  
 Leu Gly Asp Ser Leu Cys His Ile Val Glu Ser Asp Ser Leu Leu Arg  
 50 55 60  
 Arg Ala Phe Pro Met Met Thr Ser Leu Ser Leu Ser Glu Leu Gln Arg  
 65 70 75 80  
 Tyr Tyr Arg Leu Ala Glu Glu Leu Ser His Lys Glu Phe Leu Lys His  
 85 90 95

Ala Leu Glu Leu Gly Val Arg Ser Asp Asp Tyr Phe Phe Leu Ser Glu  
 100 105 110  
 Lys Phe Arg Leu Leu Val Glu Val Gly Lys Met Asp Ser Glu Glu Cys  
 115 120 125  
 Gln Arg Ile Lys Lys Arg Leu Leu Asn Lys Asp Pro Lys Asn Glu Lys  
 130 135 140  
 Gln Thr His Phe Thr Val Ala Leu Ile Glu Phe Gln Glu Leu Ala Lys  
 145 150 155 160  
 Arg Ser Arg Ala Gly Val Arg Gln Asp Ala Ser Gln Val Ile Ala Pro  
 165 170 175  
 Leu Glu Ser Tyr Ile Ser Gln Phe Gly Gln Gln Asp Lys Asp Asn Leu  
 180 185 190  
 Trp Arg Val Glu Met Met Ile Ala Gln Phe Tyr Leu Asp Ser Asp Gln  
 195 200 205  
 Trp His His Ala Leu Gln His Ala Glu Val Ala Phe Glu Ala Ala Pro  
 210 215 220  
 Asn Glu Val Arg Ser His Ile Ser Arg Ser Leu Glu Tyr Ile Arg His  
 225 230 235 240  
 Gln Ser

&lt;210&gt;1007

&lt;211&gt;139

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1007

Val His Pro Leu Thr Leu Pro Lys Gln Ser Arg Val Leu Lys Arg Lys  
 1 5 10 15  
 Gln Phe Leu Tyr Ile Thr Arg Ser Gly Phe Cys Cys Arg Gly Ser Gln  
 20 25 30  
 Ala Thr Phe Tyr Val Val Pro Ser Arg His Pro Gly Thr Cys Arg Met  
 35 40 45  
 Gly Ile Thr Val Ser Lys Lys Phe Gly Lys Ala His Glu Arg Xaa Ser  
 50 55 60  
 Phe Lys Arg Val Val Arg Glu Val Phe Arg His Val Arg His Gln Leu  
 65 70 75 80  
 Pro Asn Cys Gln Ile Val Val Phe Pro Lys Gly His Lys Gln Arg Pro  
 85 90 95  
 Val Phe Ser Lys Leu Leu Gln Asp Phe Ile Asn Gln Ile Pro Glu Gly  
 100 105 110  
 Leu His Arg Leu Gly Lys Thr Lys Ala Thr Thr Gly Gly Glu Cys Thr  
 115 120 125  
 Pro Lys Ser Glu Lys Cys Val Thr Ala Pro Arg  
 130 135

&lt;210&gt;1008

&lt;211&gt;101

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1008

Met Ala Lys Lys Ser Ser Val Ala Arg Glu Ala Lys Arg Arg Arg Leu  
 1 5 10 15  
 Val Glu Ala Asn Phe Lys Lys Arg Ser Asp Leu Arg Lys Ile Val Lys  
 20 25 30  
 Ser Leu Ser Val Ser Glu Glu Glu Lys Glu Asn Ala Arg Ile Ser Leu  
 35 40 45  
 Asn Lys Met Lys Arg Asp Thr Ser Pro Thr Arg Leu His Asn Arg Cys  
 50 55 60  
 Leu Leu Thr Gly Arg Pro Arg Gly Tyr Leu Arg Lys Phe Ala Ile Ser  
 65 70 75 80  
 Arg Ile Cys Phe Arg Gln Met Ala Ser Met Gly Glu Ile Pro Gly Val  
 85 90 95  
 Ile Lys Ala Ser Trp  
 100

&lt;210&gt;1009

&lt;211&gt;169

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1009

Gln Thr Ile Asn Leu Ser Gly Thr Leu Arg Thr Met Leu Pro Ile Ser  
 1 5 10 15  
 Ile Leu Leu Phe Tyr Val Ile Leu Gly Cys Leu Ser Ala Tyr Ile Ala  
 20 25 30  
 Asp Lys Lys Lys Arg Asn Val Ile Gly Trp Phe Phe Ala Gly Ala Phe  
 35 40 45  
 Phe Gly Phe Ile Gly Leu Val Val Leu Leu Leu Leu Pro Ser Arg Arg  
 50 55 60  
 Asn Ala Leu Glu Lys Pro Gln Asn Asp Pro Phe Asp Asn Ser Asp Leu  
 65 70 75 80  
 Phe Asp Asp Leu Lys Lys Ser Leu Ala Gly Asn Asp Glu Ile Pro Ser  
 85 90 95  
 Ser Gly Asp Leu Gln Glu Ile Val Ile Asp Thr Glu Lys Trp Phe Tyr  
 100 105 110  
 Leu Asn Lys Asp Arg Glu Asn Val Gly Pro Ile Ser Phe Glu Glu Leu  
 115 120 125  
 Val Val Leu Leu Lys Gly Lys Thr Tyr Pro Glu Glu Ile Trp Val Trp  
 130 135 140  
 Lys Lys Gly Met Lys Asp Trp Gln Arg Val Lys Asp Val Pro Ser Leu  
 145 150 155 160  
 Gln Gln Ala Leu Lys Glu Ala Ser Lys  
 165

&lt;210&gt;1010

&lt;211&gt;189

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1010

His Ile Asn Arg Trp Thr Ile Arg Leu Ser Leu Thr Leu Ile Ile Ser  
 1 5 10 15  
 Thr Val Leu Tyr Phe Phe Ser Glu Glu Ile Glu Leu Ile Gly Gly Gly  
 20 25 30  
 Lys Met Glu Lys Gln Asn Leu Lys Leu Asp Val Lys Glu Ile Glu Phe  
 35 40 45  
 Pro Glu Thr Val Phe Ser Arg Asp Ile Glu Thr Arg Val Ile Gln Val  
 50 55 60  
 Ile Ile Leu His Cys Leu Ala Lys Ile Asn Gly Val Ser Leu Leu Gly  
 65 70 75 80  
 Gly Asn Leu Ile Asp Ala Leu Phe Gly Arg Asp Ile Glu Arg Met Lys  
 85 90 95  
 Gly Ile Tyr Val Glu Gln Asp Ser Lys Asn His Leu Val Lys Val Arg  
 100 105 110  
 Val Glu Val Asn Val Asp Tyr Gly Val Ser Ile Pro Glu Lys Thr Glu  
 115 120 125  
 Glu Ile Gln Gly Cys Ile Val Ser Glu Ile Ser Glu Tyr Thr Gly Leu  
 130 135 140  
 His Val Ala Ala Val His Val Ile Ile Lys Gly Leu Thr Gln Pro Lys  
 145 150 155 160  
 Asp Arg Ile Asp Glu Glu Ile Glu Glu Val Ser Val Gln Asp Leu  
 165 170 175  
 Pro Ser Pro Glu Asp Phe Leu Leu Glu Asn Ser Glu Gly  
 180 185

&lt;210&gt;1011

&lt;211&gt;603

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1011

Met Arg Ile Glu Asp Phe Ser Leu Lys Leu Ile Pro Ser Ser Pro Gly  
 1 5 10 15  
 Val Tyr Leu Met Lys Asp Val His Asp Gln Val Leu Tyr Ile Gly Lys  
 20 25 30  
 Ala Lys Asn Leu Lys Asn Arg Leu Ala Ser Tyr Phe His Glu Lys Gly

```

      35      40      45
Asp Ser Arg Glu Arg Ile Pro Phe Leu Met Lys Lys Thr Ala Ser Ile
      50      55      60
Glu Thr Ile Val Val Ser Asn Glu Thr Glu Ala Leu Leu Leu Glu Asn
      65      70      75      80
Asn Leu Ile Lys Gln His His Pro Lys Tyr Asn Val Leu Leu Lys Asp
      85      90      95
Asp Lys Thr Phe Phe Cys Leu Ala Ile Ser Leu Ser His Ser Trp Pro
      100      105      110
Lys Val Glu Ala Ile Arg Thr Lys Ala Ile Thr Ser Ser Gln Arg Gln
      115      120      125
Leu Ile Phe Gly Pro Tyr Val Ser Ala Glu Ala Cys His Thr Leu Leu
      130      135      140
Glu Val Ile Ser Gln Trp Phe Pro Leu Arg Thr Cys Ser Asp Arg Glu
      145      150      155      160
Phe Ala Leu Arg Lys Arg Pro Cys Ile Leu Tyr Asp Met Lys Arg Cys
      165      170      175
Leu Ala Pro Cys Val Gly Tyr Cys Thr Pro Glu Glu Tyr Gln Gly Thr
      180      185      190
Leu Asp Lys Ala Ile Leu Phe Leu Lys Gly Lys Ile Glu Glu Val Val
      195      200      205
Lys Asp Leu Glu Lys Val Ile Gln Lys Ala Ser Asp Asn Leu Glu Phe
      210      215      220
Glu Gln Ala Ala Asn Tyr Tyr Arg Thr Leu Ser Leu Ile Lys Gln Ala
      225      230      235      240
Met Ala Lys Gln Gln Val Glu Lys Phe His Phe Gln Asn Ile Asp Ala
      245      250      255
Leu Gly Leu Tyr Arg His Lys Gln Arg Thr Ile Leu Thr Leu Leu Thr
      260      265      270
Val Arg Ser Gly Lys Leu Leu Gly Ala Arg His Phe Ser Phe Phe Glu
      275      280      285
Asn Ala Gln Glu Asp Gln Asp Leu Leu Ser Ser Phe Ile Leu Gln Tyr
      290      295      300
Tyr Val Ser Gln Pro Tyr Ile Pro Lys Glu Ile Leu Thr Pro Leu Pro
      305      310      315      320
Leu Glu Phe Pro Thr Leu Ser Tyr Val Leu Asn Ala Glu Ser Pro Pro
      325      330      335
Arg Leu Arg Ser Pro Lys Thr Gly Tyr Gly Lys Glu Leu Leu Asp Leu
      340      345      350
Ala Tyr Arg Asn Ala Lys Ala Tyr Ala Ala Thr Thr Leu Pro Ser Ser
      355      360      365
Ser Ser Pro Thr Lys Thr Leu Arg Ile Ile Leu Arg Met Ser Gln Tyr
      370      375      380
Pro Tyr Arg Ile Glu Cys Tyr Asp Asn Ala His Met Gln Gly Ala His
      385      390      395      400
Ala Thr Gly Val Tyr Ile Val Phe Glu Asn Asn Gly Phe Asp Pro Lys
      405      410      415
Gln Tyr Arg Thr Phe Ser Ile Asp Ser Glu Lys Thr Gln Asn Asp Leu
      420      425      430
Ala Leu Leu Glu Glu Val Leu Leu Arg Arg Phe His Ser Leu Thr Thr
      435      440      445
Ala Leu Pro Asp Met Ile Val Val Asp Gly Gly Lys Thr His Tyr Asn
      450      455      460
Lys Thr Lys Lys Ile Ile Gln Thr Leu Asn Leu Thr Gly Ile Gln Val
      465      470      475      480
Val Thr Ile Ala Lys Glu Lys Ser Asn His Ser Arg Gly Leu Asn Lys
      485      490      495
Glu Lys Ile Phe Cys Glu Thr Phe Pro Glu Gly Phe Ser Leu Pro Pro
      500      505      510
Thr Ser Asn Leu Leu Gln Phe Phe Gln Ile Leu Arg Asp Glu Ala His
      515      520      525
Arg Phe Ala Ile Ser Lys His Arg Lys Lys Arg Gly Lys Ala Leu Phe
      530      535      540
Glu Gln Glu Lys Ile Pro Gly Ile Gly Glu Val Lys Arg Lys Arg Leu

```

545 550 555 560  
 Leu Gln Lys Phe Lys Ser Trp Lys Gln Val Met Leu Ser Ser Gln Glu  
 565 570 575  
 Glu Leu Glu Ala Ile Pro Gly Leu Thr Lys Lys Asp Ile Ala Val Leu  
 580 585 590  
 Leu Ala Arg Gln Lys Asp Phe Asn Lys Ser Asp  
 595 600  
 <210>1012  
 <211>481  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1012  
 Gly Asp Pro Cys Thr Ser Arg Cys Cys Arg Ile Phe Leu Arg Gln Val  
 1 5 10 15  
 Thr Leu Arg Lys Asn Ile Lys Thr Tyr Leu Cys Gln Val Arg Asp Ile  
 20 25 30  
 Glu Arg Leu Met Thr Lys Val Thr Thr Gly Leu Ala Gly Pro Arg Asp  
 35 40 45  
 Ile Gly Thr Leu Arg Asp Ser Phe Ser Ala Gly Ala Gln Ile Tyr Glu  
 50 55 60  
 Gln Leu Ala Ser Ala Thr Leu Pro Glu Phe Phe Ile Asp Lys Cys Ser  
 65 70 75 80  
 Leu Asp Thr Lys Leu Ala Ser Leu Ile Ala Leu Leu Ser Lys Ser Leu  
 85 90 95  
 Asn Gly Asp Leu Pro Leu Arg Val Ser Asp Gly Asn Ile Phe Val Asp  
 100 105 110  
 Glu Phe His Asn Asp Leu Lys Arg Leu Arg His Asn Gln Glu His Ser  
 115 120 125  
 Gln Glu Trp Ile Trp Glu Tyr Gln Glu Arg Ile Arg Lys Glu Thr Gly  
 130 135 140  
 Ile Lys Lys Leu Lys Ile Cys Phe Ala Gln Ala Leu Gly Tyr Tyr Ile  
 145 150 155 160  
 Glu Val Ser Ser Glu Phe Ala Pro Gln Leu Pro Lys Asp Phe Ile Arg  
 165 170 175  
 Arg Gln Ser Arg Leu His Ala Glu Arg Phe Thr Thr Ile Glu Leu Gln  
 180 185 190  
 Gln Phe Gln Asp Asp Met Ser Asn Ile Ser Glu Lys Leu Gln Thr Leu  
 195 200 205  
 Glu Thr Gln Phe Phe Lys Asp Leu Cys Ser His Ile Leu Gln Leu Arg  
 210 215 220  
 Thr Glu Ile Leu Ala Leu Ser Gln Ser Leu Ala Asp Leu Asp Tyr Ile  
 225 230 235 240  
 Ile Ser Leu Ala Asp Leu Ala His Ala Gln Gly Tyr Cys Arg Pro Arg  
 245 250 255  
 Val Asp Met Ser Asp Thr Leu Cys Ile Tyr Arg Gly Cys His Pro Val  
 260 265 270  
 Ala Lys Thr Leu Val Asp Thr Gly Lys Phe Ile Pro Asn Asp Thr Glu  
 275 280 285  
 Met Arg Gly Ser Gln Thr Arg Met Ile Leu Leu Thr Gly Pro Asn Met  
 290 295 300  
 Ala Gly Lys Ser Thr Tyr Ile Arg Gln Ile Ala Leu Leu Val Ile Met  
 305 310 315 320  
 Ala Gln Met Gly Ser Tyr Ile Pro Ala Lys Ser Ala His Ile Gly Val  
 325 330 335  
 Ile Asp Lys Ile Phe Thr Arg Ile Gly Ala Gly Asp Asn Leu Ser Lys  
 340 345 350  
 Gly Met Ser Thr Phe Met Val Glu Met Ala Glu Thr Ala Asn Ile Leu  
 355 360 365  
 His Asn Ala Thr Asp Arg Ser Leu Val Ile Leu Asp Glu Val Gly Arg  
 370 375 380  
 Gly Thr Ser Thr Tyr Asp Gly Leu Ala Ile Ala Gln Ala Val Val Glu  
 385 390 395 400  
 Tyr Leu Leu Phe Thr Asp Lys Lys Lys Ala Lys Thr Leu Phe Ala Thr  
 405 410 415

His Tyr Lys Glu Leu Thr Thr Leu Glu Asp His Cys Pro His Val Glu  
 420 425 430  
 Asn Phe His Ala Gly Val Lys Asp Lys Ala Gly Gln Pro Val Phe Leu  
 435 440 445  
 Tyr Glu Ile Leu Lys Asp Ile His Lys Lys Val Ser Ala Phe Met Ser  
 450 455 460  
 Pro Gly Leu Leu Ala Phe Pro Phe Val Trp Tyr Arg Glu Leu Ser Arg  
 465 470 475 480  
 Ser

&lt;210&gt;1013

&lt;211&gt;339

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1013

Val Met Thr Glu Lys Lys Pro Thr Pro Met Met Glu Gln Trp His Gln  
 1 5 10 15  
 Cys Lys Glu Lys Ala Gly Asp Ser Val Leu Leu Phe Arg Met Gly Asp  
 20 25 30  
 Phe Tyr Glu Ala Phe Tyr Asp Asp Ala Val Leu Leu Ser Gln His Leu  
 35 40 45  
 Glu Leu Thr Leu Thr Gln Arg Gln Gly Ile Pro Met Ser Gly Ile Pro  
 50 55 60  
 Val Ser Thr Val Asp Thr Tyr Val Asp Arg Leu Ile Gly Lys Gly Phe  
 65 70 75 80  
 Lys Val Ala Val Ala Glu Gln Phe Gly Glu Pro Ala Lys Glu Lys Glu  
 85 90 95  
 Ser Lys Lys Ile Gly Pro Met Ala Arg Asp Ile Gln Arg Phe Val Thr  
 100 105 110  
 Pro Gly Thr Leu Leu Ser Ser Thr Leu Leu Gln Glu Lys Phe Asn Asn  
 115 120 125  
 Xaa Ile Val Ala Ile Thr Arg Ile Gly Ser Leu Phe Gly Phe Ala Cys  
 130 135 140  
 Leu Asp Leu Ser Thr Gly Ser Phe Phe Ile Glu Glu Cys Glu Asn Thr  
 145 150 155 160  
 Lys Glu Leu Val Asp Glu Ile Cys Arg Leu Ala Pro Ser Glu Val Leu  
 165 170 175  
 Ser Cys Asn Lys Phe Tyr Asn Lys Glu Thr Ala Ile Val Met Gln Leu  
 180 185 190  
 Gln Gln His Leu Lys Leu Thr Leu Ser Thr Tyr Ala Asp Trp Ala Phe  
 195 200 205  
 Glu His Lys Phe Ala Ser Gln Lys Leu Thr Thr His Phe Gln Val Ala  
 210 215 220  
 Ser Leu Asp Gly Phe Gly Leu Lys Gly Leu Val Pro Ala Ile Asn Ala  
 225 230 235 240  
 Ala Gly Gly Leu Leu Ser Tyr Ile Gln Asp Lys Leu Leu Leu Pro Thr  
 245 250 255  
 Lys His Ile Ala Ile Pro Gln Thr Arg Gly Lys Gln Gln Lys Leu Leu  
 260 265 270  
 Ile Asp Thr Ala Ser Gln Val Asn Leu Glu Leu Leu Ala Pro Leu Asn  
 275 280 285  
 Asp Pro Gln Gly Lys Asn Ser Leu Leu Arg Ile Met Asp His Thr Ser  
 290 295 300  
 Thr Pro Met Gly Gly Arg Leu Leu Arg Gln Ile Leu Ile Ser Pro Phe  
 305 310 315 320  
 Tyr Asn Pro Lys Glu Ile Leu Val Arg Gln Asp Ala Val Glu Phe Phe  
 325 330 335  
 Phe Gly Lys

&lt;210&gt;1014

&lt;211&gt;207

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1014

Leu Arg Thr Ala Met Tyr Thr Glu Glu Ser Leu Asp Asn Leu Arg His  
 1 5 10 15  
 Ser Ile Asp Ile Val Asp Val Leu Ser Glu His Ile His Leu Lys Arg  
 20 25 30  
 Ser Gly Ala Thr Tyr Lys Ala Cys Cys Pro Phe His Thr Glu Lys Thr  
 35 40 45  
 Pro Ser Phe Ile Val Asn Pro Ala Gly Ala His Tyr His Cys Phe Gly  
 50 55 60  
 Cys Gly Ala His Gly Asp Ala Ile Gly Phe Leu Met Gln His Leu Gly  
 65 70 75 80  
 Tyr Ser Phe Thr Glu Ala Ile Leu Val Leu Ser Lys Lys Phe Gln Val  
 85 90 95  
 Asp Leu Val Leu Gln Pro Lys Asp Ser Gly Tyr Thr Pro Pro Gln Gly  
 100 105 110  
 Leu Lys Glu Glu Leu Arg His Ile Asn Ser Glu Ala Glu Thr Phe Phe  
 115 120 125  
 Arg Tyr Cys Leu Tyr His Leu Pro Glu Ala Arg His Ala Leu Gln Tyr  
 130 135 140  
 Leu Tyr His Arg Gly Phe Ser Pro Asp Thr Ile Asp Arg Phe His Leu  
 145 150 155 160  
 Gly Tyr Gly Pro Glu Gln Ser Leu Phe Leu Gln Ala Met Glu Glu Arg  
 165 170 175  
 Lys Ile Ser Gln Glu Gln Leu His Thr Ala Gly Phe Phe Gly Asn Lys  
 180 185 190  
 Trp Phe Leu Phe Ala Arg Arg Ile Ser Phe Leu Ser Thr Met Arg  
 195 200 205

&lt;210&gt;1015

&lt;211&gt;402

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1015

Met Val Phe Val Cys Thr Lys Asn Leu Phe Pro Val His Asp Ala Leu  
 1 5 10 15  
 Gly His Thr Ile Gly Phe Ser Ala Arg Lys Phe Leu Glu Asn Ser Gln  
 20 25 30  
 Gly Gly Lys Tyr Val Asn Thr Pro Glu Thr Pro Ile Phe Lys Lys Ser  
 35 40 45  
 Arg Ile Leu Phe Gly Leu Asn Phe Ser Arg Arg Arg Ile Ala Lys Glu  
 50 55 60  
 Xaa Lys Val Ile Leu Val Glu Gly Gln Ala Asp Cys Leu Gln Met Ile  
 65 70 75 80  
 Asp Ser Gly Phe Asn Cys Thr Val Ala Ala Gln Gly Thr Ala Phe Thr  
 85 90 95  
 Glu Glu His Val Lys Glu Leu Ser Lys Leu Gly Val Leu Lys Val Phe  
 100 105 110  
 Leu Leu Phe Asp Ser Asp Glu Ala Gly Asn Lys Ala Ala Leu Arg Val  
 115 120 125  
 Gly Asp Leu Cys Gln Thr Ala Gln Met Ser Val Phe Val Cys Lys Leu  
 130 135 140  
 Pro Gln Gly His Asp Pro Asp Ser Phe Leu Met Gln Arg Gly Ser Ser  
 145 150 155 160  
 Gly Leu Ile Ala Leu Leu Glu Gln Ser Gln Asp Tyr Leu Thr Phe Leu  
 165 170 175  
 Ile Ser Glu Lys Met Ser Ser Tyr Pro Lys Phe Gly Pro Arg Glu Lys  
 180 185 190  
 Ala Leu Leu Val Glu Glu Ala Ile Arg Gln Ile Lys His Trp Gly Ser  
 195 200 205  
 Pro Ile Leu Val Tyr Glu His Leu Lys Gln Leu Ala Ser Leu Met Met  
 210 215 220  
 Val Pro Glu Asp Met Val Leu Ser Leu Ala Asn Pro Gln Val Thr Ala  
 225 230 235 240  
 Glu Pro Gln Asn Ile Pro Ile Lys Gln Lys Val Pro Lys Ile His Pro  
 245 250 255  
 His Ile Val Met Glu Thr Asp Ile Leu Arg Cys Met Leu Phe Cys Gly



```

                260                265                270
Ser Asn Thr Lys Ile Leu Tyr Thr Ala Gln Phe Tyr Phe Val Pro Glu
                275                280                285
Asp Phe Lys His Pro Glu Cys Arg Lys Leu Phe Ala Phe Met Ile Ser
                290                295                300
Tyr Tyr Glu Lys Tyr Arg Lys Asn Val Pro Phe Asp Glu Ala Cys Gln
305                310                315                320
Val Leu Ser Asp Ser Gln Ile Leu Gln Leu Leu Thr Lys Arg Arg Leu
                325                330                335
Asn Thr Glu Ala Leu Asp Thr Ile Phe Val Gln Ser Leu Gln Lys Met
                340                345                350
Ala Asp Arg Arg Trp Arg Glu Gln Cys Lys Pro Leu Ser Leu Asn Gln
                355                360                365
Asn Ile Gln Asp Lys Lys Leu Glu Ile Leu Glu Asp Tyr Val Gln Leu
370                375                380
Arg Lys Asp Arg Thr Ile Ile Thr Leu Leu Asp Pro Glu Ser Glu Leu
385                390                395                400
Ile Pro

```

&lt;210&gt;1016

&lt;211&gt;120

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1016

```

Ile Lys Ile Met Met His Arg Tyr Phe Ile Pro Leu Leu Ala Leu Leu
 1                5                10                15
Ile Phe Ser Pro Ser Leu Val Arg Ala Glu Leu Gln Pro Ser Glu Asn
                20                25                30
Arg Lys Gly Gly Trp Pro Thr Gln Leu Ser Cys Ala Glu Gly Ser Gln
                35                40                45
Leu Phe Cys Lys Phe Glu Ala Ala Tyr Asn Asn Ala Ile Glu Glu Gly
 50                55                60
Lys Pro Gly Ile Leu Val Phe Phe Ser Glu Arg Pro Thr Pro Glu Phe
 65                70                75                80
Ala Asp Leu Thr Asn Gly Ser Phe Ser Leu Ser Thr Pro Ile Ala Lys
                85                90                95
Gly Phe Asn Val Val Val Leu Cys Pro Gly Leu Ile Ser Pro Leu Asp
                100                105                110
Phe Phe His Gln Asn Gly Ile Leu
                115                120

```

&lt;210&gt;1017

&lt;211&gt;220

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1017

```

Ser Ile Phe Lys Asn Lys Ile Leu Pro Ser Tyr Phe Gly His Asn Phe
 1                5                10                15
Asp Gln Leu Arg Arg His Tyr Met Arg Ile Ala Leu Ser Leu Leu Ser
                20                25                30
Leu Leu Met Ile Phe Pro Ile Phe Gly Glu Glu Ser Arg Pro Gly Ser
                35                40                45
Glu Asp Gly Asn Ser Asn Thr Gln Glu Ile Val Gly Ser Gln Asp Thr
 50                55                60
Gln Val Cys Leu Tyr His Ser Tyr Glu Gln Gly Leu Gln Ala Ser Arg
 65                70                75                80
Ile Glu Gly Lys Pro Leu Val Ile Val Val Leu Cys Asn Ser Gly Asp
                85                90                95
Asp Gly Gln Ala Cys Thr Ile Gly Leu Ser Glu Thr Cys Glu Glu Val
                100                105                110
Leu Ser Val Leu Ser Gly Ser Ile Phe Ser Glu Leu Ala Asn Phe Val
                115                120                125
Val Leu Val Pro Ser Gly Val Asn Pro Leu Ile Tyr Pro Pro Ile Glu
                130                135                140
Asp Pro Ile Leu Ala Glu Ile Val Lys Phe Lys Glu Leu Phe Lys Asp

```

```

145          150          155          160
Glu Ser Phe Pro Thr Gly Leu Ser Ile Ile Val Val Gly Val Thr Pro
          165          170          175
Glu Gly Pro Gly Asp Ile Ile Glu Val Ser Pro Val Ser Leu Thr Val
          180          185          190
Glu Glu Glu Glu Thr Leu Pro Ser Glu Gln Thr Thr Glu Val Glu Ser
          195          200          205
Thr Ser Glu Leu Gln Ser Glu Asp Pro Ala Ile Ala
          210          215          220
<210>1018
<211>1014
<212>PRT
<213>Chlamydia pneumoniae
<400>1018
Leu Glu Ser Phe Val Ser Glu His Pro Leu Thr Leu Gln Ser Met Ile
 1          5          10          15
Ala Thr Ile Leu Arg Phe Trp Ser Glu Gln Gly Cys Val Ile His Gln
          20          25          30
Gly Tyr Asp Leu Glu Val Gly Ala Gly Thr Phe Asn Pro Ala Thr Phe
          35          40          45
Leu Arg Ala Leu Gly Pro Glu Pro Tyr Lys Ala Ala Tyr Val Glu Pro
          50          55          60
Ser Arg Arg Pro Gln Asp Gly Arg Tyr Gly Val His Pro Asn Arg Leu
          65          70          75          80
Gln Asn Tyr His Gln Leu Gln Val Ile Leu Lys Pro Val Pro Glu Asn
          85          90          95
Phe Leu Ser Leu Tyr Thr Glu Ser Leu Arg Ala Ile Gly Leu Asp Leu
          100          105          110
Arg Asp His Asp Ile Arg Phe Ile His Asp Asp Trp Glu Asn Pro Thr
          115          120          125
Ile Gly Ala Trp Gly Leu Gly Trp Glu Val Trp Leu Asn Gly Met Glu
          130          135          140
Ile Thr Gln Leu Thr Tyr Phe Gln Ala Ile Gly Ser Lys Pro Leu Asp
          145          150          155          160
Thr Ile Ser Gly Glu Ile Thr Tyr Gly Ile Glu Arg Ile Ala Met Tyr
          165          170          175
Leu Gln Lys Lys Thr Ser Ile Tyr Asp Val Leu Trp Asn Asp Thr Leu
          180          185          190
Thr Tyr Gly Gln Ile Thr Gln Ala Ser Glu Lys Ala Trp Ser Glu Tyr
          195          200          205
Asn Phe Asp Tyr Ala Asn Thr Glu Met Trp Phe Lys His Phe Glu Asp
          210          215          220
Phe Ala Glu Glu Ala Leu Arg Thr Leu Lys Asn Gly Leu Ser Val Pro
          225          230          235          240
Ala Tyr Asp Phe Val Ile Lys Ala Ser His Ala Phe Asn Ile Leu Asp
          245          250          255
Ala Arg Gly Thr Ile Ser Val Thr Glu Arg Thr Arg Tyr Ile Ala Arg
          260          265          270
Ile Arg Gln Leu Thr Arg Leu Val Ala Asp Ser Tyr Val Glu Trp Arg
          275          280          285
Ala Ser Leu Asn Tyr Pro Leu Leu Ser Leu Ser Ser Thr Ser Glu Pro
          290          295          300
Lys Glu Thr Ser Glu Ser Val Val Pro Met Ile Ser Ser Thr Glu Asp
          305          310          315          320
Leu Leu Leu Glu Ile Gly Ser Glu Glu Leu Pro Ala Thr Phe Val Pro
          325          330          335
Ile Gly Ile Gln Gln Leu Glu Ser Leu Ala Arg Gln Val Leu Thr Asp
          340          345          350
His Asn Ile Val Tyr Glu Gly Leu Glu Val Leu Gly Ser Pro Arg Arg
          355          360          365
Leu Ala Leu Leu Val Lys Asn Val Ala Pro Glu Val Val Gln Lys Ala
          370          375          380
Phe Glu Lys Lys Gly Pro Met Leu Thr Ser Leu Phe Ser Pro Asp Gly
          385          390          395          400

```

Asp Val Ser Pro Gln Gly Gln Gln Phe Phe Ala Ser Gln Gly Val Asp  
 405 410 415  
 Ile Ser His Tyr Gln Asp Leu Ser Arg His Ala Ser Leu Ala Ile Arg  
 420 425 430  
 Thr Val Asn Gly Ser Glu Tyr Leu Phe Leu Leu His Pro Glu Ile Arg  
 435 440 445  
 Leu Arg Thr Ala Asp Ile Leu Met Gln Glu Leu Pro Leu Leu Ile Gln  
 450 455 460  
 Arg Met Lys Phe Pro Lys Lys Met Val Trp Asp Asn Ser Gly Val Glu  
 465 470 475 480  
 Tyr Ala Arg Pro Ile Arg Trp Leu Val Ala Leu Tyr Gly Glu His Ile  
 485 490 495  
 Leu Pro Ile Thr Leu Gly Thr Ile Ile Ala Ser Arg Asn Ser Phe Gly  
 500 505 510  
 His Arg Gln Leu Asp Pro Arg Lys Ile Ser Ile Ser Ser Pro Gln Asp  
 515 520 525  
 Tyr Val Glu Thr Leu Arg Gln Ala Cys Val Val Val Ser Gln Lys Glu  
 530 535 540  
 Arg Arg Met Ile Ile Glu Gln Gly Leu Arg Ala His Ser Ser Asp Thr  
 545 550 555 560  
 Ile Ser Ala Ile Pro Leu Pro Arg Leu Ile Glu Glu Ala Thr Phe Leu  
 565 570 575  
 Ser Glu His Pro Phe Val Ser Cys Gly Gln Phe Ser Glu Gln Phe Cys  
 580 585 590  
 Ala Leu Pro Lys Glu Leu Leu Ile Ala Glu Met Val Asn His Gln Lys  
 595 600 605  
 Tyr Phe Pro Thr His Glu Thr Ser Ser Gly Ala Ile Ser Asn Phe Phe  
 610 615 620  
 Ile Val Val Cys Asp Asn Ser Pro Asn Asp Thr Ile Ile Glu Gly Asn  
 625 630 635 640  
 Glu Lys Ala Leu Thr Pro Arg Leu Thr Asp Gly Glu Phe Leu Phe Lys  
 645 650 655  
 Gln Asp Leu Gln Thr Pro Leu Thr Thr Phe Ile Glu Lys Leu Lys Ser  
 660 665 670  
 Val Thr Tyr Phe Glu Ala Leu Gly Ser Leu Tyr Asp Lys Val Glu Arg  
 675 680 685  
 Leu Lys Ala His Gln Arg Val Phe Ser Thr Phe Ser Ser Leu Ala Ala  
 690 695 700  
 Ser Glu Asp Leu Asp Ile Ala Ile Gln Tyr Cys Lys Ala Asp Leu Val  
 705 710 715 720  
 Ser Ala Val Val Asn Glu Phe Pro Glu Leu Gln Gly Ile Met Gly Glu  
 725 730 735  
 Tyr Tyr Leu Lys His Ala Asn Leu Pro Thr Ala Ser Ala Val Ala Val  
 740 745 750  
 Gly Glu His Leu Arg His Ile Thr Met Gly Gln Lys Leu Ser Thr Ile  
 755 760 765  
 Gly Thr Leu Leu Ser Leu Leu Asp Arg Leu Asp Asn Leu Leu Ala Cys  
 770 775 780  
 Phe Ile Leu Gly Leu Lys Pro Thr Ser Ser His Asp Pro Tyr Ala Leu  
 785 790 795 800  
 Arg Arg Gln Ser Leu Glu Val Leu Thr Leu Val Ser Ala Ser Arg Leu  
 805 810 815  
 Pro Ile Asp Leu Ala Ser Leu Leu Asp Arg Leu Ala Asp His Phe Pro  
 820 825 830  
 Ser Thr Ile Glu Glu Lys Val Trp Asp Lys Ser Lys Thr Ile His Glu  
 835 840 845  
 Ile Leu Glu Phe Ile Trp Gly Arg Leu Lys Thr Phe Met Gly Ser Leu  
 850 855 860  
 Glu Phe Arg Lys Asp Glu Ile Ala Ala Val Leu Ile Asp Ser Ala Thr  
 865 870 875 880  
 Xaa Asn Pro Ile Glu Ile Leu Asp Thr Ala Glu Ala Leu Gln Leu Leu  
 885 890 895  
 Lys Glu Glu His Thr Glu Lys Leu Ala Val Ile Thr Thr Thr His Asn  
 900 905 910

Arg Leu Lys Lys Ile Leu Ser Ser Leu Lys Leu Ser Met Thr Ser Ser  
 915 920 925  
 Pro Ile Glu Val Leu Gly Asp Arg Glu Ser Asn Phe Lys Gln Val Leu  
 930 935 940  
 Asp Ala Phe Pro Gly Phe Pro Lys Glu Thr Ser Ala His Ala Phe Leu  
 945 950 955 960  
 Glu Tyr Phe Leu Ser Leu Ala Asp Leu Ser Asn Asp Ile Gln Asp Phe  
 965 970 975  
 Leu Asn Thr Val His Ile Ala Asn Asp Asp Gly Ala Ile Arg Asn Leu  
 980 985 990  
 Arg Ile Ser Leu Leu Leu Thr Ala Met Asp Lys Phe Ser Leu Cys His  
 995 1000 1005  
 Trp Glu Ser Val Ala Val  
 1010

&lt;210&gt;1019

&lt;211&gt;97

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1019

Asn Gly Asn Asp Val Leu Lys Thr Cys Ser Leu Ile Leu Leu Asn Leu  
 1 5 10 15  
 Cys Arg Tyr Phe Leu Leu Val Phe Cys Thr Ala Val Phe Phe Lys Arg  
 20 25 30  
 Tyr Ile Leu Ile Leu Thr Arg Thr Val Arg His Thr Glu Ile Tyr Ala  
 35 40 45  
 Cys Gly Glu Gly Val Thr Val Ala Leu Lys Ser Met Leu Pro Ser Met  
 50 55 60  
 Lys Gln Glu Ser Pro Ala Leu Ala Lys Glu Asn Val Lys Arg Lys Asn  
 65 70 75 80  
 Val Ile Pro Trp Ser His Leu Cys Gln Asn Ile Pro Ser Pro Tyr Ser  
 85 90 95  
 Leu

&lt;210&gt;1020

&lt;211&gt;207

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1020

Arg Val Gly Leu Pro Asn Tyr Ile Thr Phe Ser Arg Leu Phe Ile Thr  
 1 5 10 15  
 Pro Ile Phe Met Ile Leu Tyr Leu Lys Gly Lys Trp Phe Gly Ile Thr  
 20 25 30  
 Pro Val Val Leu Pro Tyr Val Leu Leu Ala Leu Leu Ala Ile Ser Glu  
 35 40 45  
 Leu Thr Asp Ala Ile Asp Gly Tyr Val Ala Arg Lys Phe Ser Gln Val  
 50 55 60  
 Thr Asp Leu Gly Lys Leu Leu Asp Pro Met Ala Asp Ser Ile Tyr Arg  
 65 70 75 80  
 Ile Ser Ile Tyr Leu Thr Phe Thr Gln Pro Pro Val Asn Leu Pro Leu  
 85 90 95  
 Leu Leu Val Phe Ile Phe Leu Ala Arg Asp Ser Val Ile Ser Thr Leu  
 100 105 110  
 Arg Thr Val Cys Ala Phe Arg Gly Arg Val Val Ala Ala Arg Ala Ser  
 115 120 125  
 Gly Lys Leu Lys Ala Ile Leu Gln Gly Val Ser Phe Phe Leu Ile Leu  
 130 135 140  
 Leu Val Met Ile Pro His Ser Leu Gly Leu Leu Ser Gln Asn Gly Leu  
 145 150 155 160  
 Glu Ile Phe Ala Ser Val Thr Val Ser Ile Ile Ala Val Tyr Ser Ile  
 165 170 175  
 Ala Ser Gly Ile Glu Tyr Phe Trp Met Asn Lys Asn Phe Leu Ser Gln  
 180 185 190  
 Arg Ala Lys Thr Lys Asp Ser Glu Lys Asn His Glu Ser Lys Asp  
 195 200 205

&lt;210&gt;1021

&lt;211&gt;476

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1021

```

Met Arg Ile Val Gln Val Ala Val Glu Phe Thr Pro Ile Val Lys Val
 1           5           10           15
Gly Gly Leu Gly Asp Ala Val Ala Ser Leu Ser Lys Glu Leu Ala Lys
 20           25           30
Gln Asn Asp Val Glu Val Leu Leu Pro His Tyr Pro Leu Ile Ser Lys
 35           40           45
Phe Ser Ser Ser Gln Val Leu Ser Glu Arg Ser Phe Tyr Tyr Glu Phe
 50           55           60
Leu Gly Lys Gln Gln Ala Ser Ala Ile Ser Tyr Ser Tyr Glu Gly Leu
 65           70           75           80
Thr Leu Thr Ile Ile Thr Leu Asp Ser Gln Ile Glu Leu Phe Ser Thr
 85           90           95
Thr Ser Val Tyr Ser Glu Asn Asn Val Val Arg Phe Ser Ala Phe Ala
 100          105          110
Ala Ala Ala Ala Ala Tyr Leu Gln Glu Ala Asp Pro Ala Asp Ile Val
 115          120          125
His Leu His Asp Trp His Val Gly Leu Leu Ala Gly Leu Leu Lys Asn
 130          135          140
Pro Leu Asn Pro Val His Ser Lys Ile Val Phe Thr Ile His Asn Phe
 145          150          155          160
Gly Tyr Arg Gly Tyr Cys Ser Thr Gln Leu Leu Ala Ala Ser Gln Ile
 165          170          175
Asp Asp Phe His Leu Ser His Tyr Gln Leu Phe Arg Asp Pro Gln Thr
 180          185          190
Ser Val Leu Met Lys Gly Ala Leu Tyr Cys Ser Asp Tyr Ile Thr Thr
 195          200          205
Val Ser Leu Thr Tyr Val Gln Glu Ile Ile Asn Asp Tyr Ser Asp Tyr
 210          215          220
Glu Leu His Asp Ala Ile Leu Ala Arg Asn Ser Val Phe Ser Gly Ile
 225          230          235          240
Ile Asn Gly Ile Asp Glu Asp Val Trp Asn Pro Lys Thr Asp Pro Ala
 245          250          255
Leu Ala Val Gln Tyr Asp Ala Ser Leu Leu Ser Glu Pro Asp Val Leu
 260          265          270
Phe Thr Lys Lys Glu Glu Asn Arg Ala Val Leu Tyr Glu Lys Leu Gly
 275          280          285
Ile Ser Ser Asp Tyr Phe Pro Leu Ile Cys Val Ile Ser Arg Ile Val
 290          295          300
Glu Glu Lys Gly Pro Glu Phe Met Lys Glu Ile Ile Leu His Ala Met
 305          310          315          320
Glu His Ser Tyr Ala Phe Ile Leu Ile Gly Thr Ser Gln Asn Glu Val
 325          330          335
Leu Leu Asn Glu Phe Arg Asn Leu Gln Asp Cys Leu Ala Ser Ser Pro
 340          345          350
Asn Ile Arg Leu Ile Leu Asp Phe Asn Asp Pro Leu Ala Arg Leu Thr
 355          360          365
Tyr Ala Ala Ala Asp Met Ile Cys Ile Pro Ser His Arg Glu Ala Cys
 370          375          380
Gly Leu Thr Gln Leu Ile Ala Met Arg Tyr Gly Thr Val Pro Leu Val
 385          390          395          400
Arg Lys Thr Gly Gly Leu Ala Asp Thr Val Ile Pro Gly Val Asn Gly
 405          410          415
Phe Thr Phe Phe Asp Thr Asn Asn Phe Asn Glu Phe Arg Ala Met Leu
 420          425          430
Ser Asn Ala Val Thr Thr Tyr Arg Gln Glu Pro Asp Val Trp Leu Asn
 435          440          445
Leu Ile Glu Ser Gly Met Leu Arg Ala Ser Gly Leu Asp Ala Met Ala
 450          455          460
Lys His Tyr Val Asn Leu Tyr Gln Ser Leu Leu Ser

```

465 470 475  
 <210>1022  
 <211>185  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1022  
 Met Glu Leu Val Val Thr Ser Arg Glu Thr Gly Lys Lys Ser Phe Leu  
 1 5 10 15  
 Lys Lys Ile Arg Gln Gln Gly Gly Ile Pro Ala Val Val Tyr Ser Ala  
 20 25 30  
 Gly Lys Ser Leu Ala Asn Ile Thr Val Asp Ala Leu Val Phe Lys Lys  
 35 40 45  
 Phe Leu Ser Asn Leu Glu Ser Gly Ala Leu Ser Ser Thr Val Phe Ser  
 50 55 60  
 Leu Ser Tyr Glu Gly Arg Ile Ile Lys Ala Leu Val Lys Asp Ile Gln  
 65 70 75 80  
 Tyr Gln Ile Thr Thr Tyr Asp Val Ile His Leu Asp Phe Glu Glu Leu  
 85 90 95  
 Val Glu Asp Arg Pro Val Lys Leu Asn Ile Pro Ile Arg Cys Ile Asn  
 100 105 110  
 Ala Val Asp Cys Ile Gly Val Lys Leu Gly Gly Ser Leu Arg Gln Val  
 115 120 125  
 Ile Arg Ala Val Arg Val Val Cys Lys Pro Lys Asp Ile Val Pro Phe  
 130 135 140  
 Leu Glu Leu Asp Val Arg Ser Val Gly Leu Ser Gln Thr Arg Lys Leu  
 145 150 155 160  
 Ser Asp Ile Lys Ile Pro Ala Gly Ile Glu Thr Ile Thr Pro Leu Lys  
 165 170 175  
 Glu Val Ala Ile Thr Val Ser Arg Arg  
 180 185

<210>1023  
 <211>150  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1023  
 Met Ala Lys Leu Ile Val Ala Ile Gly Asn Pro Arg His Gly Tyr Ala  
 1 5 10 15  
 Asn Thr Arg His Asn Ala Gly Phe Leu Leu Ala Asp Arg Leu Val Glu  
 20 25 30  
 Glu Leu Gln Gly Pro Pro Phe Lys Pro Leu Ser Lys Cys His Ala Leu  
 35 40 45  
 Met Thr Leu Val Glu Ser Ser Ser Gly Pro Leu Val Phe Ile Lys Pro  
 50 55 60  
 Thr Thr Phe Val Asn Leu Ser Gly Lys Ala Val Val Leu Ala Lys Lys  
 65 70 75 80  
 Tyr Phe Asn Val Ala Leu Ser His Ile Leu Val Leu Ala Asp Asp Val  
 85 90 95  
 Asn Arg Ser Phe Gly Lys Leu Arg Leu Cys Phe Asn Gly Gly Ser Gly  
 100 105 110  
 Gly His Asn Gly Leu Lys Ser Ile Thr Ala Ser Leu Gly Ser Asn Glu  
 115 120 125  
 Tyr Trp Gln Leu Arg Phe Gly Val Gly Arg Pro Leu Glu Glu Val Leu  
 130 135 140  
 Ser Tyr Leu Ile Ser Phe  
 145 150

<210>1024  
 <211>112  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1024  
 Met Gly Lys Lys Glu Asn Gln Leu Tyr Glu Gly Ala Tyr Val Phe Ser  
 1 5 10 15  
 Val Thr Leu Ser Glu Glu Ala Arg Arg Lys Ala Leu Asp Lys Val Ile  
 20 25 30

Ser Gly Ile Thr Asn Tyr Gly Gly Glu Ile His Lys Ile His Asp Gln  
                   35                  40                  45  
 Gly Arg Lys Lys Leu Ala Tyr Thr Ile Arg Gly Ala Arg Glu Gly Tyr  
           50                  55                  60  
 Tyr Tyr Phe Ile Tyr Phe Ser Val Ser Pro Gly Ala Ile Thr Glu Leu  
       65                  70                  75                  80  
 Trp Lys Glu Tyr His Leu Asn Glu Asp Leu Leu Arg Phe Met Thr Leu  
                   85                  90                  95  
 Arg Ala Asp Ser Val Lys Glu Val Leu Glu Phe Ala Ser Leu Pro Glu  
                   100                  105                  110

&lt;210&gt;1025

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1025

Met Asn Lys Pro Val His Asn Asn Glu His Arg Arg Lys Arg Phe Asn  
   1                  5                  10                  15  
 Lys Lys Cys Pro Phe Val Ser Ala Gly Trp Lys Thr Ile Asp Tyr Lys  
           20                  25                  30  
 Asp Val Glu Thr Leu Lys Lys Phe Ile Thr Glu Arg Gly Lys Val Leu  
           35                  40                  45  
 Pro Arg Arg Ile Thr Gly Val Ser Ser Arg Phe Gln Gly Val Leu Ser  
           50                  55                  60  
 Gln Ala Ile Lys Arg Ala Arg His Leu Gly Leu Leu Pro Phe Val Gly  
       65                  70                  75                  80  
 Glu Asp

&lt;210&gt;1026

&lt;211&gt;169

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1026

Met Lys Gln Gln Leu Leu Leu Leu Glu Asp Val Asp Gly Leu Gly Arg  
   1                  5                  10                  15  
 Ser Gly Asp Leu Ile Thr Ala Arg Pro Gly Tyr Val Arg Asn Tyr Leu  
           20                  25                  30  
 Ile Pro Lys Lys Lys Ala Val Ile Ala Gly Ala Gly Thr Leu Arg Leu  
           35                  40                  45  
 Gln Ala Lys Leu Lys Glu Gln Arg Leu Ile Gln Ala Ala Ala Asp Lys  
       50                  55                  60  
 Ala Asp Ser Glu Arg Ile Ala Gln Ala Leu Lys Asp Ile Val Leu Glu  
       65                  70                  75                  80  
 Phe Gln Val Arg Val Asp Pro Asp Asn Asn Met Tyr Gly Ser Val Thr  
                   85                  90                  95  
 Ile Ala Asp Ile Ile Ala Glu Ala Ala Lys Lys Asn Ile Phe Leu Val  
           100                  105                  110  
 Arg Lys Asn Phe Pro His Ala His Tyr Ala Ile Lys Asn Leu Gly Lys  
           115                  120                  125  
 Lys Asn Ile Pro Leu Lys Leu Lys Glu Glu Val Thr Ala Thr Leu Leu  
           130                  135                  140  
 Val Glu Val Thr Ser Asp Asn Glu Tyr Val Thr Val Leu Ala Gln Gly  
       145                  150                  155                  160  
 Lys Gln Thr Glu Glu Asn Gln Glu Gly  
                   165

&lt;210&gt;1027

&lt;211&gt;81

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1027

Val Gly Arg Glu Cys Glu Gly Leu Phe Met Ser Tyr Lys Ile Thr Leu  
   1                  5                  10                  15  
 Pro Lys Ala Asp Glu Thr Thr Ala Lys Lys Val Thr Lys Ile Ser Glu  
           20                  25                  30  
 Ala Ser Thr Leu Ile Phe Ser Val Leu Lys Glu Lys Ala Ser Leu Gly

```

      35              40              45
Asn Val His Gly Phe Cys Gln Ala Glu Asn Ser Leu Ser Val Glu Ala
      50              55              60
Asn Lys Ile Ile Ser Val Ala Glu Asn Thr Leu Ala Gly Cys Phe Cys
      65              70              75              80
Lys

<210>1028
<211>455
<212>PRT
<213>Chlamydia pneumoniae
<400>1028
Leu Val Trp Phe Ser Met Ile Leu Pro Pro Tyr Ser Tyr Ser Leu Lys
  1              5              10              15
Ile Gly Ala Ala Val Leu Phe Phe Cys Ser Ile Leu His Thr Phe Leu
      20              25              30
Thr Pro Trp Leu Tyr Thr Leu Cys Gln Ser Tyr Glu His Lys Lys Leu
      35              40              45
Val Phe Pro Glu Cys Trp Lys Arg Tyr Ala Arg Leu Ser Glu Leu Phe
      50              55              60
Arg Ile Leu Ser Arg Val Glu Ile Val Phe Phe Leu Trp Ala Val Pro
      65              70              75              80
Leu Phe Phe Trp Phe Leu Tyr Thr Glu Gly Tyr Arg Ile Ser Met Ala
      85              90              95
Tyr Phe Asn Ser Arg Asn Tyr Gly Phe Ala Val Phe Ile Met Val Ile
      100              105              110
Leu Ile Leu Leu Glu Ser Arg Pro Ile Val Tyr Phe Ala Glu Leu Val
      115              120              125
Leu Ser Ser Ile Ala Lys Leu Gly Lys Thr Ser Pro Lys Ser Trp Trp
      130              135              140
Trp Thr Leu Met Ile Ala Pro Pro Leu Leu Ser Cys Leu Leu Lys Glu
      145              150              155              160
Thr Gly Ala Met Ile Ile Gly Ala Thr Leu Leu Met Arg His Phe Tyr
      165              170              175
Val Phe Thr Pro Ser Arg Arg Phe Ala Tyr Ala Thr Ile Gly Leu Leu
      180              185              190
Phe Ser Asn Ile Ser Ile Gly Gly Leu Thr Ser Tyr Val Ser Ser Arg
      195              200              205
Ala Leu Phe Leu Ile Phe Pro Ala Leu Lys Trp Glu His Ser Phe Phe
      210              215              220
Leu Ser His Phe Ala Trp Lys Ala Ile Val Ala Ile Leu Ile Ser Thr
      225              230              235              240
Thr Ile Tyr Tyr Phe Ile Phe Arg Lys Glu Phe Lys Lys Phe Pro Asp
      245              250              255
Ile Pro Ser Asp Lys Asp Pro Ser Val Glu Lys Val Pro Trp Trp Ile
      260              265              270
Ile Cys Val Asn Ile Ile Phe Val Gly Ser Ile Ile Leu Ser Arg Ser
      275              280              285
Thr Pro Leu Phe Met Gly Ala Leu Leu Leu Phe Tyr Leu Gly Phe Gln
      290              295              300
Lys Phe Thr Ile Phe Tyr Gln Asp Pro Ile Asn Leu Ser Lys Val Cys
      305              310              315              320
Tyr Val Gly Leu Phe Tyr Ala Gly Leu Val Phe Gly Asp Leu Gln
      325              330              335
Glu Trp Trp Val Leu Asn Leu Met Gln Gly Leu Ser Asp Phe Gly Tyr
      340              345              350
Met Thr Val Ser Tyr Thr Leu Ser Ile Phe Leu Asp Asn Ala Leu Val
      355              360              365
Asn Tyr Leu Val His Asn Leu Ser Val Ala Thr Asp Cys Tyr His Tyr
      370              375              380
Leu Val Val Ala Gly Cys Met Ala Ala Gly Gly Leu Thr Leu Val Ser
      385              390              395              400
Asn Ile Pro Asn Ile Val Gly Tyr Leu Ile Leu Arg Ser Ala Phe Pro
      405              410              415

```



Ser Ser Thr Ile His Met Gly Trp Leu Phe Leu Gly Ala Leu Gly Pro  
 420 425 430  
 Ser Ile Ile Ser Leu Gly Val Phe Trp Leu Leu Lys Asn Val Pro Glu  
 435 440 445  
 Phe Leu Tyr Cys Phe Phe Arg  
 450 455  
 <210>1029  
 <211>362  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1029  
 Pro Val Asn His Gln Leu Leu Arg Glu Tyr Tyr Pro Ala Thr Gln Ala  
 1 5 10 15  
 Gly Phe Ser Phe Thr Ser Ala Leu Gly Gly Asp Gly Ile Asp Leu Arg  
 20 25 30  
 Val Ser Gly Tyr Thr Thr Thr Val Pro Ala Leu Leu Asn Ser Ile Leu  
 35 40 45  
 Thr Ser Leu Pro Asn Leu Glu Ile Arg Tyr Glu Thr Phe Leu Val Tyr  
 50 55 60  
 Lys Lys Gln Leu Leu Glu Leu Tyr Gln Gly Ala Leu Leu Asn Cys Pro  
 65 70 75 80  
 Val Arg Ser Gly Leu Asp Glu Leu Ala Ser Gln Val Met Lys Glu Thr  
 85 90 95  
 Tyr Ser Asn Thr Thr Lys Leu Ser Ala Leu Glu Lys Leu Ser Phe Ser  
 100 105 110  
 Glu Phe Gln Ala Phe Ala Ser Asn Leu Phe Asn Ser Val His Leu Glu  
 115 120 125  
 Val Met Val Leu Gly Asn Leu Ser Glu Gln Gln Lys Lys Asp Tyr Leu  
 130 135 140  
 Glu Met Leu Gln Val Phe Thr Ala Ser Arg Ser Ser His Ala Thr Lys  
 145 150 155 160  
 Pro Phe Tyr Tyr Glu Leu Gln Ser Gln Glu Ile Ser Glu Ile His His  
 165 170 175  
 Asp Tyr Pro Leu Thr Ala Asn Gly Met Leu Leu Leu Leu Gln Asp Lys  
 180 185 190  
 Ser Ser Pro Ser Ile Gln Gly Lys Val Cys Ala Glu Met Leu Phe Glu  
 195 200 205  
 Trp Leu His His Ile Thr Phe Glu Glu Leu Arg Thr Gln Gln Gln Leu  
 210 215 220  
 Gly Tyr Met Val Gly Ala Arg Tyr Arg Glu Phe Ala Ser Arg Pro Phe  
 225 230 235 240  
 Gly Phe Leu Tyr Ile Arg Ser Asp Ala Tyr Ser Pro Glu Glu Leu Leu  
 245 250 255  
 Ala Lys Thr Ser Leu Phe Leu Asn Lys Val Ser Ala Ser Pro Glu Lys  
 260 265 270  
 Phe Gly Ile Ser Gln Glu Lys Phe Ala Asn Ile Arg Lys Ala Tyr Ile  
 275 280 285  
 Asn Lys Ile Leu Glu Pro Glu His Ser Leu Asp Met Met Asn Ser Ala  
 290 295 300  
 Leu Phe Ser Leu Ala Phe Glu Arg Pro Phe Val Glu Phe Ser Thr Pro  
 305 310 315 320  
 Asp Leu Lys Ile Ala Ile Ala Glu Thr Leu Thr Tyr Glu Glu Phe Leu  
 325 330 335  
 Lys Tyr Cys Gln Cys Phe Leu Ser Asn Glu Leu Gly Thr Gln Thr Ser  
 340 345 350  
 Val Tyr Ile Arg Gly Thr Gln Lys Thr Ser  
 355 360  
 <210>1030  
 <211>945  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1030  
 Ile Tyr Arg Ala Ile Tyr Met Gln Phe Ser Arg Tyr Leu Arg Tyr Ala  
 1 5 10 15

Phe Asp Asn Gln Tyr Leu Pro Glu Pro Leu Tyr Gln Lys Phe Ser Val  
 20 25 30  
 Phe His Gln Asn Tyr Ile Asp Ala Ala Thr Lys Lys Ala Ala Ala Asp  
 35 40 45  
 Gln Ala Glu Val Leu Cys Leu Gln Trp Val Lys Val Ile Ile Glu Asp  
 50 55 60  
 Leu Lys Asn Pro Phe Ile Phe Pro Pro Tyr His Lys Lys Ile Arg Ala  
 65 70 75 80  
 Pro Ile Asp Leu Phe Arg Leu Ser Ile Asp Phe Phe Ser Leu Val Ile  
 85 90 95  
 Asp Asp Lys Asn Ser Arg Ile Leu Asn Leu His Arg Leu Lys Glu Ile  
 100 105 110  
 Glu Glu Tyr Ile Ala Arg Gly Asp Asn Val Val Leu Leu Ala Asn His  
 115 120 125  
 Gln Thr Glu Cys Asp Pro Gln Leu Met Tyr Tyr Ala Leu Gly Lys Thr  
 130 135 140  
 His Pro Glu Leu Met Glu Asn Met Ile Phe Val Ala Gly Asp Arg Val  
 145 150 155 160  
 Thr Ser Asp Pro Leu Ala Arg Pro Phe Ser Met Gly Cys Asp Leu Leu  
 165 170 175  
 Cys Ile Tyr Ser Lys Arg His Ile Ala Thr Pro Pro Glu Leu Arg Glu  
 180 185 190  
 Glu Lys Leu Leu His Asn Gln Lys Ser Met Gln Ile Leu Lys Thr Leu  
 195 200 205  
 Leu Asn Glu Gly Gly Lys Phe Ile Tyr Val Ala Pro Ala Gly Gly Arg  
 210 215 220  
 Asp Arg Lys Asn Ala Glu Gly Arg Leu Tyr Pro Ser Glu Phe Ser Pro  
 225 230 235 240  
 Glu Ser Ile Glu Val Phe Arg Leu Leu Ala Lys Ala Ser Asn Gln Thr  
 245 250 255  
 Thr His Phe Tyr Pro Phe Ala Leu Lys Thr Tyr Asp Ile Leu Pro Pro  
 260 265 270  
 Pro Pro Lys Ile Glu Asn Ala Ile Gly Glu Gln Arg Ala Ile Phe Phe  
 275 280 285  
 Ala Pro Val Phe Phe Asn Phe Gly Ala Glu Leu Phe Phe Asp Ala Leu  
 290 295 300  
 Cys Ser Lys Glu Glu Leu Ile His Cys Asp Lys His Ala Gln Arg Thr  
 305 310 315 320  
 Leu Arg Ala Glu Lys Val Phe Ser Ile Cys Lys Lys Ser Ile Arg Gly  
 325 330 335  
 Ile Val Arg Cys Phe Gly Asn Phe Phe Val Pro Ile Leu Ile Cys Thr  
 340 345 350  
 Ser Leu Ser Ile Thr Ser Cys Glu Gln Gln Phe Lys Val Val Pro Asn  
 355 360 365  
 Gln Cys Pro Leu Gln Val Ser Thr Pro Ala Ala Ala Asp Gln Lys Ile  
 370 375 380  
 Glu Lys Ile Ile Cys Ser Asn Gly Leu Pro Leu Leu Ile Ile Ser Asp  
 385 390 395 400  
 Pro Asn Leu Pro Thr Ser Gly Ala Ala Leu Leu Val Lys Thr Gly Asn  
 405 410 415  
 Asn Ala Asp Pro Glu Glu Tyr Pro Gly Met Ala His Phe Thr Glu His  
 420 425 430  
 Cys Val Phe Leu Gly Asn Glu Lys Tyr Pro Glu Val Ser Gly Phe Pro  
 435 440 445  
 Gly Phe Leu Ser Glu Asn Asn Gly Val His Asn Ala Phe Thr Tyr Pro  
 450 455 460  
 Asn Lys Thr Val Phe Val Phe Ser Val Glu His Ser Ala Phe Ser Asp  
 465 470 475 480  
 Ala Leu Asp Gln Phe Val His Leu Phe Ile Asn Pro Lys Phe Arg Gln  
 485 490 495  
 Glu Asp Leu Asp Arg Glu Lys Tyr Ala Val His Gln Glu Phe Ala Ala  
 500 505 510  
 His Pro Leu Ser Asp Gly Arg Arg Val His Arg Ile Gln Gln Leu Val  
 515 520 525

Ala Pro Gln Gly His Pro Cys Ala Arg Phe Gly Cys Gly Asn Ala Ser  
 530 535 540  
 Thr Leu Thr Pro Val Thr Thr Glu Lys Met Ala Glu Trp Phe Lys Leu  
 545 550 555 560  
 His Tyr Ser Pro Glu Asn Met Cys Ala Ile Ala Tyr Thr Ser Ala Pro  
 565 570 575  
 Leu Ser Lys Ala Lys Lys Gln Phe Ser Lys Ile Phe Ser Gln Ile Pro  
 580 585 590  
 Arg Ser Lys Asn Tyr Glu Arg Gln Glu Pro Phe Leu Pro Ser Gly Asp  
 595 600 605  
 Thr Ser Ser Leu Lys Asn Leu Tyr Ile Asn Gln Ala Ile Gln Pro Thr  
 610 615 620  
 Ser Asn Leu Glu Ile Tyr Trp His Ile Tyr Glu Ser Ser His Pro Ile  
 625 630 635 640  
 Pro Leu Gly Cys Tyr Lys Ala Leu Ala Glu Val Leu Arg Asn Glu Ser  
 645 650 655  
 Lys Asn Ser Leu Val Ser Leu Leu Lys Asn Glu Gln Leu Ile Thr Asp  
 660 665 670  
 Leu Asp Val Glu Phe Phe Arg Ser Ser Leu Asn Thr Gly Glu Phe Tyr  
 675 680 685  
 Ile Ser Tyr Glu Leu Thr Glu Lys Gly Asp Lys His Tyr Ser Gln Val  
 690 695 700  
 Ile Asp Ser Thr Phe Gln Tyr Leu Arg Tyr Ile Gln Glu His Gly Ile  
 705 710 715 720  
 Pro Asn Tyr Thr Leu Glu Glu Ile Ser Thr Ile Asn Ala Leu Asn Tyr  
 725 730 735  
 Cys Tyr Ser Ser Lys Ser Pro Leu Phe Asp Leu Leu Cys Lys Gln Ile  
 740 745 750  
 Val Ser Leu Gly Asn Glu Asp Leu Ser Thr Tyr Pro Tyr His Ser Leu  
 755 760 765  
 Val Tyr Pro Lys Tyr Ser Ser Glu Asp Glu Ser Ala Leu Leu Asn Leu  
 770 775 780  
 Val Ser Asp Pro Glu Gln Ala Arg Phe Val Leu Ser Ser Lys Asn Ser  
 785 790 795 800  
 Glu His Trp Glu Glu Ala Thr Gln Leu His Asp Pro Ile Phe Asp Met  
 805 810 815  
 Thr Tyr Tyr Val Lys Ala Leu Asp Gly Val Gln Asp Tyr Gly Lys Val  
 820 825 830  
 Gln Ser Leu Lys Pro Ile Ala Leu Pro Lys Pro Asn Leu Phe Ile Pro  
 835 840 845  
 Lys Glu Val Thr Leu Pro Gly Val His Leu Leu Lys Lys Gln Glu Phe  
 850 855 860  
 Pro Phe Ala Pro Ala Leu Ser Tyr Gln Asp Asp Lys Leu Thr Leu Tyr  
 865 870 875 880  
 His Cys Glu Asp His Tyr Tyr Thr Ala Pro Lys Leu Ser Ser Gln Ile  
 885 890 895  
 Arg Ile Arg Ser Pro Gln Ile Ser Arg Ser Ser Pro Gln Phe Leu Val  
 900 905 910  
 Ala Thr Glu Leu Tyr Cys Leu Ala Cys Glu Pro Ser Ala Phe Glu Gly  
 915 920 925  
 Val Leu Ser Arg Asn Ala Ser Trp Phe Phe Phe Tyr Phe Cys Phe Arg  
 930 935 940  
 Trp  
 945  
 <210>1031  
 <211>521  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1031  
 Ile Gly Thr Arg Lys Val Met Glu Asn Glu Ile Leu Leu Asn Ile Glu  
 1 5 10 15  
 Ser Lys Glu Ile Arg Tyr Ala His Leu Lys Asn Gly Gln Leu Phe Asp  
 20 25 30  
 Leu Thr Ile Glu Arg Lys Lys Val Arg Gln Leu Lys Gly Asn Ile Tyr

```

      35      40      45
Arg Gly Arg Val Thr Asn Ile Leu Arg Asn Ile Gln Ser Ala Phe Ile
  50      55      60
Asn Ile Asp Glu Arg Glu Asn Gly Phe Ile His Ile Ser Asp Ile Leu
  65      70      75      80
Glu Asn Ser Lys Lys Phe Glu Gln Met Phe Asp Met Asp Val Asp Ala
      85      90      95
Leu Pro Glu Glu Ala Ser Glu Ala Pro Leu Leu Ser Ser Glu Glu Ala
  100      105      110
Pro Ile Glu Glu Phe Leu Lys Leu Asp Ser Pro Val Leu Val Gln Val
  115      120      125
Val Lys Glu Pro Ile Gly Ser Lys Gly Ala Arg Leu Thr Ser Asn Ile
  130      135      140
Ser Ile Pro Gly Arg Tyr Leu Val Leu Leu Pro Asn Ser Pro His Arg
  145      150      155      160
Gly Val Ser Arg Lys Ile Glu Asp Pro His Met Arg Glu Gln Leu Lys
      165      170      175
Gln Leu Ile Arg Ser Phe Glu Met Pro Gln Asp Met Gly Leu Ile Cys
  180      185      190
Arg Thr Ala Ser Thr Thr Ala Ser Thr Glu Ala Leu Ile Asn Glu Ala
  195      200      205
His Asp Leu Leu Leu Thr Trp Lys Thr Ile Leu Glu Lys Phe Tyr Ser
  210      215      220
Thr Glu Gln Pro Cys Leu Tyr Ser Glu Thr Asp Ile Leu Lys Lys
  225      230      235      240
Ala Val Ile Thr Cys Ile Asp Lys Asn Tyr Lys Arg Leu Leu Ile Asp
      245      250      255
Asp Tyr Ala Thr Tyr Gln Lys Cys Lys His Met Leu Lys Lys Tyr Ser
  260      265      270
Pro Asp Ala Ser Ile Lys Ile Glu Tyr Tyr Arg Asp Ser Ile Pro Met
  275      280      285
Phe Glu Arg Phe Asn Ile Glu Lys Glu Ile Asp Lys Ala Thr Arg Arg
  290      295      300
Lys Ile Trp Leu Ser Ser Gly Gly Tyr Leu Phe Phe Asp Lys Thr Glu
  305      310      315      320
Ala Met His Thr Ile Asp Val Asn Ser Gly Arg Ser Thr Gln Leu Glu
      325      330      335
Ser Gly Val Glu Thr Leu Val Gln Ile Asn Leu Glu Ala Ala Glu
  340      345      350
Glu Ile Ala Arg Gln Leu Arg Leu Arg Asn Val Gly Gly Leu Val Ile
  355      360      365
Ile Asp Phe Ile Asp Met Lys Ser Arg Lys Asn Gln Arg Arg Val Leu
  370      375      380
Glu Arg Leu Lys Glu His Met Lys Tyr Asp Ala Ala Arg Cys Thr Ile
  385      390      395      400
Leu Ser Met Ser Glu Phe Gly Leu Val Glu Met Thr Arg Gln Arg Asn
      405      410      415
Arg Glu Ser Leu Met Gln Thr Leu Phe Thr Leu Cys Pro Tyr Cys Ser
  420      425      430
Gly Asn Ala Ile Ile Lys Thr Pro Glu Ser Val Val Ile Glu Ile Glu
  435      440      445
Arg Asp Leu Lys Lys Val Ile Asn His Lys Glu His Ser His Leu Cys
  450      455      460
Leu Val Val His Pro Glu Ile Ala Ser Tyr Met Lys Gln Glu Asn Asp
  465      470      475      480
Asp Asn Glu Met Ile Asn Leu Ala Lys Gln Leu Lys Ala Lys Leu Gln
      485      490      495
Ile Asn Thr Ser Asp Ser Val His Leu Asn His Tyr Gln Phe Phe Ser
  500      505      510
Leu Ile Thr Gly Glu Ser Ile Asp Leu
  515      520
<210>1032
<211>176
<212>PRT

```

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1032

Ser Leu Ser Leu Val Ser Tyr Leu Ser Asn Pro Gln Lys Ala Leu Val  
 1 5 10 15  
 Leu Gly Ser Lys Gly Phe Ser Met Asp Cys Val Asp Asn Leu Lys Leu  
 20 25 30  
 Tyr Ile Phe Arg Leu Lys Leu Pro Gly Asp Thr Glu Arg Ile Ser Tyr  
 35 40 45  
 Ser Ile Ser Pro Glu Tyr Ile Arg Glu Lys Gly Glu Glu Glu Leu Leu  
 50 55 60  
 Asn Ser Pro Ile Glu Val Glu Gly Ser Leu Gly Arg Ile Asp Ser Asp  
 65 70 75 80  
 Gln Trp Ile Leu Ser Leu Ser Leu Lys Thr Gln Leu Gly Leu Cys Cys  
 85 90 95  
 Pro Val Cys Asn Asn Phe Phe Ser His Ser Val Cys Leu Pro Asp Leu  
 100 105 110  
 Gln Arg Val Ile Ser His Asp Glu Val Gly Ser Gly Val Phe Asp Cys  
 115 120 125  
 Arg Pro Leu Ile Arg Gln Glu Leu Leu Leu Glu Ser Asp Cys Phe Glu  
 130 135 140  
 Glu Cys Ser Gly Gln Gly Cys Pro Glu Arg Lys Asn Ile Leu Lys Phe  
 145 150 155 160  
 Leu Glu Asp Arg Lys Lys His Glu Gly Asn Asn Pro Phe Glu Tyr Leu  
 165 170 175

&lt;210&gt;1033

&lt;211&gt;213

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1033

Met Glu Val Gln Ile Gly Ile Asp Leu Met Gly Gly Asp His Ser Pro  
 1 5 10 15  
 Leu Val Val Trp Gln Val Leu Val Asp Val Leu Lys Ser Gln Ser Ser  
 20 25 30  
 Thr Ile Pro Phe Ala Phe Thr Leu Phe Ala Ser Glu Glu Ile Arg Lys  
 35 40 45  
 Gln Ile Gln Glu Glu Phe Ile Ser Asp Leu Pro Gln Glu Lys Phe Pro  
 50 55 60  
 Lys Ile Ile Ser Ala Glu Asn Phe Val Ala Met Glu Asp Ser Pro Leu  
 65 70 75 80  
 Ala Ala Ile Arg Lys Lys Ser Ser Ser Met Ala Leu Gly Leu Asp Tyr  
 85 90 95  
 Leu Gln Glu Asp Lys Leu Asp Ala Phe Ile Ser Thr Gly Asn Thr Gly  
 100 105 110  
 Ala Leu Val Thr Leu Ala Arg Ala Lys Ile Pro Leu Phe Pro Ala Val  
 115 120 125  
 Ser Arg Pro Ala Leu Leu Val Cys Val Pro Thr Met Arg Gly His Ala  
 130 135 140  
 Val Ile Leu Asp Val Gly Ala Asn Ile Ser Val Lys Pro Glu Glu Met  
 145 150 155 160  
 Val Gly Phe Ala Arg Met Gly Leu Ala Tyr Arg Gln Cys Leu Gly Asp  
 165 170 175  
 Ser Lys Ile Pro Thr Ile Gly Leu Leu Asn Ile Gly Ser Glu Glu Arg  
 180 185 190  
 Lys Gly Thr Glu Ala His Arg Gln Thr Phe Arg Met Leu Arg Glu Thr  
 195 200 205  
 Phe Gly Glu Leu Ser  
 210

&lt;210&gt;1034

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1034

Arg Tyr Gly Ser Pro Ser Pro Asp Ile Pro Tyr Ala Ala Arg Asp Ile  
 1 5 10 15

Trp Arg Thr Phe Leu Gly Asn Ile Glu Ser Gly Ala Val Phe Asp Gly  
                   20                  25                  30  
 Ala Ala Asp Ile Val Val Thr Asp Gly Phe Thr Gly Asn Ile Phe Leu  
                   35                  40                  45  
 Lys Thr Ala Glu Gly Val Phe Glu Phe Leu Gln Arg Ile Leu Gly Asp  
                   50                  55                  60  
 Lys Leu Glu Ala Asp Ile Gln Arg Arg Leu Asp Tyr Thr Phe Tyr Pro  
                   65                  70                  75                  80  
 Gly Ser Val Val Cys Gly Leu Ser Lys Leu Val Ile Lys Cys His Gly  
                                   85                  90                  95  
 Lys Ala Cys Gly Ser Ser Leu Phe His Gly Ile Leu Gly Ser Ile Asn  
                                   100                  105                  110  
 Leu Ala Gln Ala Arg Leu Cys Lys Arg Ile Leu Ser Asn Leu Ile  
                                   115                  120                  125  
 <210>1035  
 <211>1617  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1035  
 Thr Pro Leu Arg Phe Lys Val Ala Met Val Ala Lys Lys Thr Val Arg  
   1                  5                  10                  15  
 Ser Tyr Arg Ser Ser Phe Ser His Ser Val Ile Val Ala Ile Leu Ser  
                   20                  25                  30  
 Ala Gly Ile Ala Phe Glu Ala His Ser Leu His Ser Ser Glu Leu Asp  
                   35                  40                  45  
 Leu Gly Val Phe Asn Lys Gln Phe Glu Glu His Ser Ala His Val Glu  
                   50                  55                  60  
 Glu Ala Gln Thr Ser Val Leu Lys Gly Ser Asp Pro Val Asn Pro Ser  
                   65                  70                  75                  80  
 Gln Lys Glu Ser Glu Lys Val Leu Tyr Thr Gln Val Pro Leu Thr Gln  
                   85                  90                  95  
 Gly Ser Ser Gly Glu Ser Leu Asp Leu Ala Asp Ala Asn Xaa Leu Glu  
                   100                  105                  110  
 His Phe Gln His Leu Phe Glu Glu Thr Thr Val Phe Gly Ile Asp Gln  
                   115                  120                  125  
 Lys Leu Val Trp Ser Asp Leu Asp Thr Arg Asn Phe Ser Gln Pro Thr  
                   130                  135                  140  
 Gln Glu Pro Asp Thr Ser Asn Ala Val Ser Glu Lys Ile Ser Ser Asp  
                   145                  150                  155                  160  
 Thr Lys Glu Asn Arg Lys Asp Leu Glu Thr Glu Asp Pro Ser Lys Lys  
                   165                  170                  175  
 Ser Gly Leu Lys Glu Val Ser Ser Asp Leu Pro Lys Ser Pro Glu Thr  
                   180                  185                  190  
 Ala Val Ala Ala Ile Ser Glu Asp Leu Glu Ile Ser Glu Asn Ile Ser  
                   195                  200                  205  
 Ala Arg Asp Pro Leu Gln Gly Leu Ala Phe Phe Tyr Lys Asn Thr Ser  
                   210                  215                  220  
 Ser Gln Ser Ile Ser Glu Lys Asp Ser Ser Phe Gln Gly Ile Ile Phe  
                   225                  230                  235                  240  
 Ser Gly Ser Gly Ala Asn Ser Gly Leu Gly Phe Glu Asn Leu Lys Ala  
                   245                  250                  255  
 Pro Lys Ser Gly Ala Ala Val Tyr Ser Asp Arg Asp Ile Val Phe Glu  
                   260                  265                  270  
 Asn Leu Val Lys Gly Leu Ser Phe Ile Ser Cys Glu Ser Leu Glu Asp  
                   275                  280                  285  
 Gly Ser Ala Ala Gly Val Asn Ile Val Val Thr His Cys Gly Asp Val  
                   290                  295                  300  
 Thr Leu Thr Asp Cys Ala Thr Gly Leu Asp Leu Glu Ala Leu Arg Leu  
                   305                  310                  315                  320  
 Val Lys Asp Phe Ser Arg Gly Gly Ala Val Phe Thr Ala Arg Asn His  
                   325                  330                  335  
 Glu Val Gln Asn Leu Ala Gly Gly Ile Leu Ser Val Val Gly Asn  
                   340                  345                  350  
 Lys Gly Ala Ile Val Val Glu Lys Asn Ser Ala Glu Lys Ser Asn Gly

1055

865 870 875 880  
 Ala Gly Asp Ile Leu Phe Val Ser Asn Ser Thr Gly Ser Tyr Gly Gly  
 885 890 895  
 Ala Ile Phe Val Gly Ser Leu Val Ala Ser Glu Gly Ser Asn Pro Arg  
 900 905 910  
 Thr Leu Thr Ile Thr Gly Asn Ser Gly Asp Ile Leu Phe Ala Lys Asn  
 915 920 925  
 Ser Thr Gln Thr Ala Ala Ser Leu Ser Glu Lys Asp Ser Phe Gly Gly  
 930 935 940  
 Gly Ala Ile Tyr Thr Gln Asn Leu Lys Ile Val Lys Asn Ala Gly Asn  
 945 950 955 960  
 Val Ser Phe Tyr Gly Asn Arg Ala Pro Ser Gly Ala Gly Val Gln Ile  
 965 970 975  
 Ala Asp Gly Gly Thr Val Cys Leu Glu Ala Phe Gly Gly Asp Ile Leu  
 980 985 990  
 Phe Glu Gly Asn Ile Asn Phe Asp Gly Ser Phe Asn Ala Ile His Leu  
 995 1000 1005  
 Cys Gly Asn Asp Ser Lys Ile Val Glu Leu Ser Ala Val Gln Asp Lys  
 1010 1015 1020  
 Asn Ile Ile Phe Gln Asp Ala Ile Thr Tyr Glu Glu Asn Thr Ile Arg  
 1025 1030 1035 1040  
 Gly Leu Pro Asp Lys Asp Val Ser Pro Leu Ser Ala Pro Ser Leu Ile  
 1045 1050 1055  
 Phe Asn Ser Lys Pro Gln Asp Asp Ser Ala Gln His His Glu Gly Thr  
 1060 1065 1070  
 Ile Arg Phe Ser Arg Gly Val Pro Lys Ile Pro Gln Ile Ala Ala Ile  
 1075 1080 1085  
 Gln Glu Gly Thr Leu Ala Leu Ser Gln Asn Ala Glu Leu Trp Leu Ala  
 1090 1095 1100  
 Gly Leu Lys Gln Glu Thr Gly Ser Ser Ile Val Leu Ser Ala Gly Ser  
 1105 1110 1115 1120  
 Ile Leu Arg Ile Phe Asp Ser Gln Val Asp Ser Ser Ala Pro Leu Pro  
 1125 1130 1135  
 Thr Glu Asn Lys Glu Glu Thr Leu Val Ser Ala Gly Val Gln Ile Asn  
 1140 1145 1150  
 Met Ser Ser Pro Thr Pro Asn Lys Asp Lys Ala Val Asp Thr Pro Val  
 1155 1160 1165  
 Leu Ala Asp Ile Ile Ser Ile Thr Val Asp Leu Ser Ser Phe Val Pro  
 1170 1175 1180  
 Glu Gln Asp Gly Thr Leu Pro Leu Pro Pro Glu Ile Ile Ile Pro Lys  
 1185 1190 1195 1200  
 Gly Thr Lys Leu His Ser Asn Ala Ile Asp Leu Lys Ile Ile Asp Pro  
 1205 1210 1215  
 Thr Asn Val Gly Tyr Glu Asn His Ala Leu Leu Ser Ser His Lys Asp  
 1220 1225 1230  
 Ile Pro Leu Ile Ser Leu Lys Thr Ala Glu Gly Met Thr Gly Thr Pro  
 1235 1240 1245  
 Thr Ala Asp Ala Ser Leu Ser Asn Ile Lys Ile Asp Val Ser Leu Pro  
 1250 1255 1260  
 Ser Ile Thr Pro Ala Thr Tyr Gly His Thr Gly Val Trp Ser Glu Ser  
 1265 1270 1275 1280  
 Lys Met Glu Asp Gly Arg Leu Val Val Gly Trp Gln Pro Thr Gly Tyr  
 1285 1290 1295  
 Lys Leu Asn Pro Glu Lys Gln Gly Ala Leu Val Leu Asn Asn Leu Trp  
 1300 1305 1310  
 Ser His Tyr Thr Asp Leu Arg Ala Leu Lys Gln Glu Ile Phe Ala His  
 1315 1320 1325  
 His Thr Ile Ala Gln Arg Met Glu Leu Asp Phe Ser Thr Asn Val Trp  
 1330 1335 1340  
 Gly Ser Gly Leu Gly Val Val Glu Asp Cys Gln Asn Ile Gly Glu Phe  
 1345 1350 1355 1360  
 Asp Gly Phe Lys His His Leu Thr Gly Tyr Ala Leu Gly Leu Asp Thr  
 1365 1370 1375  
 Gln Leu Val Glu Asp Phe Leu Ile Gly Gly Cys Phe Ser Gln Phe Phe



1380 1385 1390  
 Gly Lys Thr Glu Ser Gln Ser Tyr Lys Ala Lys Asn Asp Val Lys Ser  
 1395 1400 1405  
 Tyr Met Gly Ala Ala Tyr Ala Gly Ile Leu Ala Gly Pro Trp Leu Ile  
 1410 1415 1420  
 Lys Gly Ala Phe Val Tyr Gly Asn Ile Asn Asn Asp Leu Thr Thr Asp  
 1425 1430 1435 1440  
 Tyr Gly Thr Leu Gly Ile Ser Thr Gly Ser Trp Ile Gly Lys Gly Phe  
 1445 1450 1455  
 Ile Ala Gly Thr Ser Ile Asp Tyr Arg Tyr Ile Val Asn Pro Arg Arg  
 1460 1465 1470  
 Phe Ile Ser Ala Ile Val Ser Thr Val Val Pro Phe Val Glu Ala Glu  
 1475 1480 1485  
 Tyr Val Arg Ile Asp Leu Pro Glu Ile Ser Glu Gln Gly Lys Glu Val  
 1490 1495 1500  
 Arg Thr Phe Gln Lys Thr Arg Phe Glu Asn Val Ala Ile Pro Phe Gly  
 1505 1510 1515 1520  
 Phe Ala Leu Glu His Ala Tyr Ser Arg Gly Ser Arg Ala Glu Val Asn  
 1525 1530 1535  
 Ser Val Gln Leu Ala Tyr Val Phe Asp Val Tyr Arg Lys Gly Pro Val  
 1540 1545 1550  
 Ser Leu Ile Thr Leu Lys Asp Ala Ala Tyr Ser Trp Lys Ser Tyr Gly  
 1555 1560 1565  
 Val Asp Ile Pro Cys Lys Ala Trp Lys Ala Arg Leu Ser Asn Asn Thr  
 1570 1575 1580  
 Glu Trp Asn Ser Tyr Leu Ser Thr Tyr Leu Ala Phe Asn Tyr Glu Trp  
 1585 1590 1595 1600  
 Arg Glu Asp Leu Ile Ala Tyr Asp Phe Asn Gly Gly Ile Arg Ile Ile  
 1605 1610 1615  
 Phe

&lt;210&gt;1036

&lt;211&gt;504

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1036

Gln Ser Ile Leu Glu Ser Ile Ile Lys Tyr Phe Tyr Leu Ile His Asn  
 1 5 10 15  
 Ser Lys Met His Met Ser Asn Pro Ile Ser Leu Phe Ser Pro Ala Glu  
 20 25 30  
 Leu Ile Ala Lys Tyr Asn Leu Ile Pro Lys Thr Ser Pro Ile Tyr Pro  
 35 40 45  
 Arg Arg Thr Glu Leu Ile Ile Leu Glu Glu Asn Ala Cys Gln Thr Arg  
 50 55 60  
 Leu Thr Asn Val Ala Gln Val Leu His Pro Ser Ser Leu Phe Ser Met  
 65 70 75 80  
 Ser Lys Lys Ile Leu Asn Pro Cys Gly Cys Ser Gly Gly Pro Leu Cys  
 85 90 95  
 Trp Val Ile Leu Asn Ile Leu Ala Phe Ile Ile Thr Ser Val Leu Phe  
 100 105 110  
 Ile Ile Leu Leu Pro Val Asn Leu Ile Val Ala Gly Leu Arg Leu Phe  
 115 120 125  
 Met Pro Leu Pro Pro Lys Lys Ile Val Glu Asp Leu Ser Glu Pro Thr  
 130 135 140  
 Thr Glu Glu Thr Asn Glu Val Ile Gln Pro Phe Ile Phe Ala Leu Gln  
 145 150 155 160  
 Ala Leu Leu Phe Glu Asp Asn Lys Leu Arg Ser Phe Lys Ile Val Glu  
 165 170 175  
 Gln Ser Val Gly Lys Ala Pro Leu Pro Asn Pro Phe Leu Asn Arg Leu  
 180 185 190  
 Val Ala Ile Ser Pro Gln Xaa Ser Gln Glu Ala Met Arg Lys Ile Pro  
 195 200 205  
 Asp Leu Cys Ser Gln Leu Lys Lys Val Leu Lys Ser Leu Gly Val Leu  
 210 215 220

Thr Pro Glu Trp Lys His Met Leu Lys Tyr Phe Glu Gly Leu Lys Asn  
 225 230 235 240  
 Glu His Asp Ser Asn Pro Asp Lys Lys Thr Phe Pro Ile Leu Ile Lys  
 245 250 255  
 Leu Leu Ile Glu Ala Leu Thr Gly Lys Ser Ser Leu Pro Lys Thr Pro  
 260 265 270  
 Ser Thr Lys Glu Lys Met Gln Ala Leu Phe Ile Ala Ser Ser Cys  
 275 280 285  
 Lys Thr Cys Lys Pro Thr Trp Gly Glu Val Ile Thr Arg Ser Leu Asn  
 290 295 300  
 Arg Leu Tyr Ser Ile Ala Asn Glu Gly Asp Asn Gln Leu Leu Ile Trp  
 305 310 315 320  
 Val Gln Glu Phe Lys Glu Arg Glu Leu Met Ser Ile Gln Asp Gly Asp  
 325 330 335  
 Asp Ala Glu Glu Tyr Arg Phe Ala Ala Gln Gln His Gly Glu Arg Tyr  
 340 345 350  
 Thr Glu Ala Ile Glu Gln Val Leu Arg Asn Glu Ser Ala Ala Lys Leu  
 355 360 365  
 Gln Trp His Val Ile Asn Thr Met Lys Phe Phe His Gly Lys Asn Leu  
 370 375 380  
 Gly Leu Val Thr Glu His Leu Gln Asp Thr Leu Gly Ala Leu Thr Leu  
 385 390 395 400  
 Arg Gln Thr Thr Val Asp Thr His Gln Gly Arg Glu Asp Ala Asp Leu  
 405 410 415  
 Ser Ala Ala Leu Phe Leu Asn Lys Tyr Leu Asn Ser Gly Asn Gln Leu  
 420 425 430  
 Val Asn Ser Val Phe Lys Ser Met Gln Lys Ala Asp Pro Glu Thr Lys  
 435 440 445  
 Ala Leu Ile Arg Glu Phe Ala Leu Asp Ile Leu Tyr Ala Ser Leu Arg  
 450 455 460  
 Leu Pro Gln Thr Ser Ala His Thr Glu Val Phe Ser Thr Leu Leu Met  
 465 470 475 480  
 Asp Pro Glu Thr Tyr Glu Pro Asn Lys Ala Cys Ile Ala Tyr Leu Leu  
 485 490 495  
 Tyr Val Leu Lys Ile Ile Glu Leu  
 500

&lt;210&gt;1037

&lt;211&gt;615

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1037

Lys Gly Phe Ser Phe Ser Lys Val Gly Leu Asn Met Ile Pro Ser Gly  
 1 5 10 15  
 Leu Val Tyr Leu Leu Tyr Pro Leu Gly Phe Leu Ala Ser Leu Phe Phe  
 20 25 30  
 Gly Ser Ala Phe Ser Ile Gln Trp Trp Leu Ser Lys Lys Arg Lys Glu  
 35 40 45  
 Val Tyr Ala Pro Arg Ser Phe Trp Ile Leu Ser Ser Ile Gly Ala Thr  
 50 55 60  
 Leu Met Ile Val His Gly Thr Ile Gln Ser Gln Phe Pro Val Thr Val  
 65 70 75 80  
 Leu His Val Ile Asn Leu Ile Ile Tyr Leu Arg Asn Leu Asn Ile Thr  
 85 90 95  
 Ser Ser Arg Pro Ile Ser Phe Arg Ala Thr Leu Val Leu Met Ala Leu  
 100 105 110  
 Ser Val Val Phe Val Thr Leu Pro Phe Leu Tyr Val Asn Met Glu Trp  
 115 120 125  
 Met Ala Ser Pro Asn Ile Phe His Leu Pro Leu Pro Pro Ala Gln Leu  
 130 135 140  
 Ser Trp His Leu Ile Gly Cys Leu Gly Leu Ala Ile Phe Ser Gly Arg  
 145 150 155 160  
 Phe Leu Ile Gln Trp Phe Tyr Ile Glu Ser Asn Asn Thr Lys Asp Phe  
 165 170 175  
 Pro Leu Leu Phe Trp Lys Ile Gly Leu Leu Gly Gly Leu Leu Ala Leu

180 185 190  
 Val Tyr Phe Ile Arg Ile Gly Asp Pro Ile Asn Ile Leu Cys Tyr Gly  
 195 200 205  
 Cys Gly Leu Phe Pro Ser Ile Ala Asn Leu Arg Leu Phe Tyr Lys Glu  
 210 215 220  
 Gln Arg Ser Thr Pro Tyr Leu Asp Thr His Cys Phe Leu Ser Ala Gly  
 225 230 235 240  
 Glu Ala Ser Gly Asp Ile Leu Gly Gly Lys Leu Ile Gln Ser Ile Lys  
 245 250 255  
 Ser Leu Tyr Pro Asn Ile Arg Phe Trp Gly Val Gly Gly Pro Ala Met  
 260 265 270  
 Arg Gln Glu Gly Leu Gln Pro Ile Leu Asn Met Glu Glu Phe Gln Val  
 275 280 285  
 Ser Gly Phe Ala Glu Val Leu Gly Ser Leu Phe Arg Leu Tyr Arg Asn  
 290 295 300  
 Tyr Arg Lys Ile Leu Lys Thr Ile Leu Lys His Lys Pro Ala Thr Leu  
 305 310 315 320  
 Ile Phe Ile Asp Phe Pro Asp Phe His Leu Leu Leu Ile Lys Lys Leu  
 325 330 335  
 Arg Lys His Gly Tyr Arg Gly Lys Ile Ile His Tyr Val Cys Pro Ser  
 340 345 350  
 Ile Trp Ala Trp Arg Pro Lys Arg Lys Arg Ile Leu Glu Gln His Leu  
 355 360 365  
 Asp Met Leu Leu Ile Leu Pro Phe Glu Glu Gly Leu Phe Lys Asn  
 370 375 380  
 Thr Ser Leu Glu Thr Val Tyr Leu Gly His Pro Leu Val Glu Glu Ile  
 385 390 395 400  
 Ser Asp Tyr Lys Glu Gln Ala Ser Trp Lys Glu Lys Phe Leu Asn Ser  
 405 410 415  
 Asp Arg Pro Ile Val Ala Ala Phe Pro Gly Ser Arg Arg Gly Asp Ile  
 420 425 430  
 Ser Arg Asn Leu Arg Ile Gln Val Gln Ala Phe Leu Asn Ser Ser Leu  
 435 440 445  
 Ser Gln Thr His Gln Phe Val Val Ser Ser Ser Ser Ala Lys Tyr Asp  
 450 455 460  
 Glu Ile Ile Glu Asp Thr Leu Lys Ala Glu Gly Cys Gln His Ser Gln  
 465 470 475 480  
 Ile Ile Pro Met Asn Phe Arg Tyr Glu Leu Met Arg Ser Cys Asp Cys  
 485 490 495  
 Ala Leu Ala Lys Cys Gly Thr Ile Val Leu Glu Thr Ala Leu Asn Gln  
 500 505 510  
 Thr Pro Thr Ile Val Met Cys Arg Leu Arg Pro Phe Asp Thr Phe Leu  
 515 520 525  
 Ala Lys Tyr Ile Phe Lys Ile Leu Leu Pro Ala Tyr Ser Leu Pro Asn  
 530 535 540  
 Ile Ile Met Asn Ser Val Ile Phe Pro Glu Phe Ile Gly Gly Lys Lys  
 545 550 555 560  
 Asp Phe His Pro Glu Glu Thr Ala Thr Ala Leu Asp Leu Leu Asn Gln  
 565 570 575  
 His Gly Ser Lys Glu Lys Gln Lys Glu Asp Cys Arg Lys Leu Cys Lys  
 580 585 590  
 Val Met Thr Thr Gly Gln Ile Ala Ser Glu Glu Phe Leu Lys Arg Ile  
 595 600 605  
 Phe Asp Thr Leu Pro Ala Val  
 610 615  
 <210>1038  
 <211>430  
 <212>PRT  
 <213>Chlamydia pneumoniae.  
 <400>1038  
 Met Val Cys Glu Asn Asn Ile Leu Ser Gly Arg Gly Leu Glu Leu Leu  
 1 5 10 15  
 Lys Lys Lys Ser Asn Ile Thr Leu Thr Pro Thr Ile Tyr Ser Val Ser  
 20 25 30

Asn His Asn Ile Lys Leu Lys Asp Phe Ser Pro His Ala Leu Ser Val  
 35 40 45  
 Ile Lys Thr Leu Arg Lys Ala Gly Tyr Ile Ala Tyr Ile Val Gly Gly  
 50 55 60  
 Cys Ile Arg Asp Leu Leu Leu Asn Thr Thr Pro Lys Asp Phe Asp Ile  
 65 70 75 80  
 Ser Thr Ser Ala Lys Pro Glu Glu Ile Lys Ala Ile Phe Lys Asn Cys  
 85 90 95  
 Ile Leu Val Gly Lys Arg Phe Arg Leu Ala His Ile Arg Phe Ser Lys  
 100 105 110  
 Gln Ile Ile Glu Val Ser Thr Phe Arg Ser Gly Ser Thr Asp Glu Asp  
 115 120 125  
 Val Leu Ile Thr Lys Asp Asn Leu Trp Gly Thr Pro Glu Glu Asp Val  
 130 135 140  
 Leu Arg Arg Asp Phe Thr Ile Asn Gly Leu Phe Tyr Asp Pro Glu His  
 145 150 155 160  
 Glu Glu Ile Ile Asp Tyr Thr Gly Gly Val Asn Asp Leu Arg Asn Arg  
 165 170 175  
 Tyr Leu Arg Thr Ile Gly Asp Pro Phe Thr Arg Phe Lys Gln Asp Pro  
 180 185 190  
 Val Arg Met Leu Arg Leu Leu Lys Ile Leu Ser Arg Ser Pro Phe Thr  
 195 200 205  
 Val Glu Thr Gln Thr Gln Glu Ala Leu Ile Ala Cys Arg Gln Glu Leu  
 210 215 220  
 Ile Lys Ser Ser Arg Ala Arg Val Phe Glu Glu Leu Ile Lys Met Leu  
 225 230 235 240  
 Asn Ser Gly Ala Ala Lys Asn Phe Phe Gln Leu Leu Ile Glu Asn His  
 245 250 255  
 Leu Leu Glu Ile Leu Phe Pro Tyr Met Asp Lys Ala Phe Arg Leu Asn  
 260 265 270  
 Arg Ala Leu Glu Glu Gln Thr Ala Thr Tyr Leu Lys Ala Leu Asp Asp  
 275 280 285  
 Lys Ile Leu Lys Lys Glu Ala Glu Tyr Asp Arg His Gln Leu Met Ala  
 290 295 300  
 Ile Phe Leu Phe Pro Leu Val Asn Phe Asn Val Arg Tyr Lys His Gln  
 305 310 315 320  
 Lys His Pro Tyr Leu Ser Leu Thr Ser Val Phe Asp Tyr Ile Lys Asn  
 325 330 335  
 Phe Leu Glu Gln Phe Phe Ala Asp Ser Phe Thr Ser Cys Ser Lys Lys  
 340 345 350  
 Asn Phe Ile Leu Thr Ala Leu Ile Leu Gln Met Gln Tyr Arg Leu Thr  
 355 360 365  
 Pro Leu Ile Pro Thr Lys Lys Ala Leu Phe Phe Asn Lys Lys Leu Leu  
 370 375 380  
 His His Thr Arg Phe Leu Glu Ala Leu Ser Leu Leu Glu Ile Arg Ser  
 385 390 395 400  
 Ile Val Tyr Pro Lys Leu Asp Lys Val Tyr Val Ala Trp Ile Arg His  
 405 410 415  
 His Gln Thr Leu Lys Cys Lys Lys Asp Ser His Ser Gln Lys  
 420 425 430

&lt;210&gt;1039

&lt;211&gt;395

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1039

Glu Arg Ile Asp Cys Trp Leu Asn Ser Met Gly Ile Glu Thr Leu Val  
 1 5 10 15  
 Leu Gly Pro Ile Pro Thr Pro Gly Val Ala Phe Ile Thr Arg Ala Tyr  
 20 25 30  
 Arg Ala Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Tyr Arg  
 35 40 45  
 Asp Asn Gly Ile Lys Ile Phe Ser Leu Glu Gly Phe Lys Ile Ser Asp  
 50 55 60  
 Val Leu Glu Gln Arg Ile Glu Thr Met Val Ser Glu Ala Asp Phe Gly

65 70 75 80  
 Pro Leu Pro Glu Asp His Ala Val Gly Lys Asn Lys Arg Val Ile Asp  
 85 90 95  
 Ala Met Gly Arg Tyr Val Glu Phe Val Lys Ala Thr Phe Pro Lys Gly  
 100 105 110  
 Arg Thr Leu Lys Gly Leu Lys Ile Val Leu Asp Cys Ala His Gly Ala  
 115 120 125  
 Ser Tyr Lys Val Ala Pro Ser Val Phe Glu Glu Leu Asp Ala Glu Val  
 130 135 140  
 Ile Cys Tyr Gly Cys Glu Pro Thr Gly Ile Asn Ile Asn Glu His Cys  
 145 150 155 160  
 Gly Ala Leu Phe Pro Gln Val Ile Gln Lys Ala Val Ile Glu His Gln  
 165 170 175  
 Ala His Leu Gly Ile Ala Leu Asp Gly Asp Gly Asp Arg Ile Ile Met  
 180 185 190  
 Val Asp Glu Lys Gly His Ile Val Asp Gly Asp Met Ile Leu Ser Ile  
 195 200 205  
 Cys Ala Gly Asp Leu Lys Lys Arg Ser Ala Leu Pro His Asn Arg Val  
 210 215 220  
 Val Ala Thr Ile Met Thr Asn Phe Gly Val Leu Lys Tyr Leu Glu Gly  
 225 230 235 240  
 Leu Gly Leu Gln Val Phe Thr Ser Pro Val Gly Asp Arg His Val Leu  
 245 250 255  
 His Ala Met Leu Glu His Glu Val Thr Xaa Gly Gly Glu Gln Ser Gly  
 260 265 270  
 His Met Ile Phe Leu Asp Tyr Asn Thr Thr Gly Asp Gly Ile Val Ser  
 275 280 285  
 Ala Leu Gln Val Leu Arg Ile Met Ile Glu Ser Glu Ser Met Leu Ser  
 290 295 300  
 Asp Leu Thr Ala Pro Ile Val Lys Ser Pro Gln Thr Leu Ile Asn Val  
 305 310 315 320  
 Ala Val Arg Glu Lys Ile Pro Leu Glu Thr Ile Pro Leu Ile Glu Arg  
 325 330 335  
 Thr Leu Arg Asp Val Gln Asp Ala Leu Gly Pro Ser Gly Arg Ile Leu  
 340 345 350  
 Leu Arg Tyr Ser Gly Thr Glu Asn Ile Cys Arg Val Met Val Glu Gly  
 355 360 365  
 His Lys Lys His Gln Val Asp Cys Leu Ala Lys Ala Leu Ala Asp Val  
 370 375 380  
 Ile Asp Ala Glu Leu Gly Thr Gly Ser Arg Glu  
 385 390 395

&lt;210&gt;1040

&lt;211&gt;161

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1040

Met Cys Gly Ile Phe Gly Tyr Leu Gly Asn Gln Asp Gly Val Ser Ile  
 1 5 10 15  
 Val Leu Glu Gly Leu Ala Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala  
 20 25 30  
 Gly Leu Ala Ala Val Val Glu Gln Glu Leu Phe Ile Arg Lys Thr Val  
 35 40 45  
 Gly Arg Val Gln Glu Leu Ser Asn Leu Phe Gln Glu Arg Glu Ile Pro  
 50 55 60  
 Thr Ala Ser Val Ile Gly His Thr Arg Trp Ala Thr His Gly Val Pro  
 65 70 75 80  
 Thr Glu Ile Asn Ala His Pro His Val Asp Glu Gly Arg Ser Cys Ala  
 85 90 95  
 Val Val His Asn Gly Ile Ile Glu Asn Phe Lys Glu Leu Arg Arg Glu  
 100 105 110  
 Leu Thr Ala Gln Gly Ile Ser Phe Ala Ser Asp Thr Asp Ser Glu Ile  
 115 120 125  
 Ile Val Gln Leu Phe Ser Leu Tyr Tyr Gln Glu Ser Gln Asp Leu Val  
 130 135 140

Phe Ser Phe Cys Gln Thr Leu Ala Gln Leu Arg Gly Ser Val Ala Ala  
 145 150 155 160  
 Leu

&lt;210&gt;1041

&lt;211&gt;307

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1041

Arg Ser Cys Ala Leu Ile His Lys Asp His Pro His Thr Ile Leu Cys  
 1 5 10 15  
 Ala Ser Gln Glu Ser Pro Leu Ile Leu Gly Leu Gly Lys Glu Glu Thr  
 20 25 30  
 Phe Ile Ala Ser Asp Ser Arg Ala Phe Phe Lys Tyr Thr Arg His Ser  
 35 40 45  
 Gln Ala Leu Ala Ser Gly Glu Phe Ala Ile Val Ser Gln Gly Lys Glu  
 50 55 60  
 Pro Glu Val Tyr Asn Leu Glu Leu Lys Lys Ile His Lys Asp Val Arg  
 65 70 75 80  
 Gln Ile Thr Cys Ser Glu Asp Ala Ser Asp Lys Ser Gly Tyr Gly Tyr  
 85 90 95  
 Tyr Met Leu Lys Glu Ile Tyr Asp Gln Pro Glu Val Leu Glu Gly Leu  
 100 105 110  
 Ile Gln Lys His Met Asp Glu Glu Gly His Ile Leu Ser Glu Phe Leu  
 115 120 125  
 Ser Asp Val Pro Ile Lys Ser Phe Lys Glu Ile Thr Ile Val Ala Cys  
 130 135 140  
 Gly Ser Ser Tyr His Ala Gly Tyr Leu Ala Lys Tyr Ile Ile Glu Ser  
 145 150 155 160  
 Leu Val Ser Ile Pro Val His Ile Glu Val Ala Ser Glu Phe Arg Tyr  
 165 170 175  
 Arg Arg Pro Tyr Ile Gly Lys Asp Thr Leu Gly Ile Leu Ile Ser Gln  
 180 185 190  
 Ser Gly Glu Thr Ala Asp Thr Leu Ala Ala Leu Lys Glu Leu Arg Arg  
 195 200 205  
 Arg Asn Ile Ala Tyr Leu Leu Gly Ile Cys Asn Val Pro Glu Ser Ala  
 210 215 220  
 Ile Ala Leu Gly Val Asp His Cys Leu Phe Leu Glu Ala Gly Val Glu  
 225 230 235 240  
 Ile Gly Val Ala Thr Thr Lys Ala Phe Thr Ser Gln Leu Leu Leu Leu  
 245 250 255  
 Val Phe Leu Gly Leu Lys Leu Ala Asn Val His Gly Ala Leu Thr His  
 260 265 270  
 Ala Glu Gln Cys Ser Phe Gly Gln Gly Leu Gln Ser Leu Pro Asp Leu  
 275 280 285  
 Cys Gln Lys Leu Leu Ala Gln Arg Val Ser Pro Phe Leu Gly Ala Ala  
 290 295 300  
 Leu Leu Leu  
 305

&lt;210&gt;1042

&lt;211&gt;182

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1042

Leu Thr Gln Asn Asn Val Pro Leu Ala Arg Asp Tyr Lys Ala Tyr Gln  
 1 5 10 15  
 Ile Ser Val Lys Asn Phe Leu Pro Asn Glu Ser Leu His Ser Trp Ala  
 20 25 30  
 Gln Pro Tyr Ser Tyr Glu Asp Lys Phe Leu Phe Leu Gly Arg Arg Leu  
 35 40 45  
 Met Tyr Pro Val Val Met Glu Ala Ala Leu Lys Leu Lys Glu Ile Ala  
 50 55 60  
 Tyr Ile Glu Ala Asn Ala Tyr Pro Gly Gly Glu Met Lys His Gly Pro  
 65 70 75 80

Ile Ala Leu Ile Ser Lys Gly Thr Pro Val Ile Ala Phe Cys Gly Asp  
                             85                            90                            95  
 Asp Ile Val Tyr Glu Lys Met Ile Gly Asn Met Met Glu Val Lys Ala  
                             100                            105                            110  
 Arg His Ala His Val Ile Ala Ile Ala Pro Glu Ser Arg Glu Asp Ile  
                             115                            120                            125  
 Ala Ala Val Ser Asp Gln Gln Ile Phe Val Pro Asp Cys His Phe Leu  
                             130                            135                            140  
 Ala Ala Pro Val Leu Tyr Thr Ile Val Gly Gln Val Met Ala Tyr Ala  
                             145                            150                            155                            160  
 Met Ala Leu Ala Lys Gly Met Glu Ile Asp Cys Pro Arg Asn Leu Ala  
                             165                            170                            175  
 Lys Ser Val Thr Val Glu  
                             180

&lt;210&gt;1043

&lt;211&gt;259

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1043

Ser His Asp Leu Asp Xaa Arg Ile Lys Glu Pro Ser Glu His Ala Phe  
   1                            5                            10                            15  
 Tyr Gly Gly Ile Tyr Phe Arg Ser Cys Arg Gln Asp Phe Tyr Met Pro  
                             20                            25                            30  
 Cys Leu Leu Val Ser Leu Leu Leu Pro Thr Asp Cys Tyr Phe Cys Glu  
                             35                            40                            45  
 Gly Gly Asn Ile Leu Cys Arg Val Phe Asn Cys Gln Asn Leu Gly Ile  
                             50                            55                            60  
 Ser Trp Ile Arg His Leu Gly Pro Leu Gly Phe Ala Ile Leu Met Gly  
                             65                            70                            75                            80  
 Pro Ile Ile Met Ala Gly Thr Lys Val Ile Asp Tyr Cys Asn Arg Phe  
                             85                            90                            95  
 Phe Met Phe Gly Leu Thr Val Ala Phe Gly Ile Phe Cys Ala Leu Gly  
                             100                            105                            110  
 Phe Leu Lys Ile Gln Pro Ser Phe Leu Val Arg Ser Ser Trp Leu Thr  
                             115                            120                            125  
 Thr Ile Asn Ala Phe Pro Val Phe Phe Leu Ala Phe Gly Phe Gln Ser  
                             130                            135                            140  
 Ile Ile Pro Thr Leu Tyr Tyr Met Asp Lys Lys Val Gly Asp Val  
                             145                            150                            155                            160  
 Lys Lys Ala Ile Leu Ile Gly Thr Leu Ile Pro Leu Val Leu Tyr Val  
                             165                            170                            175  
 Leu Trp Glu Val Val Val Leu Gly Ala Val Ser Leu Pro Ile Leu Ser  
                             180                            185                            190  
 Gln Ala Lys Ile Gly Gly Tyr Thr Ala Val Glu Ala Leu Lys Gln Ala  
                             195                            200                            205  
 His Arg Ser Trp Ala Phe Tyr Ile Ala Gly Glu Leu Phe Gly Phe Phe  
                             210                            215                            220  
 Ala Leu Val Ser Ser Phe Val Gly Val Ala Leu Gly Val Met Asp Phe  
                             225                            230                            235                            240  
 Leu Ala Asp Gly Leu Lys Trp Asn Lys Lys Ser His Pro Asn Phe Gln  
                             245                            250                            255  
 Phe Ser Phe

&lt;210&gt;1044

&lt;211&gt;241

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1044

Glu Gly Ser Met Gly Leu Tyr Asp Arg Asp Tyr Ile Gln Asp Ser Arg  
   1                            5                            10                            15  
 Val Gln Gly Thr Phe Ala Ser Arg Val Tyr Gly Trp Met Thr Ala Gly  
                             20                            25                            30  
 Leu Ile Val Thr Ser Cys Val Ala Leu Gly Leu Tyr Phe Ser Gly Leu  
                             35                            40                            45

Tyr Arg Ser Leu Phe Ser Phe Trp Trp Val Trp Cys Phe Ala Thr Leu  
 50 55 60  
 Gly Val Ser Phe Phe Ile Asn Ser Lys Ile Gln Thr Leu Ser Val Ser  
 65 70 75 80  
 Ala Val Gly Gly Leu Phe Leu Leu Tyr Ser Thr Leu Glu Gly Met Phe  
 85 90 95  
 Phe Gly Thr Leu Leu Pro Val Tyr Ala Ala Gln Tyr Gly Gly Gly Val  
 100 105 110  
 Ile Trp Ala Ala Phe Gly Ser Ala Ala Leu Val Phe Gly Leu Ala Ala  
 115 120 125  
 Val Tyr Gly Ala Phe Thr Lys Ser Asp Leu Thr Lys Ile Ser Lys Ile  
 130 135 140  
 Met Thr Phe Ala Leu Ile Gly Leu Leu Leu Val Thr Leu Val Phe Ala  
 145 150 155 160  
 Val Val Ser Met Phe Val Ser Met Pro Leu Ile Tyr Leu Leu Ile Cys  
 165 170 175  
 Tyr Leu Gly Leu Val Ile Phe Val Gly Leu Thr Ala Ala Asp Ala Gln  
 180 185 190  
 Ala Ile Arg Arg Ile Ser Ser Thr Ile Gly Asp Asn Asn Thr Leu Ser  
 195 200 205  
 Tyr Lys Leu Ser Leu Met Phe Ala Leu Lys Met Tyr Cys Asn Val Ile  
 210 215 220  
 Met Val Phe Trp Tyr Leu Leu Gln Ile Phe Ser Ser Ser Gly Asn Arg  
 225 230 235 240  
 Asp

&lt;210&gt;1045

&lt;211&gt;316

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1045

Arg Cys Ile Asn Asn Ser Leu Leu Phe Pro Ser Tyr Leu Val Ser Phe  
 1 5 10 15  
 Leu Leu Leu Gln Leu Thr Leu Leu Leu Ala Met Phe Lys Phe Phe Arg  
 20 25 30  
 Asn Lys Leu Gln Ser Leu Phe Lys Lys Asn Ile Ser Leu Asp Leu Ile  
 35 40 45  
 Glu Asp Ala Glu Ser Leu Phe Tyr Glu Ala Asp Phe Gly Thr Glu Leu  
 50 55 60  
 Thr Glu Glu Leu Cys Ala Arg Leu Arg Arg Thr Lys Lys Ala Asp Ala  
 65 70 75 80  
 Ser Thr Ile Lys Asp Leu Ile Thr Val Leu Leu Arg Glu Ser Leu Glu  
 85 90 95  
 Gly Leu Pro Ser Gln Ala Ser Gln Ser Ser Gln Thr Arg Pro Ile Val  
 100 105 110  
 Ser Leu Leu Leu Gly Thr Asn Gly Ser Gly Lys Thr Thr Thr Ala Ala  
 115 120 125  
 Lys Leu Ala His Tyr Tyr Lys Glu Arg Ser Glu Ser Val Met Leu Val  
 130 135 140  
 Ala Thr Asp Thr Phe Arg Ala Ala Gly Met Asp Gln Ala Arg Leu Trp  
 145 150 155 160  
 Ala Asn Glu Leu Gly Cys Gly Phe Val Ser Gly Gln Pro Gly Gly Asp  
 165 170 175  
 Ala Ala Ala Ile Ala Phe Asp Gly Ile Gln Ser Ala Ile Ala Arg Gly  
 180 185 190  
 Tyr Ser Arg Val Ile Ile Asp Thr Ser Gly Arg Leu His Val His Gly  
 195 200 205  
 Asn Leu Met Lys Glu Leu Ser Lys Ile Val Ser Val Cys Gly Lys Ala  
 210 215 220  
 Leu Glu Gly Ala Pro His Glu Ile Phe Met Thr Val Asp Ser Thr Leu  
 225 230 235 240  
 Gly Asn Asn Ala Ile Glu Gln Val Arg Val Phe His Asp Val Val Pro  
 245 250 255  
 Leu Ser Gly Leu Ile Phe Thr Lys Val Asp Gly Ser Ala Lys Gly Gly



260 265 270  
 Thr Leu Phe Gln Ile Ala Lys Arg Leu Lys Ile Pro Thr Lys Phe Ile  
 275 280 285  
 Gly Tyr Gly Glu Ser Leu Lys Asp Leu Asn Glu Phe Asp Leu Asp Leu  
 290 295 300  
 Phe Leu Asn Lys Leu Phe Pro Glu Val Glu Lys Ile  
 305 310 315  
 <210>1046  
 <211>386  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1046  
 Met His Leu His Glu Tyr Gln Ala Lys Asp Leu Leu Ala Ser Tyr Asp  
 1 5 10 15  
 Val Pro Ile Pro Tyr Trp Val Val Ser Ser Glu Glu Glu Gly Glu  
 20 25 30  
 Leu Leu Ile Thr Lys Ser Gly Leu Asp Ser Ala Val Val Lys Val Gln  
 35 40 45  
 Val His Ala Gly Gly Arg Gly Lys His Gly Gly Val Ile Val Ala Lys  
 50 55 60  
 Ser Ser Ala Gly Ile Leu Gln Ala Val Ala Lys Leu Leu Gly Met His  
 65 70 75 80  
 Phe Thr Ser Asn Gln Thr Ala Asp Gly Phe Leu Pro Val Glu Lys Val  
 85 90 95  
 Leu Ile Ser Pro Leu Val Ala Ile Gln Arg Glu Tyr Tyr Val Ala Val  
 100 105 110  
 Ile Met Asp Arg Lys His Arg Cys Pro Val Leu Met Leu Ser Lys Ala  
 115 120 125  
 Gly Gly Met Asp Ile Glu Glu Val Ala His Ser Ser Pro Glu Gln Ile  
 130 135 140  
 Leu Thr Leu Pro Leu Thr Ser Tyr Gly His Ile Tyr Ser Tyr Gln Leu  
 145 150 155 160  
 Arg Gln Ala Thr Lys Phe Met Glu Trp Glu Gly Glu Val Met His Gln  
 165 170 175  
 Gly Val Gln Leu Ile Lys Lys Leu Ala Lys Cys Phe Tyr Glu Asn Asp  
 180 185 190  
 Val Ser Leu Leu Glu Ile Asn Pro Leu Val Leu Thr Leu Glu Gly Glu  
 195 200 205  
 Leu Leu Val Leu Asp Ser Lys Ile Thr Ile Asp Asp Asn Ala Leu Tyr  
 210 215 220  
 Arg His Pro Asn Leu Glu Val Leu Tyr Asp Pro Ser Gln Glu Asn Val  
 225 230 235 240  
 Arg Asp Val Leu Ala Lys Gln Ile Gly Leu Ser Tyr Ile Ala Leu Ser  
 245 250 255  
 Gly Asn Ile Gly Cys Ile Val Asn Gly Ala Gly Leu Ala Met Ser Thr  
 260 265 270  
 Leu Asp Ile Leu Lys Leu His Gly Gly Asn Ala Ala Asn Phe Leu Asp  
 275 280 285  
 Val Gly Gly Gly Ala Ser Gln Lys Gln Ile Gln Glu Ala Val Ser Leu  
 290 295 300  
 Val Leu Ser Asp Glu Ser Val Lys Val Leu Phe Ile Asn Ile Phe Gly  
 305 310 315 320  
 Xaa Ile Met Asp Cys Ser Val Val Ala Ser Gly Leu Val Ala Val Met  
 325 330 335  
 Glu Thr Arg Asp Gln Val Val Pro Thr Val Ile Arg Leu Glu Gly Thr  
 340 345 350  
 Asn Val Glu Leu Gly Lys Glu Ile Val Gln Gln Ser Gly Ile Pro Cys  
 355 360 365  
 Gln Phe Val Ser Ser Met Glu Gly Ala Arg Arg Ala Val Glu Leu  
 370 375 380  
 Ser Met  
 385  
 <210>1047  
 <211>300

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1047

Val Cys Arg Phe Arg Arg Tyr Met Phe His Ser Leu Ser Lys Asn Thr  
 1 5 10 15  
 Pro Ile Ile Thr Gln Gly Ile Thr Gly Lys Ala Gly Ser Phe His Thr  
 20 25 30  
 Glu Gln Cys Leu Ala Tyr Gly Thr Asn Phe Val Gly Gly Val Thr Pro  
 35 40 45  
 Gly Lys Gly Gly Thr Leu Trp Leu Asp Leu Pro Val Tyr Asp Ser Val  
 50 55 60  
 Leu Glu Ala Lys Gln Ala Thr Gly Cys Arg Ala Thr Met Ile Phe Val  
 65 70 75 80  
 Pro Pro Pro Tyr Ala Ala Glu Ala Ile Leu Glu Ala Glu Glu Ala Gly  
 85 90 95  
 Ile Glu Leu Ile Val Cys Ile Thr Glu Gly Ile Pro Val Arg Asp Met  
 100 105 110  
 Leu Glu Val Ala Arg Val Met Asp Asn Ser Thr Ser Gln Leu Ile Gly  
 115 120 125  
 Pro Asn Cys Pro Gly Ile Ile Lys Pro Gly Glu Cys Lys Ile Gly Ile  
 130 135 140  
 Met Pro Gly Tyr Ile His Leu Pro Gly Asn Ile Gly Val Val Ser Arg  
 145 150 155 160  
 Ser Gly Thr Leu Thr Tyr Glu Ala Val Trp Gln Leu Thr Gln Leu Lys  
 165 170 175  
 Ile Gly Gln Ser Ile Cys Val Gly Ile Gly Gly Asp Pro Leu Asn Gly  
 180 185 190  
 Thr Ser Phe Ile Asp Val Leu Gln Ala Leu Glu Glu Asp Pro Tyr Thr  
 195 200 205  
 Glu Leu Ile Leu Met Ile Gly Glu Ile Gly Gly Ser Ala Glu Glu Glu  
 210 215 220  
 Ala Ala Ala Trp Ile Gln Ala His Cys Thr Lys Pro Val Val Ala Phe  
 225 230 235 240  
 Ile Ala Gly Val Thr Ala Pro Lys Gly Lys Arg Met Gly His Ala Gly  
 245 250 255  
 Ala Ile Ile Ser Gly Asn Ser Gly Asp Ala Lys Ser Lys Ile Gln Val  
 260 265 270  
 Leu Arg Glu Ser Gly Val Thr Val Val Glu Ser Pro Ala His Ile Gly  
 275 280 285  
 Lys Thr Val Asp Ala Val Leu Arg Ala Lys Glu Leu  
 290 295 300

&lt;210&gt;1048

&lt;211&gt;369

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1048

Ile Leu Met Leu Val Tyr Cys Phe Asp Pro Ser Val Pro Thr Ser Pro  
 1 5 10 15  
 Glu His Arg Leu Met Ala Ala Leu Asp Arg Trp Phe Phe Leu Gly Gly  
 20 25 30  
 His Arg Val Arg Ile Leu Thr Leu Glu Gly Asn His Tyr Arg Ala Phe  
 35 40 45  
 Gln Glu Asn Met Ser Ile Ser Thr Val Glu Lys Ile Leu Lys Leu Ile  
 50 55 60  
 Ser Tyr Leu Leu Ile Pro Ile Val Leu Ile Ala Leu Leu Ile Arg Cys  
 65 70 75 80  
 Phe Leu His Ser Arg Phe Lys Cys Asn Trp Lys Cys Asp Ser Leu Ser  
 85 90 95  
 Asp Ala Arg Val Pro His Asp Val Gln Pro Phe Asn Asp Phe Gln Leu  
 100 105 110  
 Phe Asn Asn Gln Glu Arg Leu Asn Ile Trp Lys Asn Arg Arg Tyr Val  
 115 120 125  
 Ser Gly Ile Asp Val Leu Met Val Pro Val Asp Tyr Leu Arg Ser Gln  
 130 135 140

Phe Pro Gly Phe Lys Glu Ile Pro Glu Ala Ile Arg Cys Glu Asn Tyr  
 145 150 155 160  
 Val Ser Asp Gly Gln Phe Ser Glu Glu Ser Lys Thr Ser Tyr Leu Arg  
 165 170 175  
 Ala Met Leu Thr Asp Ile Val Gly Tyr Ile Leu Ser Leu Asp Glu Thr  
 180 185 190  
 Tyr Trp Thr Asn Val Ile Leu Lys Ile Arg Ala Met Cys Ile Thr Phe  
 195 200 205  
 Glu Ser Phe Pro Gly Lys Glu Ala Asp Pro Asn Tyr Ser Pro Arg Val  
 210 215 220  
 Thr His His Tyr Phe Asp Glu Ser Trp Lys Ala Leu Ala Arg His Val  
 225 230 235 240  
 Leu Gly Glu Gly Asn Met Val Asn Arg Leu Asp Glu Ala Leu Ile Arg  
 245 250 255  
 Thr Glu Lys Pro Gly Lys Glu Gly Glu Cys Ile Thr Lys Gln Phe Leu  
 260 265 270  
 Lys Asp Tyr Cys Lys Lys His Leu Glu Val Met Ser Cys Pro Asp Phe  
 275 280 285  
 Ile Glu Ser Leu Val Asp Glu Lys Ile Arg Glu Phe Arg Cys Pro Ser  
 290 295 300  
 Ile Leu Asn Ser Ala Val Cys Asp Val Ile Asp Arg Lys Cys Gln Glu  
 305 310 315 320  
 His Leu Leu Lys Ala Ile Ile Asn Glu Ala Asn Arg Arg Leu Pro Gly  
 325 330 335  
 Met Lys Asn Ser Ser Phe Thr Met Arg Gly Asn Gln Val Leu Phe Tyr  
 340 345 350  
 Thr Ile Phe Ser Pro Pro Lys Leu Pro Pro Ala Ala Ser Ser Val Tyr  
 355 360 365  
 Phe

&lt;210&gt;1049

&lt;211&gt;358

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1049

Leu Tyr Ile Asn Gln Phe Ala Asn Ile Leu Lys Ser Ser Phe Leu Met  
 1 5 10 15  
 Glu Val Tyr Ser Phe Ser Pro Ser Val Arg Thr Ser Phe Gln His Arg  
 20 25 30  
 Val Met Ala Ala Leu Asp Asn Trp Phe Phe Leu Gly Gly Arg Arg Leu  
 35 40 45  
 Lys Val Val Ser Leu Asp Ser Cys Asn Ser Gly Gln Ala Cys Glu Glu  
 50 55 60  
 Tyr Val Pro Ile Ser Thr Thr Glu Lys Val Leu Lys Ile Leu Ser Tyr  
 65 70 75 80  
 Leu Leu Ile Pro Ile Val Ile Ile Ala Leu Leu Ile Arg Tyr Leu Leu  
 85 90 95  
 His Ser Asn Phe Thr Ala Lys Val Ser Gln Lys Pro Trp Leu Lys Thr  
 100 105 110  
 Leu Gln Leu Gly Ile Asp Ile Lys Ser Phe Ile Leu Pro Gly Ser His  
 115 120 125  
 Val Asn Thr Met Asp Ser Ala Thr Leu Phe Lys Ala Ile Arg Leu Glu  
 130 135 140  
 Gly Lys Arg Val Asp Val Glu Tyr His Arg Leu His Ser Ser Asp Lys  
 145 150 155 160  
 Val Val Phe Tyr Ile Pro Ala Gln Lys Leu Pro Asp Asp Leu Arg Leu  
 165 170 175  
 Thr His Trp Leu Pro Glu Lys Glu Thr Arg Lys Thr Glu Tyr Val Arg  
 180 185 190  
 His Met Leu Ala His Val Met Gly Tyr Leu Thr Ser Gln Gly Lys Glu  
 195 200 205  
 Arg Leu Gln Gln Val Val Gln Asp Ser Arg Ser Ser Thr Ser Leu Gly  
 210 215 220  
 Ala Glu Lys Val Leu Gln Tyr Arg Phe Ile Asp His Pro Gln Ser Gln

1068

Arg Ser

&lt;210&gt;1051

&lt;211&gt;245

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1051

Gly Ile Asp Met Ile Thr Lys Gln Leu Arg Ser Trp Leu Ala Val Leu  
 1 5 10 15  
 Val Gly Ser Ser Leu Leu Ala Leu Pro Leu Ser Gly Gln Ala Val Gly  
 20 25 30  
 Lys Lys Glu Ser Arg Val Ser Glu Leu Pro Gln Asp Val Leu Leu Lys  
 35 40 45  
 Glu Ile Ser Gly Gly Phe Ser Lys Val Ala Thr Lys Ala Thr Pro Ala  
 50 55 60  
 Val Val Tyr Ile Glu Ser Phe Pro Lys Ser Gln Ala Val Thr His Pro  
 65 70 75 80  
 Ser Pro Gly Arg Arg Gly Pro Tyr Glu Asn Pro Phe Asp Tyr Phe Asn  
 85 90 95  
 Asp Glu Phe Phe Asn Arg Phe Phe Gly Leu Pro Ser Gln Arg Glu Lys  
 100 105 110  
 Pro Gln Ser Lys Glu Ala Val Arg Gly Thr Gly Phe Leu Val Ser Pro  
 115 120 125  
 Asp Gly Tyr Ile Val Thr Asn Asn His Val Val Glu Asp Thr Gly Lys  
 130 135 140  
 Ile His Val Thr Leu His Asp Gly Gln Lys Tyr Pro Ala Thr Val Ile  
 145 150 155 160  
 Gly Leu Asp Pro Lys Thr Asp Leu Ala Val Ile Lys Ile Lys Ser Gln  
 165 170 175  
 Asn Leu Pro Tyr Leu Ser Phe Gly Asn Ser Asp His Leu Lys Val Gly  
 180 185 190  
 Asp Trp Ala Ile Ala Ile Gly Asn Pro Phe Gly Leu Gln Ala Thr Val  
 195 200 205  
 Thr Val Val Ser Ser Val Leu Lys Glu Glu Ile Asn Ser Thr Leu Gln  
 210 215 220  
 Ile Leu Lys Ile Leu Phe Arg Gln Met Leu Arg Leu Ile Gln Ala Thr  
 225 230 235 240  
 Leu Glu Ala Leu Phe  
 245

&lt;210&gt;1052

&lt;211&gt;317

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1052

Ile Pro Lys Pro Pro Val Ser Phe Phe Trp Lys Leu Arg Pro Leu Lys  
 1 5 10 15  
 Ser Arg Arg Leu Gly Asn Cys Asn Trp Lys Ser Leu Arg Ser Ser Ser  
 20 25 30  
 Tyr Gly His Arg Ser Val Ile Ser Ala Lys Gly Arg Asn Gln Leu His  
 35 40 45  
 Ile Ala Asp Phe Glu Asp Phe Ile Gln Thr Asp Ala Ala Ile Asn Pro  
 50 55 60  
 Gly Asn Ser Gly Gly Pro Leu Leu Asn Ile Asp Gly Gln Val Ile Gly  
 65 70 75 80  
 Val Asn Thr Ala Ile Val Ser Gly Ser Gly Gly Tyr Ile Gly Ile Gly  
 85 90 95  
 Phe Ala Ile Pro Ser Leu Met Ala Asn Arg Ile Ile Asp Gln Leu Ile  
 100 105 110  
 Arg Asp Gly Gln Val Thr Arg Gly Phe Leu Gly Val Thr Leu Gln Pro  
 115 120 125  
 Ile Asp Ala Glu Leu Ala Ala Cys Tyr Lys Leu Glu Lys Val Tyr Gly  
 130 135 140  
 Ala Leu Val Thr Asp Val Val Lys Gly Ser Pro Ala Asp Lys Ala Gly  
 145 150 155 160

Leu Lys Gln Glu Asp Val Ile Ile Ala Tyr Asn Gly Lys Glu Val Asp  
 165 170 175  
 Ser Leu Ser Met Phe Arg Asn Ala Val Ser Leu Met Asn Pro Asp Thr  
 180 185 190  
 Arg Ile Val Leu Lys Val Val Arg Glu Gly Lys Val Ile Glu Ile Pro  
 195 200 205  
 Val Thr Val Ser Gln Ala Pro Lys Glu Asp Gly Met Ser Ala Leu Gln  
 210 215 220  
 Arg Val Gly Ile Arg Val Gln Asn Leu Thr Pro Glu Thr Ala Lys Lys  
 225 230 235 240  
 Leu Gly Ile Ala Pro Glu Thr Lys Gly Ile Leu Ile Ile Ser Val Glu  
 245 250 255  
 Pro Gly Ser Val Ala Ala Ser Ser Gly Ile Ala Pro Gly Gln Leu Ile  
 260 265 270  
 Leu Ala Val Asn Arg Gln Lys Val Ser Ser Ile Glu Asp Leu Asn Arg  
 275 280 285  
 Thr Leu Lys Asp Ser Asn Asn Glu Asn Ile Leu Leu Met Val Ser Gln  
 290 295 300  
 Gly Asp Val Ile Arg Phe Ile Ala Leu Lys Pro Glu Glu  
 305 310 315

&lt;210&gt;1053

&lt;211&gt;104

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1053

Arg Phe Ser Tyr Glu Ile Leu Pro Gly Gly Ser Arg Gly Trp Arg Ser  
 1 5 10 15  
 Ser Ala Asn Leu Pro Ile Val Lys Val Leu Gln Glu Ile Tyr Ser Asp  
 20 25 30  
 Leu Tyr Asn Glu Glu Cys Leu Arg Leu Val Met Pro Ala Thr Ile Pro  
 35 40 45  
 Ile Gly Pro Leu Leu Gly Glu Ala Ala Gln Thr Ser Pro Ile Ile Cys  
 50 55 60  
 Gly Thr Ser Tyr Leu Ser Asp Asp Ile His Ala Ala Glu Glu His Phe  
 65 70 75 80  
 Ser Met Asp Gln Leu Lys Lys Gly Phe Leu Ser Ile Cys Gln Leu Leu  
 85 90 95  
 Asp Lys Leu Pro Lys Ile Lys Glu  
 100

&lt;210&gt;1054

&lt;211&gt;393

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1054

Met Leu Asn His Ala Lys Lys His Ala Lys Pro Tyr Val Leu Ile Phe  
 1 5 10 15  
 Phe Ser Thr Lys Asp Lys Leu Ser Tyr Cys Asp Ile Ile Phe Asn Asn  
 20 25 30  
 Cys Ser Gly Lys Pro Met Asn Leu Asp Ser Lys His Phe Asp Ile Asn  
 35 40 45  
 Ser Ala Asn Phe Leu Glu Glu Phe Ala Lys Phe Ile Ser Phe Pro Ser  
 50 55 60  
 Ile Ser Ala Asp Ser Asp His Leu Gln Asp Cys Glu Asn Cys Ala His  
 65 70 75 80  
 Phe Leu Val Asp His Val Asn Lys Ile Phe Asp Val Glu Leu Trp Glu  
 85 90 95  
 Thr Pro Gly His Pro Pro Ile Ile Tyr Ala Ser Tyr Lys Ser Glu Asp  
 100 105 110  
 Pro Leu Ser Pro Thr Leu Met Leu Tyr Asn His Tyr Asp Val Gln Pro  
 115 120 125  
 Ala Gln Leu Ser Asp Gly Trp Lys Gly Asp Pro Phe Ile Leu Arg Glu  
 130 135 140  
 Glu Asn Gly Asn Leu Tyr Ala Arg Gly Ala Ser Asp Asn Lys Gly Gln  
 145 150 155 160

Cys Phe Tyr Thr Leu Lys Ala Leu Gln His Tyr Tyr Glu Ser Gln Gly  
 165 170 175  
 Asn Phe Pro Leu Asn Ile Ile Trp Leu Ile Glu Gly Glu Glu Glu Ser  
 180 185 190  
 Gly Ser Leu Ala Leu Phe Thr Trp Leu Glu Lys Lys Lys Glu Ala Leu  
 195 200 205  
 Arg Ala Asp Tyr Leu Leu Ile Val Asp Gly Gly Phe Leu Ser Glu Lys  
 210 215 220  
 His Pro Tyr Val Ser Ile Gly Ala Arg Gly Ile Val Ser Met Lys Ile  
 225 230 235 240  
 Ser Leu Glu Glu Gly Asn Lys Asp Met His Ser Gly Val Leu Gly Gly  
 245 250 255  
 Ile Ala Tyr Asn Thr Asn Arg Ala Leu Ser Glu Ile Leu Ser Ser Leu  
 260 265 270  
 His His Pro Asp Asn Ser Ile Ala Ile Glu Gly Phe Tyr Asp Asp Leu  
 275 280 285  
 Ala Leu Pro Ser Asp Ser Asp Arg Pro Asp Leu Pro Lys Ser Asp Thr  
 290 295 300  
 Leu Arg Glu Cys Glu Glu Asn Leu Gly Phe Arg Pro Gln Gly Tyr Glu  
 305 310 315 320  
 Ala Ser Tyr Ser Pro Glu Glu Ser Ala Leu Arg Pro Thr Val Glu Ile  
 325 330 335  
 Asn Gly Ile Ser Gly Gly Tyr Thr Gly Pro Gly Phe Lys Thr Val Ile  
 340 345 350  
 Pro Tyr Arg Ala Thr Ala Tyr Leu Ser Cys Arg Leu Val Pro Asn Gln  
 355 360 365  
 Asp Pro Asp Lys Ala Ala His Gln Val Ile His His Leu Lys Gln Gln  
 370 375 380  
 Val Pro Ser Ser Leu Lys Val Leu Leu  
 385 390

&lt;210&gt;1055

&lt;211&gt;978

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1055

Val Thr Glu Ser Met Lys Ala Gly Asp Thr Tyr Arg Asn Phe Ile Ile  
 1 5 10 15  
 Lys Ser Cys Lys Asp Leu Pro Glu Ile Glu Ser Lys Leu Leu Glu Ala  
 20 25 30  
 Glu His Lys Pro Thr Gly Ala Ser Ile Met Met Ile Val Asn Asn Asp  
 35 40 45  
 Glu Glu Asn Val Phe Asn Ile Cys Phe Arg Thr Cys Pro Gln Thr Ser  
 50 55 60  
 Asn Gly Val Ala His Val Leu Glu His Met Val Leu Cys Gly Ser Glu  
 65 70 75 80  
 Asn Tyr Pro Val Arg Asp Pro Phe Phe Ser Met Thr Arg Arg Ser Leu  
 85 90 95  
 Asn Thr Phe Ile Asn Ala Phe Thr Gly Pro Asp Phe Thr Cys Tyr Pro  
 100 105 110  
 Ala Ala Ser Gln Ile Pro Glu Asp Phe Tyr Asn Leu Leu Ser Val Tyr  
 115 120 125  
 Ile Asp Ala Val Phe His Pro Leu Leu Thr Lys Gln Ser Phe Leu Gln  
 130 135 140  
 Glu Ala Trp Arg Tyr Glu Phe Asn Ser Glu Asn His Leu Cys Tyr Thr  
 145 150 155 160  
 Gly Val Val Phe Asn Glu Met Lys Gly Ala Met Met Ser Gly Glu Ala  
 165 170 175  
 Arg Leu Ser Glu Ala Leu Asn Ala Ala Ile Phe Pro Ser Val Thr Tyr  
 180 185 190  
 Gly Val Asn Ser Gly Gly Glu Pro Arg Glu Ile Val Thr Leu Ser His  
 195 200 205  
 Glu Asp Val Arg Ala Phe His Gln Ser Gln Tyr Ser Ile Asn Arg Cys  
 210 215 220  
 Leu Phe Tyr Phe Tyr Gly Asn Ile Lys Pro Ser Arg His Leu Asp Phe

225 230 235 240  
 Leu Glu Glu Lys Leu Leu Arg Gln Ala Thr Lys Leu Glu Lys Gln Ala  
 245 250 255  
 Val Ser Val Pro Leu Gln Lys Arg Phe Lys Glu Pro Val Arg Asn Ile  
 260 265 270  
 Leu Thr Tyr Pro Val Asp His Gln Glu Glu Asp Lys Val Leu Phe Gly  
 275 280 285  
 Ile Ser Trp Leu Thr Cys Ser Ile Leu Glu Gln Gln Glu Leu Leu Ala  
 290 295 300  
 Leu His Val Leu Glu Ile Ile Leu Met Gly Thr Asp Ala Ser Pro Leu  
 305 310 315 320  
 Lys Ser Arg Leu Leu Lys Ser Gly Phe Cys Lys Gln Thr Glu Met Ser  
 325 330 335  
 Ile Glu Asn Asp Ile Arg Glu Ile Pro Met Thr Leu Val Cys Lys Gly  
 340 345 350  
 Cys Ser Pro Ala Gly Ala Gln Lys Leu Glu Ala Leu Ile Phe Ala Ser  
 355 360 365  
 Leu Glu Glu Ile Ile Arg Glu Gly Ile Ser Glu Asn Ile Val Glu Gly  
 370 375 380  
 Ala Val His Gln Leu Glu Leu Ser Arg Lys Glu Ile Thr Gly Tyr Ser  
 385 390 395 400  
 Leu Pro Tyr Gly Leu Ser Leu Phe Phe Arg Ser Gly Leu Leu Lys Gln  
 405 410 415  
 His Gly Gly Ser Ala Glu Asp Gly Leu Arg Ile His Asn Leu Phe Ser  
 420 425 430  
 Glu Leu Arg Asn Ser Leu Lys Asn Ser Asp Tyr Leu Ala Lys Leu Ile  
 435 440 445  
 Arg Lys Tyr Phe Leu Asp Asn Pro His Phe Ala Arg Val Ile Leu Leu  
 450 455 460  
 Pro Asp Thr Glu Leu Val Ala Lys Asp Asn Lys Asp Glu Gln Gln Leu  
 465 470 475 480  
 Leu Leu Ser Val Ser Glu Lys Leu Thr Asp Glu Asn Lys Glu Lys Ile  
 485 490 495  
 Gln Gln Asn Val Arg Glu Leu Thr Glu Ser Gln Glu Gln Lys Glu Asp  
 500 505 510  
 Leu Asn Gly Ile Leu Pro Asn Leu Ala Leu Asp Lys Val Pro Thr Ser  
 515 520 525  
 Gly Lys Glu Phe Pro Leu Ile Lys Glu Gly Leu Ser Gln Gly Glu Val  
 530 535 540  
 Leu His His Glu Cys Phe Thr Asn Asp Ile Val Phe Ile Asp Val Val  
 545 550 555 560  
 Leu Asp Ile Pro Pro Leu Ser Gly Glu Glu Leu Pro Trp Leu Arg Leu  
 565 570 575  
 Leu Val Phe Leu Met Leu Gln Leu Gly Cys Gly Gly Arg Ser Tyr Lys  
 580 585 590  
 Glu His Leu Glu Phe Leu Leu Glu His Thr Gly Gly Val Asp Val Ser  
 595 600 605  
 Tyr Asp Phe Ser Pro His Ala Asn Lys Asn Ser Phe Leu Ser Pro Ser  
 610 615 620  
 Val Ser Ile Arg Gly Lys Ala Leu Ser Ser Lys Ser Glu Lys Leu Cys  
 625 630 635 640  
 Gly Ile Val Ser Asp Met Leu Thr Ser Val Asp Phe Thr Asp Ile Pro  
 645 650 655  
 Arg Ile Arg Glu Leu Leu Met Gln His Asn Glu Ala Leu Thr Asn Ser  
 660 665 670  
 Val Arg Asn Ser Pro Met Ser Tyr Ala Val Ser Met Ala Cys Ser Gly  
 675 680 685  
 Asn Ser Ile Thr Gly Ala Met Ser Tyr Leu Thr Thr Gly Leu Pro Tyr  
 690 695 700  
 Val Lys Lys Ile Arg Glu Leu Thr Lys Asn Phe Asp Gln Asn Ile Asp  
 705 710 715 720  
 Glu Ala Val Val Ile Leu Gln Arg Leu Tyr Thr Lys Cys Phe Ser Gly  
 725 730 735  
 Lys Arg Gln Ile Val Ile Ser Gly Ser Ala His Asn Tyr Gln Gln Leu



740 745 750  
 Lys Asp Asn Lys Phe Tyr Gly Leu Leu Asp Tyr Leu Ile Val Ile Pro  
 755 760 765  
 Glu Pro Trp Glu Asn Pro Ser Ile Asn Leu Tyr Val Thr Ser Arg Gly  
 770 775 780  
 Leu His Ile Pro Ala Arg Ala Ala Phe Asn Ala Leu Ala Phe Pro Ile  
 785 790 795 800  
 Gly Asp Ile Ala Tyr Asp His Pro Asp Ala Ala Ala Leu Thr Val Ala  
 805 810 815  
 Ala Glu Ile Leu Asp Asn Val Val Leu His Thr Lys Ile Arg Glu Gln  
 820 825 830  
 Gly Gly Ala Tyr Gly Ser Gly Ala Ala Ala Asn Leu Ser Arg Gly Ser  
 835 840 845  
 Phe Tyr Cys Tyr Ser Tyr Arg Asp Pro Glu Ile Ala Thr Thr Tyr Lys  
 850 855 860  
 Thr Phe Leu Lys Gly Val Ser Glu Ile Ala Ser Gly Asn Phe Thr Lys  
 865 870 875 880  
 Glu Asp Ile Tyr Glu Gly Ala Leu Gly Val Val Gln Gly Leu Asp Met  
 885 890 895  
 Pro Val Ala Pro Gly Ser Arg Ala Ser Val Ala Phe Tyr Arg Leu Lys  
 900 905 910  
 Ser Gly Arg Ile Pro Val Leu Arg Gln Ala Phe Arg Arg Ser Val Leu  
 915 920 925  
 Glu Val Thr Lys Glu His Ile Cys Met Val Met Asp Lys Tyr Leu Glu  
 930 935 940  
 Ser Thr Val Gln Glu Thr Thr Leu Ile Ser Phe Ala Gly Glu Glu Met  
 945 950 955 960  
 Leu Arg Asn Asn Val Leu Thr Leu Asp Lys Asp Phe Pro Ile Val Pro  
 965 970 975  
 Ala Ile

&lt;210&gt;1056

&lt;211&gt;418

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1056

Lys Lys Glu Leu Ala Ser Val Met Asn Leu Pro Val Ser Leu Ala Cys  
 1 5 10 15  
 Leu Leu Leu Ser Gly Cys Val Phe Phe Leu Gly Val Phe Val Ser Ser  
 20 25 30  
 Ser Leu Tyr Ala Arg Lys Lys Arg Ala Phe Leu Glu Lys Ile Gln Lys  
 35 40 45  
 Leu Glu His Glu Asn Gln Leu Leu Gln Thr Ser Leu Asn Leu Ser Arg  
 50 55 60  
 His Gln Glu Gln Leu Ile Glu Asp Phe Ser Asn Arg Leu Ala Leu Ser  
 65 70 75 80  
 Ser His Lys Leu Ile Lys Asp Met Lys Glu Glu Ala Gln Asn Tyr Phe  
 85 90 95  
 Gly Asp Thr Ser Lys Ser Phe Gln Ser Ile Leu Ser Pro Ile Gln Thr  
 100 105 110  
 Thr Leu Thr Thr Phe Lys Gln Ser Leu Glu Thr Phe Glu Thr Lys His  
 115 120 125  
 Ala Glu Asp Arg Gly Arg Leu Lys Glu Gln Ile Ser Gln Leu Leu Ala  
 130 135 140  
 Val Glu Lys Lys Leu Glu His Glu Thr His Val Leu Thr Asp Ile Leu  
 145 150 155 160  
 Lys His Pro Gly Ser Arg Gly Arg Trp Gly Glu Ile Gln Leu Glu Arg  
 165 170 175  
 Ile Leu Glu Leu Ala Gly Met Leu Lys Tyr Cys Asp Tyr Asp Ser Gln  
 180 185 190  
 Thr Thr Ser Ala Gln Gly Ala Phe Arg Ala Asp Ile Ile Ile Arg Leu  
 195 200 205  
 Pro Gln Asp Arg Cys Leu Ile Ile Asp Ala Lys Ala Pro Ile Ser Asp  
 210 215 220

Ser Tyr Phe Ser Val Glu Glu Ile Asp Lys Gly Asp Leu Val Asp Lys  
 225 230 235 240  
 Ile Lys Glu His Ile Lys Thr Leu Lys Ser Lys Ser Tyr Trp Glu Lys  
 245 250 255  
 Phe His Gln Ser Pro Glu Tyr Val Ile Leu Phe Leu Pro Gly Glu Ser  
 260 265 270  
 Leu Phe Asn Asp Ala Ile Arg Leu Ala Pro Glu Leu Met Glu Ile Gly  
 275 280 285  
 Ala Ser Ser Asn Val Ile Leu Ser Ser Pro Leu Thr Leu Ala Leu  
 290 295 300  
 Leu Lys Thr Ile Ala Tyr Met Trp Lys Gln Glu Asn Leu Gln Lys Gln  
 305 310 315 320  
 Ile Gln Glu Val Ser Leu Leu Gly Lys Glu Leu His Arg Arg Leu Gln  
 325 330 335  
 Val Val Phe Thr His Phe Gln Lys Ile Gly Lys Asn Leu Asn Gln Thr  
 340 345 350  
 Val Gln Ser Tyr Asn Asp Met Thr Ser Ser Phe Gln Tyr Arg Val Leu  
 355 360 365  
 Pro Thr Leu Arg Lys Phe Glu Gly Leu Glu Thr Ser Ser Ser His Gln  
 370 375 380  
 Ile Glu Glu Pro Thr Pro Ile Glu Ser Leu Ala Thr Ser Phe Pro His  
 385 390 395 400  
 Thr Cys Asp Ile Asp Thr Asn Leu Ala Val Ile Glu Ser Leu Glu Lys  
 405 410 415  
 Gln Asp

&lt;210&gt;1057

&lt;211&gt;265

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1057

Met Ala Gly Leu Asp Leu Glu Ala Arg Gly Lys Arg Arg Val Val Thr  
 1 5 10 15  
 Pro Asn Ala Ile Thr Ala Phe Gly Leu Cys Cys Gly Leu Phe Ile Ile  
 20 25 30  
 Phe Lys Ser Val Leu Arg Thr Ser Ser Ser Val Glu Leu Phe His Arg  
 35 40 45  
 Leu Gln Gly Leu Ser Leu Leu Ile Ser Ala Met Ile Ala Asp Phe  
 50 55 60  
 Ser Asp Gly Ala Ile Ala Arg Ile Met Lys Ala Glu Ser Ala Phe Gly  
 65 70 75 80  
 Ala Gln Phe Asp Ser Leu Ser Asp Ala Val Thr Phe Gly Ile Ala Pro  
 85 90 95  
 Pro Leu Ile Ala Ile Lys Ser Leu Asp Gly Ile Tyr Val Gly Asn Phe  
 100 105 110  
 Phe Ser Ser Leu Leu Leu Ile Thr Ser Ile Ile Tyr Ser Leu Cys Gly  
 115 120 125  
 Val Leu Arg Leu Val Arg Tyr Asn Leu Phe Ser Gln Lys Thr Val Asp  
 130 135 140  
 Val Ser Lys Pro Tyr Cys Phe Ile Gly Leu Pro Ile Pro Ala Ala Ala  
 145 150 155 160  
 Ala Ser Ile Val Ser Leu Ala Leu Phe Leu Ala Ser Asp Phe Phe Pro  
 165 170 175  
 Asp Leu Pro Ala Gln Leu Arg Val Gly Leu Leu Ser Phe Ala Leu Leu  
 180 185 190  
 Phe Ile Gly Gly Leu Met Ile Ser Pro Trp Lys Phe Pro Gly Val Lys  
 195 200 205  
 His Phe Arg Phe Asn Val Ser Ser Phe Leu Leu Val Val Thr Ile Gly  
 210 215 220  
 Leu Ala Ala Cys Leu Phe Ser Gly Leu Val Asp His Phe Val Glu  
 225 230 235 240  
 Val Phe Phe Leu Val Ser Trp Leu Tyr Thr Leu Val Gly Phe Pro Ile  
 245 250 255  
 Phe Ser Ile Ile Tyr Arg Lys Lys Ser

260

265

&lt;210&gt;1058

&lt;211&gt;1047

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1058

Gly Lys Val Met Val Glu Val Glu Glu Lys His Tyr Thr Ile Val Lys  
 1 5 10 15  
 Arg Asn Gly Met Phe Val Pro Phe Asn Gln Asp Arg Ile Phe Gln Ala  
 20 25 30  
 Leu Glu Ala Ala Phe Arg Asp Thr Arg Ser Leu Glu Thr Ser Ser Pro  
 35 40 45  
 Leu Pro Lys Asp Leu Glu Glu Ser Ile Ala Gln Ile Thr His Lys Val  
 50 55 60  
 Val Lys Glu Val Leu Ala Lys Ile Ser Glu Gly Gln Val Val Thr Val  
 65 70 75 80  
 Glu Arg Ile Gln Asp Leu Val Glu Ser Gln Leu Tyr Ile Ser Gly Leu  
 85 90 95  
 Gln Asp Val Ala Arg Asp Tyr Ile Val Tyr Arg Asp Gln Arg Lys Ala  
 100 105 110  
 Glu Arg Gly Asn Ser Ser Ser Ile Ile Ala Ile Ile Arg Arg Asp Gly  
 115 120 125  
 Gly Ser Ala Lys Phe Asn Pro Met Lys Ile Ser Ala Ala Leu Glu Lys  
 130 135 140  
 Ala Phe Arg Ala Thr Leu Gln Ile Asn Gly Met Thr Pro Pro Ala Thr  
 145 150 155 160  
 Leu Ser Glu Ile Asn Asp Leu Thr Leu Arg Ile Val Glu Asp Val Leu  
 165 170 175  
 Ser Leu His Gly Glu Glu Ala Ile Asn Leu Glu Glu Ile Gln Asp Ile  
 180 185 190  
 Val Glu Lys Gln Leu Met Val Ala Gly Tyr Tyr Asp Val Ala Lys Asn  
 195 200 205  
 Tyr Ile Leu Tyr Arg Glu Ala Arg Ala Arg Ala Asn Lys Asp  
 210 215 220  
 Gln Asp Gly Gln Glu Glu Phe Val Pro Gln Glu Glu Thr Tyr Val Val  
 225 230 235 240  
 Gln Lys Glu Asp Gly Thr Thr Tyr Leu Leu Arg Lys Thr Asp Leu Glu  
 245 250 255  
 Lys Arg Phe Ser Trp Ala Cys Lys Arg Phe Pro Lys Thr Thr Asp Ser  
 260 265 270  
 Gln Leu Leu Ala Asp Met Ala Phe Met Asn Leu Tyr Ser Gly Ile Lys  
 275 280 285  
 Glu Asp Glu Val Thr Thr Ala Cys Ile Met Ala Ala Arg Ala Asn Ile  
 290 295 300  
 Glu Arg Glu Pro Asp Tyr Ala Phe Ile Ala Ala Glu Leu Leu Thr Ser  
 305 310 315 320  
 Ser Leu Tyr Glu Glu Thr Leu Gly Cys Ser Ser Gln Asp Pro Asn Leu  
 325 330 335  
 Ser Glu Ile His Lys Lys His Phe Lys Glu Tyr Ile Leu Asn Gly Glu  
 340 345 350  
 Glu Tyr Arg Leu Asn Pro Gln Leu Lys Asp Tyr Asp Leu Asp Ala Leu  
 355 360 365  
 Ser Glu Val Leu Asp Leu Ser Arg Asp Gln Gln Phe Ser Tyr Met Gly  
 370 375 380  
 Val Gln Asn Leu Tyr Asp Arg Tyr Phe Asn Leu His Glu Gly Arg Arg  
 385 390 395 400  
 Leu Glu Thr Ala Gln Ile Phe Trp Met Arg Val Ser Met Gly Leu Ala  
 405 410 415  
 Leu Asn Glu Gly Glu Gln Lys Asn Phe Trp Ala Ile Thr Phe Tyr Asn  
 420 425 430  
 Leu Leu Ser Thr Phe Arg Tyr Thr Pro Ala Thr Pro Thr Leu Phe Asn  
 435 440 445  
 Ser Gly Met Arg His Ser Gln Leu Ser Ser Cys Tyr Leu Ser Thr Val  
 450 455 460

Lys Asp Asp Leu Ser His Ile Tyr Lys Val Ile Ser Asp Asn Ala Leu  
 465 470 475 480  
 Leu Ser Lys Trp Ala Gly Gly Ile Gly Asn Asp Trp Thr Asp Val Arg  
 485 490 495  
 Ala Thr Gly Ala Val Ile Lys Gly Thr Asn Gly Lys Ser Gln Gly Val  
 500 505 510  
 Ile Pro Phe Ile Lys Val Ala Asn Asp Thr Ala Ile Ala Val Asn Gln  
 515 520 525  
 Gly Gly Lys Arg Lys Gly Ala Met Cys Val Tyr Leu Glu Asn Trp His  
 530 535 540  
 Leu Asp Tyr Glu Asp Phe Leu Glu Leu Arg Lys Asn Thr Gly Asp Glu  
 545 550 555 560  
 Arg Arg Arg Thr His Asp Ile Asn Thr Ala Ser Trp Ile Pro Asp Leu  
 565 570 575  
 Phe Phe Lys Arg Leu Glu Lys Lys Gly Met Trp Thr Leu Phe Ser Pro  
 580 585 590  
 Asp Asp Val Pro Gly Leu His Glu Ala Tyr Gly Leu Glu Phe Glu Lys  
 595 600 605  
 Leu Tyr Glu Glu Tyr Glu Arg Lys Val Glu Ser Gly Glu Ile Arg Leu  
 610 615 620  
 Tyr Lys Lys Val Glu Ala Glu Val Leu Trp Arg Lys Met Leu Ser Met  
 625 630 635 640  
 Leu Tyr Glu Thr Gly His Pro Trp Ile Thr Phe Lys Asp Pro Ser Asn  
 645 650 655  
 Ile Arg Ser Asn Gln Asp His Val Gly Val Val Arg Cys Ser Asn Leu  
 660 665 670  
 Cys Thr Glu Ile Leu Leu Asn Cys Ser Glu Ser Glu Thr Ala Val Cys  
 675 680 685  
 Asn Leu Gly Ser Ile Asn Leu Val Glu His Ile Arg Asn Asp Lys Leu  
 690 695 700  
 Asp Glu Glu Lys Leu Lys Glu Thr Ile Ser Ile Ala Ile Arg Ile Leu  
 705 710 715 720  
 Asp Asn Val Ile Asp Leu Asn Phe Tyr Pro Thr Pro Glu Ala Lys Gln  
 725 730 735  
 Ala Asn Leu Thr His Arg Ala Val Gly Leu Gly Val Met Gly Phe Gln  
 740 745 750  
 Asp Val Leu Tyr Glu Leu Asn Ile Ser Tyr Ala Ser Gln Glu Ala Val  
 755 760 765  
 Glu Phe Ser Asp Glu Cys Ser Glu Ile Ile Ala Tyr Tyr Ala Ile Leu  
 770 775 780  
 Ala Ser Ser Leu Leu Ala Lys Glu Arg Gly Thr Tyr Ala Ser Tyr Ser  
 785 790 795 800  
 Gly Ser Lys Trp Asp Arg Gly Tyr Leu Pro Leu Asp Thr Ile Glu Leu  
 805 810 815  
 Leu Lys Glu Thr Arg Gly Glu His Asn Val Leu Val Asp Thr Ser Ser  
 820 825 830  
 Lys Lys Asp Trp Thr Pro Val Arg Asp Thr Ile Gln Lys Tyr Gly Met  
 835 840 845  
 Arg Asn Ser Gln Val Met Ala Ile Ala Pro Thr Ala Thr Ile Ser Asn  
 850 855 860  
 Ile Ile Gly Val Thr Gln Ser Ile Glu Pro Met Tyr Lys His Leu Phe  
 865 870 875 880  
 Val Lys Ser Asn Leu Ser Gly Glu Phe Thr Ile Pro Asn Thr Tyr Leu  
 885 890 895  
 Ile Lys Lys Leu Lys Glu Leu Gly Leu Trp Asp Ala Glu Met Leu Asp  
 900 905 910  
 Asp Leu Lys Tyr Phe Asp Gly Ser Leu Leu Glu Ile Glu Arg Ile Pro  
 915 920 925  
 Asn His Leu Lys Lys Leu Phe Leu Thr Ala Phe Glu Ile Glu Pro Glu  
 930 935 940  
 Trp Ile Ile Glu Cys Thr Ser Arg Arg Gln Lys Trp Ile Asp Met Gly  
 945 950 955 960  
 Val Ser Leu Asn Leu Tyr Leu Ala Glu Pro Asp Gly Lys Lys Leu Ser  
 965 970 975

Asn Met Tyr Leu Thr Ala Trp Lys Lys Gly Leu Lys Thr Thr Tyr Tyr  
 980 985 990  
 Leu Arg Ser Gln Ala Ala Thr Ser Val Glu Lys Ser Phe Ile Asp Ile  
 995 1000 1005  
 Asn Lys Arg Gly Ile Gln Pro Arg Trp Met Lys Asn Lys Ser Ala Ser  
 1010 1015 1020  
 Thr Ser Ile Val Val Glu Arg Lys Thr Thr Pro Val Cys Ser Met Glu  
 1025 1030 1035 1040  
 Glu Gly Cys Glu Ser Cys Gln  
 1045

&lt;210&gt;1059

&lt;211&gt;365

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1059

Leu Phe Asn Gly Arg Arg Leu Arg Ile Leu Ser Ile Thr Glu Lys Arg  
 1 5 10 15  
 Gly Ala Lys Met Glu Ala Asp Ile Leu Asp Gly Lys Leu Lys Arg Val  
 20 25 30  
 Glu Val Ser Lys Lys Gly Leu Val Asn Cys Asn Gln Val Asp Val Asn  
 35 40 45  
 Gln Leu Val Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn  
 50 55 60  
 Gly Cys Ala Asn Asn Trp Leu Pro Thr Glu Val Pro Met Ala Arg Asp  
 65 70 75 80  
 Ile Glu Leu Trp Lys Ser Asp Glu Leu Ser Glu Asp Glu Arg Arg Val  
 85 90 95  
 Ile Leu Leu Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly  
 100 105 110  
 Asn Asn Ile Val Leu Ala Ile Phe Lys His Ile Thr Asn Pro Glu Ala  
 115 120 125  
 Arg Gln Tyr Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His  
 130 135 140  
 Thr Phe Leu Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Gly Glu Val  
 145 150 155 160  
 Phe Asn Ala Tyr Asn Glu Arg Ala Ser Ile Arg Ala Lys Asp Asp Phe  
 165 170 175  
 Gln Met Thr Leu Thr Val Asp Val Leu Asp Pro Asn Phe Ser Val Gln  
 180 185 190  
 Ser Ser Glu Gly Leu Gly Gln Phe Ile Lys Asn Leu Val Gly Tyr Tyr  
 195 200 205  
 Ile Ile Met Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu  
 210 215 220  
 Ser Phe His Arg Gln Asn Lys Met Thr Gly Ile Gly Glu Gln Tyr Gln  
 225 230 235 240  
 Tyr Ile Leu Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu  
 245 250 255  
 Ile Asn Gly Ile Lys Glu Glu Asn Pro Glu Val Trp Thr Thr Glu Leu  
 260 265 270  
 Gln Glu Glu Ile Val Ala Leu Ile Glu Lys Ala Val Glu Leu Glu Ile  
 275 280 285  
 Glu Tyr Ala Lys Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ser  
 290 295 300  
 Ser Met Phe Ile Asp Tyr Val Arg His Ile Ala Asp Arg Arg Leu Glu  
 305 310 315 320  
 Arg Ile Gly Leu Lys Pro Ile Tyr His Ser Arg Asn Pro Phe Pro Trp  
 325 330 335  
 Met Ser Glu Thr Met Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr  
 340 345 350  
 Arg Val Thr Glu Tyr Gln Thr Ala Gly Asn Leu Ser Trp  
 355 360 365

&lt;210&gt;1060

&lt;211&gt;228

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1060

Phe Leu Leu Phe Met Lys Pro Gln Asp Leu Ser Pro Pro Phe Leu Trp  
 1 5 10 15  
 Lys Glu Arg Arg Pro Cys Ile Gln Asp Gly Val Leu Tyr Val Pro Arg  
 20 25 30  
 His Tyr Phe Glu His Gln Asn Phe Ser Thr Ser Tyr His Gln Glu Phe  
 35 40 45  
 Phe Gln Asn His Thr Ser Ile Ala Cys Glu Leu Cys Ser Gly Asn Gly  
 50 55 60  
 Asp Trp Val Val Ala Gln Ala Gln Lys Asp Pro Gln Val Leu Trp Ile  
 65 70 75 80  
 Ala Val Glu Gln Arg Phe Asp Arg Val Arg Lys Ile Trp Ser Lys Met  
 85 90 95  
 Ile Asn His Gln Ile Gln Asn Leu Arg Ile Val Cys Gly Thr Ala Glu  
 100 105 110  
 Thr Phe Phe Gln Tyr Tyr Val Pro Asp Gln Phe Leu Gln Arg Leu Val  
 115 120 125  
 Val Asn Phe Pro Asp Pro Trp Pro Lys Met Arg His Arg Lys His Arg  
 130 135 140  
 Leu Leu Gln Pro Ser Phe Val Gln Glu Ile Ser Arg Ser Leu Gln Asp  
 145 150 155 160  
 Ser Ala Val Phe Ala Leu Ala Thr Asp Asp Lys Thr Tyr Leu Leu Glu  
 165 170 175  
 Ser Ile Glu Ala Leu Gln Thr His Leu Ala Pro Arg Met Glu Thr Pro  
 180 185 190  
 Tyr Tyr Ile Lys Met Thr Asp Thr Tyr Gly Asn Ser Trp Phe Glu Asn  
 195 200 205  
 Leu Trp Arg Thr Lys Gly Gln Glu Ile Phe Tyr Thr Glu Phe Ile Lys  
 210 215 220  
 Lys Ala Gly Ile  
 225

&lt;210&gt;1061

&lt;211&gt;175

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1061

Met Phe Ala Tyr Arg Thr Leu Leu Thr His Asn Val Val Gln Val Ser  
 1 5 10 15  
 His Glu Ile Phe Lys Thr Thr Val Val Pro Gly Asp Thr Val Ile Asp  
 20 25 30  
 Ala Thr Cys Gly Asn Gly Asn Asp Ser Leu Phe Leu Ala Arg Leu Leu  
 35 40 45  
 Gln Gly Glu Gly Arg Leu Val Val Tyr Asp Ile Gln Lys Glu Ala Leu  
 50 55 60  
 Ser Asn Ala Leu Leu Leu Phe Glu Thr His Leu Ser Glu Gln Glu Arg  
 65 70 75 80  
 Ser Val Ile Glu Met Lys Glu Gln Ser His Glu His Ile Leu Glu Lys  
 85 90 95  
 Asp Val Lys Leu Ile His Tyr Asn Leu Gly Tyr Leu Pro Lys Gly Asn  
 100 105 110  
 Lys Glu Ile Thr Thr Leu Ala Arg Thr Thr Glu Ile Ser Leu Glu Tyr  
 115 120 125  
 Ala Leu Asn Ile Val Arg Pro Asp Gly Leu Ile Thr Val Val Cys Tyr  
 130 135 140  
 Pro Gly His Pro Glu Gly Glu Lys Glu Thr His Ser Val Glu Ser Leu  
 145 150 155 160  
 Ala Gln Arg Leu His Pro Lys Glu Trp Cys Val Ser His Phe Met  
 165 170 175

&lt;210&gt;1062

&lt;211&gt;97

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1062

Arg Ser Pro Ile Arg Ser Leu Leu Leu Ala Val Phe Ser Val Ile Leu  
 1 5 10 15  
 Lys Glu Leu Leu Leu Ala Ser Leu Leu Thr Gln Pro Gly Leu Lys Gly  
 20 25 30  
 Leu Ala Ile Gly Gly Ala Gln Ile Ser Pro Leu His Ala Asn Phe Ile  
 35 40 45  
 Ile Asn Thr Gly Lys Ala Thr Ser Asp Glu Val Lys Gln Leu Ile Ala  
 50 55 60  
 Ile Ile Gln Ser Thr Leu Lys Thr Gln Gly Ile Asp Leu Glu His Glu  
 65 70 75 80  
 Ile Arg Ile Ile Pro Tyr Gln Pro Lys Ile His Ser Pro Val Ser Glu  
 85 90 95

Lys

&lt;210&gt;1063

&lt;211&gt;263

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1063

Met Lys Glu Ala Ala Pro Met His Phe Pro Phe Pro Val Arg Arg Ser  
 1 5 10 15  
 Val Trp Leu Asn Arg Tyr Ser Thr Phe Arg Ile Gly Gly Pro Ala Asn  
 20 25 30  
 Tyr Phe Lys Ala Ile His Thr Ile Glu Glu Ala Arg Glu Val Ile Arg  
 35 40 45  
 Phe Leu His Ser Ile Asn Tyr Pro Phe Leu Ile Ile Gly Lys Gly Ser  
 50 55 60  
 Asn Cys Leu Phe Asp Asp Arg Gly Phe Asp Gly Phe Val Leu Tyr Asn  
 65 70 75 80  
 Ala Ile Tyr Gly Lys Gln Phe Leu Glu Asp Ala Arg Ile Lys Ala Tyr  
 85 90 95  
 Ser Gly Leu Ser Phe Ala Ala Leu Gly Lys Ala Thr Ala Tyr Asn Gly  
 100 105 110  
 Tyr Ser Gly Leu Glu Phe Ala Ala Gly Ile Pro Gly Ser Val Gly Gly  
 115 120 125  
 Ala Ile Phe Met Asn Ala Gly Thr Asn Glu Ser Asp Ile Ser Ser Val  
 130 135 140  
 Val Arg Asn Val Glu Thr Ile Asn Ser Glu Gly Glu Leu Cys Ser Tyr  
 145 150 155 160  
 Ser Val Glu Glu Leu Glu Leu Ser Tyr Arg Ser Ser Arg Phe His Arg  
 165 170 175  
 Gln Gln Glu Phe Ile Leu Ser Ala Thr Phe Gln Leu Ser Lys Lys Gln  
 180 185 190  
 Val Ser Ala Asp His Ser Lys Ser Ile Leu Gln His Arg Leu Met Thr  
 195 200 205  
 Gln Pro Tyr Thr Gln Pro Ser Ala Gly Cys Ile Phe Arg Asn Pro Glu  
 210 215 220  
 Gly Thr Ser Ala Gly Lys Leu Ile Asp Ala Ala Trp Val Glu Gly Ile  
 225 230 235 240  
 Ser Asn Arg Arg Gly Thr Asn Phe Ser Val Ala Cys Lys Leu His Tyr  
 245 250 255  
 Gln Tyr Trp Gln Gly His Phe  
 260

&lt;210&gt;1064

&lt;211&gt;179

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1064

Leu Arg Thr Ser Leu Ala Val Lys Cys Val Leu Leu Thr Ile Phe Trp  
 1 5 10 15  
 Leu Leu Val Met Ala Thr Leu Ser Pro Glu Lys Phe Ser Gly Ser Pro  
 20 25 30  
 Ile Ser Ile Ser Lys Glu Phe Pro Gln Gln Lys Met Arg Glu Ile Ile  
 35 40 45

Leu Gln Met Leu Tyr Ala Leu Asp Met Ala Pro Ser Ala Glu Asp Ser  
 50 55 60  
 Leu Val Pro Leu Leu Met Ser Gln Thr Ala Val Ser Gln Lys His Val  
 65 70 75 80  
 Leu Val Ala Leu Asn Gln Thr Lys Ser Ile Leu Glu Lys Ser Gln Glu  
 85 90 95  
 Leu Asp Leu Ile Ile Gly Asn Ala Leu Lys Asn Lys Ser Phe Asp Ser  
 100 105 110  
 Leu Asp Leu Val Glu Lys Asn Val Leu Arg Leu Thr Leu Phe Glu His  
 115 120 125  
 Phe Tyr Ser Pro Pro Ile Asn Lys Ala Ile Leu Ile Ala Glu Ala Ile  
 130 135 140  
 Arg Leu Val Lys Lys Phe Ser Tyr Ser Glu Ala Cys Pro Phe Ile Gln  
 145 150 155 160  
 Ala Ile Leu Asn Asp Ile Phe Thr Asp Ser Ser Leu Asn Glu Asn Ser  
 165 170 175  
 Leu Ser Ile

&lt;210&gt;1065

&lt;211&gt;187

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1065

Ser Val Ala Leu Asn Phe Lys Ile Asn Arg Gln Ile Arg Ala Pro Lys  
 1 5 10 15  
 Val Arg Leu Ile Gly Ser Ala Gly Glu Gln Leu Gly Ile Leu Ala Ile  
 20 25 30  
 Lys Asp Ala Leu Asp Leu Ala Arg Glu Ala Gly Leu Asp Leu Val Glu  
 35 40 45  
 Val Ala Ser Asn Ser Glu Pro Pro Val Cys Lys Ile Met Asp Tyr Gly  
 50 55 60  
 Lys Tyr Arg Tyr Gly Leu Thr Lys Lys Glu Lys Asp Ser Lys Lys Ala  
 65 70 75 80  
 Gln His Gln Val Arg Ile Lys Glu Val Lys Leu Lys Pro Asn Ile Asp  
 85 90 95  
 Glu Asn Asp Phe Ser Thr Lys Leu Lys Gln Ala Arg Thr Phe Val Glu  
 100 105 110  
 Lys Gly Asn Lys Val Lys Ile Thr Cys Met Phe Arg Gly Arg Glu Leu  
 115 120 125  
 Ala Tyr Pro Glu His Gly Phe Lys Val Val Gln Lys Met Ser Gln Gly  
 130 135 140  
 Leu Glu Asp Ile Gly Phe Val Glu Ala Glu Pro Lys Leu Ala Gly Arg  
 145 150 155 160  
 Ser Leu Ile Cys Val Val Ala Pro Gly Thr Val Lys Thr Lys Lys Lys  
 165 170 175  
 Gln Glu Lys Ser His Ala Gln Asp Glu Asn Gln  
 180 185

&lt;210&gt;1066

&lt;211&gt;121

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1066

Met Val Arg Ala Thr Gly Ser Val Ala Ser Arg Arg Arg Arg Lys Arg  
 1 5 10 15  
 Ile Leu Lys Gln Ala Lys Gly Phe Trp Gly Asp Arg Lys Gly His Ile  
 20 25 30  
 Arg Gln Ser Arg Ser Ser Val Met Arg Ala Met Ala Phe Asn Tyr Met  
 35 40 45  
 His Arg Lys Asp Arg Lys Gly Asp Phe Arg Ser Leu Trp Ile Ala Arg  
 50 55 60  
 Leu Asn Val Ala Ser Arg Ile His Ser Leu Ser Tyr Ser Arg Leu Ile  
 65 70 75 80  
 Asn Gly Leu Lys Cys Ala Asn Ile Ser Leu Asn Arg Lys Met Leu Ser  
 85 90 95



Glu Ile Ala Ile His Asn Pro Glu Gly Phe Ala Glu Ile Ala Asn Gln  
 100 105 110  
 Ala Lys Lys Ala Leu Glu Ala Thr Val  
 115 120  
 <210>1067  
 <211>339  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1067  
 Met Glu Met Lys Glu Glu Ile Glu Ala Val Lys Gln Gln Phe His Ser  
 1 5 10 15  
 Glu Leu Asp Gln Val Asn Ser Ser Gln Ala Leu Ala Asp Leu Lys Val  
 20 25 30  
 Arg Tyr Leu Gly Lys Lys Gly Ile Phe Arg Ser Phe Ser Glu Lys Leu  
 35 40 45  
 Lys Gln Cys Thr Asp Lys Ala Lys Leu Gly Ser Leu Ile Asn Asp Phe  
 50 55 60  
 Lys Thr Tyr Val Glu Asp Leu Leu Gln Glu Lys Ser Leu Val Leu Leu  
 65 70 75 80  
 Ala Ser Glu Gln Ala Glu Ala Phe Ser Lys Glu Lys Ile Asp Ser Ser  
 85 90 95  
 Leu Pro Gly Asp Ser Gln Pro Ser Gly Gly Arg His Ile Leu Lys Ser  
 100 105 110  
 Ile Leu Asp Asp Val Val Asp Ile Phe Val His Leu Gly Phe Cys Val  
 115 120 125  
 Arg Glu Ala Pro Asn Ile Glu Ser Glu Ala Asn Asn Phe Thr Leu Leu  
 130 135 140  
 Asn Phe Thr Glu Asp His Pro Ala Arg Gln Met His Asp Thr Phe Tyr  
 145 150 155 160  
 Leu Asn Ala Thr Thr Val Leu Arg Thr His Thr Ser Asn Val Gln Ala  
 165 170 175  
 Arg Glu Leu Lys Lys Gln Gln Pro Pro Ile Lys Val Val Ala Pro Gly  
 180 185 190  
 Leu Cys Phe Arg Asn Glu Asp Ile Ser Ala Arg Ser His Val Leu Phe  
 195 200 205  
 His Gln Val Glu Ala Phe Tyr Val Asp His Asn Val Thr Phe Ser Asp  
 210 215 220  
 Leu Thr Ala Ile Leu Ser Ala Phe Tyr His Ser Phe Phe Gln Arg Lys  
 225 230 235 240  
 Thr Glu Leu Arg Phe Arg His Ser Tyr Phe Pro Phe Val Glu Pro Gly  
 245 250 255  
 Ile Glu Val Asp Val Ser Cys Glu Cys Cys Gly Lys Gly Cys Ala Leu  
 260 265 270  
 Cys Lys His Thr Gly Trp Leu Glu Val Ala Gly Ala Gly Met Ile His  
 275 280 285  
 Pro Gln Val Leu Arg Asn Gly Asn Val Asp Pro Glu Ile Tyr Ser Gly  
 290 295 300  
 Tyr Ala Val Gly Met Gly Ile Glu Arg Leu Ala Met Leu Lys Tyr Gly  
 305 310 315 320  
 Val Ser Asp Ile Arg Leu Phe Ser Glu Asn Asp Leu Arg Phe Leu Gln  
 325 330 335  
 Gln Phe Ser

&lt;210&gt;1068

&lt;211&gt;690

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1068

Leu Phe Trp Phe His Arg Gly Gly Arg Met Lys Arg Ser Arg Arg Asn  
 1 5 10 15  
 Phe Glu Gln Ala Leu Glu Asn Leu Glu Lys Leu Lys Glu Ile Ser Leu  
 20 25 30  
 Ala Thr Ser Asn Asp Ser Tyr Leu Asn Asn Pro Ala Arg Phe Asn Gln  
 35 40 45

Arg Lys Gln Thr Gly Ser Ser Val Met Glu Met Lys Glu Ala Leu Lys  
 50 55 60  
 Asn Val Glu Asn Tyr Leu Leu Glu Ile Ser Cys Val Ser Lys Ser His  
 65 70 75 80  
 Ala Asp Lys Ala Leu Lys Glu Ser Asp Phe Leu Ile Ala Gly Val Gln  
 85 90 95  
 Asn Val Phe Ser Phe Leu Glu Asn Gln Glu Asp Leu Tyr Lys Ser Leu  
 100 105 110  
 Leu Asp Glu Tyr Ser Glu Val Thr Lys Ala Tyr Asp Glu Val Lys Lys  
 115 120 125  
 Asn Leu Lys Glu Val Pro Thr Tyr Asp Leu Ser Thr Asp Glu Glu Thr  
 130 135 140  
 Glu Glu His Lys Glu Pro Glu Cys Phe Leu Asn Asn Leu Val Glu Val  
 145 150 155 160  
 Lys Arg Asp Arg Ser Tyr Glu Leu Phe Tyr Met Leu Asp Glu Gln Asp  
 165 170 175  
 Lys Arg Phe Tyr Asn Asp Ala Leu Val Gln Ile Ile Tyr Lys Gln Asn  
 180 185 190  
 Lys Leu His Glu Thr Val Asn Glu Gly Asp Pro Leu Thr Lys Thr Leu  
 195 200 205  
 Leu Trp Asn Ser Glu Glu Val Lys Asn Ile Ala Ser Ser Leu Val Ile  
 210 215 220  
 Val Asn Asp Met Pro Leu Arg Leu Phe Tyr Gln Arg Ala Leu Ser His  
 225 230 235 240  
 Leu Asp Ile Glu Ala Val Val Lys Val His Asn Ala Val Met Ala Leu  
 245 250 255  
 Phe Phe Ser Arg Tyr Glu Ala Thr Met Val Phe Lys Ser Pro Lys Lys  
 260 265 270  
 His Asn Ile Trp Tyr Phe Asn Asp Phe Leu Leu Phe Leu Arg Glu Ala  
 275 280 285  
 Trp Lys Asp Leu Asn Asn Asn Val Ile Asp Ser Gln Glu Arg Lys Gln  
 290 295 300  
 Thr Lys Leu Leu Ala Ser Ala Leu Ser Leu Gly Ile Phe Glu Ser Lys  
 305 310 315 320  
 Leu Val Phe Glu Glu Ala Ser Arg Tyr Leu Tyr Phe Asn Ile Gln Thr  
 325 330 335  
 Lys Leu Glu Asn Ala Asn Gly Lys Lys Pro Leu Ser Pro Gly Gln Tyr  
 340 345 350  
 Leu Thr Asp Ala Tyr Glu Glu Leu His Arg Leu Ile Ser Lys Tyr Pro  
 355 360 365  
 Asn Gly Pro Leu Phe Lys Ala Met Asp Arg Val Leu Glu His Glu Ser  
 370 375 380  
 Arg Pro Tyr Asp Pro Met Ile Leu Gly Ile Leu Pro Ser Leu Glu Gly  
 385 390 395 400  
 Thr Leu Lys Leu His Gly Lys Ser Ile Asp Ile Ile Arg Ser Pro Ser  
 405 410 415  
 Pro Val Thr Gln Ser Ser Ile Leu Tyr Ala Asn Cys Asn Glu Glu Phe  
 420 425 430  
 Leu Gly Phe Leu Asn Ala Lys Ala His Arg Ser Glu Val Thr Leu Val  
 435 440 445  
 Leu Asn Ile Gln Asn Arg Ile Ser Arg Lys Glu Arg Ala Arg Ser Arg  
 450 455 460  
 Val Ile Glu Glu Ala Leu Glu Gln Glu Glu His Ala Pro Tyr Val His  
 465 470 475 480  
 Ala Phe Ser Phe Pro Glu Pro Glu Glu Leu Leu Gln Asn Leu Glu Ser  
 485 490 495  
 Ile His Gly Asp Ile Glu Thr Phe Ala Asp Phe Phe Ser Ile Leu Gln  
 500 505 510  
 Glu Glu Phe His Lys Pro Leu Leu Ala Ser Ser Phe Phe Leu Thr Lys  
 515 520 525  
 Glu Leu Lys Glu Phe Val Gly Ser Phe Leu Lys Glu Lys Leu Thr Ala  
 530 535 540  
 Leu Lys Asp Ile Phe Phe Ala Lys Lys Lys Ile Leu Phe Arg Asn Asp  
 545 550 555 560

Lys Leu Leu Leu Leu His Leu Leu Ser Tyr Leu Ile Val Phe Lys Leu  
 565 570 575  
 Ile Glu Arg Thr Asn Pro Asn Ser Ile Val Val Val Ser Lys Asp Gly  
 580 585 590  
 Leu Asp Tyr Val Ser Val Phe Ile Ala Gly Phe Ala Phe Phe Ser Arg  
 595 600 605  
 Glu Ala Phe Trp Asp Glu His Ser Leu Lys Leu Leu Leu Thr Asn Val  
 610 615 620  
 Leu Ser Pro Thr Leu Val Ala Arg Asp Arg Leu Val Phe Val Ser His  
 625 630 635 640  
 Ile Glu Leu Leu Ser Lys Phe Val Asn Cys Leu Lys Lys Asn Arg Gln  
 645 650 655  
 Gly Phe Ser Ser Leu Lys Ser Phe Phe Lys Asp Asp Ile Glu Gly Trp  
 660 665 670  
 Glu Phe Thr Gly Tyr Leu His Glu Leu Thr Glu Val Ser His Lys His  
 675 680 685  
 Asn Leu  
 690  
 <210>1069  
 <211>367  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1069  
 Arg Met Leu Ile Trp Lys Arg His Leu Leu Thr Arg Phe Trp Phe Ala  
 1 5 10 15  
 Leu Thr Ser Leu Leu Val Leu Ala Leu Ile Phe Tyr Ala Ser Ile His  
 20 25 30  
 His Ser Leu His Thr Leu Lys Gly Ala Ser Thr Ala Ala Ser Gly Ala  
 35 40 45  
 Ser Val Lys Leu Ser Ile Leu Tyr Tyr Leu Ala Gln Ile Ser Leu Lys  
 50 55 60  
 Ala Glu Phe Leu Met Pro Gln Leu Val Ala Val Ala Thr Thr Ser Thr  
 65 70 75 80  
 Leu Phe Ala Met Gln Asn Lys Arg Glu Ile Ile Leu Leu Gln Ala Ser  
 85 90 95  
 Gly Leu Ser Leu Lys Ser Leu Met His Pro Leu Leu Leu Ser Gly Ala  
 100 105 110  
 Val Ile Met Met Val Leu Tyr Ala Asn Phe Gln Trp Leu His Pro Ile  
 115 120 125  
 Cys Glu Lys Ile Ser Ile Thr Lys Glu Asn Met Asp Arg Gly Thr Thr  
 130 135 140  
 Asp Lys Glu Gln Gly Lys Ile Pro Ala Leu Tyr Leu Lys Asp Gln Thr  
 145 150 155 160  
 Val Leu Leu Tyr Ser Ser Ile Glu Pro Lys Thr Leu Thr Leu Asn Asn  
 165 170 175  
 Val Phe Trp Ile Lys Asp Pro Lys Thr Ile Tyr Thr Met Glu Lys Leu  
 180 185 190  
 Ala Phe Thr Thr Leu Ser Leu Pro Ile Gly Leu Asn Val Thr Gln Phe  
 195 200 205  
 Phe Ala Asn Asp Ser Glu Asn Leu Glu Leu Lys Glu Phe Phe Asp Met  
 210 215 220  
 Lys Glu Phe Pro Glu Ile Glu Phe Asn Phe Tyr Glu Asn Pro Phe Ser  
 225 230 235 240  
 Lys Leu Phe Ser Ala Gly Asn Lys Asn Arg Leu Ser Glu Phe Phe Lys  
 245 250 255  
 Ala Ile Pro Trp Asn Ala Thr Gly Leu Gly Leu Ser Thr Gln Val Pro  
 260 265 270  
 Gln Arg Ile Leu Ser Leu Leu Ala Gln Phe Tyr Tyr Val Leu Ile Ser  
 275 280 285  
 Pro Leu Ala Cys Met Ala Ala Ile Ile Leu Ser Ala Tyr Leu Cys Leu  
 290 295 300  
 Arg Phe Ser Arg Thr Pro Thr Val Thr Leu Ala Tyr Leu Ile Pro Leu  
 305 310 315 320  
 Gly Thr Val Asn Ile Phe Phe Val Phe Leu Lys Ala Gly Ile Val Leu

325 330 335  
 Ala Ser Ser Ser Val Leu Pro Thr Leu Pro Val Met Ala Phe Pro Leu  
 340 345 350  
 Ile Val Leu Phe Leu Leu Thr Asn Tyr Ala Tyr Ala Lys Leu Gln  
 355 360 365  
 <210>1070  
 <211>358  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1070  
 Ala Met Pro Ile Leu Trp Lys Val Leu Ile Phe Arg Tyr Leu Lys Thr  
 1 5 10 15  
 Ala Ala Phe Cys Thr Leu Ser Leu Ile Cys Ile Ser Ile Ile Ser Ser  
 20 25 30  
 Leu Gln Glu Ile Val Ala Tyr Ile Ala Lys Asp Val Pro Tyr Asp Thr  
 35 40 45  
 Val Leu Arg Leu Met Ala Tyr Gln Ile Pro Tyr Leu Leu Pro Phe Ile  
 50 55 60  
 Leu Pro Gly Ser Cys Phe Val Ser Ala Phe Ser Leu Phe Arg Lys Leu  
 65 70 75 80  
 Ser Asp Asn Asn His Met Thr Phe Leu Arg Ala Ser Gly Ala Ser Gln  
 85 90 95  
 Ser Ile Ile Met Phe Pro Val Leu Met Val Ser Gly Ala Ile Cys Cys  
 100 105 110  
 Leu Asn Phe Tyr Thr Cys Ser Glu Leu Ala Ser Ile Cys Arg Tyr Gln  
 115 120 125  
 Thr Cys Lys Glu Ile Ala Asn Met Ala Met Thr Ser Pro Ala Leu Leu  
 130 135 140  
 Leu Gln Thr Leu Gln Lys Lys Glu Asn Asn Arg Ile Phe Ile Ala Val  
 145 150 155 160  
 Asp His Cys Ala Lys Ser Lys Phe Asp Asn Val Ile Val Ala Leu Lys  
 165 170 175  
 Gly Asn Asn Glu Ile Ser His Val Gly Ile Ile Lys Ser Ile Ile Pro  
 180 185 190  
 Asp Thr Thr Lys Asp Thr Val Lys Ala Lys Asp Val Val Phe Ile Ser  
 195 200 205  
 Lys Leu Pro Asp Ser Leu Thr Glu Ser Ser Ser Pro Ser Ser Gln Arg  
 210 215 220  
 Phe Tyr Ile Glu Thr Leu Asp Glu Leu Leu Ile Pro Lys Ile Thr Ser  
 225 230 235 240  
 Thr Leu Phe Ala Gly Lys Ser Tyr Leu Lys Thr Arg Thr Asp Tyr Leu  
 245 250 255  
 Pro Trp Lys Gln Leu Val Lys Gln Ser Leu Lys His Ser His Leu Pro  
 260 265 270  
 Glu Thr Leu Arg Arg Val Ala Ile Gly Phe Leu Cys Ile Thr Leu Thr  
 275 280 285  
 Tyr Ala Gly Met Ile Leu Gly Ile His Lys Pro Arg Phe Arg Lys Ser  
 290 295 300  
 Ile Ala Leu Tyr Phe Ile Phe Pro Ile Leu Asp Leu Ile Leu Leu Ile  
 305 310 315 320  
 Val Gly Lys Asn Thr Lys Asn Leu Pro Leu Ala Phe Met Leu Phe Val  
 325 330 335  
 Phe Pro Gln Leu Val Ser Trp Val Val Phe Ala Ala Arg Ala Tyr Arg  
 340 345 350  
 Glu Ser Arg Gly Tyr Ala  
 355  
 <210>1071  
 <211>319  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1071  
 Met Val Leu Ser Ser Asp Leu Leu Arg Asp Asp Lys Gln Leu Asp Leu  
 1 5 10 15  
 Phe Phe Ala Ser Leu Asp Val Lys Lys Arg Tyr Leu Leu Ala Leu Ser

20 25 30  
 Gly Gly Ser Asp Ser Leu Phe Leu Phe Tyr Leu Leu Lys Glu Arg Gly  
 35 40 45  
 Val Ser Phe Thr Ala Val His Ile Asp His Gly Trp Arg Ser Thr Ser  
 50 55 60  
 Ala Gln Glu Ala Lys Glu Leu Glu Glu Leu Cys Ala Arg Glu Gly Val  
 65 70 75 80  
 Pro Phe Val Leu Tyr Thr Leu Thr Ala Glu Glu Gln Gly Asp Lys Asp  
 85 90 95  
 Leu Glu Asn Gln Ala Arg Lys Lys Arg Tyr Ala Phe Leu Tyr Glu Ser  
 100 105 110  
 Tyr Arg Gln Leu Asp Ala Gly Gly Ile Phe Leu Ala His His Ala Asn  
 115 120 125  
 Asp Gln Ala Glu Thr Val Leu Lys Arg Leu Leu Glu Ser Ala His Leu  
 130 135 140  
 Thr Asn Leu Lys Ala Met Ala Glu Arg Ser Tyr Val Glu Asp Val Leu  
 145 150 155 160  
 Leu Leu Arg Pro Leu Leu His Ile Pro Lys Ser Ser Leu Lys Glu Ala  
 165 170 175  
 Leu Asp Ala Arg Gly Ile Ser Tyr Leu Gln Asp Pro Ser Asn Glu Asp  
 180 185 190  
 Glu Arg Tyr Leu Arg Ala Arg Met Arg Lys Lys Leu Phe Pro Trp Leu  
 195 200 205  
 Glu Glu Val Phe Gly Lys Asn Ile Thr Phe Pro Leu Leu Thr Leu Gly  
 210 215 220  
 Glu Glu Ser Ala Glu Leu Ser Glu Tyr Leu Glu Lys Gln Ala Gln Pro  
 225 230 235 240  
 Phe Phe Ser Ala Ala Thr His Gln Asp Ser Gln Gly Glu Leu Pro Cys  
 245 250 255  
 Pro Asp Cys Leu Ile Gln Gln Ala Phe Leu Cys Lys Trp Val Met Lys  
 260 265 270  
 Lys Phe Phe Asn Asn Ala Gly Ile Ala Val Ser Arg His Phe Leu Gln  
 275 280 285  
 Met Val Tyr Asp His Leu Ser Arg Ser Ser Cys Ala Thr Leu Arg Met  
 290 295 300  
 Arg Asn Lys Ile Val Ile Ile Lys Pro Gly Val Val Val Ile Asp  
 305 310 315

&lt;210&gt;1072

&lt;211&gt;918

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1072

Leu Ile Ser Leu Val Val Lys Phe Met Ser Lys Asp Lys Lys Met Lys  
 1 5 10 15  
 Pro Glu Pro Lys Lys Asn Phe Pro Thr Val Phe Phe Phe Leu Leu Phe  
 20 25 30  
 Gly Val Val Phe Gly Val Val Ala Phe Gln Asn Phe Leu Ala Gly Lys  
 35 40 45  
 Lys Ala Arg Val Gly Phe Ser His Gln Ile Glu His Leu Val Asn Leu  
 50 55 60  
 Arg Leu Ile Val Pro Glu Asp Ser His Lys Ile Ala Leu Asn Asp Asn  
 65 70 75 80  
 Leu Val Ser Phe Gly Gly Arg Phe Arg Asp Val Gln Thr Gln Glu Gly  
 85 90 95  
 Gln Leu Arg Tyr His Tyr Leu Glu Leu Ile Asp Gln Gly His Arg Leu  
 100 105 110  
 Asp Leu Asp Leu Gln Glu Thr Ser Lys Ser Leu Thr Thr Leu Gly Lys  
 115 120 125  
 Glu Val Thr Asn Ser Ile Leu Trp Phe Ser Ala Ile Ser Gly Ser Pro  
 130 135 140  
 Ile Pro Glu Gln Gly Tyr Ala Ile Ser Tyr Pro Ser Glu Val Ser Gly  
 145 150 155 160  
 Ser Val Leu Thr Glu Pro Leu Val Val Thr Gly Pro Ala Thr Pro Gln  
 165 170 175

Leu Ile Asn Leu His Ser Leu Gln Glu Arg Tyr Pro Thr Leu Ser Arg  
 180 185 190  
 Ser Pro Glu Ala Leu Arg Thr Tyr Gly Ser Asp Leu Tyr Glu Leu Ile  
 195 200 205  
 Gly Lys Tyr Leu Ser Pro Val Leu Gly Ile Gly Ser Glu Thr Leu Lys  
 210 215 220  
 Arg Glu Leu Lys Asp Leu Tyr Gln Gln Val Glu Val Ser Leu Thr Gln  
 225 230 235 240  
 Glu Thr Asp Thr Glu Ala Ala Tyr Thr Leu Tyr Gly Gln Val Leu Ser  
 245 250 255  
 Thr Leu Asn Arg Ile Ser Ser Ser Leu Val Val Ser Glu Gly Gly Glu  
 260 265 270  
 Arg Phe Ser Gln Leu Arg Ser Val Arg Leu Tyr Arg Glu Glu Trp Asn  
 275 280 285  
 Lys Tyr His Lys Leu Val Glu Ala Arg Asp Leu Asn Gln Ala Gln Leu  
 290 295 300  
 Glu Lys Leu Arg Gly Glu Leu Ser Gln Thr Val Trp Tyr Phe Asn Asn  
 305 310 315 320  
 Gln Glu Leu Ser Ser Arg Ser Leu Glu Lys Gln Asp Pro Glu Val Phe  
 325 330 335  
 Gly His Trp Phe Ala Gly Ala Lys Glu Glu Trp Thr Ala Phe Lys Phe  
 340 345 350  
 Asn His Ser Leu Ser Phe Lys Ala Pro Asp Gln Pro Arg Asn Leu Val  
 355 360 365  
 Leu Glu Lys Thr Phe Lys Ser Gln Glu Pro Ser Pro His Xaa Leu Gly  
 370 375 380  
 Tyr Leu Phe Thr Xaa Leu Pro Ile Ile Leu Val Leu Leu Phe Val Tyr  
 385 390 395 400  
 Leu Val Phe Ser Arg Gln Met Arg Gly Met Ser Gly Ser Ala Met Ser  
 405 410 415  
 Phe Gly Lys Ser Pro Ala Arg Met Leu Leu Lys Gly Gln Asn Lys Val  
 420 425 430  
 Thr Phe Ala Asp Val Ala Gly Ile Glu Glu Ala Lys Glu Glu Leu Ile  
 435 440 445  
 Glu Ile Val Asp Phe Leu Lys Asn Pro Asn Lys Phe Thr Ser Leu Gly  
 450 455 460  
 Gly Arg Ile Pro Lys Gly Val Leu Leu Ile Gly Pro Pro Gly Thr Gly  
 465 470 475 480  
 Lys Thr Leu Ile Ala Lys Ala Val Ser Gly Glu Ala Asp Arg Pro Phe  
 485 490 495  
 Phe Ser Ile Ala Gly Ser Asp Phe Val Glu Met Phe Val Gly Val Gly  
 500 505 510  
 Ala Ser Arg Ile Arg Asp Met Phe Glu Gln Ala Lys Arg Asn Ala Pro  
 515 520 525  
 Cys Ile Ile Phe Ile Asp Glu Ile Asp Ala Val Gly Arg His Arg Gly  
 530 535 540  
 Ala Gly Ile Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu Asn Gln  
 545 550 555 560  
 Leu Leu Val Glu Met Asp Gly Phe Gly Thr Asn Glu Gly Val Ile Leu  
 565 570 575  
 Met Ala Ala Thr Asn Arg Pro Asp Val Leu Asp Lys Ala Leu Leu Arg  
 580 585 590  
 Pro Gly Arg Phe Asp Arg Arg Val Val Met Asn Leu Pro Asp Ile Lys  
 595 600 605  
 Gly Arg Phe Glu Ile Leu Met Val His Ala Lys Arg Ile Lys Leu Asp  
 610 615 620  
 Pro Thr Val Asp Leu Met Ala Val Ala Arg Ser Thr Pro Gly Ala Ser  
 625 630 635 640  
 Gly Ala Asp Leu Glu Asn Leu Leu Asn Glu Ala Ala Leu Leu Ala Ala  
 645 650 655  
 Arg Lys Asp Arg Thr Ala Val Thr Ala Val Asp Val Ala Glu Ala Arg  
 660 665 670  
 Asp Lys Val Leu Tyr Gly Lys Glu Arg Arg Ser Leu Glu Met Asp Ala  
 675 680 685

Glu Glu Arg Lys Thr Thr Ala Tyr His Glu Ser Gly His Ala Val Val  
 690 695 700  
 Gly Leu Cys Val Gln His Gly Asp Pro Val Asp Lys Val Thr Ile Ile  
 705 710 715 720  
 Pro Arg Gly Leu Ser Leu Gly Ala Thr His Phe Leu Pro Glu Lys Asn  
 725 730 735  
 Lys Leu Ser Tyr Trp Lys Lys Glu Leu Tyr Asp Gln Leu Ala Val Leu  
 740 745 750  
 Met Gly Gly Arg Ala Ala Glu Glu Ile Phe Leu Gly Asp Ile Ser Ser  
 755 760 765  
 Gly Ala Gln Gln Asp Ile Ser Gln Ala Thr Lys Leu Val Arg Ser Met  
 770 775 780  
 Val Cys Glu Trp Gly Met Ser Pro Gln Leu Gly Asn Val Thr Tyr Asp  
 785 790 795 800  
 Glu Arg Ser Asp Gly Leu Thr Gly Tyr Gly Gly Tyr His Glu Lys Ser  
 805 810 815  
 Tyr Ser Glu Glu Thr Ala Lys Thr Ile Asp Thr Glu Leu Arg Met Leu  
 820 825 830  
 Leu Asp Ala Ala Tyr Gln Arg Ala Leu Asp Ile Ile Asn Glu His Lys  
 835 840 845  
 Ala Glu Ile Glu Leu Met Thr Gln Met Leu Ile Glu Phe Glu Thr Leu  
 850 855 860  
 Asp Ser Lys Asp Val Lys Glu Ile Met Asp His Thr Trp Asp Pro Glu  
 865 870 875 880  
 Lys Lys Arg Ala Arg Leu Lys Glu Glu Gly Met Leu Phe Lys Lys Ser  
 885 890 895  
 Ser Asp Asp Leu Pro Pro Pro Pro Lys Glu Asp Thr Leu Pro Gly  
 900 905 910  
 Leu Gly Phe Asn Ala Thr  
 915  
 <210>1073  
 <211>568  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1073  
 Ser Ser Cys Tyr Leu Arg Xaa Ser Ala Ala Leu Ala Ile Ser Asp Ile  
 1 5 10 15  
 Pro Gln Ser Asn Ile Val Ala Gly Val Arg Ile Gly Cys Ile Asp Asn  
 20 25 30  
 Gln Trp Val Ile Asn Pro Thr Lys Thr Glu Leu Ala Ser Ser Thr Leu  
 35 40 45  
 Asp Leu Val Leu Ala Gly Thr Glu Asn Ala Ile Leu Met Ile Glu Gly  
 50 55 60  
 His Cys Asp Phe Phe Thr Glu Glu Gln Val Leu Asp Ala Ile Glu Phe  
 65 70 75 80  
 Gly His Lys His Ile Val Thr Ile Cys Lys Arg Leu Gln Leu Trp Gln  
 85 90 95  
 Glu Glu Val Gly Lys Ser Lys Asn Leu Ser Ala Val Tyr Pro Leu Pro  
 100 105 110  
 Ala Glu Val Leu Thr Ala Val Lys Glu Cys Ala Gln Asp Lys Phe Thr  
 115 120 125  
 Glu Leu Phe Asn Ile Lys Asp Lys Lys Val His Ala Ala Thr Ala His  
 130 135 140  
 Glu Ile Glu Glu Asn Ile Leu Glu Lys Leu Gln Arg Glu Asp Asp Asp  
 145 150 155 160  
 Leu Phe Ser Ser Phe Asn Ile Lys Ala Ala Cys Lys Thr Leu Lys Ser  
 165 170 175  
 Asp Thr Met Arg Ala Leu Ile Arg Asp Arg Glu Ile Arg Ala Asp Gly  
 180 185 190  
 Arg Ser Leu Thr Thr Val Arg Pro Ile Thr Ile Glu Thr Ser Tyr Leu  
 195 200 205  
 Pro Arg Thr His Gly Ser Cys Leu Phe Thr Arg Gly Glu Thr Gln Thr  
 210 215 220  
 Leu Ala Val Cys Thr Leu Gly Ser Glu Ala Met Ala Gln Arg Tyr Glu

225 230 235 240  
 Asp Leu Asn Gly Glu Gly Leu Ser Lys Phe Tyr Leu Gln Tyr Phe Phe  
 245 250 255  
 Pro Pro Phe Ser Val Gly Glu Val Gly Arg Ile Gly Ser Pro Gly Arg  
 260 265 270  
 Arg Glu Ile Gly His Gly Lys Leu Ala Glu Lys Ala Leu Ser His Ala  
 275 280 285  
 Leu Pro Asp Ser Ala Thr Phe Pro Tyr Thr Ile Arg Ile Glu Ser Asn  
 290 295 300  
 Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Gly  
 305 310 315 320  
 Cys Leu Ala Leu Met Asp Ala Gly Val Pro Ile Ser Ser Pro Ile Ala  
 325 330 335  
 Gly Ile Ala Met Gly Leu Ile Leu Asp Asp Gln Gly Ala Ile Ile Leu  
 340 345 350  
 Ser Asp Ile Ser Gly Leu Glu Asp His Leu Gly Asp Met Asp Phe Lys  
 355 360 365  
 Ile Ala Gly Ser Gly Lys Gly Ile Thr Ala Phe Gln Met Asp Ile Lys  
 370 375 380  
 Val Glu Gly Ile Thr Pro Ala Ile Met Lys Lys Ala Leu Ser Gln Ala  
 385 390 395 400  
 Lys Gln Gly Cys Asn Asp Ile Leu Asn Ile Met Asn Glu Ala Leu Ser  
 405 410 415  
 Ala Pro Lys Ala Asp Leu Ser Gln Tyr Ala Pro Arg Ile Glu Thr Met  
 420 425 430  
 Gln Ile Lys Pro Thr Lys Ile Ala Ser Val Ile Gly Pro Gly Gly Lys  
 435 440 445  
 Gln Ile Arg Gln Ile Ile Glu Glu Thr Gly Val Gln Ile Asp Val Asn  
 450 455 460  
 Asp Leu Gly Val Val Ser Ile Ser Ala Ser Ser Ala Ser Ala Ile Asn  
 465 470 475 480  
 Lys Ala Lys Glu Ile Ile Glu Gly Leu Val Gly Glu Val Glu Val Gly  
 485 490 495  
 Lys Thr Tyr Arg Gly Arg Val Thr Ser Val Val Ala Phe Gly Ala Phe  
 500 505 510  
 Val Glu Val Leu Pro Gly Lys Glu Gly Leu Cys His Ile Ser Glu Cys  
 515 520 525  
 Ser Arg Gln Arg Ile Glu Asn Ile Ser Asp Val Val Lys Glu Gly Asp  
 530 535 540  
 Ile Ile Asp Val Lys Leu Leu Ser Ile Asn Glu Lys Gly Gln Leu Lys  
 545 550 555 560  
 Leu Ser His Lys Ala Thr Leu Glu  
 565

&lt;210&gt;1074

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1074

Ser Asp Arg Ser Lys Ile Leu Val Phe Glu Thr Gly Lys Ile Ala Arg  
 1 5 10 15  
 Gln Ala Asn Gly Ala Val Leu Val Arg Ser Gly Glu Thr Cys Val Phe  
 20 25 30  
 Ala Ser Ala Cys Ala Val Asp Leu Asp Asp Lys Val Asp Phe Leu Pro  
 35 40 45  
 Leu Arg Val Asp Tyr Gln Glu Lys Phe Ser Ser Thr Gly Lys Thr Leu  
 50 55 60  
 Gly Gly Phe Ile Lys Arg Glu Gly Arg Pro Ser Glu Lys Glu Ile Leu  
 65 70 75 80  
 Val Ser Arg Leu Ile Asp Arg Ser Leu Arg Pro Ser Phe Pro Tyr Arg  
 85 90 95  
 Leu Met Gln Asp Val Gln Val Leu Ser Tyr Val Trp Ser Tyr Asp Gly  
 100 105 110  
 Gln Val Leu Pro Asp Pro Leu Ala Ile Cys Ala Xaa Leu Leu Leu  
 115 120 125



&lt;210&gt;1075

&lt;211&gt;163

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1075

Leu Gly Gly Glu Lys Leu Ile Asn Met Glu Lys Asp Ile Phe Phe Met  
 1 5 10 15  
 Gln Gln Ala Phe Lys Glu Ala Arg Lys Ala Tyr Asp Gln Asp Glu Val  
 20 25 30  
 Pro Val Gly Cys Val Ile Val Lys Asp Asp Lys Ile Ile Ala Arg Ala  
 35 40 45  
 His Asn Ser Val Glu Lys Leu Lys Asp Ala Thr Ala His Ala Glu Ile  
 50 55 60  
 Leu Cys Ile Gly Ser Ala Ala Gln Asp Leu Asp Asn Trp Arg Leu Leu  
 65 70 75 80  
 Asp Thr Val Leu Tyr Cys Thr Leu Glu Pro Cys Leu Met Cys Ala Gly  
 85 90 95  
 Ala Ile Gln Leu Ala Arg Ile Pro Arg Ile Val Trp Ala Ala Pro Asp  
 100 105 110  
 Val Arg Leu Gly Ala Gly Gly Ser Trp Val Asn Ile Phe Thr Glu Glu  
 115 120 125  
 His Pro Phe His Thr Val Ser Cys Thr Gly Gly Val Cys Ser Glu Glu  
 130 135 140  
 Ala Glu His Leu Met Lys Lys Phe Phe Val Glu Lys Arg Arg Glu Lys  
 145 150 155 160  
 Ser Glu Lys

&lt;210&gt;1076

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1076

Lys Ser Ala Glu Arg Lys Val Lys Asn Lys Ile Val Thr Leu Leu Asp  
 1 5 10 15  
 Gln Leu Tyr Glu Asp Gln Glu Ser Arg Leu Gln Lys Leu Gly Glu Glu  
 20 25 30  
 Ile Val Pro Asn Leu Thr Pro Glu Asp Leu Leu Gln Pro Met Asp Phe  
 35 40 45  
 Xaa Gln Leu Glu Gly Asn Pro Ala Phe Arg Phe Glu Gly Val Leu  
 50 55 60  
 Ser Gly Ile Gly Glu Val Arg Ala Ala Ile Phe Asn Gly Ala Leu Ser  
 65 70 75 80  
 Arg Glu Leu Glu Ser Gln Arg Ser Ser Ile Gly Val Gly Asp Leu Phe  
 85 90 95  
 Phe Phe Thr Lys  
 100

&lt;210&gt;1077

&lt;211&gt;180

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1077

His Leu Ser Ile Glu Glu Leu Met Ser Ile Gln Pro Val Ser Asn Thr  
 1 5 10 15  
 Thr Thr Lys Ala Asp Lys Val Ile Pro Asp Ser Thr Lys Val Ile Ser  
 20 25 30  
 Asp Ser Ile Thr Ile Asn Lys Gln Ser Ala Phe Tyr Phe Cys Ile Ser  
 35 40 45  
 Val Met Leu Arg Leu Ser Glu Ser Thr Thr Glu Tyr Gly Lys Ser Ile  
 50 55 60  
 Leu Ala Val Leu Glu Asp Asn Thr Ile Val Gln Gln Arg Val Lys  
 65 70 75 80  
 Glu Leu Ile Asn Leu Pro Leu Leu Lys Val Pro Asp Leu Gln Lys Lys  
 85 90 95  
 Asp Gly Ser Asp Asp Glu Tyr Lys Asn Gln Asn Glu Ile Gln Ala Tyr

100 105 110  
 Gln Ser Ser Asn Gln Gln Ile Ser Ala Asn Arg Gln Met Ile Gln Gln  
 115 120 125  
 Glu Leu Ser Ser Ala Gln Gln Arg Ala Gln Ala Asn Gln Lys Ser Val  
 130 135 140  
 Asn Ser Thr Thr Ile Glu Ser Met Gln Ile Leu Gln Ala Thr Ser Ser  
 145 150 155 160  
 Met Leu Ser Thr Leu Lys Glu Leu Thr Ile Lys Ala Asn Leu Thr Asn  
 165 170 175  
 Ser Pro Ser Asp  
 180

&lt;210&gt;1078

&lt;211&gt;181

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1078

Asn Arg Lys Pro Val Arg Leu Asn Met Trp Ile Ile Asp Pro Leu Ser  
 1 5 10 15  
 Ala Lys Xaa Pro Leu Gln Ala Ala Ile Asn Val Pro Gly Thr Pro Ile  
 20 25 30  
 Thr Gly Gly Pro Asn Thr Ala Thr Ala Asp Asp Ile Ile Ala Lys Phe  
 35 40 45  
 Ser Lys Asp Ser Asn Pro Leu Ile Val Thr Val Tyr Tyr Val Tyr Gln  
 50 55 60  
 Ser Val Leu Val Ala Gln Asp Asn Leu Ser Ile Ile Ala Gln Glu Leu  
 65 70 75 80  
 Gln Ala Asn Ser Ser Ala Gln Thr Tyr Leu Asn Asn Gln Glu Ala Leu  
 85 90 95  
 Tyr Gln Tyr Val Ser Ile Pro Lys Asn Lys Leu Asn Asp Asn Ser Ser  
 100 105 110  
 Ser Tyr Leu Gln Asn Ile Gln Ser Asp Asn Gln Ala Ile Gly Ala Ser  
 115 120 125  
 Arg Gln Ala Ile Gln Asn Gln Ile Ser Ser Leu Gly Asn Ala Ala Gln  
 130 135 140  
 Val Ile Ser Ser Asn Leu Asn Thr Asn Asn Asn Ile Ile Gln Gln Ser  
 145 150 155 160  
 Leu Gln Val Gly Gln Ala Leu Ile Gln Thr Phe Ser Gln Ile Val Ser  
 165 170 175  
 Leu Ile Ala Asn Ile  
 180

&lt;210&gt;1079

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1079

Thr Lys Val Asn Phe Phe Ile Met Ser Ile Thr Thr Leu Gly Thr Leu  
 1 5 10 15  
 Pro Thr Val Asn Thr Ile Asn Ser Ser Arg Pro Pro Leu Glu Pro Leu  
 20 25 30  
 Asn Thr Pro Lys Ile Gly Ala Val Leu Phe Ser Ile Tyr Glu Leu Leu  
 35 40 45  
 Leu Gln Ala Ile Glu Ile Arg Gln Gln Thr Val Leu Thr Gln Ser Gln  
 50 55 60  
 Gln Leu Asn Asp Asn Thr Asn Ile Gln Gln Gln Leu Asn Gln Glu Thr  
 65 70 75 80  
 Asn Gln Ile Lys Tyr Ala Ile Val Ser Ala Gly Ala Lys Glu Asp Glu  
 85 90 95  
 Ile Thr Arg Val Gln Asn Gln Asn Gln Tyr Ser Ala Gln Arg Ser  
 100 105 110  
 Asn Ile Gln Asp Glu Leu Val Thr Thr Arg Gln Asn Gly Gln Ile Ile  
 115 120 125  
 Leu Ser His Ala Ser Thr Asn Ile Asn Ile Ile Gln Gln Gln Ser Ser  
 130 135 140  
 Gln Asp Ser Ser Phe Ile Lys Thr Thr Asn Ser Ile Gly Ser Thr Val

1091

&lt;210&gt;1081

&lt;211&gt;294

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1081

Val Ile Leu Met Lys Arg Asn Asp Pro Cys Trp Cys Gly Ser Gly Arg  
 1 5 10 15  
 Lys Trp Lys Gln Cys His Tyr Pro Gln Pro Pro Lys Met Ser Pro Glu  
 20 25 30  
 Ala Leu Lys Gln His Tyr Ala Ser Gln Tyr Asn Ile Leu Lys Thr  
 35 40 45  
 Pro Glu Gln Lys Ala Lys Ile Tyr Asn Ala Cys Gln Ile Thr Ala Arg  
 50 55 60  
 Ile Leu Asp Glu Leu Cys Lys Ala Ser Gln Lys Gly Val Thr Thr Asn  
 65 70 75 80  
 Glu Leu Asp Glu Leu Ser Gln Glu Leu His Lys Lys Tyr Asp Ala Ile  
 85 90 95  
 Ala Ala Pro Phe His Tyr Gly Ser Pro Pro Phe Pro Lys Thr Ile Cys  
 100 105 110  
 Thr Ser Leu Asn Glu Val Ile Cys His Gly Ile Pro Asn Asp Ile Pro  
 115 120 125  
 Leu Lys Asp Gly Asp Ile Met Asn Ile Asp Val Ser Cys Ile Val Asp  
 130 135 140  
 Gly Tyr Tyr Gly Asp Cys Ser Arg Met Val Met Ile Gly Glu Val Pro  
 145 150 155 160  
 Glu Ile Lys Lys Lys Ile Cys Gln Ala Ala Leu Glu Cys Leu Asn Asp  
 165 170 175  
 Ser Ile Ala Ile Leu Lys Pro Gly Ile Pro Leu Cys Glu Ile Gly Glu  
 180 185 190  
 Ala Ile Glu Ala Arg Ala Asp Thr Tyr Gly Phe Ser Val Val Asp Gln  
 195 200 205  
 Phe Val Gly His Gly Val Gly Ile Glu Phe His Glu Asn Pro Tyr Val  
 210 215 220  
 Pro His Tyr Arg Asn Arg Ser Met Ile Pro Leu Ala Pro Gly Met Ile  
 225 230 235 240  
 Phe Thr Ile Glu Pro Met Ile Asn Val Gly Lys Lys Glu Gly Val Val  
 245 250 255  
 Asp Pro Lys Asn Gln Trp Glu Ala Arg Thr Cys Asp Asn Gln Pro Ser  
 260 265 270  
 Ala Gln Trp Glu His Thr Ile Ala Ile Thr Glu Thr Gly Tyr Glu Ile  
 275 280 285  
 Leu Thr Leu Leu Asn Asp  
 290

&lt;210&gt;1082

&lt;211&gt;202

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1082

Met Leu Ile Leu Leu Asn Leu Ser Leu Leu Phe Tyr Val Leu Phe Asp  
 1 5 10 15  
 Ser Pro Gly Ser Ile Pro Val Phe Val Ala Leu Leu Lys Asn Phe Ser  
 20 25 30  
 Arg Lys Lys Gln Gln Arg Val Ile Leu Arg Glu Cys Leu Phe Ala Leu  
 35 40 45  
 Gly Ala Leu Ile Leu Phe Val Thr Phe Gly Arg Ser Phe Phe Gln Phe  
 50 55 60  
 Leu Asp Ile Ser Leu Tyr Ala Phe Gln Ile Ile Gly Gly Phe Leu Leu  
 65 70 75 80  
 Phe Thr Val Ser Ile Lys Met Met Leu Ala Pro Met Pro Glu Lys Ala  
 85 90 95  
 Lys Asp Asp Thr Ser Lys Thr Glu Pro Ile Phe Phe Pro Leu Ala Phe  
 100 105 110  
 Pro Val Ile Thr Gly Pro Ala Val Ile Thr Ala Leu Leu Ser Tyr Met  
 115 120 125

Glu Glu Gly Ile Tyr Ser Arg Glu Ile Ile Phe Thr Ala Met Ile Ile  
 130 135 140  
 Ala Trp Ala Phe Ser Leu Phe Thr Leu Leu Cys Ser Ser Phe Phe Asp  
 145 150 155 160  
 Arg Leu Ser Gly Asn Phe Gly Leu Leu Ala Leu Glu Arg Leu Phe Gly  
 165 170 175  
 Ile Ala Leu Leu Leu Met Ser Val Asn Leu Met Leu Lys Gly Ile Ser  
 180 185 190  
 Ile Ala Phe Asn Ile Gly Phe Tyr Ile Gly  
 195 200

&lt;210&gt;1083

&lt;211&gt;251

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1083

Thr Ser Arg Tyr Gly Pro Leu Pro Cys Ser Arg His His Glu Asp Leu  
 1 5 10 15  
 His Lys Arg His Ala Asn Thr Asn Arg Arg Glu Ile Asp Arg Gln Phe  
 20 25 30  
 Pro Ala Arg Phe Leu Tyr Arg Ser Gln Asp Pro Ile Tyr Lys Phe Glu  
 35 40 45  
 Asp Leu Asn Gly Lys Val Leu Gly Phe Cys Leu Asn Asn Ser Arg Asp  
 50 55 60  
 Leu Asn Arg Leu Leu Glu Thr Leu Asn Arg Asn Gly Val Val Pro Ser  
 65 70 75 80  
 Glu Val Lys Asn Val Ser Ser Asp Leu Ile Ser Pro Met Leu Leu Asn  
 85 90 95  
 Lys Ile Asp Phe Leu Tyr Gly Ala Phe Tyr Asn Ile Glu Gly Val Lys  
 100 105 110  
 Leu Gln Thr Leu Gly Met Pro Val Lys Cys Phe Leu Ser Asp Thr Cys  
 115 120 125  
 Asp Leu Pro Thr Gly Pro Gln Leu Ile Val Phe Thr Lys Lys Gly Thr  
 130 135 140  
 Lys Ala Ser Glu Pro Glu Ile Val Glu Ala Phe Gln Lys Ala Leu Gln  
 145 150 155 160  
 Glu Ser Ile Ile Phe Ser Lys Asp His Pro Glu Asp Ala Phe Lys Leu  
 165 170 175  
 Tyr Ala Lys Glu Thr Lys Ser Ile Pro Lys Asn Leu Tyr Gln Glu Tyr  
 180 185 190  
 Leu Gln Trp Glu Glu Thr Phe Pro Leu Leu Ala Gln Ser Gln Asp Pro  
 195 200 205  
 Leu Ser Lys Asp Leu Val Asp Lys Leu Leu Glu Thr Ile Ile Lys Arg  
 210 215 220  
 Tyr Pro Glu Leu Ala Ser Glu Val Ala Lys Phe Ser Leu Asn Asp Leu  
 225 230 235 240  
 Tyr Asn Pro Ser Leu Pro Glu Glu Gln Ser Val  
 245 250

&lt;210&gt;1084

&lt;211&gt;303

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1084

Arg Ser Pro Thr Thr Ser Phe His Pro Ala Thr Val His Ser Tyr Val  
 1 5 10 15  
 Cys Ser Gly Ser Thr Asp Cys Thr Leu Val Trp Leu Gly Asn Arg Cys  
 20 25 30  
 Cys Asn Arg Pro Tyr Ser Thr His His Ile Leu Ser Ala His Pro Asp  
 35 40 45  
 Tyr Leu Ser Gly His Leu Ile Asn Thr Arg Arg Thr Tyr Arg Ala Ile  
 50 55 60  
 Arg Pro Leu Arg Ser Thr Lys Phe Gln Leu Leu Ile Lys Leu Arg Ile  
 65 70 75 80  
 Pro His Ala Leu Pro His Ile Phe Ser Gly Leu Lys Ile Ala Ile Gly  
 85 90 95

Ser Ala Gly Phe Ala Ala Ile Ala Gly Glu Trp Val Ala Ser Gln Ser  
 100 105 110  
 Gly Leu Gly Ile Leu Met Leu Glu Ser Arg Arg Asn Tyr Glu Met Glu  
 115 120 125  
 Leu Ala Phe Ala Gly Leu Ala Thr Leu Ser Ile Leu Thr Leu Ser Leu  
 130 135 140  
 Phe Gln Ile Thr Leu Leu Ile Glu Lys Leu Ile Phe Ser Leu Phe Arg  
 145 150 155 160  
 Val Lys Arg Met Ser Leu Lys His Lys Ser Val Ala Lys Lys Ala Leu  
 165 170 175  
 Ser Val Leu Ala Leu Ile Pro Ile Met Leu Ile Pro Trp Lys Gly Asn  
 180 185 190  
 Ser Lys Ser Pro Pro Asp Lys Lys Asn Leu Thr Ser Leu Thr Leu Leu  
 195 200 205  
 Leu Asp Trp Thr Pro Asn Pro Asn His Ile Pro Leu Tyr Ala Gly Val  
 210 215 220  
 Ala Lys Gly Tyr Phe Lys Gln His Gly Leu Asp Leu Gln Leu Gln Lys  
 225 230 235 240  
 Asn Thr Asp Ser Ser Ser Ala Val Pro His Val Leu Phe Glu Gln Val  
 245 250 255  
 Asp Met Ala Leu Tyr His Ala Leu Gly Ile Met Lys Thr Ser Ile Lys  
 260 265 270  
 Gly Met Pro Ile Gln Ile Val Gly Arg Leu Ile Asp Ser Ser Leu Gln  
 275 280 285  
 Asp Phe Ser Thr Glu Val Arg Thr Pro Ser Thr Asn Leu Lys Thr  
 290 295 300

&lt;210&gt;1085

&lt;211&gt;460

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1085

Met Arg Gln Glu Lys Asp Ser Leu Gly Ile Val Glu Val Pro Glu Asp  
 1 5 10 15  
 Lys Leu Tyr Gly Ala Gln Thr Met Arg Ser Arg Asn Phe Phe Ser Trp  
 20 25 30  
 Gly Pro Glu Leu Met Pro Tyr Glu Val Ile Arg Ala Leu Val Trp Ile  
 35 40 45  
 Lys Lys Cys Ala Ala Gln Ala Asn Gln Asp Leu Gly Phe Leu Asp Ser  
 50 55 60  
 Lys His Cys Asp Met Ile Val Ala Ala Ala Asp Glu Ile Leu Glu Gly  
 65 70 75 80  
 Gly Phe Glu Glu His Phe Pro Leu Lys Val Trp Gln Thr Gly Ser Gly  
 85 90 95  
 Thr Gln Ser Asn Met Asn Val Asn Glu Val Ile Ala Asn Leu Ala Ile  
 100 105 110  
 Arg His His Gly Gly Val Leu Gly Ser Lys Asp Pro Ile His Pro Asn  
 115 120 125  
 Asp His Val Asn Lys Ser Gln Ser Ser Asn Asp Val Phe Pro Thr Ala  
 130 135 140  
 Met His Ile Ala Ala Val Ile Ser Leu Lys Asn Lys Leu Ile Pro Ala  
 145 150 155 160  
 Leu Asp His Met Ile Arg Val Leu Asp Ala Lys Val Glu Glu Phe Arg  
 165 170 175  
 His Asp Val Lys Ile Gly Arg Thr His Leu Met Asp Ala Val Pro Met  
 180 185 190  
 Thr Leu Gly Gln Glu Phe Ser Gly Tyr Ser Ser Gln Leu Arg His Cys  
 195 200 205  
 Leu Glu Ser Ile Ala Phe Ser Leu Ala His Leu Tyr Glu Leu Ala Ile  
 210 215 220  
 Gly Ala Thr Ala Val Gly Thr Gly Leu Asn Val Pro Glu Gly Phe Val  
 225 230 235 240  
 Glu Lys Ile Ile His Tyr Leu Arg Lys Xaa Thr Asp Glu Pro Phe Ile  
 245 250 255  
 Pro Ala Xaa Asn Tyr Phe Ser Ala Leu Ser Cys His Asp Ala Leu Val

```

<211>20
<212>DNA
<400>1396
gaccttgcca gcttgggtcg      20
<210>1397
<211>20
<212>DNA
<400>1397
gctgctaaat cccatcgctt     20
<210>1398
<211>20
<212>DNA
<400>1398
gttttgtggc tttggcagtg     20
<210>1399
<211>20
<212>DNA
<400>1399
actttcctaa gaagcgtagc     20
<210>1400
<211>20
<212>DNA
<400>1400
gaggaatggc gcaggagtta     20
<210>1401
<211>20
<212>DNA
<400>1401
gcagtgaaaa cggaatccag     20
<210>1402
<211>20
<212>DNA
<400>1402
gcgtggggat tgtagggata     20
<210>1403
<211>20
<212>DNA
<400>1403
ggccggggat caatcagcta     20
<210>1404
<211>20
<212>DNA
<400>1404
gaataagatg caggcggaag     20
<210>1405
<211>20
<212>DNA
<400>1405
gggagacgtt tgtgcgtaaa     20
<210>1406
<211>20
<212>DNA
<400>1406
cgtcctgcag gtgttattgt     20
<210>1407
<211>20
<212>DNA
<400>1407
caaggggtgt agagaaagga     20
<210>1408
<211>20
<212>DNA
<400>1408
gaagacaaac cttgtcctgg     20

```

Thr Val Met Thr Thr Ile Thr Ala Ala Val Gln Val Gly Met Met Leu  
 275 280 285  
 Ala Ala Phe Leu Phe Met Lys Gln Met Ser Asp Leu Ser Asp Val Ile  
 290 295 300  
 Ser Thr Ala Lys Tyr Phe Asp Lys Asp Ser Asp Phe Leu Ser Lys Ala  
 305 310 315 320  
 Glu Val Pro Gln Asn Thr Glu Ile Tyr Glu Ile Asn Gly Pro Phe Phe  
 325 330 335  
 Phe Gly Ile Ala Asp Arg Leu Lys Asn Leu Leu Asn Asp Ile Glu Lys  
 340 345 350  
 Pro Pro Lys Ile Phe Ile Leu Cys Met Thr Arg Val Pro Thr Ile Asp  
 355 360 365  
 Ala Ser Ala Met His Ala Leu Glu Glu Phe Phe Leu Glu Cys Asp Arg  
 370 375 380  
 Gln Gly Thr Leu Leu Leu Leu Ala Gly Val Lys Lys Thr Pro Leu Ala  
 385 390 395 400  
 Asp Leu Lys Arg Tyr His Leu Asp Glu Leu Ile Gly Val Asp His Ile  
 405 410 415  
 Phe Ser Asn Ile Lys Ser Ala Leu Leu Phe Ala Gln Ala Leu Thr Asn  
 420 425 430  
 Leu Glu Ser Lys Thr Ser Thr Arg His Leu Val  
 435 440

&lt;210&gt;1087

&lt;211&gt;143

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1087

Lys Asn Phe Ile Pro Lys Leu Tyr Thr Ser Ile Lys Glu Gly Tyr Ser  
 1 5 10 15  
 Phe Asn Thr Phe Lys Lys Asp Phe Gln Ala Gly Ile Thr Val Gly Ile  
 20 25 30  
 Leu Ala Phe Pro Phe Ala Ile Ala Ile Gly Val Gly Val Ser  
 35 40 45  
 Pro Ile Gln Gly Leu Leu Ala Ser Ile Ile Gly Gly Leu Leu Ala Ser  
 50 55 60  
 Ala Met Gly Gly Ser Asn Val Leu Ile Ser Gly Pro Ser Ser Ala Phe  
 65 70 75 80  
 Ile Ser Ile Leu Tyr Cys Leu Ser Ala Lys Tyr Gly Ala Glu Ala Leu  
 85 90 95  
 Phe Thr Val Thr Leu Leu Ala Gly Val Phe Leu Ile Ala Phe Gly Leu  
 100 105 110  
 Thr Gly Leu Gly Thr Phe Ile Lys Tyr Met Pro Tyr Pro Val Val Thr  
 115 120 125  
 Gly Leu Thr His Arg Thr Cys Asp His Tyr Ile Leu Leu Ala Asn  
 130 135 140

&lt;210&gt;1088

&lt;211&gt;422

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1088

Val Thr Met Leu Lys Leu Gln Leu Cys Ala Leu Phe Leu Phe Gly Tyr  
 1 5 10 15  
 Leu Ala Ile Val Phe Glu His Ile Val Arg Val Asn Lys Ser Ala Ile  
 20 25 30  
 Ala Leu Ala Met Gly Gly Leu Met Trp Leu Val Cys Phe Ser His Ile  
 35 40 45  
 Pro Met Ala Asp His Met Ile Leu Val Glu Glu Ile Ala Asp Met Ser  
 50 55 60  
 Gln Val Ile Phe Phe Leu Phe Ser Ala Met Ala Ile Val Glu Leu Ile  
 65 70 75 80  
 Asp Ala His Lys Gly Phe Ser Val Ile Val Lys Phe Cys Arg Ile Gln  
 85 90 95  
 Ser Arg Thr Leu Leu Trp Ala Leu Ile Gly Leu Ser Phe Phe Leu  
 100 105 110



Ser Ala Ala Leu Asp Asn Leu Thr Ser Ile Ile Ile Ile Ile Ser Ile  
 115 120 125  
 Leu Lys Arg Leu Val Lys Ala Arg Glu Asp Arg Leu Leu Leu Gly Ala  
 130 135 140  
 Ile Cys Val Ile Ala Val Asn Ala Gly Gly Ala Trp Thr Pro Leu Gly  
 145 150 155 160  
 Asp Val Thr Thr Thr Met Leu Trp Ile Asn Asn Lys Ile Thr Ser Trp  
 165 170 175  
 Gly Ile Ile Arg Ala Leu Phe Val Pro Ser Leu Val Cys Val Leu Val  
 180 185 190  
 Ala Gly Phe Cys Gly Gln Phe Phe Leu Arg Lys Arg Gly Ser Thr Leu  
 195 200 205  
 Ile Ala Lys Asp Val Glu Leu Gln Ser Ala Pro Pro Lys Ser Leu Trp  
 210 215 220  
 Ile Ile Phe Ile Gly Leu Gly Ser Leu Leu Met Val Pro Val Trp Lys  
 225 230 235 240  
 Ala Cys Leu Gly Leu Pro Pro Phe Met Gly Ala Leu Leu Gly Leu Gly  
 245 250 255  
 Leu Val Trp Leu Thr Ser Asp Trp Ile His Ser Pro His Gly Glu Asp  
 260 265 270  
 Arg Tyr His Leu Arg Val Pro His Ile Leu Thr Lys Ile Asp Ile Ser  
 275 280 285  
 Ser Ile Thr Phe Phe Ile Gly Ile Leu Leu Ala Val Asn Ala Leu Ser  
 290 295 300  
 Phe Ala Asn Leu Leu Thr Asp Phe Ser Leu Trp Met Asp Lys Ile Phe  
 305 310 315 320  
 Ser Arg Asn Val Val Ala Ile Val Ile Gly Leu Leu Ser Ser Val Leu  
 325 330 335  
 Asp Asn Val Pro Leu Val Ala Xaa Thr Met Gly Met Tyr Thr Leu Pro  
 340 345 350  
 Leu Asp Asp Thr Leu Trp Lys Leu Ile Ala Tyr Ala Ala Xaa Thr Gly  
 355 360 365  
 Gly Ser Ile Leu Ile Ile Gly Ser Ala Ala Gly Val Ala Phe Met Gly  
 370 375 380  
 Leu Glu Lys Val Asp Phe Leu Trp Tyr Phe Lys Arg Ile Ser Trp Ile  
 385 390 395 400  
 Ala Leu Ala Ser Tyr Phe Gly Gly Leu Phe Ser Tyr Phe Val Leu Glu  
 405 410 415  
 Ser Leu Asn Phe Phe Ile  
 420

&lt;210&gt;1089

&lt;211&gt;624

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1089

Lys Arg Glu Val Phe Met Lys Lys Gly Lys Leu Gly Ala Ile Val Phe  
 1 5 10 15  
 Gly Leu Leu Phe Thr Ser Ser Val Ala Gly Phe Ser Lys Asp Leu Thr  
 20 25 30  
 Lys Asp Asn Ala Tyr Gln Asp Leu Asn Val Ile Glu His Leu Ile Ser  
 35 40 45  
 Leu Lys Tyr Ala Pro Leu Pro Trp Lys Glu Leu Leu Phe Gly Trp Asp  
 50 55 60  
 Leu Ser Gln Gln Thr Gln Gln Ala Arg Leu Gln Leu Val Leu Glu Glu  
 65 70 75 80  
 Lys Pro Thr Thr Asn Tyr Cys Gln Lys Val Leu Ser Asn Tyr Val Arg  
 85 90 95  
 Ser Leu Asn Asp Tyr His Ala Gly Ile Thr Phe Tyr Arg Thr Glu Ser  
 100 105 110  
 Ala Tyr Ile Pro Tyr Val Leu Lys Leu Ser Glu Asp Gly His Val Phe  
 115 120 125  
 Val Val Asp Val Gln Thr Ser Gln Gly Asp Ile Tyr Leu Gly Asp Glu  
 130 135 140  
 Ile Leu Glu Val Asp Gly Met Gly Ile Arg Glu Ala Ile Glu Ser Leu

145	150	155	160
Arg Phe Gly Arg Gly Ser Ala Thr Asp Tyr Ser Ala Ala Val Arg Ser			
	165	170	175
Leu Thr Ser Arg Ser Ala Ala Phe Gly Asp Ala Val Pro Ser Gly Ile			
	180	185	190
Ala Met Leu Lys Leu Arg Arg Pro Ser Gly Leu Ile Arg Ser Thr Pro			
	195	200	205
Val Arg Trp Arg Tyr Thr Pro Glu His Ile Gly Asp Phe Ser Leu Val			
	210	215	220
Ala Pro Leu Ile Pro Glu His Lys Pro Gln Leu Pro Thr Gln Ser Cys			
	225	230	235
Val Leu Phe Arg Ser Gly Val Asn Ser Gln Ser Ser Ser Ser Ser Leu			
	245	250	255
Phe Ser Ser Tyr Met Val Pro Tyr Phe Trp Glu Glu Leu Arg Val Gln			
	260	265	270
Asn Lys Gln Arg Phe Asp Ser Asn His His Ile Gly Ser Arg Asn Gly			
	275	280	285
Phe Leu Pro Thr Phe Gly Pro Ile Leu Trp Glu Gln Asp Lys Gly Pro			
	290	295	300
Tyr Arg Ser Tyr Ile Phe Lys Ala Lys Asp Ser Gln Gly Asn Pro His			
	305	310	315
Arg Ile Gly Phe Leu Arg Ile Ser Ser Tyr Val Trp Thr Asp Leu Glu			
	325	330	335
Gly Leu Glu Glu Asp His Lys Asp Ser Pro Trp Glu Leu Phe Gly Glu			
	340	345	350
Ile Ile Asp His Leu Glu Lys Glu Thr Asp Ala Leu Ile Ile Asp Gln			
	355	360	365
Thr His Asn Pro Gly Gly Ser Val Phe Tyr Leu Tyr Ser Leu Leu Ser			
	370	375	380
Met Leu Thr Asp His Pro Leu Asp Thr Pro Lys His Arg Met Ile Phe			
	385	390	395
Thr Gln Asp Glu Val Ser Ser Ala Leu His Trp Gln Asp Leu Leu Glu			
	405	410	415
Asp Val Phe Thr Asp Glu Gln Ala Val Ala Val Leu Gly Glu Thr Met			
	420	425	430
Glu Gly Tyr Cys Met Asp Met His Ala Val Ala Ser Leu Gln Asn Phe			
	435	440	445
Ser Gln Ser Val Leu Ser Ser Trp Val Ser Gly Asp Ile Asn Leu Ser			
	450	455	460
Lys Pro Met Pro Leu Leu Gly Phe Ala Gln Val Arg Pro His Pro Lys			
	465	470	475
His Gln Tyr Thr Lys Pro Leu Phe Met Leu Ile Asp Glu Asp Asp Phe			
	485	490	495
Ser Cys Gly Asp Leu Ala Pro Ala Ile Leu Lys Asp Asn Gly Arg Ala			
	500	505	510
Thr Leu Ile Gly Lys Pro Thr Ala Gly Ala Gly Gly Phe Val Phe Gln			
	515	520	525
Val Thr Phe Pro Asn Arg Ser Gly Ile Lys Gly Leu Ser Leu Thr Gly			
	530	535	540
Ser Leu Ala Val Arg Lys Asp Gly Glu Phe Ile Glu Asn Leu Gly Val			
	545	550	555
Ala Pro His Ile Asp Leu Gly Phe Thr Ser Arg Asp Leu Gln Thr Ser			
	565	570	575
Arg Phe Thr Asp Tyr Val Glu Ala Val Lys Thr Ile Val Leu Thr Ser			
	580	585	590
Leu Ser Glu Asn Ala Lys Lys Ser Glu Glu Gln Thr Ser Pro Gln Glu			
	595	600	605
Thr Pro Glu Val Ile Arg Val Ser Tyr Pro Thr Thr Thr Ser Ala Leu			
	610	615	620

&lt;210&gt;1090

&lt;211&gt;310

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1090

Met Arg Lys Leu Ile Leu Cys Asn Pro Arg Gly Phe Cys Ser Gly Val  
 1 5 10 15  
 Val Arg Ala Ile Gln Val Val Glu Val Ala Leu Glu Lys Trp Gly Ala  
 20 25 30  
 Pro Ile Tyr Val Lys His Glu Ile Val His Asn Arg His Val Val Asn  
 35 40 45  
 Ala Leu Arg Ala Lys Gly Ala Ile Phe Val Glu Glu Leu Val Asp Val  
 50 55 60  
 Pro Glu Gly Glu Arg Val Ile Tyr Ser Ala His Gly Ile Pro Pro Ser  
 65 70 75 80  
 Val Arg Ala Glu Ala Lys Ala Arg Lys Leu Ile Asp Ile Asp Ala Thr  
 85 90 95  
 Cys Gly Leu Val Thr Lys Val His Ser Ala Ala Lys Leu Tyr Ala Ser  
 100 105 110  
 Lys Gly Tyr Lys Ile Ile Leu Ile Gly His Lys Lys His Val Glu Val  
 115 120 125  
 Ile Gly Ile Val Gly Glu Val Pro Glu His Ile Thr Val Val Glu Lys  
 130 135 140  
 Val Ala Asp Val Glu Ala Leu Pro Phe Ser Ser Asp Thr Pro Leu Phe  
 145 150 155 160  
 Tyr Ile Thr Gln Thr Thr Leu Ser Leu Asp Asp Val Gln Glu Ile Ser  
 165 170 175  
 Ser Ala Leu Leu Lys Arg Tyr Pro Ser Ile Ile Thr Leu Pro Ser Ser  
 180 185 190  
 Ser Ile Cys Tyr Ala Thr Thr Asn Arg Gln Lys Ala Leu Arg Ser Val  
 195 200 205  
 Leu Ser Arg Val Asn Tyr Val Tyr Val Val Gly Asp Val Asn Ser Ser  
 210 215 220  
 Asn Ser Asn Arg Leu Arg Glu Val Ala Leu Arg Arg Gly Val Pro Ala  
 225 230 235 240  
 Asp Leu Ile Asn Asn Pro Glu Asp Ile Asp Thr Asn Ile Val Asn His  
 245 250 255  
 Ser Gly Asp Ile Ala Met Thr Ala Gly Ala Ser Thr Pro Glu Asp Val  
 260 265 270  
 Val Gln Ala Cys Ile Arg Lys Leu Ser Ser Leu Ile Pro Gly Leu Gln  
 275 280 285  
 Val Glu Asn Asp Ile Phe Ala Val Glu Asp Val Val Phe Gln Leu Pro  
 290 295 300  
 Lys Glu Leu Arg Cys Ser  
 305 310

&lt;210&gt;1091

&lt;211&gt;245

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1091

Arg Met Ser Tyr Phe Asn Tyr Gln Lys Asn Ser Val Val Leu Arg Ser  
 1 5 10 15  
 Leu Gly Leu Leu Ala Lys Phe Phe Ser Arg Leu Leu Tyr Arg Val Phe  
 20 25 30  
 Phe Ser Phe Arg Glu Gly Ile Tyr Leu Phe Ser Ser Leu Tyr Leu Lys  
 35 40 45  
 Tyr Pro Arg Leu Phe Phe Tyr Asp Leu Gly Lys Tyr Val Tyr Ser Leu  
 50 55 60  
 Arg His Cys Pro Tyr Ala Lys Leu Gly Arg Leu Pro Gly Ala Ser Leu  
 65 70 75 80  
 Leu Lys Glu Gly Asn Val Tyr Gly Glu Thr Pro Trp Ser Val Leu Ala  
 85 90 95  
 Lys Ile Cys Gln Ala Phe Asp Ile Thr Ser Gln Asp Ile Leu Tyr Asp  
 100 105 110  
 Leu Gly Cys Gly Leu Gly Lys Val Cys Phe Trp Phe Ser His Val Val  
 115 120 125  
 Arg Cys Gln Val Ile Gly Ile Asp Asn Gln Pro His Phe Ile Arg Phe  
 130 135 140  
 Ser Ser Asn Met His Arg Lys Leu Ser Ser Gly Phe Ala Leu Phe Asp

145 150 155 160  
 Thr Glu Glu Phe Lys Asn Val Val Leu Ser Gln Ala Ser Tyr Val Tyr  
 165 170 175  
 Phe Tyr Gly Ser Ser Phe Ser Arg Arg Leu Leu Asn Glu Ile Ile Leu  
 180 185 190  
 Lys Leu Ser Glu Met Ala Pro Gly Ser Val Val Ile Ser Ile Ser Phe  
 195 200 205  
 Pro Leu Asp Ser Phe Ser Arg Gly Lys Glu Cys Phe Phe Thr Glu Lys  
 210 215 220  
 Ser Cys Ser Val Arg Phe Pro Trp Gly Lys Thr Ile Ala Tyr Lys Asn  
 225 230 235 240  
 Ile Arg Lys Gly Ser  
 245

&lt;210&gt;1092

&lt;211&gt;385

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1092

Lys Ser Leu Ser Ala Glu Ser Thr Ser Ser Asn Ser Thr Gly Lys Ala  
 1 5 10 15  
 Ser Thr Glu Thr Thr Ser Ser Ser Phe Pro Phe Phe Ser Cys Lys Ala  
 20 25 30  
 Pro Glu Gly Asp Ser Ser Val Asp Lys Thr Phe Thr Val Ser Val Gln  
 35 40 45  
 Thr Pro Lys Ala Gln Glu Gln Glu Ala Ser Ala Ser Gln Ser Gln  
 50 55 60  
 Ala Gln Phe His Val Arg Ser Tyr Ser Ser Ser Thr Ile Lys Glu His  
 65 70 75 80  
 Ser Ala Lys Glu Lys Val Ser Gln Ser Thr Lys Ser Ala Glu Thr Gln  
 85 90 95  
 Lys His Thr Gln Thr Lys Ser Asp Ala Thr Leu Ser Pro Met Ser Leu  
 100 105 110  
 Tyr Ser Thr Leu His Lys Glu Val Pro Gln Ala Leu Ser Ser Thr Lys  
 115 120 125  
 Ser Gln Gln Lys Asp Glu Glu His Arg Asp Gln Arg Gln Gln Glu Gly  
 130 135 140  
 Tyr Glu Gln Glu Gln Glu Gln Glu Glu Gly Lys Lys Lys Thr Pro Trp  
 145 150 155 160  
 Cys Thr Val Glu Ser Leu Gln Gln Thr Ser Ser Ser Asn Gln Val Tyr  
 165 170 175  
 Glu Ser Tyr Thr Pro Ile Ile Pro Asp Pro Ile Val Glu Phe Ala Leu  
 180 185 190  
 Ser Glu Ser Gln Leu Ser Val Leu Ala Gly Lys Arg Val Thr Asn Leu  
 195 200 205  
 Asp Val Leu Arg Ile Cys Thr Glu Leu Met Lys Leu Met Leu Lys Ser  
 210 215 220  
 Arg Ala Asn Asp Thr Met Thr Arg Leu Glu Glu Arg Glu Leu Met Glu  
 225 230 235 240  
 Arg Glu Ala His Glu Leu Ala Ala Ser Tyr Ser Arg Gln Ala Lys Tyr  
 245 250 255  
 Ala Arg Trp Leu Gly Ile Ala Thr Ala Thr Leu Gly Ile Leu Gly Ala  
 260 265 270  
 Ile Ala Pro Met Val Gly Glu Ile Ser Gly Asp Ser Ile Leu Gly Phe  
 275 280 285  
 Val Gln Arg Ile Ser Gly Arg Phe Lys Asp Ala Thr Ala Lys Thr Phe  
 290 295 300  
 Phe Lys Gly Ile Gly Lys Val Phe Thr Ser Leu Ser Gln Leu Thr Glu  
 305 310 315 320  
 Ala Ala Ser Lys Val His Glu Leu Ser Glu Ser Ala Val Arg Ala Val  
 325 330 335  
 Ala Glu Tyr Arg Lys Glu Val Phe Arg Met Arg Gln Asp Glu Val Thr  
 340 345 350  
 Arg Thr Ile Glu Glu Val Lys Asp Asn Trp Lys Ser Met Asp Asn Phe  
 355 360 365

Leu Leu Asn Ile Leu Gln Thr Glu His Asp Ala Ala Arg Ser Leu Tyr  
 370 375 380  
 Gln  
 385  
 <210>1093  
 <211>112  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1093  
 Ile His Arg Arg Xaa Ile Met Thr Val Ser Tyr Gln Ser Ile Ser Thr  
 1 5 10 15  
 Pro Pro Pro Glu Gly Glu Phe Asp Ile Phe Val Asp Gly Asn Ala Thr  
 20 25 30  
 Glu Glu Ala Val Val Ala Ala Glu Val Gln Val Ala Leu Pro Ala Gly  
 35 40 45  
 Glu Gln Tyr Ala Met Leu Arg Ala Thr Ser Glu Leu Cys Phe Gly Ile  
 50 55 60  
 Xaa Thr Gln Ser Glu Cys Ala Leu Thr Gln Ala Leu Pro Pro Lys Glu  
 65 70 75 80  
 Lys Thr Ile Thr Arg Arg Ala Ile Ser Ser Lys Lys Trp His Ile Asn  
 85 90 95  
 Ala Ile Asn Ile Ser Ala Glu Pro Lys Thr Arg Thr Ile Ala Ala Asp  
 100 105 110  
 <210>1094  
 <211>515  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1094  
 Cys Gly Asn Ser Thr Met Ser Ser Trp Leu Ser Gln Ala Ser Glu Val  
 1 5 10 15  
 Leu Leu Asn Gln Asp Pro Tyr Ile Pro Asp Ala Pro Arg Ser Gln Glu  
 20 25 30  
 Ser Ser Val Pro Lys Ile Ser Tyr Ser Ile Thr Val Ala Pro Gln Glu  
 35 40 45  
 Ala Gln Lys Ser Leu Pro Lys Phe Phe Thr Gln Lys Phe Gln Ser Gln  
 50 55 60  
 Cys Lys Ser Glu Pro Pro Ile Thr His His Lys Thr Phe Ile Ile Ala  
 65 70 75 80  
 Thr Pro Arg Glu Arg Ile Leu Arg Phe Gly Ser Ser Phe Glu Ser Gln  
 85 90 95  
 Leu His Asn Thr Ser Gln Ala Gln Thr Ser Ser Pro Trp Asn Leu Phe  
 100 105 110  
 Ser Gln Lys Asn Ser Thr Glu Ala Ser Lys Ala Leu Met Gln Glu Leu  
 115 120 125  
 Thr Met Pro Lys Ser Pro Glu Lys Thr Ser Glu Lys Ala Leu Asp Lys  
 130 135 140  
 Asn Leu Ser Ser Lys Gln Glu Gly Ser Cys Lys Asn Phe Asp Thr Leu  
 145 150 155 160  
 His Leu Gln Gln His Leu Lys Leu Phe Gly Thr Val Asp Ser Leu Tyr  
 165 170 175  
 Ser Gln Ser Leu Asp Ser Glu Gln Gln Glu Leu Leu Gln Ser Arg Arg  
 180 185 190  
 Glu Glu Arg Ser Glu Thr Tyr Ala Asn Gln Gln Ser Ser Glu Lys Lys  
 195 200 205  
 Ile Glu Thr Lys Val Gln Ile Lys Asp Leu Cys Lys Asp Leu Phe Ser  
 210 215 220  
 Gln Asp Gln Asp Ser Asn Gln Lys Gln Lys Lys Ser Pro Phe Gln Gln  
 225 230 235 240  
 Asp Thr Ser Arg Lys Asn Arg Ile Ala Lys Ala Ala Gln Ala Val Pro  
 245 250 255  
 Val Ile Pro Pro Pro Ser Ile Gly Val Phe Thr Leu Ser Tyr Leu Leu  
 260 265 270  
 Thr Lys Gln Gly Ile Leu Ser Asp Phe Ser Ser Tyr Gly Cys His Lys  
 275 280 285

Asp Ser Val Glu Ser Thr Gln Arg Glu Leu Asp Ala Leu His Glu Lys  
 290 295 300  
 Arg Ile Glu Thr Ile Lys Val Ser Ile Glu Lys Glu Lys Arg Glu Arg  
 305 310 315 320  
 Leu Trp Gly Ser Leu Ser Asp Ile Ile Gly Trp Leu Ala Pro Phe Val  
 325 330 335  
 Ser Ile Gly Ile Gly Ile Val Ala Ile Leu Ser Gly Gly Gly Ile Phe  
 340 345 350  
 Ala Phe Ala Gly Phe Phe Ala Gly Leu Ile Ser Leu Val Ile Lys Cys  
 355 360 365  
 Leu Glu Lys Leu Lys Phe Trp Asp Trp Leu Glu Lys His Leu Pro Ile  
 370 375 380  
 Asn Asn Glu Glu Leu Arg Arg Lys Ile Ile Thr Ile Ile Gln Trp Val  
 385 390 395 400  
 Val Tyr Leu Thr Pro Val Ile Leu Ser Ile Cys Thr Leu Lys Val Glu  
 405 410 415  
 Asn Leu Gly Phe Ser Pro Ile Ile Glu Gly Ala Ile Lys Gly Ile Gln  
 420 425 430  
 Pro Ala Ile Glu Ser Thr Met Ala Ala Leu Arg Cys Ala Ile Leu Phe  
 435 440 445  
 Ser Gln Ala Glu Ile Tyr Lys Leu Lys Gly Lys Leu Thr Lys Ile Gln  
 450 455 460  
 Leu Asp Ile Glu Leu Lys Ser Phe Asp Arg Asp Asp His Tyr Glu Arg  
 465 470 475 480  
 Ser Gln Glu Leu Leu Asp Asn Met Glu Ser Ser Phe Glu Ala Leu Ser  
 485 490 495  
 Arg Ile Leu Asn Tyr Met Arg Glu Leu Asp Gln Val Tyr Leu His Ser  
 500 505 510  
 Leu Arg Gly  
 515

&lt;210&gt;1095

&lt;211&gt;191

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1095

Cys Ile Glu Val Ile Glu Arg Thr Tyr Gly His Leu His Leu Gln Pro  
 1 5 10 15  
 Thr Pro Leu Met Ser His Leu Asn Tyr Leu Leu Glu Lys Ile Ala Ala  
 20 25 30  
 Ser Ser Lys Glu Asp Phe Pro Phe Pro Asp Asp Leu Glu Ser Tyr Leu  
 35 40 45  
 Glu Gly Tyr Val Pro Asp Lys Asn Ile Ala Leu Asp Thr Tyr Gln Lys  
 50 55 60  
 Ile Phe Lys Ile Ser Ser Glu Asp Leu Glu Lys Val Tyr Lys Glu Gly  
 65 70 75 80  
 Tyr His Ala Tyr Leu Asp Lys Asp Tyr Ala Lys Ser Ile Thr Val Phe  
 85 90 95  
 Arg Trp Leu Val Phe Phe Asn Pro Phe Val Ser Lys Phe Trp Phe Ser  
 100 105 110  
 Leu Gly Ala Ser Leu His Met Ser Glu Gln Tyr Ser Gln Ala Leu His  
 115 120 125  
 Ala Tyr Gly Val Thr Ala Val Leu Arg Asp Lys Asp Pro Tyr Pro His  
 130 135 140  
 Tyr Tyr Ala Tyr Ile Cys Tyr Thr Leu Thr Asn Glu His Glu Glu Ala  
 145 150 155 160  
 Glu Lys Ala Leu Glu Met Ala Trp Val Arg Ala Gln His Lys Pro Leu  
 165 170 175  
 Tyr Asn Glu Leu Lys Glu Glu Ile Leu Asp Ile Arg Lys His Lys  
 180 185 190

&lt;210&gt;1096

&lt;211&gt;339

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1096

Thr Thr Ala Ser Ser Ser Asn Thr Lys Arg Leu Cys Cys Lys Lys Thr  
 1 5 10 15  
 Gln Arg Arg Pro Ser Pro Glu Thr Gln Ala Arg Ala Ser Leu Ser Gln  
 20 25 30  
 Ala Ser Ser Ser Ser Gln Arg Ser Leu Pro Pro Gln Glu Ser Ala Pro  
 35 40 45  
 Glu Arg Thr Leu Leu Glu Gln Gln Lys Ala Ser Ser Phe Ser Pro Leu  
 50 55 60  
 Ser Gln Phe Ser Ala Glu Lys Gln Lys Glu Ala Leu Thr Thr Ser Lys  
 65 70 75 80  
 Ser His Glu Leu Tyr Lys Glu Arg Asp Gln Asp Arg Gln Gln Arg Glu  
 85 90 95  
 Gln His Asp Arg Lys His Asp Gln Glu Glu Asp Ala Glu Ser Lys Lys  
 100 105 110  
 Lys Lys Lys Lys Arg Gly Leu Gly Val Glu Ala Val Ala Glu Glu Pro  
 115 120 125  
 Gly Glu Asn Leu Asp Ile Ala Ala Leu Ile Phe Ser Asp Gln Met Arg  
 130 135 140  
 Pro Pro Ala Glu Glu Thr Ser Xaa Lys Glu Thr Thr Phe Lys Lys Lys  
 145 150 155 160  
 Leu Pro Ser Pro Met Ser Val Phe Ser Arg Phe Ile Pro Ser Lys Asn  
 165 170 175  
 Pro Leu Ser Val Gly Ser Ser Ile His Xaa Pro Ile Gln Thr Pro Lys  
 180 185 190  
 Val Glu Asn Val Phe Leu Arg Phe Met Lys Leu Met Ala Arg Ile Leu  
 195 200 205  
 Gly Gln Ala Glu Ala Glu Ala Asn Glu Leu Tyr Met Arg Val Lys Gln  
 210 215 220  
 Arg Thr Asp Asp Val Asp Thr Leu Thr Val Leu Ile Ser Lys Ile Asn  
 225 230 235 240  
 Asn Glu Lys Lys Asp Ile Asp Trp Ser Glu Asn Glu Glu Met Lys Ala  
 245 250 255  
 Leu Leu Asn Arg Ala Lys Glu Ile Gly Val Thr Ile Asp Lys Glu Lys  
 260 265 270  
 Tyr Thr Trp Thr Glu Glu Glu Lys Arg Leu Leu Lys Glu Asn Val Gln  
 275 280 285  
 Met Arg Lys Glu Asn Met Glu Lys Ile Thr Gln Met Glu Arg Thr Asp  
 290 295 300  
 Met Gln Arg His Leu Gln Glu Ile Ser Gln Cys His Gln Ala Arg Ser  
 305 310 315 320  
 Asn Val Leu Lys Leu Leu Lys Glu Leu Met Asp Thr Phe Ile Tyr Asn  
 325 330 335  
 Leu Arg Pro

&lt;210&gt;1097

&lt;211&gt;211

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1097

Phe Ser Phe Phe Phe Tyr Ala Leu Lys Leu Gln Ile Met Asn Met Pro  
 1 5 10 15  
 Val Pro Ser Ala Val Pro Ser Ala Asn Ile Thr Leu Lys Glu Asp Ser  
 20 25 30  
 Ser Thr Val Ser Thr Ala Ser Gly Ile Leu Lys Thr Ala Thr Gly Glu  
 35 40 45  
 Val Leu Val Ser Cys Thr Ala Leu Glu Gly Ser Ser Thr Asp Ala  
 50 55 60  
 Leu Ile Ser Leu Ala Leu Gly Gln Ile Ile Leu Ala Thr Gln Gln Glu  
 65 70 75 80  
 Leu Leu Leu Gln Ser Thr Asn Val His Gln Leu Leu Phe Leu Pro Pro  
 85 90 95  
 Glu Val Val Glu Leu Glu Ile Gln Val Val Asp Leu Leu Val Gln Leu  
 100 105 110  
 Glu His Ala Glu Thr Ile Thr Ser Glu Pro Gln Glu Thr Gln Thr Gln

```

      115      120      125
Ser Arg Ser Glu Gln Thr Leu Pro Gln Gln Ser Ser Ser Lys Gln Ser
      130      135      140
Ala Leu Ser Pro Arg Ser Leu Lys Pro Glu Ile Ser Asp Ser Lys Gln
145      150      155      160
Gln Gln Ala Leu Gln Thr Pro Lys Asp Ser Ala Val Arg Lys His Ser
      165      170      175
Glu Asp Arg His Leu Arg His Lys Leu Ala Leu Pro Tyr Leu Arg Gln
      180      185      190
Ala Gln Val Leu Arg Asp Pro Tyr Leu Arg Lys Lys Val Arg Gln Lys
      195      200      205
Glu His Tyr
      210
<210>1098
<211>106
<212>PRT
<213>Chlamydia pneumoniae
<400>1098
Ile Phe Leu Glu Ile Phe Ile Met Lys Lys Val Val Thr Leu Ser Ile
1      5      10      15
Ile Phe Phe Ala Thr Tyr Cys Ala Ser Glu Leu Ser Ala Val Thr Val
      20      25      30
Val Ala Val Pro Leu Ser Glu Ala Pro Gly Lys Ile Gln Val Arg Pro
      35      40      45
Val Val Gly Leu Gln Phe Gln Glu Glu Gln Gly Ser Val Pro Tyr Ser
      50      55      60
Phe Tyr Tyr Pro Tyr Asp Tyr Gly Tyr Tyr Tyr Pro Glu Thr Tyr Gly
      65      70      75      80
Tyr Thr Lys Asn Thr Gly Gln Glu Ser Arg Glu Cys Tyr Thr Arg Phe
      85      90      95
Glu Asp Gly Thr Ile Phe Tyr Glu Cys Asp
      100      105
<210>1099
<211>301
<212>PRT
<213>Chlamydia pneumoniae
<400>1099
Met Thr Met Pro Ser Thr Gln Phe His Thr Thr Ile Leu Glu Gln Phe
1      5      10      15
Ser Leu Phe Leu Ser Val Asp Arg Gly Leu Cys Gln Gln Ser Ile Ala
      20      25      30
Ala Tyr Arg Gln Asp Ile Ser Ser Phe Leu Thr Ile Ser Ala Ile Ser
      35      40      45
Ser Pro Gln Asp Ile Ser Gln Asn Ser Val Tyr Ile Phe Ala Glu Glu
      50      55      60
Leu Tyr Arg Arg Lys Glu Ala Glu Thr Thr Leu Ala Arg Arg Leu Ile
      65      70      75      80
Ala Leu Lys Val Phe Phe Leu Phe Leu Lys Asp Gln Gln Leu Leu Pro
      85      90      95
Tyr Pro Pro Ile Ile Glu His Pro Lys Ile Trp Lys Arg Leu Pro Ser
      100      105      110
Val Leu Thr Pro Gln Glu Val Asp Ala Leu Leu Ala Val Pro Leu Gln
      115      120      125
Met Glu Lys Asn Pro Arg His Leu Ala Phe Arg Asp Thr Ala Ile Leu
      130      135      140
His Thr Leu Tyr Ser Thr Gly Val Arg Val Ser Glu Leu Cys Asp Leu
145      150      155      160
Arg Leu Gly His Val Ser Asp Asp Cys Ile Arg Val Thr Gly Lys Gly
      165      170      175
Ser Lys Thr Arg Leu Val Pro Leu Gly Ser Arg Ala Arg Glu Ala Ile
      180      185      190
Asp Ala Tyr Leu Cys Pro Phe Arg Asp Gln Tyr Gln Lys Lys Asn Pro
      195      200      205
His Glu Asp His Leu Phe Leu Ser Thr Arg Gly His Lys Leu Glu Arg

```



210 215 220  
 Ser Cys Val Trp Arg Arg Ile His Asn Tyr Ala Lys Gln Val Thr Ser  
 225 230 235 240  
 Lys Pro Val Ser Pro His Ser Leu Arg His Ala Phe Ala Thr His Leu  
 245 250 255  
 Leu Asp Asn Lys Ala Asp Leu Arg Val Ile Gln Glu Met Leu Gly His  
 260 265 270  
 Ala Arg Ile Ala Ser Thr Glu Val Tyr Thr His Val Ala Ala Asp Ser  
 275 280 285  
 Leu Ile Glu Lys Phe Leu Ala His His Pro Arg Asn Leu  
 290 295 300  
 <210>1100  
 <211>553  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1100  
 Val Glu Gly Ile Val Ile Leu Ala Asn Glu Cys Asn Phe Ser Ile Gly  
 1 5 10 15  
 Ser Gly Glu Phe Ser Ser Tyr Arg Glu Lys Thr Met Glu Arg Lys Arg  
 20 25 30  
 Phe Ile Asp Cys Asp Ser Thr Lys Ile Leu Gln Glu Leu Ala Leu Asn  
 35 40 45  
 Pro Leu Asp Leu Thr Ala Pro Gly Val Leu Ser Ala Glu Arg Ile Lys  
 50 55 60  
 Lys Phe Ser Leu Leu Gly Gly Gly Phe Thr Phe Ser Phe Ala Thr Glu  
 65 70 75 80  
 Arg Leu Asp Asp Ala Ile Leu Ala Ala Leu Ile Ser Leu Ala Glu Glu  
 85 90 95  
 Arg Gly Leu His Glu Ser Met Leu Ala Met Gln Gln Gly Gln Val Val  
 100 105 110  
 Asn Tyr Ile Glu Gly Phe Pro Ser Glu Met Arg Pro Ala Leu His Thr  
 115 120 125  
 Ala Thr Arg Ala Trp Val Thr Asp Ser Ser Phe Thr Gly Glu Ala Glu  
 130 135 140  
 Asp Ile Ala Val Arg Ser Arg Val Glu Ala Gln Arg Leu Lys Asp Phe  
 145 150 155 160  
 Leu Thr Lys Val Arg Ser Gln Phe Thr Thr Ile Val Gln Ile Gly Ile  
 165 170 175  
 Gly Gly Ser Glu Leu Gly Pro Lys Ala Leu Tyr Arg Ala Leu Arg Ala  
 180 185 190  
 Tyr Cys Pro Thr Asp Lys His Val His Phe Ile Ser Asn Ile Asp Pro  
 195 200 205  
 Asp Asn Gly Ala Glu Val Leu Asp Thr Ile Asp Cys Ala Lys Ala Leu  
 210 215 220  
 Val Val Val Val Ser Lys Ser Gly Thr Thr Ile Glu Thr Ala Val Asn  
 225 230 235 240  
 Glu Ala Phe Phe Ala Asp Tyr Phe Ala Lys Lys Gly Leu Ser Phe Lys  
 245 250 255  
 Asp His Phe Ile Ala Val Thr Cys Glu Gly Ser Pro Met Asp Asp Thr  
 260 265 270  
 Gly Lys Tyr Leu Glu Val Phe His Leu Trp Glu Ser Ile Gly Gly Arg  
 275 280 285  
 Phe Ser Ser Thr Ser Met Val Gly Gly Val Val Leu Gly Phe Ala Tyr  
 290 295 300  
 Gly Phe Glu Val Phe Leu Gln Leu Leu Gln Gly Ala Ser Ala Met Asp  
 305 310 315 320  
 Gln Ile Ala Leu Gln Pro Asn Ala Arg Glu Asn Leu Pro Met Leu Ser  
 325 330 335  
 Ala Leu Ile Ser Ile Trp Asn Arg Asn Phe Leu Gly Tyr Pro Thr Glu  
 340 345 350  
 Ala Val Ile Pro Tyr Ser Ser Gly Leu Glu Phe Phe Pro Ala His Leu  
 355 360 365  
 Gln Gln Cys Cys Met Glu Ser Asn Gly Lys Ser Ile Val Gln Asp Gly  
 370 375 380

Arg Arg Val Gly Phe Ser Thr Ser Pro Val Ile Trp Gly Glu Pro Gly  
 385 390 395 400  
 Thr Asn Gly Gln His Ser Phe Phe Gln Cys Leu His Gln Gly Thr Asp  
 405 410 415  
 Ile Ile Pro Val Glu Phe Ile Gly Phe Glu Lys Ser Gln Lys Gly Glu  
 420 425 430  
 Asp Ile Ser Phe Gln Gly Thr Thr Ser Ser Gln Lys Leu Phe Ala Asn  
 435 440 445  
 Met Ile Ala Gln Ala Ile Ala Leu Ala Cys Gly Ser Glu Asn Thr Asn  
 450 455 460  
 Pro Asn Lys Asn Phe Asp Gly Asn Arg Pro Ser Ser Val Leu Val Ser  
 465 470 475 480  
 Ser Gln Leu Asn Pro Tyr Ser Leu Gly Glu Leu Leu Ser Tyr Tyr Glu  
 485 490 495  
 Asn Lys Ile Val Phe Gln Gly Phe Cys Trp Gly Ile Asn Ser Phe Asp  
 500 505 510  
 Gln Glu Gly Val Ser Leu Gly Lys Ala Leu Ala Asn Arg Val Leu Glu  
 515 520 525  
 Leu Leu Glu Gly Ala Asp Ala Ser Asn Phe Pro Glu Ala Ala Ser Leu  
 530 535 540  
 Leu Thr Leu Phe Asn Ile Lys Phe Arg  
 545 550  
 <210>1101  
 <211>523  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1101  
 Asn Met Pro Gly Ser Val Ser Ser Pro Pro Leu Ser Pro Val Ile Val  
 1 5 10 15  
 Arg Glu Arg Val Pro Ser Ser Ser Gly Ser Asp Leu Ile Gln Pro His  
 20 25 30  
 Ala Val Leu Lys Ile Ser Ile Leu Ile Phe Ala Leu Val Thr Ile Leu  
 35 40 45  
 Gly Ile Val Leu Val Val Ser Ser Ala Leu Gly Ala Leu Pro Ser Leu  
 50 55 60  
 Val Leu Thr Val Ser Gly Cys Ile Ala Ile Ala Val Gly Leu Ile Gly  
 65 70 75 80  
 Leu Gly Ile Leu Val Thr Arg Leu Ile Leu Ser Thr Ile Arg Lys Val  
 85 90 95  
 Asp Ala Met Gly Tyr Asp Ala Ala Val Lys Glu Glu Gln Tyr Leu Ser  
 100 105 110  
 Arg Ile Arg Glu Leu Glu Ser Glu Asn Arg Glu Ile Arg Asp Arg Asn  
 115 120 125  
 Arg Ala Val Glu Asp Gln Cys Ala His Leu Ser Glu Glu Asn Lys Asp  
 130 135 140  
 Leu Arg Asp Pro Glu Tyr Leu His Gly Met Thr Glu Arg Leu Ile Ala  
 145 150 155 160  
 Ser Leu Glu Ile Glu Asn Gln Ala Leu Val Ala Glu Asn Ile Leu Leu  
 165 170 175  
 Lys Asp Trp Asn Ala Ser Leu Ser Arg Asp Phe Arg Ala Tyr Lys Gln  
 180 185 190  
 Lys Phe Pro Leu Gly Ala Leu Glu Pro Trp Lys Glu Asp Ile Ala Cys  
 195 200 205  
 Ile Met Glu Gln Asn Leu Phe Leu Lys Pro Glu Cys Ile Ala Met Val  
 210 215 220  
 Lys Ser Leu Pro Leu Glu Thr Gln Arg Leu Phe Leu Tyr Pro Lys Gly  
 225 230 235 240  
 Phe Gln Ser Leu Val Asn Arg Phe Ala Pro Arg Ser Arg Phe Phe Gln  
 245 250 255  
 Thr Pro Lys Tyr Glu Tyr Asn Ser Arg Asn Glu Asn Glu Asp Gly Lys  
 260 265 270  
 Val Ala Ala Val Cys Ala Arg Leu Lys Lys Glu Phe Phe Ser Ala Val  
 275 280 285  
 Leu Gly Ala Cys Ser Tyr Glu Glu Leu Gly Gly Ile Cys Glu Arg Ala

290 295 300  
 Val Ala Leu Lys Glu Thr Leu Pro Leu Pro Glu Ala Val Tyr Asp Thr  
 305 310 315 320  
 Leu Val Gln Glu Phe Pro Asn Leu Leu Thr Ala Glu Ser Leu Trp Lys  
 325 330 335  
 Glu Trp Cys Phe Tyr Ser Tyr Pro Tyr Leu Arg Pro Tyr Leu Ser Val  
 340 345 350  
 Asp Tyr Cys Lys Arg Leu Phe Val Gln Leu Phe Glu Glu Leu Cys Leu  
 355 360 365  
 Lys Leu Phe Thr Thr Gly Ser Pro Glu Asp Gln Ala Leu Val Arg Leu  
 370 375 380  
 Phe Ser Tyr Tyr Arg Asn His Ile Pro Ala Val Leu Ala Ser Phe Gly  
 385 390 395 400  
 Leu Pro Pro Pro Glu Thr Gly Gly Ser Val Phe Val Leu Leu Pro Lys  
 405 410 415  
 Gln Glu Asn Leu Leu Trp Ser Gln Ile Glu Val Leu Ala Thr Arg Tyr  
 420 425 430  
 Leu Lys Asp Thr Phe Val Arg Asn Ser Glu Trp Thr Gly Ser Phe Glu  
 435 440 445  
 Met Met Phe Ser Tyr Asn Glu Met Cys Lys Glu Ile Ser Glu Gly Arg  
 450 455 460  
 Ile Arg Phe Ala Glu Asp Tyr Glu Thr Arg His Ser Glu Glu Phe Pro  
 465 470 475 480  
 Pro Ser Pro Leu Ser Glu Glu Gly Glu Gly Glu Glu Phe Leu Pro Pro  
 485 490 495  
 Cys Ser Glu Glu Glu Val Ser Val Leu Glu Arg Pro Asp Leu Asp Val  
 500 505 510  
 Asp Ser Met Trp Val Trp His Pro Ser Gly Pro  
 515 520  
 <210>1102  
 <211>335  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1102  
 Phe Phe Leu Lys Gly Val Arg Met Ala Phe Lys Glu Val Val Arg Val  
 1 5 10 15  
 Ala Val Thr Gly Gly Lys Gly Gln Ile Ala Tyr Asn Phe Leu Phe Ala  
 20 25 30  
 Leu Ala His Gly Asp Val Phe Gly Val Asp Arg Gly Val Asp Leu Arg  
 35 40 45  
 Ile Tyr Asp Val Pro Gly Thr Glu Arg Ala Leu Ser Gly Val Arg Met  
 50 55 60  
 Glu Leu Asp Asp Gly Ala Tyr Pro Leu Xaa His Arg Leu Arg Val Thr  
 65 70 75 80  
 Thr Ser Leu Asn Asp Ala Phe Asp Gly Ile Asp Ala Ala Phe Leu Ile  
 85 90 95  
 Gly Ala Val Pro Arg Gly Pro Gly Met Glu Arg Gly Asp Leu Leu Lys  
 100 105 110  
 Gln Asn Gly Gln Ile Phe Ser Leu Gln Gly Ala Ala Leu Asn Thr Ala  
 115 120 125  
 Ala Lys Arg Asp Ala Lys Ile Phe Val Val Gly Asn Pro Val Asn Thr  
 130 135 140  
 Asn Cys Trp Ile Ala Met Lys His Ala Pro Arg Leu His Arg Lys Asn  
 145 150 155 160  
 Phe His Ala Met Leu Arg Leu Asp Gln Asn Arg Met His Ser Met Leu  
 165 170 175  
 Ala His Arg Ala Glu Val Pro Leu Glu Val Ser Arg Val Val Ile  
 180 185 190  
 Trp Gly Asn His Ser Ala Lys Gln Val Pro Asp Phe Thr Gln Ala Arg  
 195 200 205  
 Ile Ser Gly Lys Pro Ala Ala Glu Val Ile Gly Asp Arg Asp Trp Leu  
 210 215 220  
 Glu Asn Ile Leu Val His Ser Val Gln Asn Arg Gly Ser Ala Val Ile  
 225 230 235 240

Glu Ala Arg Gly Lys Ser Ser Ala Ala Ser Ala Ser Arg Ala Leu Ala  
 245 250 255  
 Glu Ala Ala Arg Ser Ile Phe Cys Pro Lys Ser Asp Glu Trp Phe Ser  
 260 265 270  
 Ser Gly Val Cys Ser Asp His Asn Pro Tyr Gly Ile Pro Glu Asp Leu  
 275 280 285  
 Ile Phe Gly Phe Pro Cys Arg Met Leu Pro Ser Gly Asp Tyr Glu Ile  
 290 295 300  
 Ile Pro Gly Leu Pro Trp Glu Pro Phe Ile Arg Asn Lys Ile Gln Ile  
 305 310 315 320  
 Ser Leu Asp Glu Ile Ala Gln Glu Lys Ala Ser Val Ser Ser Leu  
 325 330 335

&lt;210&gt;1103

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1103

Ser Glu His Thr Pro Glu Glu Asn His Ser Ser Leu Leu Gly Gln Lys  
 1 5 10 15  
 Ile Asp Arg Ala Ala Ser Ala Ser Ala Arg Asp Ala Asp Ala Ala Glu  
 20 25 30  
 Asp Phe Pro Leu Ala Ser Ile Thr Ala Leu Pro Arg Phe Cys Thr Glu  
 35 40 45  
 Cys Thr Lys Met Phe Ser Asn Gln Ser Arg Ser Pro Ile Thr Ser Ala  
 50 55 60  
 Ala Gly Phe Pro Glu Ile Arg Ala Cys Val Lys Ser Gly Thr Cys Phe  
 65 70 75 80  
 Ala Glu

&lt;210&gt;1104

&lt;211&gt;275

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1104

Ser Xaa Cys Ala Ser Lys Ala Leu Asn Val Pro Ile Val Ile Ser Gln  
 1 5 10 15  
 Gly Ile Leu Arg Pro Ala Ile Asp Glu Asp Gln Ala Gln Leu Phe Thr  
 20 25 30  
 Glu Arg Val Glu Glu Phe Pro Lys Glu Val Glu Trp Trp Glu Xaa Ala  
 35 40 45  
 Arg Cys Glu Ile Ser Ile Pro Ser Met Val Ile Pro Pro Asn Leu Gly  
 50 55 60  
 Ala Leu Phe Ile Lys Ser Gly Val Thr Leu Asn Asn Asp Leu Tyr Ile  
 65 70 75 80  
 Gln Gly Leu Ala Asp Ala Cys Met Lys Leu Gly Thr Gln Phe Tyr Asp  
 85 90 95  
 Glu Leu Ile Glu Asp Leu Ala Asp Ile Glu Glu Phe Tyr Asp His Ile  
 100 105 110  
 Ile Val Thr Pro Gly Ala Asn Ala Ser Ile Leu Pro Glu Leu Lys Asp  
 115 120 125  
 Met Pro Val Asn Lys Val Lys Gly Gln Leu Leu Glu Ile Ser Trp Pro  
 130 135 140  
 Lys Asp Leu Ala Met Leu Ser Phe Ser Ile Asn Ala His Lys Tyr Met  
 145 150 155 160  
 Val Ala Asn Thr Gln Lys Asn Thr Cys Ile Leu Gly Ala Thr Phe Glu  
 165 170 175  
 His Asn Gln Pro Glu Glu Thr Pro Asp Pro Ala Ile Ala Tyr Gln Glu  
 180 185 190  
 Ile Met Pro Pro Val Leu Ser Leu Phe Pro Gly Leu Lys Asp Ala Gln  
 195 200 205  
 Val Leu His Cys Tyr Ala Gly Met Arg Ser Ser Ser Lys Ser Arg Leu  
 210 215 220  
 Pro Val Ile Ser Arg Ile Arg Glu Lys Leu Trp Phe Leu Gly Gly Leu  
 225 230 235 240

1109

420 425 430  
 Val Leu Leu Ala Leu Gly Ile Pro Phe Tyr Ile Asp Ala Gly Lys Lys  
 435 440 445  
 Lys Lys Asn Ala Lys Thr Phe Phe Ala Lys Lys Glu Ile Val Gly Met  
 450 455 460  
 Thr Phe Ile Gly Leu Leu Ala Leu Thr Ala Ile Phe Leu Phe Ser Thr  
 465 470 475 480  
 Gly Arg Ile Lys Ile  
 485

&lt;210&gt;1106

&lt;211&gt;196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1106

Leu Met Ala Tyr Gly Thr Arg Tyr Pro Thr Leu Ala Phe His Thr Gly  
 1 5 10 15  
 Gly Ile Gly Glu Ser Asp Asp Gly Met Pro Pro Gln Pro Phe Glu Thr  
 20 25 30  
 Phe Cys Tyr Asp Ser Ala Leu Leu Gln Ala Lys Ile Glu Asn Phe Asn  
 35 40 45  
 Ile Val Pro Tyr Thr Ser Val Leu Pro Lys Glu Leu Phe Gly Asn Ile  
 50 55 60  
 Val Pro Val Asp Thr Cys Val Lys Ser Phe Lys His Gly Ala Val Leu  
 65 70 75 80  
 Glu Val Ile Met Ala Gly Arg Gly Ala Leu Ser Asp Gly Thr His  
 85 90 95  
 Ala Ile Ala Thr Gly Ile Gly Ile Cys Trp Gly Lys Asp Lys Asn Gly  
 100 105 110  
 Glu Leu Ile Gly Gly Trp Ala Ala Glu Tyr Val Glu Phe Phe Pro Thr  
 115 120 125  
 Trp Ile Asn Asp Glu Ile Ala Glu Thr His Ala Lys Met Trp Leu Lys  
 130 135 140  
 Lys Ser Leu Gln His Glu Leu Asp Leu Arg Ser Ile Ala Lys His Ser  
 145 150 155 160  
 Glu Phe Gln Phe Phe His Asn Tyr Ile Asn Ile Lys Gln Lys Phe Gly  
 165 170 175  
 Phe Cys Leu Thr Ala Leu Gly Phe Leu Asn Phe Glu Asn Ala Glu Pro  
 180 185 190  
 Ala Lys Val Asn  
 195

&lt;210&gt;1107

&lt;211&gt;165

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1107

Gln Lys Ala Thr Tyr Asn Phe Tyr Gly Tyr Ala Ser Trp Thr Pro Lys  
 1 5 10 15  
 Pro Ser Cys Gly Asp Gly Gln Tyr Ser Val Leu Leu Tyr Ser Thr Arg  
 20 25 30  
 Lys Val Pro Glu Gln Asn Ser Gln Val Thr Gly Trp Ser Leu Asn Ala  
 35 40 45  
 Ala Gln His Ile His Glu Lys Leu Tyr Leu Phe Gly Arg Ile Asn Gly  
 50 55 60  
 Ala Thr Gly Thr Ala Leu Pro Ile Asn Arg Ser Tyr Val Leu Gly Leu  
 65 70 75 80  
 Val Ser Glu Asn Pro Leu Asn Arg His Ser Gln Asp Leu Leu Gly Ile  
 85 90 95  
 Gly Phe Ala Thr Asn Lys Val Asn Ala Lys Ala Ile Ser Asn Val Asn  
 100 105 110  
 Lys Leu Arg Arg Tyr Glu Ser Val Met Glu Ala Phe Ala Thr Ile Gly  
 115 120 125  
 Phe Gly Pro Tyr Ile Ser Leu Thr Pro Asp Phe Gln Leu Tyr Ile His  
 130 135 140  
 Pro Ala Leu Arg Pro Glu Arg Arg Thr Ser Gln Val Tyr Gly Leu Arg

145 150 155 160  
Ala Asn Leu Ser Leu  
165  
<210>1108  
<211>354  
<212>PRT  
<213>Chlamydia pneumoniae  
<400>1108  
Asn Asn Lys Lys Lys Asp Tyr Ser Gly Glu Phe Leu Thr Thr Asp Thr  
1 5 10 15  
Val Asp Ser Ile Ala Phe Leu Ser Ser Glu Glu Asn Phe Cys Tyr Ile  
20 25 30  
Lys Thr Ile Leu Phe Phe Arg Val Lys Lys Lys His Tyr Ala Phe Phe  
35 40 45  
Tyr Gly Glu Phe Met Ile Xaa Phe Arg Phe Leu Leu Leu Ser Gly Leu  
50 55 60  
Cys Ala Leu Gly Ile Ser Ser Tyr Ala Glu Thr Pro Lys Glu Thr Thr  
65 70 75 80  
Gly His Tyr His Arg Tyr Lys Ala Arg Ile Gln Lys Lys His Pro Glu  
85 90 95  
Ser Ile Lys Glu Ser Ala Pro Ser Glu Thr Pro His His Asn Ser Leu  
100 105 110  
Leu Ser Pro Val Thr Asn Ile Phe Cys Ser His Pro Trp Lys Asp Gly  
115 120 125  
Ile Ser Val Ser Asn Leu Leu Thr Ser Val Glu Lys Ala Thr Asn Thr  
130 135 140  
Gln Ile Ser Leu Asp Phe Ser Ile Leu Pro Gln Trp Phe Tyr Pro His  
145 150 155 160  
Lys Ala Leu Gly Gln Thr Gln Ala Leu Glu Ile Pro Ser Trp Gln Phe  
165 170 175  
Tyr Phe Ser Pro Ser Thr Thr Trp Thr Leu Tyr Asp Ser Pro Thr Ala  
180 185 190  
Gly Gln Gly Ile Val Asp Phe Ser Tyr Thr Leu Ile His Tyr Trp Gln  
195 200 205  
Thr Asn Gly Val Asp Ala Asn Gln Ala Ala Gly Thr Ala Ser Ser Met  
210 215 220  
Asn Asp Tyr Ser Asn Arg Glu Asn Asn Leu Ala Gln Leu Thr Phe Ser  
225 230 235 240  
Gln Thr Phe Pro Gly Asp Phe Leu Thr Leu Ala Ile Gly Gln Tyr Ser  
245 250 255  
Leu Tyr Ala Ile Asp Gly Thr Leu Tyr Asp Asn Asp Gln Tyr Ser Gly  
260 265 270  
Phe Ile Ser Tyr Ala Leu Ser Gln Asn Ala Ser Ala Thr Tyr Ser Leu  
275 280 285  
Gly Ser Thr Gly Ala Tyr Leu Gln Phe Thr Pro Asn Ser Glu Ile Lys  
290 295 300  
Val Gln Leu Gly Phe Gln Asp Ser Tyr Asn Ile Asp Gly Thr Asn Phe  
305 310 315 320  
Ser Ile Tyr Asn Leu Thr Lys Ser Asn Ile Gln Leu Leu Arg Leu Arg  
325 330 335  
Leu Leu Asp Ser Lys Thr Phe Val Trp Arg Trp Thr Val Leu Cys Ile  
340 345 350  
Ala Leu

&lt;210&gt;1109

&lt;211&gt;286

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1109

Lys Thr Ser Trp Gln Lys Tyr Lys Lys Tyr Leu Ser Tyr Ser Ile Leu  
1 5 10 15  
Val Gln Lys Ile Ala Arg Tyr Val Met Lys Thr Trp Leu Phe Thr  
20 25 30  
Phe Leu Phe Ser Cys Ser Ser Phe Tyr Ala Ser Cys Arg Tyr Ala Glu

35 40 45  
 Val Arg Ser Ile His Glu Val Ala Gly Asp Ile Leu Tyr Asp Glu Glu  
 50 55 60  
 Asn Phe Trp Leu Ile Leu Asp Leu Asp Asp Thr Leu Leu Gln Gly Gly  
 65 70 75 80  
 Glu Ala Leu Ser His Ser Ile Trp Lys Ser Lys Ala Ile Gln Gly Leu  
 85 90 95  
 Gln Lys Gln Gly Thr Pro Glu Gln Glu Ala Trp Glu Ala Val Val Pro  
 100 105 110  
 Phe Trp Ile Glu Ile Gln Glu Met Gly Thr Val Gln Pro Ile Glu Ser  
 115 120 125  
 Ala Ile Phe Leu Leu Ile Glu Lys Ile Gln Lys Gln Gly Lys Thr Thr  
 130 135 140  
 Phe Val Tyr Thr Glu Arg Pro Lys Thr Ala Lys Asp Leu Thr Leu Lys  
 145 150 155 160  
 Gln Leu His Met Leu Asn Val Ser Leu Glu Asp Thr Ala Pro Gln Pro  
 165 170 175  
 Gln Ala Pro Leu Pro Lys Asn Leu Leu Tyr Thr Ser Gly Ile Leu Phe  
 180 185 190  
 Ser Gly Asp Tyr His Lys Gly Pro Gly Leu Asp Leu Phe Leu Glu Ile  
 195 200 205  
 Cys Thr Pro Leu Pro Ala Lys Ile Ile Tyr Ile Asp Asn Gln Lys Glu  
 210 215 220  
 Asn Val Leu Arg Ile Gly Asp Leu Cys Gln Lys Tyr Gly Ile Ala Tyr  
 225 230 235 240  
 Phe Gly Ile Thr Tyr Lys Ala Gln Glu Leu His Pro Pro Ile Tyr Phe  
 245 250 255  
 Asp Asn Ile Ala Gln Val Gln Tyr Asn Tyr Ser Lys Lys Leu Leu Ser  
 260 265 270  
 Asn Glu Ala Ala Ala Leu Leu Leu Arg His Gln Met His Glu  
 275 280 285

&lt;210&gt;1110

&lt;211&gt;504

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1110

Val Val Gln Leu Pro Leu Met Val Pro Ile Val His Leu Gln Ile Trp  
 1 5 10 15  
 Arg Phe Ser Met Ile Tyr Tyr Gly Val Ser Val Met Leu Cys Ala Thr  
 20 25 30  
 Val Ser Gly Pro Ser Phe Cys Glu Ala Lys Gln Gln Ile Leu Lys Ser  
 35 40 45  
 Leu His Leu Val Asp Ile Ile Glu Leu Arg Leu Asp Leu Ile Asn Glu  
 50 55 60  
 Leu Asp Asp Gln Glu Leu His Thr Leu Ile Thr Thr Ala Gln Asn Pro  
 65 70 75 80  
 Ile Leu Thr Phe Arg Gln His Lys Glu Met Ser Thr Ala Leu Trp Ile  
 85 90 95  
 Gln Lys Leu Tyr Ser Leu Ala Lys Leu Glu Pro Lys Trp Met Asp Ile  
 100 105 110  
 Asp Val Ser Leu Pro Lys Thr Ala Leu Gln Thr Ile Arg Lys Ser His  
 115 120 125  
 Pro Lys Ile Lys Leu Ile Leu Ser Tyr His Thr Asp Lys Asn Glu Asp  
 130 135 140  
 Leu Asp Ala Ile Tyr Asn Glu Met Leu Ala Thr Pro Ala Glu Ile Tyr  
 145 150 155 160  
 Lys Ile Val Leu Ser Pro Glu Asn Ser Ser Glu Ala Leu Asn Tyr Ile  
 165 170 175  
 Lys Lys Ala Arg Leu Leu Pro Lys Pro Ser Thr Val Leu Cys Met Gly  
 180 185 190  
 Thr His Gly Leu Pro Ser Arg Val Leu Ser Pro Leu Ile Ser Asn Ala  
 195 200 205  
 Met Asn Tyr Ala Ala Gly Ile Ser Ala Pro Gln Val Ala Pro Gly Gln  
 210 215 220



Pro Lys Leu Glu Glu Leu Leu Ser Tyr Asn Tyr Ser Lys Leu Ser Glu  
 225 230 235 240  
 Lys Ser His Ile Tyr Gly Leu Ile Gly Asp Pro Val Asp Arg Ser Ile  
 245 250 255  
 Ser His Leu Ser His Asn Phe Leu Leu Ser Lys Leu Ser Leu Asn Ala  
 260 265 270  
 Thr Tyr Ile Lys Phe Pro Val Thr Ile Gly Glu Val Val Thr Phe Phe  
 275 280 285  
 Ser Ala Ile Arg Asp Leu Pro Phe Ser Gly Leu Ser Val Thr Met Pro  
 290 295 300  
 Leu Lys Thr Ala Ile Phe Asp His Val Asp Ala Leu Asp Ala Ser Ala  
 305 310 315 320  
 Gln Leu Cys Glu Ser Ile Asn Thr Leu Val Phe Arg Asn Gln Lys Ile  
 325 330 335  
 Leu Gly Tyr Asn Thr Asp Gly Glu Gly Val Ala Lys Leu Leu Lys Gln  
 340 345 350  
 Lys Asn Ile Ser Val Asn Asn Lys His Ile Ala Ile Val Gly Ala Gly  
 355 360 365  
 Gly Ala Ala Lys Ala Ile Ala Ala Thr Leu Ala Met Gln Gly Ala Asn  
 370 375 380  
 Leu His Ile Phe Asn Arg Thr Leu Ser Ser Ala Ala Ala Leu Ala Thr  
 385 390 395 400  
 Cys Cys Lys Gly Lys Ala Tyr Pro Leu Gly Ser Leu Glu Asn Phe Lys  
 405 410 415  
 Thr Ile Asp Ile Ile Ile Asn Cys Leu Pro Pro Glu Val Thr Phe Pro  
 420 425 430  
 Trp Arg Phe Pro Pro Ile Val Met Asp Ile Asn Thr Lys Pro His Pro  
 435 440 445  
 Ser Pro Tyr Leu Glu Arg Ala Gln Lys His Gly Ser Leu Ile Ile His  
 450 455 460  
 Gly Tyr Glu Met Phe Ile Glu Gln Ala Leu Leu Gln Phe Ala Leu Trp  
 465 470 475 480  
 Phe Pro Asp Phe Leu Thr Pro Glu Ser Cys Asp Ser Phe Arg Asn Tyr  
 485 490 495  
 Val Lys Asn Phe Met Ala Lys Val  
 500

&lt;210&gt;1111

&lt;211&gt;384

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1111

Met Leu Gln Thr Ile Met Ser Glu Thr Ile Ile Thr Thr Pro His Val  
 1 5 10 15  
 Val Lys Leu Ile Ser Asn Phe Phe Gln Lys Lys Leu Phe Ser Ser Ile  
 20 25 30  
 Ser Thr Ala Tyr Pro Leu Val Ile Ile Thr Asp Val Ser Val Gln Gln  
 35 40 45  
 His Leu Leu Gly Pro Ile Leu Asp His Ile Lys Met Leu Gly Tyr Gln  
 50 55 60  
 Val Ile Val Leu Thr Phe Pro Pro Gly Glu Pro Asn Lys Thr Trp Glu  
 65 70 75 80  
 Thr Phe Ile Ser Leu Gln Tyr Gln Leu Val Asp Gln Asn Ile Ser Pro  
 85 90 95  
 Lys Ser Ser Ile Ile Gly Ile Gly Gly Thr Val Leu Asp Met Thr  
 100 105 110  
 Gly Phe Leu Ala Ala Thr Tyr Cys Arg Gly Leu Pro Leu Tyr Leu Ile  
 115 120 125  
 Pro Thr Thr Ile Thr Ala Met Val Asp Thr Ser Ile Gly Gly Lys Asn  
 130 135 140  
 Gly Ile Asn Leu Arg Gly Ile Lys Asn Arg Leu Gly Thr Phe Tyr Leu  
 145 150 155 160  
 Pro Lys Glu Val Trp Met Cys Pro Gln Phe Leu Ser Thr Leu Pro Arg  
 165 170 175  
 Glu Glu Trp Tyr His Gly Ile Ala Glu Ala Ile Lys His Gly Phe Ile

180 185 190  
 Ala Asp Ala Tyr Leu Trp Glu Phe Leu Asn Ser His Ser Lys Met Leu  
 195 200 205  
 Phe Ser Ser Ser Gln Ile Leu His Glu Phe Ile Lys Arg Asn Cys Gln  
 210 215 220  
 Ile Lys Ala Ala Ile Val Ala Glu Asp Pro Tyr Asp Arg Ser Leu Arg  
 225 230 235 240  
 Lys Ile Leu Asn Phe Gly His Ser Ile Ala His Ala Ile Glu Thr Leu  
 245 250 255  
 Ala Lys Gly Thr Val Asn His Gly Gln Ala Val Ser Val Gly Met Met  
 260 265 270  
 Ile Glu Thr Arg Ile Ser Leu Ala Glu Gly Val Met Lys Thr Pro Gln  
 275 280 285  
 Leu Ile Asp Gln Leu Glu Arg Leu Leu Lys Arg Phe Asn Leu Pro Ser  
 290 295 300  
 Thr Leu Lys Asp Leu Gln Ser Ile Val Pro Glu His Leu His Asn Ser  
 305 310 315 320  
 Leu Tyr Ser Pro Glu Asn Ile Ile Tyr Thr Leu Gly Tyr Asp Lys Lys  
 325 330 335  
 Asn Leu Ser Gln His Glu Leu Lys Met Ile Met Ile Glu His Leu Gly  
 340 345 350  
 Arg Ala Ala Pro Phe Asn Gly Thr Tyr Cys Ala Ser Pro Asn Met Glu  
 355 360 365  
 Ile Leu Tyr Asp Ile Leu Trp Ser Glu Cys His Val Met Arg His Cys  
 370 375 380  
 <210>1112  
 <211>376  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1112  
 Thr Ser Val Ser Arg Ser His Tyr Leu Val Lys Val Met Lys Asn Ser  
 1 5 10 15  
 Phe Gly Ser Leu Phe Ser Phe Thr Thr Trp Gly Glu Ser His Gly Pro  
 20 25 30  
 Ser Ile Gly Val Val Ile Asp Gly Cys Pro Ala Gly Leu Glu Leu His  
 35 40 45  
 Glu Ser Asp Phe Val Pro Ala Met Lys Arg Arg Arg Pro Gly Asn Pro  
 50 55 60  
 Gly Thr Ser Ser Arg Lys Glu Asn Asp Ile Val Gln Ile Leu Ser Gly  
 65 70 75 80  
 Val Tyr Lys Gly Lys Thr Thr Gly Thr Pro Leu Ser Leu Gln Ile Leu  
 85 90 95  
 Asn Thr Asp Val Asp Ser Ser Pro Tyr Glu Asn Ser Glu Arg Leu Tyr  
 100 105 110  
 Arg Pro Gly His Ser Gln Tyr Thr Tyr Glu Lys Lys Phe Gly Ile Val  
 115 120 125  
 Asp Pro Asn Gly Gly Gly Arg Ser Ser Ala Arg Glu Thr Ala Cys Arg  
 130 135 140  
 Val Ala Ala Gly Val Val Ala Glu Lys Phe Leu Ala Asn Gln Asn Ile  
 145 150 155 160  
 Phe Thr Leu Ala Tyr Leu Ser Ser Leu Gly Ser Leu Thr Leu Pro His  
 165 170 175  
 Tyr Leu Lys Ile Ser Pro Glu Leu Ile His Lys Ile His Thr Ser Pro  
 180 185 190  
 Phe Tyr Ser Pro Leu Pro Asn Glu Lys Ile Gln Glu Ile Leu Thr Ser  
 195 200 205  
 Leu His Asp Asp Ser Asp Ser Leu Gly Gly Val Ile Ser Phe Ile Thr  
 210 215 220  
 Ser Pro Ile His Asp Phe Leu Gly Glu Pro Leu Phe Gly Lys Val His  
 225 230 235 240  
 Ala Leu Leu Ala Ser Ala Leu Met Ser Ile Pro Ala Ala Lys Gly Phe  
 245 250 255  
 Glu Ile Gly Lys Gly Phe Ala Ser Ala Gln Met Arg Gly Ser Gln Tyr  
 260 265 270

Thr Asp Pro Phe Val Met Glu Gly Glu Asn Ile Thr Leu Lys Ser Asn  
 275 280 285  
 Asn Cys Gly Gly Thr Leu Gly Gly Ile Thr Ile Gly Val Pro Ile Glu  
 290 295 300  
 Gly Arg Ile Ala Phe Lys Pro Thr Ser Ser Ile Lys Arg Pro Cys Ala  
 305 310 315 320  
 Thr Val Thr Lys Thr Lys Lys Glu Thr Thr Tyr Arg Thr Pro Gln Thr  
 325 330 335  
 Gly Arg His Asp Pro Cys Val Ala Ile Arg Ala Val Pro Val Val Glu  
 340 345 350  
 Ala Met Ile Asn Leu Val Leu Ala Asp Leu Val Leu Tyr Gln Arg Cys  
 355 360 365  
 Ser Lys Leu Ser Cys Gln Arg Gln  
 370 375

&lt;210&gt;1113

&lt;211&gt;184

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1113

Trp Lys Leu Glu Leu Arg Asn Val Met Thr Ile Ile Leu Cys Gly Leu  
 1 5 10 15  
 Pro Thr Ser Gly Lys Ser Ser Leu Gly Lys Ala Leu Ala Lys Phe Leu  
 20 25 30  
 Asn Leu Pro Phe Tyr Asp Leu Asp Asp Leu Ile Val Ser Asn Tyr Ser  
 35 40 45  
 Ser Ala Leu Tyr Ser Ser Ser Ala Glu Ile Tyr Lys Ala Tyr Gly Asp  
 50 55 60  
 Gln Lys Phe Ser Glu Cys Glu Ala Arg Ile Leu Glu Thr Leu Pro Pro  
 65 70 75 80  
 Glu Asp Ala Leu Ile Ser Leu Gly Gly Gly Thr Leu Met Tyr Glu Ala  
 85 90 95  
 Ser Tyr Arg Ala Ile Gln Thr Arg Gly Ala Leu Val Phe Leu Ser Val  
 100 105 110  
 Glu Leu Pro Leu Ile Tyr Glu Arg Leu Glu Lys Arg Gly Leu Pro Glu  
 115 120 125  
 Arg Leu Lys Glu Ala Met Lys Thr Lys Pro Leu Ser Glu Ile Leu Thr  
 130 135 140  
 Glu Arg Ile Asp Arg Met Lys Glu Ile Ala Asp Tyr Ile Phe Pro Val  
 145 150 155 160  
 Asp His Val Asp His Ser Ser Lys Ser Ser Leu Glu Gln Ala Ser Gln  
 165 170 175  
 Asp Leu Ile Thr Leu Leu Lys Ser  
 180

&lt;210&gt;1114

&lt;211&gt;449

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1114

Val Cys Phe Thr Met Leu Thr Tyr Lys Val Ser Pro Ser Ser Val Tyr  
 1 5 10 15  
 Gly Asn Ala Phe Ile Pro Ser Ser Lys Ser His Thr Leu Arg Ala Ile  
 20 25 30  
 Leu Trp Ala Ser Val Ala Glu Gly Lys Ser Thr Ile Tyr Asn Tyr Leu  
 35 40 45  
 Asp Ser Pro Asp Thr Glu Ala Met Ile Cys Ala Cys Lys Gln Met Gly  
 50 55 60  
 Ala Ser Ile Lys Lys Phe Pro Gln Ile Leu Glu Ile Val Gly Asn Pro  
 65 70 75 80  
 Leu Ala Ile Phe Pro Lys Tyr Thr Leu Ile Asp Ala Gly Asn Ser Gly  
 85 90 95  
 Ile Val Leu Arg Phe Met Thr Ala Leu Ala Cys Val Phe Ser Lys Glu  
 100 105 110  
 Ile Thr Val Thr Gly Ser Ser Gln Leu Gln Arg Arg Pro Met Ala Pro  
 115 120 125

Leu Leu Gln Ala Leu Arg Asn Phe Gly Ala Ser Phe His Phe Ser Ser  
 130 135 140  
 Asp Lys Ser Val Leu Pro Phe Thr Met Ser Gly Pro Leu Arg Ser Ala  
 145 150 155 160  
 Tyr Ser Asp Val Glu Gly Ser Asp Ser Gln Phe Ala Ser Ala Leu Ala  
 165 170 175  
 Val Ala Cys Ser Leu Ala Glu Gly Pro Cys Ser Phe Thr Ile Ile Glu  
 180 185 190  
 Pro Lys Glu Arg Pro Trp Phe Asp Leu Ser Leu Trp Trp Leu Glu Lys  
 195 200 205  
 Leu His Leu Pro Tyr Ser Cys Ser Asp Thr Thr Tyr Ser Phe Pro Gly  
 210 215 220  
 Ser Ser His Pro Gln Gly Phe Ser Tyr His Val Thr Gly Asp Phe Ser  
 225 230 235 240  
 Ser Ala Ala Phe Ile Ala Ala Ala Ala Leu Leu Ser Lys Ser Leu Gln  
 245 250 255  
 Pro Ile Arg Leu Arg Asn Leu Asp Ile Leu Asp Ile Gln Gly Asp Lys  
 260 265 270  
 Ile Phe Phe Ser Leu Met Gln Asn Leu Gly Ala Ser Ile Gln Tyr Asp  
 275 280 285  
 Asn Glu Glu Ile Leu Val Phe Pro Ser Ser Phe Ser Gly Gly Ser Ile  
 290 295 300  
 Asp Met Asp Gly Cys Ile Asp Ala Leu Pro Ile Leu Thr Val Leu Cys  
 305 310 315 320  
 Cys Phe Ala Asp Ser Pro Ser His Leu Tyr Asn Ala Arg Ser Ser Lys  
 325 330 335  
 Asp Lys Glu Ser Asp Arg Ile Leu Ala Ile Thr Glu Glu Leu Gln Lys  
 340 345 350  
 Met Gly Ala Cys Ile Gln Pro Thr His Asp Gly Leu Leu Val Asn Pro  
 355 360 365  
 Ser Pro Leu Tyr Gly Ala Val Leu Asp Ser His Asp Asp His Arg Ile  
 370 375 380  
 Ala Met Ala Leu Thr Ile Ala Ala Leu Tyr Ala Ser Gly Asp Ser Arg  
 385 390 395 400  
 Ile His Asn Thr Ala Cys Val Arg Lys Thr Phe Pro Asn Phe Val Gln  
 405 410 415  
 Thr Leu Asn Ile Met Glu Ala Arg Ile Glu Glu Cys His Asp Asn Tyr  
 420 425 430  
 Ser Met Trp Ser Thr His Lys Arg Lys Val Phe Ala Arg Glu Ser Phe  
 435 440 445  
 Gly

&lt;210&gt;1115

&lt;211&gt;96

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1115

Arg Cys Glu Gly Glu Ser Ala Lys Gln Gln Arg Thr Val Arg Met Gly  
 1 5 10 15  
 Arg Ala Ser Ile Gln Pro Ser Ile Ser Ile Glu Pro Pro Glu Asn Asp  
 20 25 30  
 Glu Gly Asn Thr Lys Ile Ser Ser Leu Ser Tyr Cys Ile Glu Ala Pro  
 35 40 45  
 Lys Phe Cys Met Arg Glu Lys Lys Ile Leu Ser Pro Trp Ile Ser Lys  
 50 55 60  
 Met Ser Lys Leu Arg Arg Ile Gly Trp Ser Asp Phe Glu Ser Arg  
 65 70 75 80  
 Ala Ala Ala Ala Met Lys Ala Ala Leu Leu Lys Ser Pro Val Thr Trp  
 85 90 95

&lt;210&gt;1116

&lt;211&gt;283

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1116

Arg Pro Ser Gln Ser Leu Phe Leu Arg Thr Trp Ser Pro Ser Ser Ser  
 1 5 10 15  
 Phe Arg Glu His Thr Val Cys Ala Ala Pro Leu Leu Tyr Pro Arg Arg  
 20 25 30  
 Arg Ser Pro Asp Tyr Leu Phe Ser Pro Thr Gly Cys Pro Met Ser Thr  
 35 40 45  
 Thr Thr Val Lys His Phe Ile His Thr Ala Ser Arg Trp Glu Pro Val  
 50 55 60  
 Leu Lys Glu Ile Val Ala Ser Asn Tyr Trp His Ala Gln Trp Ile Asn  
 65 70 75 80  
 Thr Leu Ser Phe Leu Glu Asn Ser Gly Ala Lys Lys Ile Ser Ala Ser  
 85 90 95  
 Glu His Pro Thr Glu Val Lys Glu Glu Val Leu Lys His Ala Ala Glu  
 100 105 110  
 Glu Phe Arg His Gly His Tyr Leu Lys Thr Gln Ile Ser Arg Ile Ser  
 115 120 125  
 Glu Thr Ser Leu Pro Asp Tyr Thr Ser Lys Asn Leu Leu Gly Gly Leu  
 130 135 140  
 Leu Thr Lys Tyr Tyr Leu His Leu Leu Asp Leu Arg Thr Cys Arg Val  
 145 150 155 160  
 Leu Glu Asn Glu Tyr Ser Leu Ser Gly Gln Thr Leu Lys Thr Ala Ala  
 165 170 175  
 Tyr Ile Leu Val Thr Tyr Ala Ile Glu Leu Arg Ala Ser Glu Leu Tyr  
 180 185 190  
 Pro Leu Tyr His Asp Ile Leu Lys Glu Ala Gln Ser Lys Ile Thr Val  
 195 200 205  
 Lys Ser Ile Ile Leu Glu Glu Gln Gly His Leu Gln Glu Met Glu Arg  
 210 215 220  
 Glu Leu Lys Asp Leu Pro His Gly Glu Gly Thr Leu Arg Leu Cys Leu  
 225 230 235 240  
 Pro Ile Arg Arg Gly Ala Leu Leu Ala Val Cys Arg Glu Ile Arg Thr  
 245 250 255  
 Asn Asp Leu Arg Ser Phe Leu Asp Phe Tyr Lys Val Leu Glu Phe Phe  
 260 265 270  
 Leu Asp Asp Lys Ser Glu Val Arg Gln Ile Thr  
 275 280

&lt;210&gt;1117

&lt;211&gt;505

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1117

Leu Val Met Phe Leu Asp Phe Ser Glu Pro Ser Ile Ser Arg Lys Tyr  
 1 5 10 15  
 Gln Ser His Leu Phe Asn Gly Arg Ser Asn Ala Leu Thr Lys Pro Gln  
 20 25 30  
 Tyr Leu Arg Tyr Gly Gly Lys Trp Val Ser Arg Gly Arg Arg Ala Leu  
 35 40 45  
 Ala Asn Ser Arg Asn Gln Ala Ser Tyr Asn Arg Asp Ser Cys Gln Gly  
 50 55 60  
 Lys Arg Asn His Lys Asp Asn His Lys Leu Leu Cys Arg Thr Met Glu  
 65 70 75 80  
 Gly Ser Met Asp Lys Gln Ser Ser Gly Asn Ser Gly Cys Ile Trp His  
 85 90 95  
 Pro Phe Thr Gln Ser Ala Leu Asp Ser Thr Pro Ile Lys Ile Val Arg  
 100 105 110  
 Gly Glu Gly Ala Tyr Leu Tyr Ala Glu Ser Gly Thr Arg Tyr Leu Asp  
 115 120 125  
 Ala Ile Ser Ser Trp Trp Cys Asn Leu His Gly His Gly His Pro Tyr  
 130 135 140  
 Ile Thr Lys Lys Leu Cys Glu Gln Ala Gln Lys Leu Glu His Val Ile  
 145 150 155 160  
 Phe Ala Asn Phe Thr His Glu Pro Ala Leu Glu Leu Val Ser Lys Leu  
 165 170 175  
 Ala Pro Leu Leu Pro Glu Gly Leu Glu Arg Phe Phe Phe Ser Asp Asn

180 185 190  
 Gly Ser Thr Ser Ile Glu Ile Ala Met Lys Ile Ala Val Gln Tyr Tyr  
 195 200 205  
 Tyr Asn Gln Asn Lys Ala Lys Ser His Phe Val Gly Leu Ser Asn Ala  
 210 215 220  
 Tyr His Gly Asp Thr Phe Gly Ala Met Ser Ile Ala Gly Thr Ser Pro  
 225 230 235 240  
 Thr Thr Val Pro Phe His Asp Leu Phe Leu Pro Ser Ser Thr Ile Ala  
 245 250 255  
 Ala Pro Tyr Tyr Gly Lys Glu Glu Leu Ala Ile Ala Gln Ala Lys Thr  
 260 265 270  
 Val Phe Ser Glu Ser Asn Ile Ala Ala Phe Ile Tyr Glu Pro Leu Leu  
 275 280 285  
 Gln Gly Ala Gly Gly Met Leu Met Tyr Asn Pro Glu Gly Leu Lys Glu  
 290 295 300  
 Ile Leu Lys Leu Ala Lys His Tyr Gly Val Leu Cys Ile Ala Asp Glu  
 305 310 315 320  
 Ile Leu Thr Gly Phe Gly Arg Thr Gly Pro Leu Phe Ala Ser Glu Phe  
 325 330 335  
 Thr Asp Ile Pro Pro Asp Ile Ile Cys Leu Ser Lys Gly Leu Thr Gly  
 340 345 350  
 Gly Tyr Leu Pro Leu Ala Leu Thr Val Thr Thr Lys Glu Ile His Asp  
 355 360 365  
 Ala Phe Val Ser Gln Asp Arg Met Lys Ala Leu Leu His Gly His Thr  
 370 375 380  
 Phe Thr Gly Asn Pro Leu Gly Cys Ser Ala Ala Leu Ala Ser Leu Asp  
 385 390 395 400  
 Leu Thr Leu Ser Pro Glu Cys Leu Gln Gln Arg Gln Met Ile Glu Arg  
 405 410 415  
 Cys His Gln Glu Phe Gln Glu Ala His Gly Ser Leu Trp Gln Arg Cys  
 420 425 430  
 Glu Val Leu Gly Thr Val Leu Ala Leu Asp Tyr Pro Ala Glu Ala Thr  
 435 440 445  
 Gly Tyr Phe Ser Gln Tyr Arg Asp His Leu Asn Arg Phe Phe Leu Glu  
 450 455 460  
 Arg Gly Val Leu Leu Arg Pro Leu Gly Asn Thr Leu Tyr Val Leu Pro  
 465 470 475 480  
 Pro Tyr Cys Ile Gln Glu Glu Asp Leu Arg Ile Ile Tyr Ser His Leu  
 485 490 495  
 Gln Asp Ala Leu Cys Leu Gln Pro Gln  
 500 505

&lt;210&gt;1118

&lt;211&gt;219

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1118

Met Gln Arg Ile Ile Ile Val Gly Ile Asp Thr Gly Val Gly Lys Thr  
 1 5 10 15  
 Ile Val Ser Ala Ile Leu Ala Arg Ala Leu Asn Ala Glu Tyr Trp Lys  
 20 25 30  
 Pro Ile Gln Ala Gly Asn Leu Glu Asn Ser Asp Ser Asn Ile Val His  
 35 40 45  
 Glu Leu Ser Gly Ala Tyr Cys His Pro Glu Ala Tyr Arg Leu His Lys  
 50 55 60  
 Pro Leu Ser Pro His Lys Ala Ala Gln Ile Asp Asn Val Ser Ile Glu  
 65 70 75 80  
 Glu Ser His Ile Cys Ala Pro Lys Thr Thr Ser Asn Leu Ile Ile Glu  
 85 90 95  
 Thr Ser Gly Gly Phe Leu Ser Pro Cys Thr Ser Lys Arg Leu Gln Gly  
 100 105 110  
 Asp Val Phe Ser Ser Trp Ser Cys Ser Trp Ile Leu Val Ser Gln Ala  
 115 120 125  
 Tyr Leu Gly Ser Ile Asn His Thr Cys Leu Thr Val Glu Ala Met Arg  
 130 135 140

Ser Arg Asn Leu Asn Ile Leu Gly Met Val Val Asn Gly Tyr Pro Glu  
 145 150 155 160  
 Asp Glu Glu His Trp Leu Thr Gln Glu Ile Lys Leu Pro Ile Ile Gly  
 165 170 175  
 Thr Leu Ala Lys Glu Lys Glu Ile Thr Lys Thr Ile Ile Ser Cys Tyr  
 180 185 190  
 Ala Glu Gln Trp Lys Glu Val Trp Thr Ser Asn His Gln Gly Ile Gln  
 195 200 205  
 Gly Val Ser Gly Thr Pro Ser Leu Asn Leu His  
 210 215  
 <210>1119  
 <211>383  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1119  
 Pro Met Leu Cys Gln Gln Phe Leu Ile Glu Ala Leu Ala Arg Arg Lys  
 1 5 10 15  
 Ser Lys His Thr Tyr Arg Ser Leu Ser Leu Asn Ser His Leu Ile Asp  
 20 25 30  
 Phe Thr Ser Asn Asp Tyr Leu Gly Phe Ala Ser Ser Pro Glu Leu Arg  
 35 40 45  
 Lys Glu Tyr Ile Thr Lys Leu His Ala Ile Glu Ser Leu Gly Ala Thr  
 50 55 60  
 Gly Ser Arg Leu Leu Thr Gly His Ser Gln Leu Cys Gln Arg Ile Glu  
 65 70 75 80  
 Glu Gln Leu Ala Ala Tyr His Asn Phe Glu Ser Cys Leu Ile Phe Asn  
 85 90 95  
 Thr Gly Tyr Thr Ala Asn Leu Gly Leu Tyr Ala Leu Ala Thr Asp  
 100 105 110  
 Gln Asp Arg Ile Leu His Asp Leu Tyr Ile His Ala Ser Ile Tyr Asp  
 115 120 125  
 Gly Ile Arg Leu Ser Lys Ala Gln Ser Phe Pro Phe Asn His Asn Asp  
 130 135 140  
 Leu Asn His Leu Glu Lys Arg Leu Ala Ser Ser His Leu Gly Arg Thr  
 145 150 155 160  
 Phe Val Cys Val Glu Ser Val Tyr Ser Leu His Gly Ser Val Ala Pro  
 165 170 175  
 Leu Gln Ala Ile Ser Glu Leu Cys Glu Arg Tyr Ser Ala Tyr Leu Ile  
 180 185 190  
 Val Asp Glu Ala His Ala Val Gly Val Phe Gly Asp Gln Gly Glu Gly  
 195 200 205  
 Leu Val Ser Ala Leu Gly Leu Gln Asp Lys Val Leu Ala Thr Val Tyr  
 210 215 220  
 Thr Phe Gly Lys Ala Leu Gly Thr His Gly Ala Ala Ile Ala Gly Ser  
 225 230 235 240  
 Ser Ile Leu Lys Asp Tyr Leu Ile Asn Phe Cys Arg Pro Phe Ile Tyr  
 245 250 255  
 Thr Thr Ala Gln Pro Pro His Ala Leu Thr Ala Ile Glu Leu Ala Tyr  
 260 265 270  
 Glu His Asn Gln Arg Ala Phe Asn Gln Arg Glu His Leu Ser Ala Leu  
 275 280 285  
 Ile His His Phe Arg Glu Lys Ala Gln Asn Leu Gly Leu Gln Leu Met  
 290 295 300  
 Lys Asp Asn Thr Thr Thr Pro Ile Gln Ser Ile Cys Val Ser Gly Ser  
 305 310 315 320  
 His Arg Ala Arg Gln Ala Ala Leu Gln Ile Gln Asn Ser Gly Tyr Asp  
 325 330 335  
 Val Arg Pro Ile Val Ser Pro Thr Val Lys Gln Arg Glu Glu Leu Leu  
 340 345 350  
 Arg Ile Cys Leu His Ala Phe Asn Thr Lys Asn Glu Ile Asp His Leu  
 355 360 365  
 Leu His Thr Leu Glu Gln Ile Phe Leu Cys Asn Val Ser Ser Leu  
 370 375 380  
 <210>1120

&lt;211&gt;334

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1120

Ala Lys His Met Arg Glu Glu Thr Val Ser Trp Ser Leu Glu Asp Ile  
 1 5 10 15  
 Arg Glu Ile Tyr His Thr Pro Val Phe Glu Leu Ile His Lys Ala Asn  
 20 25 30  
 Ala Ile Leu Arg Ser Asn Phe Leu His Ser Glu Leu Gln Thr Cys Tyr  
 35 40 45  
 Leu Ile Ser Ile Lys Thr Gly Gly Cys Val Glu Asp Cys Ala Tyr Cys  
 50 55 60  
 Ala Gln Ser Ser Arg Tyr His Thr His Val Thr Pro Glu Pro Met Met  
 65 70 75 80  
 Lys Ile Val Asp Val Val Glu Arg Ala Lys Arg Ala Val Glu Leu Gly  
 85 90 95  
 Ala Thr Arg Val Cys Leu Gly Ala Ala Trp Arg Asn Ala Lys Asp Asp  
 100 105 110  
 Arg Tyr Phe Asp Arg Val Leu Ala Met Val Lys Ser Ile Thr Asp Leu  
 115 120 125  
 Gly Ala Glu Val Cys Cys Ala Leu Gly Met Leu Ser Glu Glu Gln Ala  
 130 135 140  
 Lys Lys Leu Tyr Asp Ala Gly Leu Tyr Ala Tyr Asn His Asn Leu Asp  
 145 150 155 160  
 Ser Ser Pro Glu Phe Tyr Glu Thr Ile Ile Thr Thr Arg Ser Tyr Glu  
 165 170 175  
 Asp Arg Leu Asn Thr Leu Asp Val Val Asn Lys Ser Gly Ile Ser Thr  
 180 185 190  
 Cys Cys Gly Gly Ile Val Gly Met Gly Glu Ser Glu Glu Asp Arg Ile  
 195 200 205  
 Lys Leu Leu His Val Leu Ala Thr Arg Asp His Ile Pro Glu Ser Val  
 210 215 220  
 Pro Val Asn Leu Leu Trp Pro Ile Asp Gly Thr Pro Leu Gln Asp Gln  
 225 230 235 240  
 Pro Pro Ile Ser Phe Trp Glu Val Leu Arg Thr Ile Ala Thr Ala Arg  
 245 250 255  
 Val Val Phe Pro Arg Ser Met Val Arg Leu Ala Ala Gly Arg Ala Phe  
 260 265 270  
 Leu Thr Val Glu Gln Gln Thr Leu Cys Phe Leu Ala Gly Ala Asn Ser  
 275 280 285  
 Ile Phe Tyr Gly Asp Lys Leu Leu Thr Val Glu Asn Asn Asp Ile Asp  
 290 295 300  
 Glu Asp Ala Glu Met Ile Lys Leu Leu Gly Leu Ile Pro Arg Pro Ser  
 305 310 315 320  
 Phe Gly Ile Glu Arg Gly Asn Pro Cys Tyr Ala Asn Asn Ser  
 325 330

&lt;210&gt;1121

&lt;211&gt;259

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1121

Ser Glu Phe Met Val Ser Thr Pro Phe Leu Thr Val Phe Ser Met Glu  
 1 5 10 15  
 Lys Leu Leu Ser Lys Ile Phe Leu Asp Tyr Leu Glu Ala Phe Gly Leu  
 20 25 30  
 Leu Ser Asp Phe Leu Asp His Gln Ala Val Ile Lys Phe Phe Glu Leu  
 35 40 45  
 Glu Thr His Phe Ser Tyr Tyr Pro Val Ser Gly Phe Val Ala Pro His  
 50 55 60  
 Gln Tyr Leu Ser Leu Leu Gln Asp Arg Tyr Phe Pro Ile Ala Ser Val  
 65 70 75 80  
 Met Arg Thr Leu Asp Lys Asp Asn Phe Ser Leu Thr Pro Asp Leu Ile  
 85 90 95  
 His Asp Leu Leu Gly His Val Pro Trp Leu Leu His Pro Ser Phe Ser



100 105 110  
 Glu Phe Phe Ile Asn Met Gly Arg Leu Phe Thr Lys Val Ile Glu Lys  
 115 120 125  
 Val Gln Ala Leu Pro Ser Lys Lys Gln Arg Ile Gln Thr Leu Gln Ser  
 130 135 140  
 Asn Leu Ile Ala Ile Val Arg Cys Phe Trp Phe Thr Val Glu Ser Gly  
 145 150 155 160  
 Leu Ile Glu Asn His Glu Gly Arg Lys Ala Tyr Gly Ala Val Leu Ile  
 165 170 175  
 Ser Ser Pro Gln Glu Leu Gly His Ala Phe Ile Asp Asn Val Arg Val  
 180 185 190  
 Leu Pro Leu Glu Leu Asp Gln Ile Ile Arg Leu Pro Phe Asn Thr Ser  
 195 200 205  
 Thr Pro Gln Glu Thr Leu Phe Ser Ile Arg His Phe Asp Glu Leu Val  
 210 215 220  
 Glu Leu Thr Ser Lys Leu Glu Trp Met Leu Asp Gln Gly Leu Leu Glu  
 225 230 235 240  
 Ser Ile Pro Leu Tyr Asn Gln Glu Lys Tyr Leu Ser Gly Phe Glu Val  
 245 250 255  
 Leu Cys Gln

&lt;210&gt;1122

&lt;211&gt;264

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1122

Met Gly Ser Ser Met His Val Gly Val Ile Gly Cys Ser Gly Arg Thr  
 1 5 10 15  
 Gly Lys Val Ile Val Ser Ala Leu Glu Gln Ser Ser Glu Tyr Thr Leu  
 20 25 30  
 Gly Pro Gly Phe Ser Arg Ser Ser Ala Leu Thr Leu Phe Gln Val Ile  
 35 40 45  
 Ala His Asn Asp Val Leu Val Asp Phe Ser His Pro Leu Leu Thr Lys  
 50 55 60  
 Glu Val Val Ala His Leu Leu Ile Ser Pro Lys Pro Leu Ile Ile Gly  
 65 70 75 80  
 Thr Thr Gly Phe Pro Gly Lys Cys Lys Glu Ala His Asp Ser Leu Glu  
 85 90 95  
 Glu Leu Thr His Ile Val Pro Val Val Val Cys Pro Asn Ala Ser Leu  
 100 105 110  
 Gly Ala Tyr Ile His Lys Arg Leu Val Met Leu Leu Ser Gln Leu Cys  
 115 120 125  
 Asn Pro Gln Phe Asp Ile Arg Ile Arg Glu Thr His His Arg Tyr Lys  
 130 135 140  
 Lys Asp Ser Leu Ser Gly Thr Ala Gln Asp Leu Leu Asp Thr Ile Gln  
 145 150 155 160  
 Gln Val Lys Gln Glu Asp Trp Gly Glu Glu Tyr Glu Val Gly Gln Arg  
 165 170 175  
 Asp Ser Ser Lys Lys Thr Ile Glu Val Gln Ser Ser Arg Val Gly Asp  
 180 185 190  
 Ile Pro Gly Glu His Glu Val Ala Phe Ile Ser Ser Gly Glu Gln Ile  
 195 200 205  
 Leu Val Arg His Thr Val Phe Ser Arg Asn Val Phe Gly Arg Gly Ile  
 210 215 220  
 Leu Ser Ile Leu Asp Trp Leu Lys Thr Leu Asn Pro Gln Pro Gly Leu  
 225 230 235 240  
 Tyr Ser Leu Gly Asp Thr Leu Glu Leu Val Leu Arg Asn Glu His Cys  
 245 250 255  
 Leu Leu Lys Lys Thr Thr Asp His  
 260

&lt;210&gt;1123

&lt;211&gt;295

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1123

```

Ile Trp Ala Ile Val Trp Arg Cys Leu Tyr Leu Ala Gly Ala Ile Gly
 1           5           10           15
Pro Met Pro Glu Met Val Arg Asp Leu Pro Ile Arg Lys Ile Glu Glu
      20           25           30
Val Gln Ser Asp Ile Val Val Ser Phe Leu Pro Ser Ser Ala Glu Ser
      35           40           45
Met Glu Ala Tyr Cys Leu Ser Gln Gly Lys Val Val Phe Ser Asn Ala
      50           55           60
Ser Thr Tyr Arg Met His Ser Ser Val Pro Ile Ile Ile Pro Glu Val
      65           70           75           80
Asn Ser Asp His Phe Gln Leu Leu Glu Glu Gln Pro Tyr Pro Gly Lys
      85           90           95
Ile Ile Thr Ser Pro Asn Cys Cys Val Ser Gly Ile Thr Leu Ala Leu
      100           105           110
Ala Pro Leu Arg Lys Phe Ser Leu Asp His Val His Ile Val Thr Leu
      115           120           125
Gln Ser Ala Ser Gly Ala Gly Tyr Pro Gly Val Pro Ser Leu Asp Leu
      130           135           140
Leu Ala Asn Thr Val Pro His Ile Val Gly Glu Glu Glu Lys Ile Leu
      145           150           155           160
Arg Glu Thr Val Lys Ile Leu Gly Ser Ser Lys Gln Pro Leu Pro Cys
      165           170           175
Lys Leu Ser Val Thr Val His Arg Val Pro Val Ala Tyr Gly His Thr
      180           185           190
Leu Ser Leu His Val Thr Phe Ser Lys Asp Val Asp Leu Asp Glu Ile
      195           200           205
Leu Tyr Ser Tyr Gln Glu Lys Asn Lys Glu Phe Pro Asn Thr Tyr Gln
      210           215           220
Leu Tyr Asp Asn Pro Trp Ser Pro Gln Ala Arg Lys His Leu Ser His
      225           230           235           240
Asp Asp Met Arg Val His Leu Gly Pro Ile Thr Tyr Gly Gly Asp Phe
      245           250           255
Arg Thr Ile Lys Met Asn Val Leu Ile His Asn Leu Val Arg Gly Ala
      260           265           270
Ala Gly Thr Leu Leu Ala Ser Met Glu Asn Tyr Phe Phe Asp Tyr Leu
      275           280           285
Lys Arg Glu Met Cys Leu Arg
      290           295

```

&lt;210&gt;1124

&lt;211&gt;441

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1124

```

Asn Val Ser Lys Ile Val Tyr Lys Phe Gly Gly Thr Ser Leu Ala Thr
 1           5           10           15
Ala Glu Asn Ile Cys Leu Val Cys Asp Ile Ile Cys Lys Asp Lys Pro
      20           25           30
Ser Phe Val Val Val Ser Ala Ile Ala Gly Val Thr Asp Leu Leu Val
      35           40           45
Asp Phe Cys Ser Ser Ser Leu Arg Glu Arg Glu Glu Val Leu Arg Lys
      50           55           60
Ile Glu Gly Lys His Glu Glu Ile Val Lys Asn Leu Ala Ile Pro Phe
      65           70           75           80
Pro Val Ser Thr Trp Thr Ser Arg Leu Leu Pro Tyr Leu Gln His Leu
      85           90           95
Glu Ile Ser Asp Leu Asp Phe Ala Arg Ile Leu Ser Leu Gly Glu Asp
      100           105           110
Ile Ser Ala Ser Leu Val Arg Ala Val Cys Ser Thr Arg Gly Trp Asp
      115           120           125
Leu Gly Phe Leu Glu Ala Arg Ser Val Ile Leu Thr Asp Asp Ser Tyr
      130           135           140
Arg Arg Ala Ser Pro Asn Leu Asp Leu Met Lys Ala His Trp His Gln
      145           150           155           160

```

Leu Glu Leu Asn Gln Pro Ser Tyr Ile Ile Gln Gly Phe Ile Gly Ser  
 165 170 175  
 Asn Gly Leu Gly Glu Thr Val Leu Leu Gly Arg Gly Gly Ser Asp Tyr  
 180 185 190  
 Ser Ala Thr Leu Ile Ala Glu Leu Ala Arg Ala Thr Glu Val Arg Ile  
 195 200 205  
 Tyr Thr Asp Val Asn Gly Ile Tyr Thr Met Asp Pro Lys Val Ile Ser  
 210 215 220  
 Asp Ala Gln Arg Ile Pro Glu Leu Ser Phe Glu Glu Met Gln Asn Leu  
 225 230 235 240  
 Ala Ser Phe Gly Ala Lys Val Leu Tyr Pro Pro Met Leu Phe Pro Cys  
 245 250 255  
 Met Arg Ala Gly Ile Pro Ile Phe Val Thr Ser Thr Phe Asp Pro Glu  
 260 265 270  
 Lys Gly Gly Thr Trp Val Tyr Ala Val Asp Lys Ser Val Ser Tyr Glu  
 275 280 285  
 Pro Arg Ile Lys Ala Leu Ser Leu Ser Gln Tyr Gln Ser Phe Cys Ser  
 290 295 300  
 Val Asp Tyr Thr Val Leu Gly Cys Gly Gly Leu Glu Glu Ile Leu Gly  
 305 310 315 320  
 Ile Leu Glu Ser His Gly Ile Asp Pro Glu Leu Met Ile Ala Gln Asn  
 325 330 335  
 Asn Val Val Gly Phe Val Met Asp Asp Ile Ile Ser Gln Glu Ala  
 340 345 350  
 Gln Glu His Leu Val Asp Val Leu Ser Leu Ser Ser Val Thr Arg Leu  
 355 360 365  
 His His Ser Val Ala Leu Ile Thr Met Ile Gly Asp Asn Leu Ser Ser  
 370 375 380  
 Pro Lys Val Val Ser Thr Ile Thr Glu Lys Leu Arg Gly Phe Gln Gly  
 385 390 395 400  
 Pro Val Phe Cys Phe Cys Gln Ser Ser Met Ala Leu Ser Phe Val Val  
 405 410 415  
 Ala Ser Glu Leu Ala Glu Gly Ile Ile Glu Glu Leu His Asn Asp Tyr  
 420 425 430  
 Val Lys Gln Lys Ala Ile Val Ala Thr  
 435 440  
 <210>1125  
 <211>271  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1125  
 Lys Ser Tyr Ser Arg His Val Gly Arg Ile Met His Leu Leu Thr Ala  
 1 5 10 15  
 Thr Val Thr Pro Phe Phe Pro Asn Gly Thr Ile Asp Phe Ala Ser Leu  
 20 25 30  
 Glu Arg Leu Leu Ser Phe Gln Asp Ala Val Gly Asn Gly Val Val Leu  
 35 40 45  
 Leu Gly Ser Thr Gly Glu Gly Leu Ser Leu Thr Lys Lys Glu Lys Gln  
 50 55 60  
 Ala Leu Ile Cys Phe Ala Cys Asp Leu Gln Leu Lys Val Pro Leu Phe  
 65 70 75 80  
 Val Gly Thr Ser Gly Thr Leu Leu Glu Glu Val Leu Asp Trp Ile His  
 85 90 95  
 Phe Cys Asn Asp Leu Pro Ile Ser Gly Phe Leu Met Thr Thr Pro Ile  
 100 105 110  
 Tyr Thr Lys Pro Lys Leu Cys Gly Gln Ile Leu Trp Phe Glu Ala Val  
 115 120 125  
 Leu Asn Ala Ala Lys His Pro Ala Ile Leu Tyr Asn Ile Pro Ser Arg  
 130 135 140  
 Ala Ala Thr Pro Leu Tyr Leu Asp Thr Val Lys Ala Leu Ala His His  
 145 150 155 160  
 Pro Gln Phe Leu Gly Ile Lys Asp Ser Gly Gly Ser Val Glu Glu Phe  
 165 170 175  
 Gln Ser Tyr Lys Ser Ile Ala Pro His Ile Gln Leu Tyr Cys Gly Asp

180 185 190  
 Asp Val Phe Trp Ser Glu Met Ala Ala Cys Gly Ala His Gly Leu Ile  
 195 200 205  
 Ser Val Leu Ser Asn Ala Trp Pro Glu Glu Ala Arg Glu Tyr Val Leu  
 210 215 220  
 Asn Pro Gln Glu Gln Asp Tyr Arg Ser Leu Trp Met Glu Thr Cys Arg  
 225 230 235 240  
 Trp Val Tyr Thr Thr Thr Asn Pro Ile Gly Ile Lys Ala Ile Leu Ala  
 245 250 255  
 Tyr Lys Lys Ala Ile Thr His Ala His Cys Ala Cys Pro Cys Leu  
 260 265 270

&lt;210&gt;1126

&lt;211&gt;256

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1126

Phe Phe Ile Gln Lys Met Lys Tyr Asn Ser Arg Glu Lys Ile Lys Ser  
 1 5 10 15  
 Ala Leu Arg Ile Cys Ser Ser Tyr Cys Ile Thr Val Phe Arg Asn Asn  
 20 25 30  
 Phe Ser Leu Ser Cys Tyr Asp Lys Ile Phe Tyr Ser Leu Ser Cys Tyr  
 35 40 45  
 Val Phe Asn Gly Pro Asn Ser Ile Gly Arg Cys Arg Ser Phe Cys Phe  
 50 55 60  
 Phe Arg Gly Lys Lys Thr Glu Val Glu Thr Lys Glu Val Lys Ile Lys  
 65 70 75 80  
 Asp Glu Ile Arg Pro Ser Leu Glu Gly Asn Asp Pro Val Lys Val Ala  
 85 90 95  
 Glu Ser Phe Pro Lys Arg Arg Ala Ala Leu Glu Ser Leu Ser Ser Gln  
 100 105 110  
 Ser Ser Ile Gly Asn Leu Cys Ala Ile Ser Asn Phe Leu Asp Ser Gln  
 115 120 125  
 Met Leu Ser Arg Asn Phe Ser Lys Glu Ile Trp Gly Ser Thr Ile Phe  
 130 135 140  
 Thr Arg Ser Lys Ser Thr Cys Asp Ala Glu Gly Ser Glu Pro Phe Arg  
 145 150 155 160  
 Tyr Thr Ala Cys Gly Tyr Leu Ala Gly Leu Arg Ser Lys Leu Ala Gly  
 165 170 175  
 Ser Tyr Glu Leu Gly Val Thr Ala Gly Leu Leu Gln Gly Arg Leu Lys  
 180 185 190  
 Asp Val Ser Asp Ser His Arg Thr Arg Ala Thr Ser Ser Ile Leu Ser  
 195 200 205  
 Val His Gly Ser Met Val Thr Arg Pro Leu Ser Cys Thr Lys Tyr Ile  
 210 215 220  
 Val Gly Lys Ala Arg Pro Leu Leu Phe Phe Phe Arg Leu Thr Ser Asp  
 225 230 235 240  
 Val Arg Arg Asp Leu Lys Lys Lys Phe Arg Leu Glu Phe Cys Lys Asp  
 245 250 255

&lt;210&gt;1127

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1127

His Ile Leu Phe Tyr Ser Lys Phe Thr Tyr Arg Thr Pro Leu Arg Val  
 1 5 10 15  
 Thr Ser Pro Ser Gly Arg His Asp Phe Asn Ile Asp Met His Val Ala  
 20 25 30  
 Pro Lys Ile Gly Ala Val Leu Ser His Gly Thr Arg Glu Ala Lys Glu  
 35 40 45  
 Ile Pro Gly Ser Ser Lys Asp Tyr Ala Phe Phe Ser Leu Thr Ala Arg  
 50 55 60  
 Glu Ser Leu Met Ile Ser Glu Lys Leu Ala Met Thr Phe Gln Val Ser  
 65 70 75 80  
 Glu Val Ile Gln Asn Cys Tyr Ser Gln Cys Thr Lys Val Thr Lys Thr

85 90 95  
 Asn Leu Lys Glu Gln Tyr Arg His Leu Ser His Asn Thr Gly Phe Glu  
 100 105 110  
 Leu Ser Val Lys Ser Ala Phe  
 115  
 <210>1128  
 <211>810  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1128  
 Cys Lys Tyr Phe Tyr Leu Arg Ser Tyr Pro Pro Pro Gln His Ser Val  
 1 5 10 15  
 Gly Ser Ile Ser Ser Pro Ser Lys Leu Arg Val Leu Ala Ile Thr Phe  
 20 25 30  
 Leu Val Phe Gly Met Leu Leu Leu Ile Ser Gly Ala Leu Phe Leu Thr  
 35 40 45  
 Leu Gly Ile Pro Gly Leu Ser Ala Ala Ile Ser Phe Gly Leu Gly Ile  
 50 55 60  
 Gly Leu Ser Ala Leu Gly Gly Val Leu Met Ile Ser Gly Leu Leu Cys  
 65 70 75 80  
 Leu Leu Val Lys Arg Glu Ile Pro Thr Val Arg Pro Glu Glu Ile Pro  
 85 90 95  
 Glu Gly Val Ser Leu Ala Pro Ser Glu Glu Pro Ala Leu Gln Ala Ala  
 100 105 110  
 Gln Lys Thr Leu Ala Gln Leu Pro Lys Glu Leu Asp Gln Leu Asp Thr  
 115 120 125  
 Asp Ile Gln Glu Val Phe Ala Cys Leu Arg Lys Leu Lys Asp Ser Lys  
 130 135 140  
 Tyr Glu Ser Arg Ser Phe Leu Asn Asp Ala Lys Lys Glu Leu Arg Val  
 145 150 155 160  
 Phe Asp Phe Val Val Glu Asp Thr Leu Ser Glu Ile Phe Glu Leu Arg  
 165 170 175  
 Gln Ile Val Ala Gln Glu Gly Trp Asp Leu Asn Phe Leu Ile Asn Gly  
 180 185 190  
 Gly Arg Ser Leu Met Met Thr Ala Glu Ser Glu Ser Leu Asp Leu Phe  
 195 200 205  
 His Val Ser Lys Arg Leu Gly Tyr Leu Pro Ser Gly Asp Val Arg Gly  
 210 215 220  
 Glu Gly Leu Lys Lys Ser Ala Lys Glu Ile Val Ala Arg Leu Met Ser  
 225 230 235 240  
 Leu His Cys Glu Ile His Lys Val Ala Val Ala Phe Asp Arg Asn Ser  
 245 250 255  
 Tyr Ala Met Ala Glu Lys Ala Phe Ala Lys Ala Leu Gly Ala Leu Glu  
 260 265 270  
 Glu Ser Val Tyr Arg Ser Leu Thr Gln Ser Tyr Arg Asp Lys Phe Leu  
 275 280 285  
 Glu Ser Glu Arg Ala Lys Ile Pro Trp Asn Gly His Ile Thr Trp Leu  
 290 295 300  
 Arg Asp Asp Ala Lys Ser Gly Cys Ala Glu Lys Lys Leu Arg Asp Ala  
 305 310 315 320  
 Glu Glu Arg Trp Lys Lys Phe Arg Lys Ala Val Phe Trp Val Glu Glu  
 325 330 335  
 Asp Gly Gly Phe Asp Ile Asn Asn Leu Leu Gly Asp Trp Gly Thr Val  
 340 345 350  
 Leu Asp Pro Tyr Arg Gln Glu Arg Met Asp Glu Ile Thr Phe His Glu  
 355 360 365  
 Leu Tyr Glu Lys Thr Thr Phe Leu Lys Arg Leu His Arg Lys Cys Ala  
 370 375 380  
 Leu Ala Lys Thr Thr Phe Glu Lys Xaa Arg Ser Lys Lys Asn Leu Gln  
 385 390 395 400  
 Ala Val Xaa Glu Ala Asn Ala Arg Arg Leu Lys Tyr Val Arg Asp Trp  
 405 410 415  
 Tyr Asp Gln Xaa Phe Gln Lys Ala Gly Glu Arg Leu Glu Lys Leu His  
 420 425 430

Ala Leu Tyr Pro Glu Val Ser Val Ser Ile Arg Glu Asn Lys Ile Gln  
 435 440 445  
 Glu Thr Arg Ser Asn Leu Xaa Lys Ala Tyr Glu Ala Ile Glu Xaa Asn  
 450 455 460  
 Tyr Arg Cys Cys Val Arg Glu Gln Glu Asp Tyr Trp Lys Glu Glu Glu  
 465 470 475 480  
 Lys Arg Glu Ala Xaa Phe Arg Glu Arg Gly Asn Xaa Ile Leu Ser Pro  
 485 490 495  
 Glu Glu Leu Glu Xaa Ser Leu Glu Gln Phe Asp His Gly Leu Lys Asn  
 500 505 510  
 Phe Ser Glu Lys Leu Met Glu Leu Glu Gly His Ile Leu Lys Leu Gln  
 515 520 525  
 Lys Glu Ala Thr Ala Glu Val Glu Asn Lys Ile Leu Ser Asp Ala Glu  
 530 535 540  
 Ser Arg Leu Glu Ile Val Phe Glu Asp Val Lys Glu Met Pro Cys Arg  
 545 550 555 560  
 Ile Glu Glu Ile Glu Lys Thr Leu Arg Met Ala Xaa Leu Pro Leu Leu  
 565 570 575  
 Pro Thr Lys Lys Ala Phe Glu Lys Ala Cys Ser Gln Tyr Asn Ser Cys  
 580 585 590  
 Ala Glu Met Leu Glu Lys Val Lys Pro Tyr Cys Lys Glu Ser Leu Ala  
 595 600 605  
 Tyr Val Thr Ser Lys Glu Arg Leu Val Ser Leu Asp Glu Asp Leu Arg  
 610 615 620  
 Arg Ala Tyr Thr Glu Cys Gln Lys Arg Phe Gln Gly Asp Ser Gly Leu  
 625 630 635 640  
 Glu Ser Glu Val Arg Ala Cys Arg Glu Gln Leu Arg Glu Arg Ile Gln  
 645 650 655  
 Glu Phe Glu Thr Gln Gly Leu Asp Leu Val Glu Lys Glu Leu Leu Cys  
 660 665 670  
 Val Ser Ser Arg Leu Arg Asn Thr Glu Cys Asp Cys Val Ser Gly Val  
 675 680 685  
 Lys Lys Glu Ala Pro Pro Gly Lys Lys Phe Tyr Ala Gln Tyr Tyr Asp  
 690 695 700  
 Glu Ile Tyr Arg Val Arg Val Gln Ser Arg Trp Met Thr Met Ser Glu  
 705 710 715 720  
 Arg Leu Arg Glu Gly Val Gln Ala Cys Asn Lys Met Leu Lys Ala Gly  
 725 730 735  
 Leu Ser Glu Glu Asp Lys Val Leu Lys Glu Glu Glu Tyr Trp Leu Tyr  
 740 745 750  
 Arg Glu Glu Arg Lys Asn Lys Glu Lys Arg Leu Val Gly Thr Lys Ile  
 755 760 765  
 Val Ala Thr Gln Gln Arg Val Ala Ala Phe Glu Ser Ile Glu Val Pro  
 770 775 780  
 Glu Ile Pro Glu Ala Pro Glu Glu Lys Pro Ser Leu Leu Asp Lys Ala  
 785 790 795 800  
 Arg Ser Leu Phe Thr Arg Glu Asp His Thr  
 805 810

&lt;210&gt;1129

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1129

Val Ala Cys Arg Ala Gly Ser Ser Glu Gly Ala Thr Glu Thr Pro Ser  
 1 5 10 15  
 Gly Ile Ser Ser Gly Arg Thr Val Gly Thr Ser Arg Phe Ala Lys Arg  
 20 25 30  
 His Arg Ser Pro Glu Thr Thr Ser Thr Pro Pro Asn Ala Glu Arg Pro  
 35 40 45  
 Met Pro Asn Pro Lys Glu Ile Ala Ala Leu Asn Pro Glu Ile Pro Asn  
 50 55 60  
 Val Arg Lys Arg Ala Pro Glu Ile Lys Lys Ser Thr Pro Arg Thr Lys  
 65 70 75 80  
 Lys Val Ile Ala Lys Thr Arg Asn Leu Asp Arg Gln Lys Lys Ala Pro

85 90 95  
 Thr Glu Trp Ser Gly Gly Gly Gly Ser Cys Gly Asp Arg Gly Thr  
 100 105 110  
 Cys Ile Met Asn Leu Trp Arg His His Ala Gln Thr His Lys Leu Asn  
 115 120 125  
 Pro Leu Ser Tyr  
 130  
 <210>1130  
 <211>320  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1130  
 Trp Arg His Arg Phe Ile Met Gln Val Pro Leu Ser Pro Gln Leu Pro  
 1 5 10 15  
 Pro Pro Pro Pro Asp His Ser Val Gly Ala Phe Phe Cys Leu Ser Lys  
 20 25 30  
 Phe Arg Val Leu Ala Ile Thr Phe Leu Val Leu Gly Val Leu Phe Leu  
 35 40 45  
 Ile Ser Gly Ala Leu Phe Leu Thr Leu Gly Ile Ser Gly Leu Ser Ala  
 50 55 60  
 Ala Ile Ser Phe Gly Leu Gly Ile Gly Leu Ser Ala Leu Gly Gly Val  
 65 70 75 80  
 Leu Val Val Ser Gly Leu Leu Cys Leu Leu Ala Lys Arg Glu Val Pro  
 85 90 95  
 Thr Val Arg Pro Glu Glu Ile Pro Glu Gly Val Ser Val Ala Pro Ser  
 100 105 110  
 Glu Glu Pro Ala Leu Gln Ala Thr Gln Lys Thr Leu Ala Gln Leu Pro  
 115 120 125  
 Lys Glu Leu Asp Gln Leu Asp Arg Tyr Ile Gln Glu Val Val Ser Cys  
 130 135 140  
 Leu Gly Lys Leu Lys Asp Leu Arg Cys Glu Asp Gln Gly Leu Leu Lys  
 145 150 155 160  
 Asp Ala Lys Glu Lys Leu Gln Val Phe Asp Phe Val Trp Lys Asp Met  
 165 170 175  
 Met Thr Glu Phe Val Glu Leu Gln Gln Ile Met Asp Gln Glu Gly Trp  
 180 185 190  
 Tyr Leu Lys Cys Leu Ile Gln Glu Met Arg Asp Ile Gly Ser Thr Leu  
 195 200 205  
 Phe Met Ser Gln Val Ser Leu Phe Lys Leu Trp Glu Trp Leu Gly Tyr  
 210 215 220  
 Leu Pro Ser Gly Asp Val Arg Gly Glu Arg Leu Lys Lys Ser Ala Arg  
 225 230 235 240  
 Glu Val Val Asp Arg Phe Met Arg Arg Ile Cys Asp Thr Arg Lys Val  
 245 250 255  
 Ala Met Thr Phe Asp Arg Asn Ala Tyr Gly Val Ala Lys Thr Ala Phe  
 260 265 270  
 Glu Lys Ala Phe Gly Ala Leu Glu Thr Cys Val Tyr Lys Ser Met Thr  
 275 280 285  
 Glu Ser Tyr Arg Glu Ala Phe Cys Glu Tyr Lys Lys Thr Lys Ile Leu  
 290 295 300  
 Arg Asp Glu Glu Lys Ile Leu Arg Ile Cys Tyr Leu Glu Leu Arg Arg  
 305 310 315 320  
 <210>1131  
 <211>249  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1131  
 Gly Glu Asp Ile Lys Asp Met Leu Ser Arg Val Glu Glu Ile Glu Met  
 1 5 10 15  
 Met Leu Arg Val Ile Glu Leu Pro Leu Leu Pro Ile Lys Gln Ala Leu  
 20 25 30  
 Glu Lys Ala Phe Val Gln Tyr Asn Ser Tyr Lys Ala Lys Leu Thr Lys  
 35 40 45  
 Val Glu Pro Cys Phe Arg Glu Ser Pro Ala Tyr Ile Thr Ser Glu Glu

50	55	60																	
Arg	Leu	Xaa	Ser	Leu	Asp	Gln	Thr	Leu	Glu	Arg	Ala	Tyr	Lys	Glu	Tyr				
65					70					75					80				
Gln	Lys	Arg	Phe	Gln	Glu	Pro	Ser	Arg	Leu	Glu	Ser	Glu	Val	Ser	Gly				
				85					90					95					
Cys	Arg	Glu	His	Leu	Arg	Glu	Gln	Val	Lys	Gln	Phe	Glu	Thr	Gln	Gly				
			100					105					110						
Leu	Asp	Leu	Ile	Lys	Glu	Glu	Leu	Ile	Phe	Val	Ser	Asp	Val	Leu	Phe				
	115						120					125							
Arg	Lys	Met	Val	Ser	Cys	Leu	Val	Ser	Thr	Val	His	Val	Pro	Phe	Met				
	130					135					140								
Glu	Phe	Tyr	Tyr	Glu	Tyr	Phe	Glu	Leu	His	Arg	Leu	Arg	Leu	Arg	Ala				
145					150					155					160				
Gln	Trp	Met	Ala	Asn	Ala	Glu	Ile	Tyr	Ser	Lys	Val	Arg	Lys	Ala	Phe				
				165					170					175					
Pro	Glu	Met	Leu	Lys	Glu	Thr	Leu	Glu	Lys	Ala	Lys	Ala	Pro	Arg	Glu				
			180					185					190						
Glu	Glu	Tyr	Trp	Leu	Leu	Cys	Glu	Glu	Arg	Lys	Ser	Lys	Glu	Lys	Arg				
	195						200					205							
Leu	Ile	Leu	Asn	Lys	Ile	Glu	Ala	Ala	Gln	Gln	Arg	Val	Lys	Asp	Leu				
	210					215				220									
Glu	Pro	Pro	Pro	Ile	Lys	Glu	Thr	Gly	Lys	Gln	Lys	Arg	Lys	Lys	Glu				
225					230					235					240				
Tyr	Ser	Phe	Phe	Ile	Arg	Leu	Lys	Ser											
				245															

&lt;210&gt;1132

&lt;211&gt;679

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1132

Met	Pro	Glu	Pro	Leu	Tyr	Thr	Asn	Lys	Leu	Ile	Thr	Glu	Lys	Ser	Pro				
1				5					10					15					
Tyr	Leu	Leu	Leu	Tyr	Ala	His	Thr	Pro	Val	Asn	Trp	Tyr	Pro	Trp	Gly				
			20					25					30						
Ala	Glu	Ala	Phe	His	Ile	Ala	Ala	Ile	Glu	Asn	Lys	Pro	Val	Phe	Leu				
		35				40					45								
Ser	Ile	Gly	Cys	Lys	His	Ser	Arg	Trp	Cys	Gln	Val	Met	Leu	Gln	Glu				
	50					55				60									
Ser	Tyr	Thr	Asn	Pro	Glu	Ile	Ala	Ala	Met	Leu	Asn	Glu	Tyr	Phe	Val				
65				70					75					80					
Asn	Val	Lys	Val	Asp	Lys	Glu	Glu	Leu	Pro	Tyr	Val	Ala	Lys	Leu	Tyr				
			85					90					95						
Gly	Asp	Leu	Ala	Gln	Met	Leu	Ala	Val	Ser	Gly	Asp	His	Gln	Glu	Thr				
		100					105					110							
Val	Ser	Trp	Pro	Leu	Asn	Val	Phe	Leu	Thr	Pro	Asp	Leu	Val	Pro	Phe				
	115					120					125								
Phe	Ser	Val	Asn	Tyr	Leu	Gly	Asn	Glu	Gly	Lys	Leu	Gly	Leu	Pro	Ser				
	130					135				140									
Phe	Pro	Gln	Ile	Ile	Asp	Lys	Leu	His	Phe	Met	Trp	Glu	Asp	Ala	Glu				
145				150					155					160					
Glu	Arg	Glu	Ala	Leu	Val	Glu	Gln	Ala	Met	Arg	Phe	Leu	Glu	Ile	Ala				
			165					170					175						
Ser	Phe	Leu	Glu	Gly	Cys	Val	Arg	Lys	Glu	Ile	Leu	Asp	Glu	Ser	Ser				
		180					185					190							
Leu	Lys	Arg	Thr	Val	Ala	Ala	Leu	Tyr	Gln	Asp	Ile	Asp	Pro	His	Tyr				
	195					200				205									
Gly	Gly	Val	Lys	Ala	Phe	Pro	Lys	Arg	Leu	Pro	Gly	Leu	Leu	Leu	Gln				
	210					215				220									
Phe	Phe	Leu	Arg	Tyr	Ser	Leu	Glu	Tyr	Gln	Glu	Ser	Arg	Gly	Leu	Phe				
225					230				235					240					
Phe	Val	Asp	Arg	Ser	Leu	Ser	Met	Val	Ala	Leu	Gly	Gly	Val	Arg	Asp				
			245					250					255						
His	Ile	Gly	Gly	Gly	Val	Tyr	Ser	Tyr	Thr	Ile	Asp	Asp	Lys	Trp	Leu				
		260					265						270						



Ile Pro Ala Phe Glu Lys Arg Leu Ile Asp Asn Ala Leu Met Ala Leu  
 275 280 285  
 Asn Tyr Leu Glu Ala Trp Ala Cys Leu Gly Lys Glu Glu Tyr Arg Gly  
 290 295 300  
 Ile Gly Lys Gln Ile Leu Ser Tyr Ile Leu Ser Glu Leu Tyr Ser Pro  
 305 310 315 320  
 Glu Val Gly Ala Phe Tyr Ser Ser Glu Gln Ala Glu Asn Trp Gly Ala  
 325 330 335  
 Gly Gly Gln Asn Phe Tyr Thr Trp Ser Val Glu Glu Ile Ser Asn Ala  
 340 345 350  
 Leu Gly Glu Asp Ala Glu Ile Phe Cys Asp Tyr Tyr Gly Ile Ser Arg  
 355 360 365  
 Glu Gly Phe Phe Asn Gly Arg Asn Ile Leu His Ile Pro Val His Arg  
 370 375 380  
 Glu Ile Glu Glu Leu Ser Glu Lys Tyr His Arg Ser Ile Glu Ala Ile  
 385 390 395 400  
 Glu Asp Ile Val Asp Arg Ser Arg Asp Ile Leu Lys Gly Ile Arg Ala  
 405 410 415  
 Gln Arg Ser His Arg Ser Lys Asp Asp Leu Ser Leu Thr Phe Asn Asn  
 420 425 430  
 Gly Trp Met Ile Tyr Thr Phe Ala Tyr Ala Gly Arg Leu Leu Gly Glu  
 435 440 445  
 Val Glu Tyr Ile Glu Ile Glu Lys Lys Cys Gly Glu Phe Val Arg Asn  
 450 455 460  
 Ser Leu Tyr Lys His His Glu Leu Tyr Arg Arg Trp Arg Glu Gly Glu  
 465 470 475 480  
 Ala Lys Tyr Arg Ala Ser Leu Glu Asp Tyr Gly Ala Leu Ile Leu Gly  
 485 490 495  
 Val Leu Ala Leu Tyr Glu Ser Gly Cys Gly Ser Phe Trp Leu Ser Phe  
 500 505 510  
 Ala Glu Glu Leu Met Gln Glu Val Leu Ser Phe Arg Ser Glu Glu  
 515 520 525  
 Gly Gly Phe Tyr Ser Asp Asp Gly Arg Asp Ser Thr Leu Leu Ile Lys  
 530 535 540  
 Gln Ser Pro Leu Ser Asp Gly Glu Thr Ile Ser Gly Asn Ala Leu Ile  
 545 550 555 560  
 Cys Gln Cys Leu Leu Ser Leu His Leu Ile Thr Glu Lys Lys His Tyr  
 565 570 575  
 Leu Thr Tyr Ala Glu Asp Ile Leu Gln Ile Ala Gln Ala Cys Ala His  
 580 585 590  
 Thr His Lys Phe Ser Ser Leu Gly Leu Leu Ile Ala Ser Gln Asn Tyr  
 595 600 605  
 Phe Ser Arg Lys His Val Lys Val Leu Ile Pro Leu Gly Asp Gln Glu  
 610 615 620  
 Asp Arg Ser Pro Val Leu Lys Cys Leu Ser Gly Leu Phe Leu Pro Tyr  
 625 630 635 640  
 Leu Ser Leu Ile Trp Met Thr Gln Glu Asn Gln Glu His Leu Glu Thr  
 645 650 655  
 Val Leu Pro Glu Tyr Glu His Cys Leu Ile Pro Lys Arg Gly Ile Ala  
 660 665 670  
 Gln Leu Arg Gln Phe Met Phe  
 675  
 <210>1133  
 <211>365  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1133  
 Glu Val Met Lys Leu Tyr Gln Thr Leu Arg Gly Ile Val Leu Val Ser  
 1 5 10 15  
 Thr Gly Cys Ile Phe Leu Gly Met His Gly Gly Tyr Ala Ala Glu Val  
 20 25 30  
 Pro Val Thr Ser Ser Gly Tyr Glu Asn Leu Leu Glu Ser Lys Glu Gln  
 35 40 45  
 Asp Pro Ser Gly Leu Ala Ile His Asp Arg Ile Leu Phe Lys Val Asp

50 55 60  
 Glu Glu Asn Val Val Thr Ala Leu Asp Val Ile His Lys Leu Asn Leu  
 65 70 75 80  
 Leu Phe Tyr Asn Ser Tyr Pro His Leu Ile Asp Ser Phe Pro Ala Arg  
 85 90 95  
 Ser Gln Tyr Tyr Thr Ala Met Trp Pro Val Val Leu Glu Ser Val Ile  
 100 105 110  
 Asp Glu Phe Leu Met Val Ala Asp Ala Lys Ala Lys Arg Ile Ala Thr  
 115 120 125  
 Asp Pro Thr Ala Val Asn Gln Glu Ile Glu Glu Met Phe Gly Arg Asp  
 130 135 140  
 Leu Ser Pro Leu Tyr Ala His Phe Glu Met Ser Pro Asn Asp Ile Phe  
 145 150 155 160  
 Asn Val Ile Asp Arg Thr Leu Thr Ala Gln Arg Val Met Gly Met Met  
 165 170 175  
 Val Arg Ser Lys Val Met Leu Lys Val Thr Pro Gly Lys Ile Arg Glu  
 180 185 190  
 Tyr Tyr Arg Lys Leu Glu Glu Glu Ala Ser Arg Lys Val Ile Trp Lys  
 195 200 205  
 Tyr Arg Val Leu Thr Ile Lys Ala Asn Thr Glu Ser Leu Ala Ser Gln  
 210 215 220  
 Ile Ala Asp Lys Val Arg Ala Arg Leu Asn Glu Ala Lys Thr Trp Asp  
 225 230 235 240  
 Lys Asp Arg Leu Thr Ala Leu Val Ile Ser Gln Gly Gly Gln Leu Val  
 245 250 255  
 Cys Ser Glu Glu Phe Ser Arg Glu Asn Ser Glu Leu Ser Gln Ser His  
 260 265 270  
 Lys Gln Glu Leu Asp Leu Ile Gly Tyr Pro Lys Glu Leu Cys Gly Leu  
 275 280 285  
 Pro Lys Ala His Lys Ser Gly Tyr Lys Leu Tyr Met Leu Leu Asp Lys  
 290 295 300  
 Thr Ser Gly Ser Ile Glu Pro Leu Asp Val Met Glu Ser Lys Ile Lys  
 305 310 315 320  
 Gln His Leu Phe Ala Leu Glu Ala Glu Ser Val Glu Lys Gln Tyr Lys  
 325 330 335  
 Asp Arg Leu Arg Lys Arg Tyr Gly Tyr Asp Ala Ser Met Ile Ala Lys  
 340 345 350  
 Leu Leu Ser Glu Glu Ala Pro Pro Leu Phe Ser Leu Leu  
 355 360 365  
 <210>1134  
 <211>277  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1134  
 Val Thr Arg Ser Ser Pro Ala Gln Leu Ser Arg Phe Leu Ser Glu Ile  
 1 5 10 15  
 Gln Asn Lys Pro Lys Lys Ser Leu Ser Gln Asn Phe Leu Val Asp Gln  
 20 25 30  
 Asn Ile Val Lys Lys Ile Val Ala Thr Ser Glu Val Ile Pro Gln Asp  
 35 40 45  
 Trp Val Leu Glu Ile Gly Pro Gly Phe Gly Ala Leu Thr Glu Glu Leu  
 50 55 60  
 Ile Ala Ala Gly Ala Gln Val Ile Ala Ile Glu Lys Asp Pro Met Phe  
 65 70 75 80  
 Ala Pro Ser Leu Glu Glu Leu Pro Ile Arg Leu Glu Ile Ile Asp Ala  
 85 90 95  
 Cys Lys Tyr Pro Leu Asp Gln Leu Gln Glu Tyr Lys Thr Leu Gly Lys  
 100 105 110  
 Gly Arg Val Val Ala Asn Leu Pro Tyr His Ile Thr Thr Pro Leu Leu  
 115 120 125  
 Thr Lys Leu Phe Leu Glu Ala Pro Asp Phe Trp Lys Thr Val Thr Val  
 130 135 140  
 Met Val Gln Asp Glu Val Ala Arg Arg Ile Val Ala Gln Pro Gly Gly  
 145 150 155 160

Arg Asp Tyr Gly Ser Leu Thr Ile Phe Leu Gln Phe Phe Ala Asp Ile  
 165 170 175  
 His Tyr Ala Phe Lys Val Ser Ala Ser Cys Phe Tyr Pro Lys Pro Gln  
 180 185 190  
 Val Gln Ser Ala Val Ile His Met Lys Val Lys Glu Thr Leu Pro Leu  
 195 200 205  
 Ser Asp Glu Glu Ile Pro Val Phe Phe Thr Leu Thr Arg Thr Ala Phe  
 210 215 220  
 Gln Gln Arg Arg Lys Val Leu Ala Asn Thr Leu Lys Gly Leu Tyr Pro  
 225 230 235 240  
 Lys Glu Gln Val Glu Gln Ala Leu Lys Glu Leu Gly Leu Leu Leu Asn  
 245 250 255  
 Val Arg Pro Glu Val Leu Ser Leu Asn Asp Tyr Leu Ala Leu Phe His  
 260 265 270  
 Lys Met Gln Ala Gly  
 275  
 <210>1135  
 <211>644  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1135  
 Met Thr Ser Ser Ser Cys Pro Leu Leu Asp Leu Ile Leu Ser Pro Ala  
 1 5 10 15  
 Asp Leu Lys Lys Leu Ser Ile Ser Gln Leu Pro Gly Leu Ala Glu Glu  
 20 25 30  
 Ile Arg Tyr Arg Ile Ile Ser Val Leu Ser Gln Thr Gly Gly His Leu  
 35 40 45  
 Ser Ser Asn Leu Gly Ile Val Glu Leu Thr Ile Ala Leu His Tyr Val  
 50 55 60  
 Phe Ser Ser Pro Lys Asp Lys Phe Ile Phe Asp Val Gly His Gln Thr  
 65 70 75 80  
 Tyr Pro His Lys Leu Thr Gly Arg Asn Asn Glu Gly Phe Asp His  
 85 90 95  
 Ile Arg Asn Asp Asn Gly Leu Ser Gly Phe Thr Asn Pro Thr Glu Ser  
 100 105 110  
 Asp His Asp Leu Phe Phe Ser Gly His Ala Gly Thr Ala Leu Ser Leu  
 115 120 125  
 Ala Leu Gly Met Ala Gln Thr Thr Pro Leu Glu Ser Arg Thr His Val  
 130 135 140  
 Ile Pro Ile Leu Gly Asp Ala Ala Phe Ser Cys Gly Leu Thr Leu Glu  
 145 150 155 160  
 Ala Leu Asn Asn Ile Ser Thr Asp Leu Ser Lys Phe Val Val Ile Leu  
 165 170 175  
 Asn Asp Asn Asn Met Ser Ile Ser Lys Asn Val Gly Ala Met Ser Arg  
 180 185 190  
 Ile Phe Ser Arg Trp Leu His His Pro Ala Thr Asn Lys Leu Thr Lys  
 195 200 205  
 Gln Val Glu Lys Trp Leu Ala Lys Ile Pro Arg Tyr Gly Asp Ser Leu  
 210 215 220  
 Ala Lys His Ser Arg Arg Leu Ser Gln Cys Val Lys Asn Leu Phe Cys  
 225 230 235 240  
 Pro Thr Pro Leu Phe Glu Gln Phe Gly Leu Ala Tyr Val Gly Pro Ile  
 245 250 255  
 Asp Gly His Asn Val Lys Lys Leu Ile Pro Ile Leu Gln Ser Val Arg  
 260 265 270  
 Asn Leu Pro Phe Pro Ile Leu Val His Val Cys Thr Thr Lys Gly Lys  
 275 280 285  
 Gly Leu Asp Gln Ala Gln Asn Asn Pro Ala Lys Tyr His Gly Val Arg  
 290 295 300  
 Ala Asn Phe Asn Lys Arg Glu Ser Ala Lys His Leu Pro Ala Ile Lys  
 305 310 315 320  
 Pro Lys Pro Ser Phe Pro Asp Ile Phe Gly Gln Thr Leu Cys Glu Leu  
 325 330 335  
 Gly Glu Val Ser Ser Arg Leu His Val Thr Pro Ala Met Ser Ile

340 345 350  
 Gly Ser Arg Leu Glu Gly Phe Lys Gln Lys Phe Pro Glu Arg Phe Phe  
 355 360 365  
 Asp Val Gly Ile Ala Glu Gly His Ala Val Thr Phe Ser Ala Gly Ile  
 370 375 380  
 Ala Lys Ala Gly Asn Pro Val Ile Cys Ser Ile Tyr Ser Thr Phe Leu  
 385 390 395 400  
 His Arg Ala Leu Asp Asn Val Phe His Asp Val Cys Met Gln Asp Leu  
 405 410 415  
 Pro Val Ile Phe Ala Ile Asp Arg Ala Gly Leu Ala Tyr Gly Asp Gly  
 420 425 430  
 Arg Ser His His Gly Ile Tyr Asp Met Ser Phe Leu Arg Ala Met Pro  
 435 440 445  
 Gln Met Ile Ile Cys Gln Pro Arg Ser Gln Val Val Phe Gln Gln Leu  
 450 455 460  
 Leu Tyr Ser Ser Leu His Trp Ser Ser Pro Ser Ala Ile Arg Tyr Pro  
 465 470 475 480  
 Asn Ile Pro Ala Pro His Gly Asp Pro Leu Thr Gly Asp Pro Asn Phe  
 485 490 495  
 Leu Arg Ser Pro Gly Asn Ala Glu Thr Leu Ser Gln Gly Glu Asp Val  
 500 505 510  
 Leu Ile Ile Ala Leu Gly Thr Leu Cys Phe Thr Ala Leu Ser Ile Lys  
 515 520 525  
 His Gln Leu Leu Ala Tyr Gly Ile Ser Ala Thr Val Val Asp Pro Ile  
 530 535 540  
 Phe Ile Lys Pro Phe Asp Asn Asp Leu Phe Ser Leu Leu Leu Met Ser  
 545 550 555 560  
 His Ser Lys Val Ile Thr Ile Glu Glu His Ser Ile Arg Gly Gly Leu  
 565 570 575  
 Ala Ser Glu Phe Asn Asn Phe Val Ala Thr Phe Asn Phe Lys Val Asp  
 580 585 590  
 Ile Leu Asn Phe Ala Ile Pro Asp Thr Phe Leu Ser His Gly Ser Lys  
 595 600 605  
 Glu Ala Leu Thr Lys Ser Ile Gly Leu Asp Glu Ser Ser Met Thr Asn  
 610 615 620  
 Arg Ile Leu Thr His Phe Asn Phe Arg Ser Lys Lys Gln Thr Val Gly  
 625 630 635 640  
 Asp Val Arg Val

&lt;210&gt;1136

&lt;211&gt;127

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1136

Ala Ser Pro Ala Arg Ser Ile Ala Lys Ile Thr Gly Arg Ser Cys Met  
 1 5 10 15  
 Gln Thr Ser Trp Lys Thr Leu Ser Arg Ala Arg Cys Lys Asn Val Glu  
 20 25 30  
 Tyr Ile Glu Gln Ile Thr Gly Leu Pro Ala Phe Ala Met Pro Ala Leu  
 35 40 45  
 Lys Val Thr Ala Trp Pro Ser Ala Ile Pro Thr Ser Lys Lys Arg Ser  
 50 55 60  
 Gly Asn Phe Cys Leu Lys Pro Ser Lys Arg Asp Pro Ile Asp Ile Ala  
 65 70 75 80  
 Gly Val Thr Thr Trp Arg Arg Glu Glu Thr Ser Pro Ser Ser His Ser  
 85 90 95  
 Val Trp Pro Asn Ile Ser Gly Lys Glu Gly Leu Gly Leu Ile Ala Gly  
 100 105 110  
 Arg Cys Phe Ala Asp Ser Arg Leu Leu Lys Phe Ala Leu Thr Pro  
 115 120 125

&lt;210&gt;1137

&lt;211&gt;554

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1137

```

Met Ser Ser Pro Pro Gln Ala Val Ala Ser Leu Thr Glu Arg Ile Lys
 1          5          10          15
Thr Leu Leu Glu Ser Asn Phe Cys Gln Ile Ile Val Lys Gly Glu Leu
 20          25          30
Ser Asn Val Ser Leu Gln Pro Ser Gly His Leu Tyr Phe Gly Ile Lys
 35          40          45
Asp Ser Gln Ala Phe Leu Asn Gly Ala Phe Phe His Phe Lys Ser Lys
 50          55          60
Tyr Tyr Asp Arg Lys Pro Lys Asp Gly Asp Ala Val Ile Ile His Gly
 65          70          75          80
Lys Leu Ala Val Tyr Ala Pro Arg Gly Gln Tyr Gln Ile Val Ala His
 85          90          95
Ala Leu Val Tyr Ala Gly Glu Gly Asp Leu Leu Gln Lys Phe Glu Glu
100          105          110
Thr Lys Arg Arg Leu Thr Ala Glu Gly Tyr Phe Ala Thr Glu Lys Lys
115          120          125
Lys Pro Leu Pro Phe Ala Pro Gln Cys Ile Gly Val Ile Thr Ser Pro
130          135          140
Thr Gly Ala Val Ile Gln Asp Ile Leu Arg Val Leu Ser Arg Arg Ala
145          150          155          160
Arg Asn Tyr Lys Ile Leu Val Tyr Pro Val Thr Val Gln Gly Asn Ser
165          170          175
Ala Ala His Glu Ile Ser Lys Ala Ile Glu Val Met Asn Ala Glu Asn
180          185          190
Leu Ala Asp Val Leu Ile Ile Ala Arg Gly Gly Gly Ser Ile Glu Asp
195          200          205
Leu Trp Ala Phe Asn Glu Glu Ile Leu Val Lys Ala Ile His Ala Ser
210          215          220
Thr Ile Pro Ile Val Ser Ala Val Gly His Glu Thr Asp Tyr Thr Leu
225          230          235          240
Cys Asp Phe Ala Ser Asp Val Arg Ala Pro Thr Pro Ser Ala Ala Ala
245          250          255
Glu Ile Val Cys Lys Ser Ser Glu Glu Gln Val Gln Val Phe Glu Gly
260          265          270
Tyr Leu Arg His Leu Leu Ser His Ser Arg Gln Leu Leu Thr Ser Lys
275          280          285
Lys Gln Gln Leu Leu Pro Trp Arg Arg Phe Leu Asp Arg Ala Glu Phe
290          295          300
Tyr Thr Thr Ala Gln Gln Leu Asp Ser Ile Glu Ile Ala Ile Gln
305          310          315          320
Lys Gly Val Gln Gly Lys Ile His Glu Ser Lys Gln Arg Tyr Asp Asn
325          330          335
Ile Ser Arg Trp Leu Gln Gly Asp Leu Val Ser Arg Met Thr Cys Arg
340          345          350
Leu Gln Ser Leu Lys Lys Met Leu Ser Gln Ala Leu Ser His Lys Ala
355          360          365
Leu Ser Leu Gln Val Arg Cys His Gln Leu Lys Lys Ser Leu Thr Tyr
370          375          380
Pro Arg Gln Ile Gln Gln Ala Ser Gln Lys Leu Ser Pro Trp Arg Gln
385          390          395          400
Gln Leu Asp Thr Leu Ile Ser Arg Arg Leu His Tyr Gln Lys Glu Glu
405          410          415
Tyr Phe His Lys His Thr Arg Leu Lys His Ala His Asn Val Leu Glu
420          425          430
Gln Gln Leu Arg Ser His Val Gln Lys Leu Glu Leu Leu Gly Arg Arg
435          440          445
Leu Ser Arg Gly Cys Glu Leu Asn Leu Gln Asn Gln Lys Ile Ala Tyr
450          455          460
Ala Asn Val Lys Glu Thr Leu Ala Thr Ile Leu Glu Arg Arg Tyr Glu
465          470          475          480
Asn Ser Val Ala Arg Tyr Ser Ala Leu Lys Glu Gln Leu His Ser Leu
485          490          495
Asn Pro Lys Asn Val Leu Lys Arg Gly Tyr Ala Met Leu Phe Asp Phe

```

500 505 510  
 Asn Glu Asn Ser Ala Met Ile Ser Val Asp Ser Leu Gln Glu Asn Ala  
 515 520 525  
 Arg Val Arg Ile Gln Leu Gln Asp Gly Glu Ala Ile Leu Thr Val Thr  
 530 535 540  
 Asn Ile Glu Ile Cys Lys Leu Ile Lys Gly  
 545 550  
 <210>1138  
 <211>184  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1138  
 Met Thr Tyr Ala Gln Val Glu Val Leu Met Ala Thr Pro Asp Ile Ser  
 1 5 10 15  
 Lys Tyr His Gly Leu Arg Asp Arg Cys Leu Met Glu Leu Phe Tyr Ser  
 20 25 30  
 Ser Gly Leu Arg Ile Ser Glu Ile Val Ala Val Asn Lys Gln Asp Phe  
 35 40 45  
 Asp Leu Ser Thr His Leu Ile Arg Ile Arg Gly Lys Gly Lys Lys Glu  
 50 55 60  
 Arg Ile Ile Pro Val Thr Ser Asn Ala Ile Gln Trp Ile Gln Ile Tyr  
 65 70 75 80  
 Leu Asn His Pro Asp Arg Lys Arg Leu Glu Lys Asp Pro Gln Ala Ile  
 85 90 95  
 Phe Leu Asn Arg Phe Gly Arg Arg Ile Ser Thr Arg Ser Ile Asp Arg  
 100 105 110  
 Ser Phe Gln Glu Tyr Leu Arg Arg Ser Gly Leu Ser Gly His Ile Thr  
 115 120 125  
 Pro His Thr Ile Arg His Thr Ile Ala Thr His Trp Leu Glu Ser Gly  
 130 135 140  
 Met Asp Leu Lys Thr Ile Gln Ala Leu Leu Gly His Ser Ser Leu Glu  
 145 150 155 160  
 Thr Thr Thr Val Tyr Thr Gln Val Ser Val Lys Leu Lys Lys Gln Thr  
 165 170 175  
 His Gln Glu Ala His Pro His Ala  
 180  
 <210>1139  
 <211>288  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1139  
 Met Ser His Leu Ile Pro Ser Leu Arg Asn Ser Val Thr Ser Tyr Phe  
 1 5 10 15  
 His Lys Pro Gln Pro Ile Lys Gln Ala Ala Pro Ser Lys Ser Ile Arg  
 20 25 30  
 Asp Ile Cys Asn Ile Ala Tyr Leu Ile Ile Ile Cys Val Leu Val Val  
 35 40 45  
 Val Val Leu Val Gly Ala Met Leu Cys Met Phe Ile Pro Ser Val Gly  
 50 55 60  
 Ile Pro Leu Cys Leu Ser Ser Leu Ala Leu Leu Val Leu Leu Ser Ile  
 65 70 75 80  
 Phe Asn Pro Cys Leu Ile Asn Trp Ile Ser Thr Lys Lys Thr Lys Glu  
 85 90 95  
 Ile Ala Pro Lys Asp Ala Ser Glu Ser Gln Pro Thr Lys Ser Ala Ser  
 100 105 110  
 Arg Lys Gly Ser Pro Gln Leu Ser Pro His His Asp His Glu Pro Lys  
 115 120 125  
 Asn Phe Ile Arg Thr Gln Leu Glu Lys Gly Val Asn Tyr Val Thr Asn  
 130 135 140  
 Lys Phe Lys Ser Gly Glu Glu Ser Pro His Ile Ser Asp Glu His His  
 145 150 155 160  
 Ser Pro Arg Gln Ser Lys Arg Ser Ser Glu Ile Glu Ser Ser Asp Glu  
 165 170 175  
 Ser Ser Pro Glu Leu His Arg Lys Ala Lys Gly Lys Ala Pro His Thr

180 185 190  
 Ala Thr Thr Lys Gly Ser Lys Thr Ser Thr Thr Glu Ser Ser Lys Lys  
 195 200 205  
 Lys Lys Lys Thr Lys His Ser Leu His Arg Thr Thr Ser Ser Ile His  
 210 215 220  
 Lys Arg Ser Ala Pro Lys Pro Met Val Pro Ser Lys Lys Arg Lys Pro  
 225 230 235 240  
 Val Leu Leu Lys Lys Thr Val Pro Leu Pro Ile Glu Asp Leu Glu His  
 245 250 255  
 Gln Ser Ser Gly Asn Glu Ser Ser Asp Ser Ser Ser Pro Pro Pro Val  
 260 265 270  
 Gln Arg Lys Ala Ile Leu Pro Trp Phe Cys Lys Gln Pro Thr Asp Pro  
 275 280 285

&lt;210&gt;1140

&lt;211&gt;153

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1140

Met Leu Arg Arg Arg Ile Trp Lys Lys Thr Leu Thr Pro Asp Gln Glu  
 1 5 10 15  
 Asn Leu Ser Leu Pro Leu Pro Ser Pro Thr Thr Leu Lys Lys Ile His  
 20 25 30  
 Ala Leu His Ile Leu Val Arg Ser Gly Lys Thr Tyr Asn Glu Leu Ile  
 35 40 45  
 Gln Glu Gly Phe Ser Phe Thr Lys Ile Thr Asp Leu Gly Gln Ala Pro  
 50 55 60  
 Ser Pro Lys Gln Asp Ile Gly Phe Ser Tyr Asn Ser Leu Leu Pro Asn  
 65 70 75 80  
 Phe Tyr Phe His Ser Leu Val Ser Val Pro Asn Ile Ser Gly Glu Glu  
 85 90 95  
 Arg Ala Leu Asn Tyr His Lys Glu Gln Gln Glu Glu Met Ala Val Lys  
 100 105 110  
 Leu Lys Thr Met Gln Ala Cys Ser Phe Val Phe Arg Ser Leu His Leu  
 115 120 125  
 Pro Ser Met Gln Thr Lys Asp Lys Lys Ala Gly Phe Gly Leu Leu Thr  
 130 135 140  
 Phe Phe Pro Trp Lys Ile Tyr Pro Leu  
 145 150

&lt;210&gt;1141

&lt;211&gt;136

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1141

Leu Ala Met Ala Lys Asn Val Pro Leu Leu Gly Tyr Ser Ser Leu Glu  
 1 5 10 15  
 Gly Tyr Leu Leu Ser Lys Asp Glu Lys Lys Ala Leu Met Leu Pro Leu  
 20 25 30  
 Gly Lys Arg Gly Gly Val Leu Thr Ser Ser Glu Ile Pro Glu Glu  
 35 40 45  
 Gly Leu Asn Glu Lys Arg Arg Gly Val Gly Pro Gly Ala Leu Leu Ser  
 50 55 60  
 Tyr Glu Glu Ala Ser Asp Tyr Cys Val Ala His Gly Tyr Tyr His Val  
 65 70 75 80  
 Ile Ser Pro Asn Pro Gln Leu Phe Ala Ser Ser Phe Ser Asp Lys Ile  
 85 90 95  
 Thr Val Glu Glu Val Ala Pro Ser Val Glu Gln Ile Arg Arg His Val  
 100 105 110  
 Ile Ser Gln Phe Met Phe Val Glu Tyr Asp Lys Gln Leu Ser Pro Asp  
 115 120 125  
 Tyr Arg Ser Tyr Ser Cys Ile Phe  
 130 135

&lt;210&gt;1142

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1142

```

Met Ile Glu Phe Pro Ser Ala Val Trp Met Ile Glu Glu Ile Leu Pro
 1           5           10           15
Glu Cys Asp Phe Leu Ser Ile Gly Thr Asn Asp Leu Val Gln Tyr Thr
           20           25           30
Leu Gly Ile Ser Arg Glu Ser Ala Leu Pro Lys His Leu Asn Val Thr
           35           40           45
Leu Pro Pro Ala Val Ile Arg Met Ile His His Val Leu Gln Ala Ala
           50           55           60
Asn Lys Ile Arg Phe Leu Ala Phe Val Glu Arg Pro Gln Gly Ser
           65           70           75           80
Ser Val

```

&lt;210&gt;1143

&lt;211&gt;108

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1143

```

Leu Phe Asp Ala Leu His Ile Ser Leu His Arg Asn Ile Pro Arg Met
 1           5           10           15
Gly Asn His Glu Thr Tyr Ile His Pro Gly Val Leu Pro Ser Ser His
           20           25           30
Ala Gln Asp Val Ser Arg Ser Thr Val Tyr Pro Ser Arg Ser Phe Ile
           35           40           45
Met Arg Arg Met Leu Met Gly Trp Asn Phe Asn Arg Val Pro Ser Lys
           50           55           60
Ser Ser Glu Gln Leu Met Asp Gly His Arg Ile Pro Leu Ile Phe Phe
           65           70           75           80
Gly Lys His His Pro Thr Ile Ser Ile Leu Asn Val Asn Arg Phe Ser
           85           90           95
Trp Leu Ser Ile Phe Tyr Asn Gly Glu Arg Gly Phe
           100           105

```

&lt;210&gt;1144

&lt;211&gt;141

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1144

```

Met Ala Thr Lys Thr Lys Thr Gln Trp Thr Cys Asn Gln Cys Gly Ala
 1           5           10           15
Thr Ala Pro Lys Trp Leu Gly Gln Cys Pro Gly Cys His Asn Trp Asn
           20           25           30
Ser Leu Val Glu Glu Tyr Val Pro Gln Ala Arg Ser Gly Thr Ser Ser
           35           40           45
Arg Ser Ser Thr Ser Ala Ile Ala Leu Ser Ser Ile Glu Leu Glu Asn
           50           55           60
Glu Ser Arg Ile Phe Ile Asp His Ala Gly Trp Asp Arg Ile Leu Gly
           65           70           75           80
Gly Gly Val Val Arg Gly Ser Leu Thr Leu Gly Gly Asp Pro Gly
           85           90           95
Ile Gly Lys Ser Thr Leu Leu Leu Gln Thr Ala Glu Arg Leu Ala Ser
           100           105           110
Gln Lys Tyr Lys Val Leu Tyr Val Cys Gly Glu Glu Ser Val Thr Gln
           115           120           125
Thr Ser Leu Arg Ala Lys Arg Ser Ile Ser His His Leu
           130           135           140

```

&lt;210&gt;1145

&lt;211&gt;77

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1145

```

Met Thr Lys Ile Gln Cys Ser Ala Gln Tyr Tyr Arg Ser Arg Pro Ala
 1           5           10           15
Glu Arg Ala Gln Thr Pro Pro Gln Pro Phe Leu Ala Arg Asp Arg Ala

```



20 25 30  
 Asp Phe Trp Glu Arg His Pro Arg Phe Ser Ala Cys Cys Arg Val Leu  
 35 40 45  
 Leu Leu Val Ala Trp Val Val Leu Ala Leu Leu Phe Leu Phe Val Met  
 50 55 60  
 Leu Leu Pro Leu Ala Ala Gly Ser Tyr Leu Leu Ala Phe  
 65 70 75

&lt;210&gt;1146

&lt;211&gt;121

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1146

Leu Thr Tyr Thr Arg Val Asn Asp Gly His Leu Ala Pro Phe Arg Ala  
 1 5 10 15  
 Gly Ala Lys Trp Ile Leu Ile His Tyr Val Arg Leu Arg Arg Gln His  
 20 25 30  
 Asn Gln Asn Asp Phe Phe Thr Pro Gly His Ser Cys Tyr Tyr Ala Arg  
 35 40 45  
 Leu Ala Phe Asn Gln Thr Gln Arg Leu Tyr His Gln Leu Phe Asn Val  
 50 55 60  
 Glu Lys Leu Arg Ser Ile Tyr Ala Asn Met Asp Lys Asp Pro Leu Cys  
 65 70 75 80  
 His Pro Trp Ala Xaa Ile Pro Ile Tyr Asp Leu Leu Lys Thr Glu Asp  
 85 90 95  
 His Gly Asp Gly Phe Leu Glu Gln Gln Glu Asp Arg Glu Tyr Pro Ser  
 100 105 110  
 Arg Ala Ala Gln Asp Gln Phe Trp Gly  
 115 120

&lt;210&gt;1147

&lt;211&gt;170

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1147

Val Ser Ala Glu Phe Lys Leu Met Leu Asp Leu Arg Gln Tyr Met Gly  
 1 5 10 15  
 Ser Val Met Gln Arg Leu Gly Leu Ser Asn Leu Phe His Cys Leu Leu  
 20 25 30  
 Leu Phe Leu Arg Tyr Tyr Tyr Ser Lys Leu Val Phe Gly Leu Thr Val  
 35 40 45  
 Leu Leu Ala Ala Ile Ser Val Ile Cys Leu Leu Gly Cys Ser Glu Pro  
 50 55 60  
 Ser Leu Ser Ser Phe Thr Glu Tyr Val Gly Pro Glu Tyr Ser Ala Ala  
 65 70 75 80  
 Ala Gln Leu Ser Ile Glu Gln Ser Cys His Asp Glu Val Tyr Gly Gln  
 85 90 95  
 Gln Val Val Val Thr Trp Ser Leu Pro Ser Arg Met Arg Lys Cys Leu  
 100 105 110  
 Pro Val Thr Leu Tyr Leu Trp Val Tyr Tyr Gly Asn Gly Lys Val Glu  
 115 120 125  
 Lys Leu Thr Tyr Glu Val Asn Gln Ser Ala Gly Tyr Arg Val Tyr Cys  
 130 135 140  
 Leu Lys Gly Leu Glu Tyr Lys Glu Leu Gln Gly Ile Ile Ser Tyr Pro  
 145 150 155 160  
 Leu Arg Tyr Val Ala Gly Ile Lys Arg Leu  
 165 170

&lt;210&gt;1148

&lt;211&gt;101

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1148

Met Val Ser Pro Leu Ser Leu Phe His Lys Met Leu Leu Glu Asn Trp  
 1 5 10 15  
 Thr Pro Val Glu Pro Phe Pro Trp Pro Pro Ala Glu Lys Asn Gln  
 20 25 30

Lys Ile Phe Ala Trp Ala Leu Asn Gln Ser Lys Leu Ile Phe Val Ser  
                   35                  40                  45  
 Thr Ser Gly Asn Ile Ala Gln Pro Arg Leu Val Thr Asp Ser Met Ser  
           50                  55                  60  
 Met Met Ile Val Asn Ala Ala Asn Arg Thr Met Ser Arg Asp Gly Ala  
       65                  70                  75                  80  
 Gly Thr Asn Gln Val Leu Ser Ala Ala Val Ser Val Asp Ser Trp Gly  
                   85                  90                  95  
 Cys Arg Asn Asp Leu  
                   100

&lt;210&gt;1149

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1149

Val Ala Leu Lys Ile Arg Leu Arg Gln Gln Gly Arg Arg Asn His Val  
   1                  5                  10                  15  
 Val Tyr Arg Leu Val Leu Ala Asp Val Glu Ser Pro Arg Asp Gly Lys  
           20                  25                  30  
 Tyr Ile Glu Leu Leu Gly Trp Tyr Asp Pro His Ser Ser Ile Asn Tyr  
           35                  40                  45  
 Gln Leu Lys Ser Glu Arg Ile Phe Tyr Trp Leu Glu Arg Gly Ala Gln  
       50                  55                  60  
 Leu Ser Ser Lys Ala Glu Ala Leu Val Lys Gln Gly Ala Pro Gly Val  
       65                  70                  75                  80  
 Tyr Ser Ala Leu Leu Ser Lys Gln Glu Ala Arg Lys Leu Val Val Arg  
                   85                  90                  95  
 Lys Lys Arg Arg Ala Tyr Arg Gln Arg Arg Ser Thr Gln Arg Glu Glu  
                   100                  105                  110  
 Ala Ala Lys Asp Ala Thr Lys  
                   115

&lt;210&gt;1150

&lt;211&gt;170

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1150

Met Ser Glu Val Lys Pro Leu Phe Leu Lys Asn Asp Ser Phe Asp Leu  
   1                  5                  10                  15  
 Ala Thr Gln Arg Phe Gln Asn Leu Ile Asn Met Leu Gln Glu Gln Ala  
           20                  25                  30  
 Glu Ile Tyr Asn Glu Tyr Glu Glu Lys Asn Ala Arg Val Gln Asn Glu  
           35                  40                  45  
 Ile Lys Glu Gln Lys Asp Phe Val Lys Arg Cys Ile Glu Asp Phe Glu  
       50                  55                  60  
 Ala Arg Gly Leu Gly Val Leu Lys Glu Glu Leu Ala Ser Leu Thr Arg  
       65                  70                  75                  80  
 Asp Phe His Asp Lys Ala Lys Ala Glu Thr Ser Met Leu Ile Glu Cys  
                   85                  90                  95  
 Pro Cys Ile Gly Phe Tyr Tyr Ser Ile His Gln Glu Glu Gln Arg Gln  
           100                  105                  110  
 Arg Gln Glu Arg Leu Gln Lys Met Ala Glu Arg Tyr Arg Asp Cys Lys  
           115                  120                  125  
 Gln Val Leu Glu Ala Val Gln Val Glu Gln Lys Asp Met Ile Ser Ser  
       130                  135                  140  
 Arg Val Val Val Asp Asp Ser Tyr Phe Glu Glu Glu Lys Glu Glu Gln  
       145                  150                  155                  160  
 Lys Val Asp Asn Arg Lys Lys Glu Gln Asp  
                   165                  170

&lt;210&gt;1151

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1151

Leu Val Phe Ser Tyr Tyr Cys Met Gly Leu Phe Phe Phe Ser Gly Ala

1 5 10 15  
 Ile Ser Ser Cys Gly Leu Leu Val Ser Leu Gly Val Gly Leu Gly Leu  
 20 25 30  
 Ser Val Leu Gly Val Leu Leu Leu Leu Ala Gly Leu Leu Leu Phe  
 35 40 45  
 Lys Ile Gln Ser Met Leu Arg Glu Val Pro Lys Ala Pro Asp Leu Leu  
 50 55 60  
 Asp Leu Glu Asp Ala Ser Glu Arg Leu Arg Val Lys Ala Ser Arg Ser  
 65 70 75 80  
 Leu Ala Ser Leu Pro Lys Lys Ser Val Ser  
 85 90

&lt;210&gt;1152

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1152

Leu Leu Leu Cys Ser Ala Met Gly Ile Phe Ser Ser Ala Lys Ala Leu  
 1 5 10 15  
 Ile Ala Trp Asn Lys Ala Ser Leu Asn Leu Ser Pro Ala Leu Leu Gly  
 20 25 30  
 Ala Ile Leu Ile Phe Glu Pro Ile Phe Gly Leu Val Leu Thr Tyr Leu  
 35 40 45  
 Tyr Ser Gln Ser Leu Pro Ser Leu Gln Glu Gly Ile Gly Ile Phe Leu  
 50 55 60  
 Met Leu Gly Gly Ser Leu Cys Leu Val Leu Phe Gly Arg Lys Val  
 65 70 75 80  
 Gln Lys Ser Leu Glu Asn Ser Gln Val Ser Ser Ser Asn Glu  
 85 90

&lt;210&gt;1153

&lt;211&gt;248

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1153

Met Phe Pro Ser Ala Asn Gln Glu Ser Arg Thr Arg Asn Val Pro Leu  
 1 5 10 15  
 Gly Ile Phe His Gly Leu Val Ala Cys Leu Tyr Trp Gly Ile Val Phe  
 20 25 30  
 Val Ile Pro Asn Phe Leu Gly Ser Phe Gly Asp Leu Asp Ile Val Leu  
 35 40 45  
 Thr Arg Tyr Thr Ile Phe Gly Ile Phe Ser Leu Ile Ala Cys Ala Ile  
 50 55 60  
 Lys Asn Pro Ser Val Ile Lys Lys Thr Pro Leu Tyr Ile Trp Arg Lys  
 65 70 75 80  
 Ser Leu Leu Trp Thr Leu Leu Ile Asn Pro Val Tyr Tyr Phe Gly Ile  
 85 90 95  
 Thr Leu Gly Ile Arg Tyr Val Gly Ser Ala Ile Thr Val Val Ile Ala  
 100 105 110  
 Ser Leu Ala Pro Thr Ala Val Leu Tyr His Ser Asn Thr Lys Gln Lys  
 115 120 125  
 Glu Leu Pro Tyr Ser Leu Leu Phe Ala Ile Ser Ser Val Ile Ile Thr  
 130 135 140  
 Gly Val Ile Leu Thr His Leu Ser Ala Leu Asn Leu Pro Thr Ala Ala  
 145 150 155 160  
 Ser Pro Leu Tyr Ser Ile Leu Gly Val Ile Ala Val Ile Leu Ser Thr  
 165 170 175  
 Ser Leu Trp Val Ile Tyr Val Ile Arg Asn Gln Ser Leu Leu Glu Lys  
 180 185 190  
 His Pro Xaa Leu Thr Pro Asp Tyr Leu Glu Leu Pro His Arg Asn Gln  
 195 200 205  
 Arg Phe Asp His Leu Pro Pro Tyr Asp Tyr Tyr Ser Arg Ser Leu Trp  
 210 215 220  
 Asn Tyr Pro Arg Asn Thr Gln Ser Tyr Leu Ala Tyr Thr Gly Ile Arg  
 225 230 235 240  
 Ala Thr Ala Leu Leu Val Ala Met

245

&lt;210&gt;1154

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1154

```

Met Ala Val Gln Ser Ile Lys Glu Ala Val Thr Ser Ala Ala Thr Ser
 1           5           10           15
Val Gly Cys Val Asn Cys Ser Arg Glu Ala Ile Pro Ala Phe Asn Thr
           20           25           30
Glu Glu Arg Ala Thr Ser Ile Ala Arg Ser Val Ile Ala Ala Ile Ile
           35           40           45
Ala Val Val Ala Ile Ser Leu Leu Gly Leu Gly Leu Val Val Leu Ala
           50           55           60
Gly Cys Cys Pro Leu Gly Met Ala Ala Gly Ala Ile Thr Met Leu Leu
           65           70           75           80
Gly Val Ala Leu Leu Ala Trp Ala Ile Leu Ile Thr Leu Arg Leu Leu
           85           90           95
Asn Ile Pro Lys Ala Glu Ile Pro Ser Pro Gly Asn Asn Gly Glu Pro
           100          105          110
Asn Glu Arg Asn Ser Ala Thr Pro Pro Leu Glu Gly Gly Val Ala Gly
           115          120          125
Glu Ala Gly Arg Gly Gly Gly Ser Pro Leu Thr Gln Leu Asp Leu Asn
           130          135          140
Ser Gly Ala Gly Ser
145

```

&lt;210&gt;1155

&lt;211&gt;124

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1155

```

Met Gly Asn Ser Cys Phe Trp Arg Gly Gly Leu Leu Arg Tyr Pro Cys
 1           5           10           15
Gly Glu Glu Ile Glu Lys Ser Arg Ala Asn Phe Phe Thr Ala Asp Thr
           20           25           30
Thr Thr Val Met Ser Tyr Pro Pro Asn Pro Tyr Gly Leu Tyr Asp Met
           35           40           45
Ala Gly Asn Val Tyr Glu Trp Cys Gln Asp Trp Tyr Gly Tyr Asp Phe
           50           55           60
Tyr Glu Ile Ser Ala Gln Glu Pro Glu Ser Pro Gln Gly Pro Ala Gln
           65           70           75           80
Gly Val Tyr Arg Val Leu Arg Gly Gly Cys Trp Lys Ser Leu Lys Asp
           85           90           95
Asp Leu Arg Cys Ala His Arg His Arg Asn Asn Pro Gly Ala Val Asn
           100          105          110
Ser Thr Tyr Gly Phe Arg Cys Ala Lys Asn Ile Asn
           115          120

```

&lt;210&gt;1156

&lt;211&gt;181

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1156

```

Lys Leu Lys Leu Leu Lys Ala Ser Phe Ile Lys Leu Leu Leu Thr Leu
 1           5           10           15
Asp Trp Pro Thr Glu Leu Leu Leu Lys Asn Arg Pro Phe Asp Phe Thr
           20           25           30
Gly His Pro Glu Glu Glu Lys Leu Ile Lys Asp Ile Leu Leu Lys Glu
           35           40           45
Glu Gly Asn Lys Tyr Phe Ser Leu Glu Ser Lys Lys Leu Leu Ala Arg
           50           55           60
His Met Met His Asn Ile Val Val Leu Ser Glu Glu Pro Gly Arg Ser
           65           70           75           80
Ala Phe Leu Gly Arg Thr Ala Phe Phe Pro Asn Lys Tyr Pro Ile Ala
           85           90           95

```

Gln Gly Gly Val Gly Ile Pro Ser Thr Ile Gly Asn Leu Phe Thr Ile  
 100 105 110  
 Trp Tyr Cys Phe Tyr Phe Tyr Arg Ala Ala Thr Pro Gln Ser Asp His  
 115 120 125  
 Pro Asp Gly Cys Gly Phe Ile Leu Leu Glu Arg Leu Lys Glu Leu Gly  
 130 135 140  
 Ala Gly Phe Phe Tyr Cys Asp Leu Arg Glu Ser Asn Thr Thr Gly Phe  
 145 150 155 160  
 Thr Leu Phe Phe Glu Gly Ser Asn Lys Gly Val Leu Lys Asn His Leu  
 165 170 175  
 Phe Ile Arg Asp Glu  
 180

&lt;210&gt;1157

&lt;211&gt;131

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1157

Met Asn Ile Tyr Gln Phe Ser Pro Gly Ala Ser Pro Asn Trp Gln Ala  
 1 5 10 15  
 Ser Leu Met Ala Gln Leu Asn Ser Tyr Phe Cys Leu Gly Gly Glu Thr  
 20 25 30  
 Val Thr Arg Ile Ile Ser Leu Arg Pro Ser Gly Leu Ile Leu Ala Lys  
 35 40 45  
 Lys Glu Lys Ala Val Val Ser Thr Ala Glu Lys Ile Leu Lys Ile Leu  
 50 55 60  
 Ser Phe Ile Leu Phe Pro Leu Val Leu Ile Ala Leu Ala Ile Arg Tyr  
 65 70 75 80  
 Leu Leu Tyr Asn Lys Phe Asn Lys Asp Leu Asp Arg Ala Val Phe Phe  
 85 90 95  
 Ile Pro Thr Glu Ile Thr Lys Ala Glu Glu Leu Ile Ile Ala Lys Asn  
 100 105 110  
 Ser Cys Ala Ser Glu Arg Ser Gly Ser Asn Cys Phe Ser Ala Leu Leu  
 115 120 125  
 Phe Ser Ser  
 130

&lt;210&gt;1158

&lt;211&gt;111

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1158

Met Leu Gln His Leu Phe Ile Asp Gly Ile Thr Gln Glu Asn Pro Glu  
 1 5 10 15  
 Ala Leu Pro Asn Asn Thr Ser Gly Arg Leu Thr Leu Phe Pro Ser Val  
 20 25 30  
 Arg Tyr Ile Tyr Ser His Phe Thr Pro Gln Asn Pro Thr Ile Trp Pro  
 35 40 45  
 Gln Val Phe Phe Arg Gln Gly Pro Leu Asp Glu Asp Arg Gly Gly Gly  
 50 55 60  
 Phe Glu Ile Leu Glu Gln Leu Glu Leu Gly Val Arg Phe Pro Ile  
 65 70 75 80  
 Cys Pro Ser Gln Gly Pro Asp Asn Pro Asn Phe Gln Gly Phe Gln Gly  
 85 90 95  
 Ile Arg Ile Tyr Trp Glu Asp Ser Tyr Gln Pro Asn Lys Glu Val  
 100 105 110

&lt;210&gt;1159

&lt;211&gt;111

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1159

Met Ser Glu Ser Ile Asn Arg Ser Ile His Leu Glu Ala Ser Thr Pro  
 1 5 10 15  
 Phe Phe Ile Lys Leu Thr Asn Leu Cys Glu Ser Arg Leu Val Lys Ile  
 20 25 30  
 Thr Ser Leu Val Ile Ser Leu Leu Ala Leu Val Gly Ala Gly Val Thr

35 40 45  
 Leu Val Val Leu Phe Val Ala Gly Ile Leu Pro Leu Leu Pro Val Leu  
 50 55 60  
 Ile Leu Glu Ile Ile Leu Ile Thr Val Leu Val Leu Leu Phe Cys Leu  
 65 70 75 80  
 Val Leu Glu Pro Tyr Leu Ile Glu Lys Pro Ser Lys Ile Lys Glu Leu  
 85 90 95  
 Pro Lys Val Asp Glu Leu Ser Val Val Glu Thr Asp Ser Thr Leu  
 100 105 110

&lt;210&gt;1160

&lt;211&gt;75

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1160

Leu Ala Phe Asn Glu Ser Val Arg Ile Tyr Arg Lys Leu Phe Asn Thr  
 1 5 10 15  
 Ala Glu Leu Lys Gln Met Tyr Gly Ala Gly Asp Tyr Glu Gln Gln Asn  
 20 25 30  
 Glu Asp Asn Leu Lys Ser Ile Leu Ser Phe Val Gln Ile Leu Asp Glu  
 35 40 45  
 Lys Asp Gly Phe Asp Asp Phe Leu Ala Thr His Lys Asp Thr Thr Phe  
 50 55 60  
 Ile Gly Arg Gly Gly Ala Asp Ile Phe Cys Ser  
 65 70 75

&lt;210&gt;1161

&lt;211&gt;87

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1161

Met Glu Glu Ala Leu Thr Phe Asp Asp Val Leu Leu Ile Pro Gln Tyr  
 1 5 10 15  
 Ser Glu Ile Leu Pro Ser Glu Val Ser Leu Lys Thr Ala Ile Ser Lys  
 20 25 30  
 Thr Leu Ser Leu Asn Ile Pro Ile Leu Ser Ala Ala Met Asp Ser Val  
 35 40 45  
 Thr Glu Thr Ala Met Ala Leu Ala Leu Ala Gln Glu Gly Gly Leu Gly  
 50 55 60  
 Ile Leu His Lys Asn Met Ser Glu Val Glu Gln Ser Ser Ser Val Arg  
 65 70 75 80  
 Lys Ile Lys Glu Ala Tyr Pro  
 85

&lt;210&gt;1162

&lt;211&gt;91

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1162

Met Asp Phe Ser Val Phe Pro Asp Arg Phe Val Glu Ser Thr Ser Pro  
 1 5 10 15  
 Ser Pro Ile Glu Asp Ile Asp Ala Lys Thr Leu Val Ser Asn Cys Cys  
 20 25 30  
 His Tyr Cys Ser Arg Cys Leu Phe Ile Phe Leu Ser Leu Leu Ser Ile  
 35 40 45  
 Ile Ile Cys Phe Ser Val Tyr Gly Thr Ser Gly Glu Thr Ala Ser Leu  
 50 55 60  
 Val Phe Gly Ile Leu Ser Leu Ile Val Leu Val Leu Leu Ile Ile Glu  
 65 70 75 80  
 Cys Arg Asn Arg Glu Cys Cys Arg Arg Ile Ser  
 85 90

&lt;210&gt;1163

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1163

Leu Gln Ala Gly Arg Ser Gly Ile Ile Pro Gly Lys Lys Ala Ile Leu

1 5 10 15  
 Leu Asn Val Asn Asp Ala Lys Thr Pro Asn Tyr Ser Cys Ile Phe Glu  
 20 25 30  
 Ser Ile Gly Phe Phe Asn Glu Gln Asp Leu Glu Ala Gln His Asn Gln  
 35 40 45  
 Gln Ala Ala Leu Val Arg Lys Ile Leu Lys Val Val Pro His His Phe  
 50 55 60  
 Leu Lys Gly Leu Ile Ala Lys Leu Pro Arg Ser Leu Lys Lys Asp Arg  
 65 70 75 80  
 Lys Phe Met Ser Ser Leu Ile Phe Thr Lys Leu Ser Tyr Cys Phe  
 85 90 95

&lt;210&gt;1164

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1164

Met Met Lys Ile Lys Lys Ala Ile Ser Arg His Ile Asp Arg Tyr Leu  
 1 5 10 15  
 Ser Pro Met Lys Ile Pro Ile Met Ala His Pro Gly Gln Lys Asp Ser  
 20 25 30  
 Pro Ser Thr Leu Ser Phe His Phe Pro Leu Ser Tyr Trp Phe Lys Glu  
 35 40 45  
 Leu Ser Ser His Gly Phe Leu Val Ser Gly Leu Glu Glu Trp Thr Ser  
 50 55 60  
 Ser Lys Thr Ser Thr Gly Lys Arg Ala Lys Ala Glu Asn Leu Cys Arg  
 65 70 75 80  
 Lys Glu Phe Pro Leu Phe Leu Met Ile Ser Cys Ile Lys Ile Lys  
 85 90 95

&lt;210&gt;1165

&lt;211&gt;238

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1165

Met Glu Asn Leu Ser Ser Ala Pro Ser Arg Ser Ile Trp Lys Ser Ile  
 1 5 10 15  
 Ile Gln Asn Lys Met Leu Val Leu Gly Leu Thr Thr Leu Ile Ile Leu  
 20 25 30  
 Met Leu Gly Ala Leu Leu Leu Pro Trp Phe Tyr Gln Asp Tyr Glu Gln  
 35 40 45  
 Thr Ser Leu Lys Asp Ile Leu Val Ser Pro Cys Ser Arg Phe Pro Phe  
 50 55 60  
 Gly Thr Asp Thr Leu Gly Arg Cys Met Phe Ala Arg Thr Leu Arg Gly  
 65 70 75 80  
 Leu Arg Leu Ser Leu Leu Ile Ala Thr Ile Ala Thr Leu Ile Asp Val  
 85 90 95  
 Cys Val Gly Leu Leu Trp Ala Thr Val Ala Ile Ser Gly Gly Lys Lys  
 100 105 110  
 Ile Asp Phe Leu Met Met Arg Thr Thr Glu Ile Leu Phe Ser Leu Pro  
 115 120 125  
 Arg Ile Pro Ile Ile Ile Leu Leu Leu Val Ile Phe His His Gly Leu  
 130 135 140  
 Leu Pro Leu Ile Leu Ala Met Thr Ile Thr Gly Trp Ile Pro Ile Ser  
 145 150 155 160  
 Arg Ile Ile Tyr Gly Gln Phe Leu Leu Lys Asn Lys Pro Phe Val  
 165 170 175  
 Leu Ser Ala Lys Ala Met His Ala Ser Thr Phe His Ile Leu Lys Lys  
 180 185 190  
 His Leu Leu Pro Asn Thr Leu Ala Pro Ile Ile Ser Thr Leu Ile Phe  
 195 200 205  
 Thr Ile Pro Asn Ala Ile Tyr Thr Glu Ala Phe Ile Ser Phe Leu Gly  
 210 215 220  
 Leu Gly Ile Gln Pro Pro Gln Ala Lys Pro Arg His Leu Ser  
 225 230 235  
 <210>1166

&lt;211&gt;211

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1166

```

Met Gly Pro Leu Lys Lys Glu Glu Lys Thr Ile Leu Met Ile Phe Phe
 1           5           10           15
Leu Leu Val Val Leu Trp Thr Phe Gly Asp Leu Leu Gly Ile Ser Ala
           20           25           30
Thr Thr Ala Ala Leu Ile Gly Leu Ser Leu Leu Ile Leu Thr Asn Ile
           35           40           45
Leu Asp Trp Gln Lys Asp Val Ile Ala Asn Thr Thr Ala Trp Glu Thr
           50           55           60
Phe Ile Trp Phe Gly Ala Leu Ile Met Met Ala Ser Phe Leu Asn Gln
           65           70           75           80
Leu Gly Phe Ile Pro Leu Val Gly Asp Ser Ala Ala Ala Leu Val Ser
           85           90           95
Gly Leu Ser Trp Lys Ile Gly Phe Pro Leu Leu Phe Leu Ile Tyr Phe
           100          105          110
Tyr Ser His Tyr Leu Phe Ala Ser Asn Thr Ala His Ile Gly Ala Met
           115          120          125
Tyr Pro Ile Phe Leu Ala Val Ser Ile Ser Leu Gly Thr Asn Pro Ile
           130          135          140
Phe Ala Ala Leu Thr Leu Ala Phe Ala Ser Asn Leu Phe Gly Gly Leu
           145          150          155          160
Thr His Tyr Gly Ser Gly Pro Ala Pro Leu Tyr Phe Gly Ser His Leu
           165          170          175
Val Thr Val Gln Glu Trp Trp Arg Ser Gly Phe Ala Leu Ser Ile Val
           180          185          190
Asn Ile Val Ile Trp Ile Gly Ile Gly Ser Leu Trp Trp Lys Ala Leu
           195          200          205
Gly Leu Ile
           210

```

&lt;210&gt;1167

&lt;211&gt;81

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1167

```

Leu Lys Met Glu Thr Tyr Ser Phe Ser Thr Glu Leu Gln Lys Asn Thr
 1           5           10           15
Ser Leu Tyr Ile Met Glu Lys Leu Asp Ser Tyr Phe Ser Phe Gln Gly
           20           25           30
Lys Arg Thr Arg Val Ile Ala Ile Thr Pro Ala Gly Leu Ala Ile Ala
           35           40           45
Tyr Glu Gln Asn Ile His Leu Ser Met Thr Val Lys Ile Leu Lys Val
           50           55           60
Leu Ser Phe Pro Arg Ser Leu Leu Arg Thr Thr Ser Leu Trp Tyr Arg
           65           70           75           80
Pro

```

&lt;210&gt;1168

&lt;211&gt;228

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1168

```

Leu Lys Gly Phe Leu Ser Val Asn Glu Leu Ile Phe Gly Phe Gln Thr
 1           5           10           15
Phe Ser Val Val Leu Gly Val Phe Phe Ala Ser Arg Gly Lys Ala
           20           25           30
Trp Leu Thr Gly Trp Leu Ser Leu Leu Ser Ser Ile Met Asn Val Phe
           35           40           45
Val Leu Lys Gln Ile His Leu Trp Gly Phe Glu Val Thr Ser Ala Asp
           50           55           60
Val Tyr Val Ile Gly Leu Leu Thr Cys Leu Asn Tyr Ala Arg Glu His
           65           70           75           80

```



Tyr Glu Lys Asn Asp Ile Asn Asp Ala Met Leu Cys Ser Trp Val Ile  
 85 90 95  
 Ser Ile Ala Phe Leu Val Leu Thr Gln Leu His Leu Phe Leu Ile Pro  
 100 105 110  
 Ser Pro Asn Asp Ser Ser Gln Glu His Phe Leu Ala Leu Phe Ser Ser  
 115 120 125  
 Thr Pro Arg Ile Val Val Ala Ser Leu Val Thr Leu Ile Phe Val Gln  
 130 135 140  
 Ile Val Asp Ile Lys Leu Phe Thr Phe Leu Gln Arg Val Phe Ser Lys  
 145 150 155 160  
 Lys Tyr Phe Ala Met Arg Ser Thr Ile Ser Leu Leu Phe Ser Gln Leu  
 165 170 175  
 Ile Asp Thr Ile Ile Phe Ser Phe Leu Gly Leu Tyr Gly Leu Val Ser  
 180 185 190  
 Asn Leu Cys Asp Val Met Ile Phe Ala Met Leu Val Lys Gly Ile Val  
 195 200 205  
 Ile Thr Leu Ala Ile Pro Thr Leu Thr Val Thr Lys Ala Val Leu Asp  
 210 215 220  
 Arg Arg Ser Ser  
 225

&lt;210&gt;1169

&lt;211&gt;189

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1169

Leu Gly Ile Phe Cys Phe Lys Lys Ile Asn Leu Phe Lys Thr Phe Ile  
 1 5 10 15  
 Leu Met Asn Asn Asn Val Tyr Leu Phe Cys Phe Leu Ile Phe Leu Ser  
 20 25 30  
 Lys Lys Val Phe Phe Glu Ser Tyr Glu Asp Phe Ala Asn Val Ala Ser  
 35 40 45  
 Ser Trp Pro Lys Ser Leu Arg Ala Leu Val Gln Gly Arg Tyr Phe Val  
 50 55 60  
 Asp Ser Glu Leu Lys Glu Thr Pro Tyr Arg Ile His Asp Phe Lys Lys  
 65 70 75 80  
 Thr Pro Ile His His Arg Leu Tyr Arg Ser Leu Pro Ile Ile Ser Thr  
 85 90 95  
 Ile Gly Gly Ile Ile Arg Leu Ile Glu Ala His Ser Gly Pro Ile His  
 100 105 110  
 Pro Arg Asp Lys Met Lys Tyr Arg Phe Glu Val Leu Gln Ala Val Ile  
 115 120 125  
 Glu Ile Leu Gly Leu Gly Val Leu Ile Leu Val Phe Asp Ile Ile Gly  
 130 135 140  
 Cys Phe Leu Ala Phe Leu Val Ala Ile Ile Leu Ser Leu Leu Leu Tyr  
 145 150 155 160  
 Cys Asn Ser Thr Phe Thr Cys Val Gln Asn Leu Ser Phe Thr Glu Arg  
 165 170 175  
 Met Leu Glu Gly Ile Gly Glu Ala Val Asn Phe Leu Ala  
 180 185

&lt;210&gt;1170

&lt;211&gt;92

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1170

Val Gly Leu Ser Tyr Trp Asp Ser Gly Phe Val Val Leu Ala Cys Lys  
 1 5 10 15  
 Val Leu Ala Thr Ala Leu Lys Phe Leu Phe Ser Lys Ala Ser Ser Lys  
 20 25 30  
 Ile Lys Gln Met Lys Trp Arg Glu Lys Ala Arg Asn Leu Ala Ala Lys  
 35 40 45  
 Asp Thr Val Gln Ser Ile Lys Glu Phe Cys Ser Val Asp Leu Thr Ser  
 50 55 60  
 Cys Phe Thr Arg Cys Phe Arg Leu Arg Asn Arg Val Val Glu Glu Gly  
 65 70 75 80

Ala Ser Glu Asn Gln Thr Val Arg Glu Ile Ile Val  
85 90

<210>1171

<211>130

<212>PRT

<213>Chlamydia pneumoniae

<400>1171

Met Val Asn Arg Tyr Lys Ser Ser Ala Glu Phe Ser Ala Asp His Tyr  
1 5 10 15  
Tyr Asp Asp Asn Leu Val Arg Met Gly Tyr Lys Arg Asn Leu Arg Gly  
20 25 30  
Leu Ala Pro Val Glu Asn Glu Val Cys Leu Phe Glu Glu Asn Asn Leu  
35 40 45  
Leu Glu Ser Val Met Ala Ser Ile Pro Ile Met Gly Ser Ile Leu Gly  
50 55 60  
Leu Gly Arg Leu His Ser Val Trp Ser Thr Gln Asp Pro Lys Asp Ser  
65 70 75 80  
Lys Ile Ser Ile Ile Phe His Thr Ala Leu Gly Ile Leu Glu Thr Leu  
85 90 95  
Gly Leu Gly Ile Ile Val Leu Leu Ile Lys Ile Thr Ile Thr Ile Leu  
100 105 110  
Leu Ile Leu Phe Thr Pro Cys Leu Leu Cys Tyr Phe Met Tyr Ser Cys  
115 120 125  
Cys Leu  
130

<210>1172

<211>125

<212>PRT

<213>Chlamydia pneumoniae

<400>1172

Met Thr Lys Asn Ala Ile Asn Ser Gln Thr Thr Thr Pro Gln Pro Asn  
1 5 10 15  
Leu Thr Asp Ala Glu Pro Ile Ala Ser Arg Ala Gln Cys Lys Ser Ile  
20 25 30  
Ala Val Ile Ile Ser Leu Phe Ala Leu Gly Met Leu Leu Leu Cys Leu  
35 40 45  
Gly Ile Ile Leu Ile Ser Ile Pro Ile Pro Gly Leu Ala Ala Gln Val  
50 55 60  
Ala Leu Gly Leu Gly Ile Val Ser Leu Ile Leu Gly Ile Ala Leu Ala  
65 70 75 80  
Asn Ile Gly Phe Leu Cys Leu Leu Leu Arg Cys Lys Gln Phe Pro Lys  
85 90 95  
Asn Pro Ile His Cys Pro Leu Lys Ala Leu Asn Ser Leu Pro Arg Glu  
100 105 110  
Ala Leu Pro Pro His Ser His Gly Lys Leu Glu Asn Phe  
115 120 125

<210>1173

<211>141

<212>PRT

<213>Chlamydia pneumoniae

<400>1173

Leu Lys Glu Ile Met Met Ile Asn Phe Ile Arg Ser Tyr Ala Leu Tyr  
1 5 10 15  
Phe Ala Trp Ala Ile Ser Cys Ala Gly Thr Leu Ile Ser Ile Phe Tyr  
20 25 30  
Ser Tyr Ile Leu Asn Val Glu Pro Cys Ile Leu Cys Tyr Tyr Gln Arg  
35 40 45  
Ile Cys Leu Phe Pro Leu Thr Val Ile Leu Gly Ile Ser Ala Tyr Arg  
50 55 60  
Glu Asp Ser Ser Ile Lys Leu Tyr Ile Leu Pro Gln Ala Val Leu Gly  
65 70 75 80  
Leu Gly Ile Ser Ile Tyr Gln Val Phe Leu Gln Glu Ile Pro Gly Met  
85 90 95  
Gln Leu Asp Ile Cys Gly Arg Val Ser Cys Ser Thr Lys Ile Phe Leu

100 105 110  
 Phe Ser Tyr Val Thr Ile Pro Met Ala Ser Val Val Ala Phe Gly Ala  
 115 120 125  
 Ile Val Cys Leu Leu Val Leu Thr Lys Asn Tyr Arg Gly  
 130 135 140

&lt;210&gt;1174

&lt;211&gt;146

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1174

Leu Xaa Ile Glu Gln Glu Asn Phe Ser Phe Lys Phe Lys Lys Ser Ala  
 1 5 10 15  
 Leu Ser Phe Thr Tyr Asn Thr Ala Asn Leu Thr Lys Ser Thr Phe Thr  
 20 25 30  
 Phe Ile Leu Leu Leu Leu Leu Arg Lys Lys Asp Gln Gly Leu Arg Phe  
 35 40 45  
 Met Asp Lys Glu Thr Leu Glu Asn Ile Tyr Arg His Phe Arg Tyr Arg  
 50 55 60  
 Phe Leu Lys Leu Asn Ile Leu Pro Ala Phe Leu Gly Leu Leu Leu Leu  
 65 70 75 80  
 Cys Ser Pro Asn Thr Leu Asn Tyr Thr Gln Val Asp Val Ile Phe Ser  
 85 90 95  
 Asp Arg Leu Cys Ser Cys Leu Leu Ile Phe Leu Ala Ile Ala Ser Leu  
 100 105 110  
 Thr Lys Arg Ser Leu Leu Trp Leu Gly Ala Pro Leu Gly Ile Trp Val  
 115 120 125  
 Thr Leu Phe Ala Cys Val Ala Asp Asp Leu Leu Leu Phe Leu Gln Met  
 130 135 140

Ile Leu

145

&lt;210&gt;1175

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1175

Leu Leu Val Phe Val Lys Val Asn Ser Ser Met Gly Leu Pro Thr Phe  
 1 5 10 15  
 Pro Xaa Xaa Phe Leu Asn Ile Cys Cys Trp Phe Ile Ile Val Leu Phe  
 20 25 30  
 Ile Leu Ala Phe Ala Glu Ser Leu Arg His Leu Arg Trp Met Asn Leu  
 35 40 45  
 Ile Phe Ser Ala Ala Ile Leu Phe Ser Pro Val Leu Phe His Ile Pro  
 50 55 60  
 Val Glu Ser Pro Met Phe Leu Pro Ile Ile Val Thr Gly Leu Ile Leu  
 65 70 75 80  
 Ile Ile Leu Ser Ile Gly Lys Arg Arg Arg Thr Lys Arg Lys Leu  
 85 90 95

&lt;210&gt;1176

&lt;211&gt;85

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1176

Leu Val Tyr Phe Met Val Phe Ser Pro Ser Ser Glu Ser Val Val Lys  
 1 5 10 15  
 Ala Asn Ser Val Val Arg Ser Asn Phe Cys Tyr Phe Leu Glu Asn Lys  
 20 25 30  
 Phe Val Ser Pro Ser Glu Ser Thr Glu Val Met Phe Ser Glu Ile Met  
 35 40 45  
 Lys Gly Arg Val Pro Asp Ile Glu Ser Leu Phe Asp Arg Pro Thr Asp  
 50 55 60  
 Met Met Met Thr Gly Phe Lys Xaa Arg Arg Ile Trp Gly Ile Cys Ser  
 65 70 75 80  
 Ile Ala Ser Glu Tyr  
 85

&lt;210&gt;1177

&lt;211&gt;114

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1177

Met Leu Tyr Pro Val Ile Ala Val Val Cys Ala Val Val Ser Val Val  
 1 5 10 15  
 Leu Leu Ile Leu Lys Val Leu Phe Leu Leu Leu Ser Phe Pro Phe Lys  
 20 25 30  
 Leu Cys Ser Ala Ser Ser Ala Leu Pro Gly Glu Arg Val Ser Leu Gly  
 35 40 45  
 Ser His Phe Lys Cys Leu Tyr Gly Gly Gly Leu Pro Tyr Leu Leu Ala  
 50 55 60  
 Cys Leu Leu Ile Val Pro Val Ile Gly Thr Ala Ile His Gly Phe Ile  
 65 70 75 80  
 Ile Ser His Arg Thr Ser Glu Asp Ala Arg Leu Ser Ser Ala Ile Val  
 85 90 95  
 Phe Met Gln Ala Pro Ile Leu Gln Leu Ala Gly Met Ser Gly Leu Ile  
 100 105 110  
 Lys Pro

&lt;210&gt;1178

&lt;211&gt;79

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1178

Leu Phe Phe Tyr Ile Tyr Ser Ile Leu Lys Arg Tyr Ile Val Val Leu  
 1 5 10 15  
 Gly Lys Ile Leu Gly Leu Ile Thr Ile Gln Phe Tyr Gln Asn Leu Gly  
 20 25 30  
 Gly Met Ser Ser Glu Arg Tyr Ser Ala Leu His Ser Arg Lys Ser Leu  
 35 40 45  
 Ser Val Leu Pro His Val Val Arg Lys Val Leu Leu Ser Phe Pro Asp  
 50 55 60  
 Phe Arg Gly Asn Gly Asp Val Asn Leu Arg Asn Ile Arg Ser Asp  
 65 70 75

&lt;210&gt;1179

&lt;211&gt;163

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1179

Leu Lys Ala Lys Ala Tyr Leu Asp Lys Gly Ala Phe Val Pro Ser Asp  
 1 5 10 15  
 Phe Val Trp Glu Ile Leu Lys Glu Lys Leu Gln Ser Gln Ala Cys Ser  
 20 25 30  
 Lys Gly Cys Ile Ile Asp Gly Phe Pro Arg Thr Leu Asp Gln Ala His  
 35 40 45  
 Leu Leu Asp Ser Phe Leu Met Asp Val His Ser Asn Tyr Thr Val Ile  
 50 55 60  
 Phe Leu Glu Ile Ser Glu Asp Glu Ile Leu Lys Arg Val Cys Ser Arg  
 65 70 75 80  
 Phe Leu Cys Pro Ser Cys Ser Arg Ile Tyr Asn Thr Ser Gln Gly His  
 85 90 95  
 Thr Glu Cys Pro Asp Cys His Val Pro Leu Ile Arg Arg Ser Asp Asp  
 100 105 110  
 Thr Pro Glu Ile Ile Lys Glu Arg Leu Thr Lys Tyr Gln Glu Arg Thr  
 115 120 125  
 Ala Pro Val Ile Ala Tyr Tyr Asp Ser Leu Gly Lys Leu Cys Arg Val  
 130 135 140  
 Ser Ser Glu Asn Lys Glu Asp Leu Val Phe Glu Asp Ile Leu Lys Cys  
 145 150 155 160  
 Ile Tyr Lys

&lt;210&gt;1180

&lt;211&gt;128

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1180

```

Met Ser Gln Cys Gln Ser Ser Ser Thr Ser Thr Trp Glu Trp Met Lys
 1              5              10              15
Ser Phe Val Pro Asn Trp Lys Asn Pro Thr Pro Pro Leu Ser Pro Ile
              20              25              30
Pro Ser Glu Asp Glu Phe Ile Leu Ala Tyr Glu Pro Phe Val Leu Pro
              35              40              45
Lys Thr Asp Pro Glu Asn Ala Gln Ala Asn Pro Pro Gly Thr Ser Thr
              50              55              60
Pro Asn Val Glu Asn Gly Ile Asp Asp Leu Asn Pro Leu Leu Gly Gln
              65              70              75              80
Pro Asn Glu Gln Asn Asn Ala Asn Asn Pro Gly Thr Ser Gly Ser Asn
              85              90              95
Pro Thr Ser Leu Pro Ala Pro Glu Arg Leu Pro Glu Thr Glu Glu Asn
              100              105              110
Ser Gln Glu Glu Glu Gln Gly Ser Gln Asn Asn Glu Asp Leu Ile Gly
              115              120              125

```

&lt;210&gt;1181

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1181

```

Leu Lys Ser Met Leu Asp Pro Lys Lys His Ser Thr Leu Gly Ile Glu
 1              5              10              15
Ile Ser Ser Glu Thr Ala Glu Thr Ile Glu Ser Cys Ser Leu Gly Leu
              20              25              30
Ile Ser Ile Asn Leu Leu Leu Ser Gly Leu Cys Leu Arg Ser Ser His
              35              40              45
Asp Arg Ser Gln Ala Val Lys Ile Ile Gln Gln Phe Cys Pro Gln Phe
              50              55              60
Ser Ser Glu Glu Val Gln Asn Phe Val Glu Gln Arg Asn Ile Leu Leu
              65              70              75              80
His Phe Tyr Ile Ile Cys Leu Lys Gly Thr Lys Ser Pro Cys
              85              90

```

&lt;210&gt;1182

&lt;211&gt;314

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1182

```

Met Asn Lys Lys His Ala Ser Phe Ser Ser Arg Leu Gly Phe Ile Phe
 1              5              10              15
Ser Met Ile Gly Ile Ala Val Gly Ala Gly Asn Ile Trp Arg Phe Pro
              20              25              30
Arg Val Ala Ala Gln Asn Gly Gly Gly Ala Phe Leu Ile Leu Trp Leu
              35              40              45
Cys Phe Leu Phe Leu Trp Ser Ile Pro Leu Ile Ile Glu Leu Ser
              50              55              60
Ile Gly Lys Leu Thr Lys Lys Ala Pro Ile Gly Ala Leu Ile Lys Thr
              65              70              75              80
Ala Gly Lys Lys Phe Ala Trp Ala Gly Gly Phe Ile Thr Leu Val Thr
              85              90              95
Thr Cys Ile Leu Ala Tyr Tyr Ser Thr Ile Val Gly Trp Gly Leu Ser
              100              105              110
Tyr Phe Tyr Tyr Ala Val Ser Gly Lys Ile His Leu Gly Asn Asp Phe
              115              120              125
Ala Lys Leu Trp Thr Ser His Tyr Gln Ser Ser Ile Pro Leu Trp Ala
              130              135              140
His Leu Thr Ser Leu Gly Leu Ala Tyr Leu Val Ile Arg Lys Gly Ile
              145              150              155              160
Val His Gly Ile Glu Lys Cys Asn Lys Ile Leu Ile Pro Ala Phe Phe
              165              170              175

```

Leu Cys Thr Ile Ala Leu Leu Leu Arg Ala Val Thr Leu Pro Gly Ala  
 180 185 190  
 Val Gln Gly Ile Lys Gln Leu Phe Ser Cys Asp Lys Ser Cys Phe Ser  
 195 200 205  
 Asn Tyr Lys Val Trp Ile Glu Ala Leu Thr Gln Asn Ala Trp Asp Thr  
 210 215 220  
 Gly Ala Gly Trp Gly Leu Leu Leu Val Tyr Ala Gly Phe Ala Ser Lys  
 225 230 235 240  
 Lys Thr Gly Val Val Ser Asn Gly Ala Leu Thr Ala Ile Cys Asn Asn  
 245 250 255  
 Leu Val Ser Leu Ile Met Gly Asp His Tyr Leu Phe His Met Cys Phe  
 260 265 270  
 Phe Arg His Phe Arg Asn His Ala Ala Thr Arg Trp Ser Arg Ser Xaa  
 275 280 285  
 Lys His Arg Asp Tyr Leu Tyr Leu Pro Thr Arg Val Ile Tyr Pro Phe  
 290 295 300  
 Ala Trp Arg Asn Leu Ser Asn His Pro Val  
 305 310

&lt;210&gt;1183

&lt;211&gt;132

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1183

Met Arg Ala Glu Met Ala Val Ile Tyr Trp Asp Arg Ser Lys Ile Val  
 1 5 10 15  
 Trp Ser Phe Glu Pro Trp Ser Leu Arg Leu Thr Trp Tyr Gly Val Phe  
 20 25 30  
 Phe Thr Val Gly Ile Phe Leu Ala Cys Leu Ser Ala Arg Tyr Leu Ala  
 35 40 45  
 Leu Ser Tyr Tyr Gly Leu Lys Asp His Leu Ser Phe Ser Lys Ser Gln  
 50 55 60  
 Leu Arg Val Ala Leu Glu Asn Phe Phe Ile Tyr Ser Ile Leu Phe Ile  
 65 70 75 80  
 Val Pro Gly Ala Arg Leu Ala Tyr Val Ile Phe Tyr Gly Trp Ser Phe  
 85 90 95  
 Tyr Leu Gln His Pro Glu Glu Ile Ile Gln Ile Trp His Gly Gly Leu  
 100 105 110  
 Ser Ser His Gly Gly Val Leu Trp Leu Ser Phe Val Gly Gly His Phe  
 115 120 125  
 Phe Leu Asp Ile  
 130

&lt;210&gt;1184

&lt;211&gt;171

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1184

Met Ser Val His Ile Thr Pro Arg Lys Cys Phe Ile Leu Cys Ile Leu  
 1 5 10 15  
 Ser Met Phe Thr Leu Pro Thr Leu Phe Pro Lys Ala His Leu Ile Leu  
 20 25 30  
 Phe Ser Pro Tyr Ile Val Leu Cys Phe Tyr Cys Phe Ser Lys Asp Lys  
 35 40 45  
 Gly Leu Val Leu Ala Leu Gly Cys Gly Val Leu Ser Asp Leu Ala Leu  
 50 55 60  
 Gly Ser Arg Gly Val Phe Leu Leu Leu Tyr Pro Leu Thr Ala Leu Ile  
 65 70 75 80  
 Thr His Lys Ala His Leu Ile Phe Ser Lys Glu Ser Lys Ala Ala Leu  
 85 90 95  
 Val Ile Val Asn Met Ile Phe Tyr Gly Val Phe Leu Leu Leu Thr Ile  
 100 105 110  
 Pro Met Cys Ala Leu Phe Gly His Glu Val Arg Trp Ser Ile Asp Val  
 115 120 125  
 Leu Met Ile Pro Leu Lys Cys Ser Phe Leu Asp Asn Leu Ile Phe Thr  
 130 135 140

Ser Val Ile Tyr Ile Leu Pro Cys Ala Ile Asn Ser Gly Ile His Lys  
 145 150 155 160  
 Met Ile Ser Phe Phe Arg Arg Leu Val Cys Tyr  
 165 170

&lt;210&gt;1185

&lt;211&gt;205

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1185

Met Phe Met Lys Ile Cys Ser Leu Lys Leu Lys Asn Phe Arg Asn His  
 1 5 10 15  
 Ser Asp Leu Glu Ile Ser Leu Ala Pro Lys Leu Asn Tyr Ala Gln Gly  
 20 25 30  
 Lys Thr Asn Leu Leu Glu Ala Leu Tyr Val Leu Ser Leu Gly Arg Ser  
 35 40 45  
 Phe Arg Thr Gln His Leu Thr Asp Thr Ile Thr Phe Gly Ser Ser His  
 50 55 60  
 Phe Phe Leu Glu Thr Gln Phe Glu Lys Asp His Leu Pro Gln Ala Leu  
 65 70 75 80  
 Ser Ile Tyr Thr Asp Lys Gln Gly Lys Lys Ile Cys Tyr Asn Gln Leu  
 85 90 95  
 Pro Ile Lys Thr Leu Ser Gln Leu Ile Gly Lys Val Pro Ile Val Leu  
 100 105 110  
 Phe Ser Ser Lys Asp Arg Leu Leu Ile Ser Gly Ala Pro Ala Asp Arg  
 115 120 125  
 Arg Leu Phe Leu Asn Leu Leu Leu Ser Gln Cys Asp Asn His Tyr Thr  
 130 135 140  
 Leu Cys Leu Ser Tyr Tyr His Arg Ala Leu Gln Gln Arg Asn Ala Leu  
 145 150 155 160  
 Leu Lys Ser Lys Gln Thr Ser Thr Val Ala Ser Gly Met Asn Ser Trp  
 165 170 175  
 Ser Asn Thr Ala Pro Thr Tyr Pro Ser Asn Gly Phe Ser Val Val Arg  
 180 185 190  
 Asn Phe Gln Ile Tyr Pro Lys Asn Phe Gly Leu Thr Thr  
 195 200 205

&lt;210&gt;1186

&lt;211&gt;81

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1186

Leu Arg Phe Arg Asn Ile Lys Lys Ser Leu Ile Phe Ile Lys Arg Ile  
 1 5 10 15  
 Arg Tyr Ser Gln Ser Gly Lys Glu Gln Lys Gly Ala Arg Pro Phe Phe  
 20 25 30  
 Lys Lys Ser Ile Thr Ser Ser Leu Val Ile Leu Leu Leu Glu Ala Ile  
 35 40 45  
 Phe Asn Glu Asn Phe Ser Ser Ile Ile Gln Asn Asn Phe Asn Lys Asn  
 50 55 60  
 Phe Lys Asn Lys Asn Ile Ser Ile Asn Arg Ile Phe Val Lys Phe Thr  
 65 70 75 80  
 Ile

&lt;210&gt;1187

&lt;211&gt;79

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1187

Val Gln Leu Phe Gln Tyr Met Asn Glu Ser Gly Trp Asp Trp Leu Cys  
 1 5 10 15  
 Asp Phe Asp Ser Gln Gly Glu Gly Phe Gln Leu Ser Arg Leu Val Gly  
 20 25 30  
 Leu Leu His Ser Ser Trp Ala Leu Tyr Glu Ala Lys Glu Gln Phe Tyr  
 35 40 45  
 Leu Pro Glu Val Ser Leu Leu Thr Trp Glu Glu Leu Ile Glu Met Gln

1152



Ala Val Glu Val Asp Tyr Ser His Glu Asp Asp Glu Asp Pro Phe Ser  
 130 135 140  
 Asp Arg Asn Arg Trp Arg Arg Gly Gly Ile Ile Asp Pro Asp Ala Asn  
 145 150 155 160  
 Glu Trp

&lt;210&gt;1191

&lt;211&gt;83

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1191

Leu Val Ile Gln Ile Gly Val Leu Pro Pro Leu Val Ala Thr Lys Lys  
 1 5 10 15  
 Ile Asp Ile Asn Arg Phe Met Gln Asp Ala Asp Asn Trp Ile Pro Met  
 20 25 30  
 Phe Ser His Pro Phe Phe Leu Arg Glu Lys Thr Leu Ser Asp Gly Lys  
 35 40 45  
 Asp Ile His Ile Leu Ser Arg Leu Lys Gly Leu Gln Thr Cys Ala Pro  
 50 55 60  
 Cys Ser Pro His Glu Glu Arg Thr Ile Thr Leu Leu Ser His Ser Asn  
 65 70 75 80  
 Ser Val Ser

&lt;210&gt;1192

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1192

Met Asn Lys Ser Arg Phe Leu Arg Leu Cys Cys Cys Leu Cys Phe Cys  
 1 5 10 15  
 Gly Ser Leu Phe Tyr Phe Tyr Ile Asn Lys Gln Asn Ser Leu Thr Lys  
 20 25 30  
 Leu Arg Leu Glu Ile Pro Cys Leu Ser Val Arg Leu Arg Gln Leu Glu  
 35 40 45  
 Gln Gln Asn Ile Ser Leu Arg Phe Leu Ile Asp Lys Ile Glu Arg Pro  
 50 55 60  
 Asp His Leu Met Glu Ile Ala Ala Leu Pro Glu Tyr Gln Tyr Leu Glu  
 65 70 75 80  
 Tyr Pro Ser Glu Glu Ser Ile Ser Leu Leu Ser Tyr Glu Leu Pro  
 85 90 95

&lt;210&gt;1193

&lt;211&gt;101

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1193

Met Asp Pro Ala Ser Pro Val Ala Pro His Val Leu Gln Asp His Val  
 1 5 10 15  
 Gln Leu Ser Ser Glu Glu Leu Ser Ala Leu Ser Ser Gly Val Ser Arg  
 20 25 30  
 Val Lys Lys Leu Thr Ile Ala Ile Met Val Leu Ser Leu Ile Ala Ile  
 35 40 45  
 Ser Leu Val Ala Cys Gly Leu Phe Leu Thr Gly Ser Ala Pro Leu Gln  
 50 55 60  
 Leu Ser Ile Trp Ile Ala Ala Ser Cys Ile Thr Leu Ser Met Leu Val  
 65 70 75 80  
 Cys Ala Cys Trp Arg Tyr Lys Ile Ser Asn Ala Leu Glu Lys Thr Lys  
 85 90 95  
 Val Ala His Glu Ser  
 100

&lt;210&gt;1194

&lt;211&gt;77

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1194

Val Met Trp Tyr Ser Asp Tyr His Val Trp Ile Leu Pro Val His Glu  
 1 5 10 15  
 Arg Val Val Arg Leu Gly Leu Thr Glu Lys Met Gln Lys Asn Leu Gly  
 20 25 30  
 Ala Ile Leu His Val Asp Leu Pro Ser Val Gly Ser Leu Cys Lys Glu  
 35 40 45  
 Gly Glu Val Leu Val Ile Leu Glu Ser Ser Lys Ser Ala Ile Arg Gly  
 50 55 60  
 Val Lys Ser Cys Ile Arg Arg Gly Tyr Arg Tyr Gln Pro  
 65 70 75

&lt;210&gt;1195

&lt;211&gt;172

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1195

Met Gly Phe Lys Asn Ile Cys Lys Gln Gly Ser Gln Leu Tyr Leu Asn  
 1 5 10 15  
 Gly Ile Phe Pro Glu Arg Ile Leu Ala Arg Lys Leu Lys Asn Cys Ala  
 20 25 30  
 Lys Ser Tyr Pro Arg Thr Ala Leu Thr Ile Glu Val Leu Val Ser Ser  
 35 40 45  
 Val Leu Gly Ala Leu Lys Val Ile Leu Ile Pro Cys Ala Ser Thr Tyr  
 50 55 60  
 Ala Ala Leu Thr Leu Pro Leu Arg Ala Leu Phe Asn Ala Ile Lys Thr  
 65 70 75 80  
 Lys Ser Cys Gln His Leu Ala Ser Tyr Ala Met Ala Trp Leu Leu His  
 85 90 95  
 Ile Leu Thr Ile Ala Val Ile Ile Gly Leu Val Phe Ser Leu Val Phe  
 100 105 110  
 Ile Pro Pro Pro Val Val Phe Ile Ser Leu Gly Leu Leu Met Ser Val  
 115 120 125  
 Thr Thr Ser Val Thr Leu Phe Gln Val His Lys Asn Leu Phe Pro Pro  
 130 135 140  
 Tyr Glu Pro Pro Pro Ser Arg Pro His Thr Pro Pro Phe Ala Asp  
 145 150 155 160  
 Glu Tyr Val Pro Leu Ile Ser Glu Ser Tyr Phe Asp  
 165 170

&lt;210&gt;1196

&lt;211&gt;224

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1196

Val Thr Pro Ser Ala Asp Asp Ala Lys Lys Ile Ala Val Glu Lys Lys  
 1 5 10 15  
 Lys Asp Leu Ser Ala Ser Ala Arg Met Glu Glu His Glu Ala Ser Gln  
 20 25 30  
 Arg Gln Asp Ala Arg His Arg Arg Ile Gly Arg Glu Ala Gln Gly Ser  
 35 40 45  
 Phe Phe Tyr Ser Ser Arg Asn Pro Glu His Arg Arg Ser Phe Gly Ser  
 50 55 60  
 Leu Ser Arg Phe Lys Thr Lys Pro Ser Asp Ala Ala Ser Thr Arg Pro  
 65 70 75 80  
 Ala Ser Ile Ser Pro Pro Phe Lys Asp Asp Phe Gln Pro Tyr His Phe  
 85 90 95  
 Lys Asp Leu Arg Ser Ser Ser Phe Gly Ser Gly Ala Ser Ser Ala Phe  
 100 105 110  
 Thr Pro Ile Met Pro Ala Ser Ser Arg Ser Pro Asn Phe Ser Thr Gly  
 115 120 125  
 Thr Val Leu His Pro Glu Pro Val Tyr Pro Lys Gly Gly Lys Glu Pro  
 130 135 140  
 Ser Ile Pro Arg Val Ser Ser Ser Ser Arg Arg Ser Pro Arg Asp Arg  
 145 150 155 160  
 Gln Asp Lys Gln Gln Gln Gln Asn Gln Asp Glu Glu Gln Lys Gln  
 165 170 175

Gln Ser Lys Lys Lys Ser Gly Lys Ser Asn Gln Ser Leu Lys Thr Pro  
 180 185 190  
 Pro Pro Asp Gly Lys Ser Thr Ala Asn Leu Ser Pro Ser Asn Pro Phe  
 195 200 205  
 Ser Asp Gly Tyr Asp Glu Arg Glu Lys Arg Lys His Arg Lys Asn Lys  
 210 215 220

&lt;210&gt;1197

&lt;211&gt;139

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1197

Leu Ile Lys Lys Arg Ala Ile Phe Glu Arg Met Phe Pro Ile Pro Pro  
 1 5 10 15  
 Pro His Cys Pro Pro Asn Asn Lys Asn Asn Phe Tyr His Leu Thr Thr  
 20 25 30  
 Asp Thr Lys Asp Pro Leu Leu Leu Arg Ile Leu Arg Thr Ile Gly Tyr  
 35 40 45  
 Val Leu Leu His Ile Ile Thr Leu Gly Leu Leu Leu Leu Ile His Tyr  
 50 55 60  
 Tyr Lys His His Arg Val Val Arg Lys Glu Gly Leu Pro Thr Pro Pro  
 65 70 75 80  
 Thr Leu Pro Lys Gly Pro Glu Pro Lys Thr Ile Glu Ile Ala Lys Gln  
 85 90 95  
 Pro Pro Lys Asp Gly Glu Asp Lys Lys Pro Asp Val Pro Lys Pro Gly  
 100 105 110  
 Thr Pro Pro Pro Glu Asp Thr Pro Pro Pro Pro Pro Lys Ala Pro Ser  
 115 120 125  
 Pro Ala Ser Pro Lys Val Pro Lys Thr Thr Cys  
 130 135

&lt;210&gt;1198

&lt;211&gt;79

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1198

Val Val Glu Ser Ala Phe Tyr Gln Gln Val Val Leu Gly Thr Phe Gly  
 1 5 10 15  
 Leu Ala Gly Glu Gly Ala Leu Gly Gly Gly Gly Val Ser Ser Gly  
 20 25 30  
 Gly Gly Val Pro Gly Leu Gly Thr Ser Gly Phe Leu Ser Ser Pro Ser  
 35 40 45  
 Leu Gly Gly Cys Leu Ala Ile Ser Ile Val Phe Gly Ser Gly Pro Leu  
 50 55 60  
 Gly Arg Val Gly Gly Val Gly Lys Pro Ser Phe Leu Thr Thr Arg  
 65 70 75

&lt;210&gt;1199

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1199

Leu Asp Asp Ser Trp Ile Leu Glu Val Lys Val Thr Pro Lys Ala Lys  
 1 5 10 15  
 Glu Asn Lys Ile Val Gly Phe Asp Gly Gln Ala Leu Lys Val Arg Val  
 20 25 30  
 Thr Glu Pro Pro Glu Lys Gly Lys Ala Asn Asp Ala Val Ile Ser Leu  
 35 40 45  
 Leu Ala Lys Ala Leu Ser Leu Pro Lys Arg Asp Val Thr Leu Ile Ala  
 50 55 60  
 Gly Glu Thr Ser Arg Lys Lys Phe Leu Leu Pro Asn Arg Val Gln  
 65 70 75 80  
 Asp Ile Ile Phe Ser Leu His Ile Asp Val  
 85 90

&lt;210&gt;1200

&lt;211&gt;107

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1200

Leu Gln Asn Ser Met His Lys Val Phe Ala Asp Pro Ser Leu Thr Asp  
 1 5 10 15  
 Thr Ile Thr Leu Pro Ile Asp Ala Pro Gly Asp Pro Ala Tyr Pro His  
 20 25 30  
 Val Leu Gly Glu Ala Phe Ile Ser Pro Gln Ala Ala Leu Arg Phe Leu  
 35 40 45  
 Glu Asn Thr Ser Pro Asn Gln Glu Asp Ile Tyr Glu Glu Ile Ser Arg  
 50 55 60  
 Tyr Leu Val His Ser Ile Leu His Met Leu Gly Tyr Asp Asp Thr Ser  
 65 70 75 80  
 Ser Glu Glu Lys Arg Lys Met Arg Val Lys Glu Asn Gln Ile Leu Cys  
 85 90 95  
 Met Leu Arg Lys Lys His Ala Leu Leu Thr Ala  
 100 105

&lt;210&gt;1201

&lt;211&gt;279

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1201

Met Ser Ser Leu Leu Ser Cys Gly Arg Ile Glu Pro Thr Arg Val Thr  
 1 5 10 15  
 Cys Ser Leu Lys Thr Tyr Leu Glu Asp Thr Ser Gln Asn Gln Leu Ser  
 20 25 30  
 Thr Arg Leu Val Arg Ala Ser Val Ile Phe Leu Cys Ala Leu Leu Ile  
 35 40 45  
 Ile Leu Val Cys Val Ala Leu Ser Ser Leu Ile Pro Ser Ile Met Ala  
 50 55 60  
 Leu Ala Thr Ser Phe Thr Val Met Gly Leu Ile Leu Phe Val Met Ser  
 65 70 75 80  
 Leu Leu Gly Asp Val Ala Ile Ile Ser Tyr Leu Thr Tyr Ser Thr Val  
 85 90 95  
 Thr Ser Tyr Arg Gln Asn Lys Arg Ala Phe Glu Ile His Lys Pro Ala  
 100 105 110  
 Arg Ser Val Tyr Tyr Glu Gly Val Arg His Trp Asp Leu Gly Arg Ser  
 115 120 125  
 Ser Leu Gly Thr Gly Glu Ile Pro Ile Val Arg Thr Leu Phe Ser Pro  
 130 135 140  
 Phe Gln Asn His Gly Leu Asn His Ala Leu Ala Ala Lys Ile Phe Leu  
 145 150 155 160  
 Phe Met Glu His Phe Ser Pro Glu Pro Pro Asn Glu Pro Leu Val Asp  
 165 170 175  
 Trp Ala Cys Leu Ile Arg Asp Phe Arg Pro His Val Ser Ser Leu Cys  
 180 185 190  
 Phe Val Ile Glu Lys Gln Gly Ser Ser Leu Arg Thr Lys Glu Gly Asn  
 195 200 205  
 Thr Ile Cys Glu Ala Phe Arg Ser Asp Tyr Asp Ala His Phe Ala Met  
 210 215 220  
 Val Asp Cys Tyr Arg Leu Ile His Ser Lys Leu Ile Ile Glu Lys Met  
 225 230 235 240  
 Gly Leu Lys Asn Ile Asp Ile Ile Pro Ser Val Met Val Arg Glu Asp  
 245 250 255  
 Tyr Pro Ser Arg Pro Gly Glu Gly Tyr Arg Glu Gly Leu Leu Arg Met  
 260 265 270  
 Tyr Gly Gly Lys Gly Ala Leu  
 275

&lt;210&gt;1202

&lt;211&gt;239

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1202

Leu Lys Val Gln Lys Leu Arg Gln Pro Ser Phe Tyr Pro Lys Arg Leu  
 1 5 10 15

Met Thr Leu Tyr Leu Gly Leu Asn Gln Lys Thr Ala Arg Lys Tyr Gln  
 20 25 30  
 Ala His Tyr Leu Pro Ile Leu Thr Leu Phe Pro Tyr Ala Lys Ser Thr  
 35 40 45  
 Pro Gln Asn Lys Arg Ala Leu Gln Phe Leu Pro Gln Ala Thr His Val  
 50 55 60  
 Ile Leu Thr Ser Pro Ser Ser Thr His Leu Phe Leu Ser Arg Met Thr  
 65 70 75 80  
 Ser Leu Leu Ser Lys Ala Thr Leu Lys Thr Lys Thr Tyr Leu Cys Ile  
 85 90 95  
 Gly Glu Ser Thr Lys Glu Arg Leu Leu Ser Phe Leu Gly Gln Val Lys  
 100 105 110  
 Tyr Val Val Ala Thr Gln Glu Ile Ala Glu Gly Ile Phe Pro Leu Leu  
 115 120 125  
 Gln Ala Leu Pro Ser Ser Ala Arg Ile Leu Tyr Pro His Ser Ser Leu  
 130 135 140  
 Ala Arg Pro Val Ile Arg Glu Phe Leu Tyr Asn Arg Phe Thr Phe Phe  
 145 150 155 160  
 Ser Tyr Pro His Tyr Thr Val Lys Pro Arg Lys Leu Lys Lys Asn Ile  
 165 170 175  
 Leu Ser Lys Tyr Lys Lys Ile Ile Phe Thr Ser Pro Ser Thr Val Arg  
 180 185 190  
 Ala Phe Ala Lys Ile Phe Pro Arg Phe Pro Glu Lys Thr Tyr Trp Cys  
 195 200 205  
 Gln Gly Arg Met Thr Leu Gln Glu Phe Gln Lys Phe Ser Ser Gln Lys  
 210 215 220  
 Gln Val Ser Leu Leu Glu Thr Leu Gly Lys Ser Arg Thr Ser Pro  
 225 230 235

&lt;210&gt;1203

&lt;211&gt;110

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1203

Met Ala Ser Ser Ala Thr Pro Gly Phe Asp Gly Thr Ala Pro Ser Leu  
 1 5 10 15  
 Phe Pro Pro Ala Thr Arg Pro Arg Tyr Asn Phe Lys Leu Ala Leu Phe  
 20 25 30  
 Val Thr Ile Ala Ile Ala Leu Val Trp Ile Ala Leu Ile Ala Thr Thr  
 35 40 45  
 Ile Ala Ile Gly Leu Cys Ile His Pro Leu Cys Ser Phe Ile Phe Leu  
 50 55 60  
 Thr Ala Ile Pro Leu Tyr Phe Ile Ser Arg Tyr Ile Cys Ser His Tyr  
 65 70 75 80  
 Ala Arg Asn Val Tyr Ile Ala Leu Asp Val Val Pro Asp His Ser Lys  
 85 90 95  
 Leu Gln Asp Met Arg Ser His Ser Pro Ile Phe Ser Asp Arg  
 100 105 110

&lt;210&gt;1204

&lt;211&gt;196

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1204

Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr  
 1 5 10 15  
 Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly Trp  
 20 25 30  
 Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys  
 35 40 45  
 Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Xaa Lys  
 50 55 60  
 Tyr Lys Xaa Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Asn Val  
 65 70 75 80  
 Gly Leu Ser Asp His His His His Cys Phe Ala His Leu Ser Gly Gly  
 85 90 95

Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro Glu  
 100 105 110  
 Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn Gln  
 115 120 125  
 Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr Ile  
 130 135 140  
 Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn Lys  
 145 150 155 160  
 Val Phe Tyr Met Asn Lys Thr Leu Thr Ser Leu Ala Asp Thr Ser Thr  
 165 170 175  
 Leu Thr Asp Gln Phe Cys Cys His Pro Tyr Lys Asn Gln Glu Phe Ser  
 180 185 190  
 Cys Ser Pro His  
 195

&lt;210&gt;1205

&lt;211&gt;92

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1205

Met Leu Ser Ser Leu Ile Arg Asp Ser Phe Pro Leu Leu Ile Leu Leu  
 1 5 10 15  
 Pro Thr Phe Leu Ala Ala Leu Gly Ala Ser Val Ala Gly Gly Val Met  
 20 25 30  
 Gly Thr Tyr Ile Val Val Lys Arg Ile Val Ser Ile Ser Gly Ser Ile  
 35 40 45  
 Ser His Ala Ile Leu Gly Gly Ile Gly Leu Thr Leu Trp Ile Gln Tyr  
 50 55 60  
 Lys Leu His Leu Ser Phe Phe Pro Met Tyr Gly Ala Ile Val Gly Ala  
 65 70 75 80  
 Ile Phe Leu Ala Leu Cys Ile Gly Lys Arg Ser Thr  
 85 90

&lt;210&gt;1206

&lt;211&gt;188

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1206

Leu His Arg Gln Lys Ile His Leu Lys Tyr Gln Glu Arg Glu Asp Ser  
 1 5 10 15  
 Leu Ile Ala Met Ile Trp Ser Val Gly Met Ala Ile Gly Ile Ile Phe  
 20 25 30  
 Ile Ser Arg Leu Pro Thr Phe Asn Gly Glu Leu Ile Asn Phe Leu Phe  
 35 40 45  
 Gly Asn Ile Leu Trp Val Thr Pro Ser Asp Leu Tyr Ser Leu Xaa Ile  
 50 55 60  
 Phe Asp Leu Leu Val Leu Gly Ile Val Val Leu Cys His Thr Arg Phe  
 65 70 75 80  
 Leu Ala Leu Cys Phe Asp Glu Arg Tyr Thr Ala Leu Asn His Cys Ser  
 85 90 95  
 Val Gln Leu Trp Tyr Phe Leu Leu Leu Val Leu Thr Ala Ile Thr Ile  
 100 105 110  
 Val Met Leu Ile Tyr Val Met Gly Thr Ile Leu Met Leu Ser Met Leu  
 115 120 125  
 Val Leu Pro Val Ala Ile Ala Cys Arg Phe Ser Tyr Lys Met Thr Arg  
 130 135 140  
 Ile Met Phe Ile Ser Val Leu Leu Asn Ile Leu Cys Ser Phe Ser Gly  
 145 150 155 160  
 Ile Cys Ile Ala Tyr Cys Leu Asp Phe Pro Val Gly Pro Thr Ile Ser  
 165 170 175  
 Leu Leu Met Gly Leu Xaa Tyr Thr Ala Ser Leu Val  
 180 185

&lt;210&gt;1207

&lt;211&gt;112

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1207

Val Phe Ser Tyr Leu Leu Leu Cys Ile Ile Leu Val Tyr Val Arg Phe  
 1 5 10 15  
 Met Tyr Glu Gly Lys Ser Arg Met Ala Ser Pro Thr Pro Gly Gln Leu  
 20 25 30  
 His Leu Gln Gln Lys Val Glu Ser Lys Ala Tyr Asp Tyr Ser Arg Ser  
 35 40 45  
 Leu Ala Met Ile Ala Thr Ala Leu Leu Phe Phe Ile Val Ala Leu Ile  
 50 55 60  
 Leu Ser Gly Leu Ser Leu Leu Pro Gln Val Phe Leu Pro Phe Ser Gly  
 65 70 75 80  
 Ala Tyr Phe Ile Ile Gly Ser Phe Leu Ala Phe Ile Ala Leu Gly Ile  
 85 90 95  
 Leu Leu Ile Asn Cys Val Cys Asp Leu Lys Gln Tyr Leu Thr Ser Ser  
 100 105 110

&lt;210&gt;1208

&lt;211&gt;320

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1208

Val Leu Ile Ser Ile Ser Leu Ala Thr Leu Pro Ile Leu Ala Phe Ser  
 1 5 10 15  
 Trp Ala Ser Phe Ile Glu Pro Asn Trp Leu Arg Thr Thr Ala Ile Pro  
 20 25 30  
 Trp Arg Leu Pro Lys Lys His Ala His Leu His Gly Leu Arg Ile Ala  
 35 40 45  
 Gln Ile Ser Asp Leu His Phe His Lys Arg Val Pro Glu Lys Phe Leu  
 50 55 60  
 Asn Lys Val Ser Lys Ser Ile Lys Asn Phe Ser Pro Asp Leu Ile Val  
 65 70 75 80  
 Phe Cys Gly Asp Leu Leu Cys Arg Ala Arg Leu Glu Asp Lys Glu Arg  
 85 90 95  
 Leu Glu Thr Phe Leu Asn Thr Leu Glu Ala Pro Leu Gly Val Phe Ala  
 100 105 110  
 Ile Leu Gly Asn His Asp Tyr Ser Ser Tyr Ile Ser Arg Asn Thr Lys  
 115 120 125  
 Gly Glu Ile Thr Cys Ile Pro Glu Glu Lys Ser Arg Pro Ile Gln Arg  
 130 135 140  
 Ala Ile Ile Ala Val Met Gln Gly Leu Phe Ser Ser Pro Ser Tyr Arg  
 145 150 155 160  
 Tyr Asp Pro Asn Leu Thr Pro Gln Glu Pro His Pro Asp Leu Leu Lys  
 165 170 175  
 Leu Leu Lys Asn Thr Pro Leu Thr Leu Leu His Asn Thr Thr His Val  
 180 185 190  
 Ile Pro Asn Thr Leu Asn Ile Val Gly Leu Gly Asp Leu Phe Ala Arg  
 195 200 205  
 Gln Phe His Pro Glu Gln Ala Phe Lys Asn Tyr Asp Pro Ser Leu Pro  
 210 215 220  
 Gly Leu Leu Leu Ser His Asn Pro Asp Gly Ile Thr Arg Leu Gln Gln  
 225 230 235 240  
 Tyr Pro Gly Asp Phe Val Leu Ser Gly His Ser His Gly Pro Gln Val  
 245 250 255  
 Thr Leu Ser Trp Pro Lys Phe Ala Arg Lys Phe Phe Glu Arg Leu Ser  
 260 265 270  
 Gly Leu Glu Asn Pro Tyr Leu Ala Arg Gly Tyr Phe Val Thr Lys Glu  
 275 280 285  
 Gly Lys Gln Leu Tyr Val Asn Arg Gly Leu Gly Gly Leu Lys Arg Ile  
 290 295 300  
 Arg Phe Cys Ser Pro Pro Glu Ile Cys Tyr Ile Thr Cys Ser Tyr Asp  
 305 310 315 320

&lt;210&gt;1209

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1209

```

Met Thr Ala Thr Met Ser Leu Leu Asn Leu Pro Ser Ser Gln Asp Ser
 1          5          10          15
Ala Ser Glu Asp Ser Thr Ser Gln Ser Gln Ile Phe Asp Pro Ile Arg
          20          25          30
Asn Arg Glu Leu Val Ser Thr Pro Glu Glu Lys Val Arg Gln Arg Leu
          35          40          45
Leu Ser Phe Leu Met His Lys Leu Asn Tyr Pro Lys Lys Leu Ile Ile
          50          55          60
Ile Glu Lys Glu Leu Lys Thr Leu Phe Pro Leu Leu Met Arg Lys Gly
        65          70          75          80
Thr Leu Ile Pro Lys Arg Arg Pro Asp Ile Leu Ile Ile Thr Pro Pro
          85          90          95
Thr Tyr Thr Asp Ala Gln Gly Asn Thr His Asn Leu Gly Asp Pro Lys
          100          105          110
Pro Leu Leu Leu Ile Glu Cys Lys Ala Leu Ala Val Asn Gln Asn Ala
          115          120          125
Leu Lys Gln Leu Leu Ser Tyr Asn Tyr Ser Ile Gly Ala Thr Cys Ile
          130          135          140
Ala Met Ala Gly Lys His Ser Gln Val Ser Ala Leu Phe Asn Pro Lys
        145          150          155          160
Thr Gln Thr Leu Asp Phe Tyr Pro Gly Leu Pro Glu Tyr Ser Gln Leu
          165          170          175
Leu Asn Tyr Phe Ile Ser Leu Asn Leu
          180          185

```

&lt;210&gt;1210

&lt;211&gt;173

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1210

```

Met Ala Asp Asp Thr Leu Ile Pro Lys Leu Met Lys Asn Ser Leu Ser
 1          5          10          15
Gln Ala Cys Ser Glu Gly Leu Leu Ile Ala Lys Tyr Pro Pro Leu Gln
          20          25          30
Val Ile Val His Phe Asp Asn Asn Leu Val Val Lys Thr His Leu Ser
          35          40          45
Val Ala Pro Val Phe Ser Cys Leu Phe Leu Gly Pro Ala Ala His Lys
          50          55          60
Ala Met Gln Glu Ile Val Leu Trp Cys Ser Arg Tyr Ala Asn Lys Glu
        65          70          75          80
His Pro Pro Phe Ser Ser His Phe Ala Lys Asp Leu Ile Pro Ser Gln
          85          90          95
Tyr Leu Glu Ile Leu Asn Cys Val Ala Glu Ile Pro Phe Gly Glu Gln
          100          105          110
Gln Thr Tyr Ala Glu Ile Ala Lys Lys Thr Asp Thr His Pro Arg Thr
          115          120          125
Val Gly Ala Ala Cys Lys Gln Asn Pro Phe Leu Leu Phe Phe Pro Cys
          130          135          140
His Arg Val Val Gly Ser His Gly Glu Arg Asn Tyr Val Leu Gly Pro
        145          150          155          160
Val Ile His Glu Ile Leu Leu Lys Phe Glu Asn Ser Tyr
          165          170

```

&lt;210&gt;1211

&lt;211&gt;137

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1211

```

Met Ile Glu Asn Asp Phe Pro Glu Ala Ser Asn Phe Glu Ser Ser His
 1          5          10          15
Phe Tyr Arg Asp Lys Val Gly Val Ile Ile Leu Cys Gly Gly Glu Gly
          20          25          30
Lys Arg Leu Ser Pro Leu Thr Asn Cys Arg Cys Lys Pro Thr Val Ser
          35          40          45
Phe Gly Gly Arg Tyr Lys Leu Ile Asp Ile Pro Ile Ser His Ala Ile

```



50 55 60  
 Ser Ala Gly Phe Ser Lys Ile Phe Val Ile Gly Gln Tyr Leu Thr Tyr  
 65 70 75 80  
 Thr Leu Gln Gln His Leu Phe Lys Thr Tyr Phe Tyr His Gly Val Leu  
 85 90 95  
 Gln Asp Gln Ile His Leu Leu Ala Pro Glu Ala Arg Gln Gly Asp Gln  
 100 105 110  
 Ile Trp Tyr Gln Gly Thr Gln Met Gln Phe Glu Lys Thr Tyr Phe Ile  
 115 120 125  
 Ser Lys Ile Gln Lys Ser Asn Thr Phe  
 130 135

&lt;210&gt;1212

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1212

Met Leu Ile Arg Leu Phe Leu Gly Ile Ser Leu Pro Lys Gly Phe Pro  
 1 5 10 15  
 Leu Tyr Leu Glu Pro Pro Leu Val Leu Ala Thr Phe Gln Gly Thr Gln  
 20 25 30  
 Phe Val Gly Thr Tyr Ser Glu Ala Thr Asn Pro Leu Tyr Ile Asp Asn  
 35 40 45  
 Leu Asn Leu Asn Tyr His Tyr Thr Gln Glu Leu Leu Tyr Lys Ala Val  
 50 55 60  
 Pro Cys Asn Tyr Lys Ser Ile Tyr Arg Glu Ile Pro Leu Ile Ile Phe  
 65 70 75 80  
 Pro Glu Val Leu Ile Gly Ser Thr Pro Thr Gln Ser Thr Glu  
 85 90

&lt;210&gt;1213

&lt;211&gt;168

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1213

Met Arg Gln Phe Cys Asn Leu Leu Ser Leu Ser Arg Leu Trp Leu Ala  
 1 5 10 15  
 Leu Tyr Phe Cys Gln Glu Lys Leu His Ile Arg Leu Leu Ala Ile Val  
 20 25 30  
 Gly Ala Met Leu Ser Asp Val Leu Asp Gly Tyr Leu Ala Arg Arg Tyr  
 35 40 45  
 Lys Ala Thr Ser Arg Leu Gly Ser Ile Leu Asp Pro Ile Thr Asp Lys  
 50 55 60  
 Val Phe Val Phe Val Cys Ile Thr Val Leu Tyr Met Glu Gly Ser Leu  
 65 70 75 80  
 Ser Ile Ala His Leu Phe Phe Ile Cys Ala Arg Asp Leu Phe Leu Xaa  
 85 90 95  
 Thr Phe Val Phe Tyr Leu Ser Leu Val Lys Gly Trp Lys Gly Tyr Asp  
 100 105 110  
 Tyr Gly Ser Leu Phe Trp Gly Lys Ile Phe Thr Val Val Gln Phe Ile  
 115 120 125  
 Ile Leu Leu Gly Val Thr Ala Gly Gly Glu Ile Pro Trp Thr Gly Leu  
 130 135 140  
 Val Pro Leu Val Ala Leu Gly Phe Leu Tyr Phe Leu Glu Arg Ile Met  
 145 150 155 160  
 Asp Tyr Lys Lys Gln Phe Leu Arg  
 165

&lt;210&gt;1214

&lt;211&gt;88

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1214

Met Ser Arg Ser Leu Arg Lys Gly Pro Phe Val Asp His His Leu Leu  
 1 5 10 15  
 Lys Lys Val Arg Ala Met Asn Ile Glu Lys Lys Thr Pro Ile Lys  
 20 25 30

Thr Trp Ser Arg Arg Ser Met Ile Thr Pro Glu Met Ile Gly His Thr  
                   35                  40                  45  
 Phe Glu Val His Asn Gly Lys Lys Phe Leu Thr Val Phe Val Ser Glu  
           50                  55                  60  
 Thr Met Val Gly His Lys Leu Gly Glu Phe Ser Pro Thr Arg Ile Phe  
           65                  70                  75                  80  
 Lys Ser His Pro Val Lys Lys Gly  
                                   85

&lt;210&gt;1215

&lt;211&gt;252

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1215

Met Leu Ile Val Leu Ala Phe Arg Gln Val Phe Phe Ser His Ser Arg  
   1                  5                  10                  15  
 Ser Gln Leu Asp Arg Leu Lys Asn Tyr Leu Arg Leu Leu Lys Gln Asn  
                   20                  25                  30  
 Phe Ala Ile Thr Leu Pro Lys Glu Arg Thr Ser Lys Gly His Ser Leu  
           35                  40                  45  
 Met Leu Thr Phe Asp Phe Ala Ser Phe Asp Phe Tyr Thr Asn Ile Phe  
           50                  55                  60  
 Pro Phe Leu Glu Glu Gln Lys Ile Pro Ala Val Val Gly Val Ala Ser  
           65                  70                  75                  80  
 Arg Tyr Ile Pro Ser Asn Ala Ala Gln Asp Leu His Pro Ser His Arg  
                   85                  90                  95  
 Leu Lys Pro Ser Glu Thr Leu Ala Phe Gln Asp Glu Ile Phe Ser Asn  
                   100                  105                  110  
 Tyr Met Pro Phe Cys Cys Gln Asn Glu Leu Ile Glu Met Ala Lys Ser  
           115                  120                  125  
 Pro Tyr Ile Gln Leu Ala Ser Ser Gly Phe Ala Ile Arg Asn Leu Met  
           130                  135                  140  
 Asn Asn Pro Pro Tyr Leu Thr Thr Glu Ile Leu Leu Ser Arg His His  
   145                  150                  155                  160  
 Ile Glu Thr Ile Thr Gly Ala Lys Pro Leu Ala Phe Leu Phe Pro Phe  
                   165                  170                  175  
 Gly Lys Ser Asp Pro Thr Ser Arg Lys Leu Ala Ala Asp His Tyr Pro  
                   180                  185                  190  
 Tyr Ser Phe Leu Leu Gly Asn Thr Ile Asn Arg Lys Leu Lys Thr His  
                   195                  200                  205  
 Asn Ile Tyr Arg Leu Asp Ile Lys Pro Met Gln Tyr Val Cys Pro Ser  
           210                  215                  220  
 Leu Phe Gln Ser Ser Arg Tyr Leu Lys Asn Trp Ile Lys Glu Lys Ser  
   225                  230                  235                  240  
 Lys Gln Leu Tyr Leu Lys Lys Gln Leu Pro Lys Arg  
                                   245                  250

&lt;210&gt;1216

&lt;211&gt;149

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1216

Met Ala Asp Leu Glu Val Phe Gln Ala Asp Phe Ala Leu Leu Phe Glu  
   1                  5                  10                  15  
 Ala Gly Leu Leu Ala Ile Lys Gln Gly Asp Glu Asp Ser Ala Arg Lys  
                   20                  25                  30  
 Leu Phe Gln Ser Leu His Ile Leu Asn Pro Asn His Tyr Gly His Asp  
           35                  40                  45  
 Leu Gly Leu Ala Leu Ile Ser Leu His Lys Met Asp Leu Phe Asp Ala  
           50                  55                  60  
 Glu Glu Arg Leu Ser Ala Leu Ile Lys Gly Asn Glu Asp Asn Trp Ser  
           65                  70                  75                  80  
 Ile Lys Ala Phe Leu Ser Leu Thr His Met Leu Ile Val Leu His Gln  
                   85                  90                  95  
 Gly Ser Ser Phe Glu Val Arg Arg Glu Ser Leu Glu Ser Cys Leu Lys  
                   100                  105                  110

Phe Ala Asp Gln Val Ile Ala Asn Cys Lys Ile Glu Ser Thr Arg Ala  
           115                  120                  125  
 Leu Ala Gln Ser Val Leu Asp Trp His Asp Thr Leu Val Ala Lys Ser  
           130                  135                  140  
 Ala Gly Pro Leu Gly  
 145  
 <210>1217  
 <211>75  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1217  
 Met Phe Phe Ala Pro Leu Leu Tyr Glu Ser Leu Arg Arg Gly Leu Met  
       1                  5                  10                  15  
 His Pro Thr Ser His Met Gln Gln Gln Leu Ala Arg Leu Glu Phe Ile  
           20                  25                  30  
 Asn Asp Gln Leu Thr Thr Glu Leu Glu His Val Asn Glu Leu Leu Cys  
           35                  40                  45  
 Ser Leu Gly Phe Pro Glu Gly Leu Thr Thr Ile Lys Ala Ile Ala Glu  
           50                  55                  60  
 Glu Val Leu Ser Asp Asp Glu Pro Leu Leu Asp  
           65                  70                  75  
 <210>1218  
 <211>467  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1218  
 Leu Pro Ser Asn Arg Lys Asn Ala Lys Arg Asn Leu Tyr Lys Leu Ser  
       1                  5                  10                  15  
 Phe Ile Ile Val Arg Lys Cys Val Val Thr Ser Ala Leu Asn Asp Phe  
           20                  25                  30  
 Phe Leu Thr Glu Thr Val Met Asn Ala Thr Lys His Cys Arg Ala Ser  
           35                  40                  45  
 Phe Ser Asn Ser Pro Arg His Leu Leu Ala Gln Leu Ala Glu Asp Ile  
           50                  55                  60  
 Thr Ser Thr His Gln Lys Pro Phe Thr Lys Arg Trp Ile Leu Val Ala  
           65                  70                  75                  80  
 Asn Ala Thr Thr Gly His Trp Ile Lys Asn Gln Leu Val His Val Leu  
           85                  90                  95  
 Ser Asp His Ile Phe Met Gly Ser Thr Ile Phe Thr Ala Ser Asp Ser  
           100                  105                  110  
 Ile Val Lys His Leu Phe Leu Gly Ser Gly Cys Ser Gln Pro Asn Ile  
           115                  120                  125  
 Pro Asp Tyr Leu Thr Leu Pro Leu Leu Ile Asn Asn Ile Leu Glu Glu  
           130                  135                  140  
 Ile Ser Lys Ala Ser Lys Phe Glu Asn Gly Arg Glu Phe Leu Ser Pro  
           145                  150                  155                  160  
 Pro Thr Tyr Gly Thr Thr Lys Lys Leu Ala Ala Ala Phe Lys Gln Phe  
           165                  170                  175  
 His Thr Phe Ser Gln Arg Pro Thr Lys Asn Ala Ser His Tyr Gln Glu  
           180                  185                  190  
 Leu Phe Gln Ile Leu Glu Ser His Phe Ser Ser Tyr Glu Glu Met Phe  
           195                  200                  205  
 Thr Thr Ile Leu Asn Asn Arg Thr Gln Glu Glu Asp Cys Ser Leu His  
           210                  215                  220  
 Ile Phe Gly Tyr Ala His Leu Pro Lys His Leu Ala Glu Phe Phe Ile  
           225                  230                  235                  240  
 Asn Leu Ser Thr Tyr Phe Pro Val Tyr Phe Tyr Cys Phe Ser Pro Cys  
           245                  250                  255  
 Arg Glu Tyr Phe Gly Asp Leu Leu Ser Asp Arg Ala Ile Asp Phe Phe  
           260                  265                  270  
 Trp Asn Gln Leu Pro Asp Ser Pro Ile Lys Asn Ala Trp Glu His Tyr  
           275                  280                  285  
 Val Leu Ser Asp Arg Gln Ala Leu Leu Ala Asn Leu Ala His Lys Ser  
           290                  295                  300

Gln Ser Ser Gln Asn Phe Phe Leu Asp Arg Glu Ile Asp Tyr Gln Glu  
 305 310 315 320  
 Met Phe Leu Pro Ser Lys His Asp Ser Ser Leu Gly Val Ile Gln Asn  
 325 330 335  
 Ser Ile Leu Asp Leu Lys Pro Thr Ser Pro Gln Asp Phe Ser Gln Thr  
 340 345 350  
 Lys Gln Thr Ile Cys Ile Tyr Arg Ala Leu Asn Ile Pro Arg Glu Val  
 355 360 365  
 Gln Glu Val Phe Cys Lys Val Thr Glu Leu Leu His Arg Gly Val Ser  
 370 375 380  
 Pro Glu Glu Ile Phe Ile Leu Ser Ser His Ile Glu Ser Tyr Lys Val  
 385 390 395 400  
 His Leu Asn Ala Ile Phe Asn Pro His Val Pro Ile Tyr Phe Thr Asp  
 405 410 415  
 Glu Val Asp Pro Arg Ala Glu Asp Leu Arg Asn Lys Asn Pro Pro Thr  
 420 425 430  
 Phe Phe Tyr Phe Thr Asn Thr Arg Gly Phe Thr Leu His Ser Ser Thr  
 435 440 445  
 Pro Tyr Ala Pro Thr Thr Thr Thr Tyr Arg Ser Lys Gln Gly Ser  
 450 455 460  
 Leu Ser Asp  
 465

&lt;210&gt;1219

&lt;211&gt;81

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1219

Leu Glu Ala Pro Met Asn Glu Gly Ile His Ser Val Cys Phe Gln Lys  
 1 5 10 15  
 Thr Pro Arg Leu Thr Ala Lys Ser Val Val Ser Met Glu Met Leu Leu  
 20 25 30  
 Thr Thr Gln Gln Leu Pro Ser Ala Glu Gly Met Pro Ser Val Ala Asn  
 35 40 45  
 Leu Glu Ala Asp Phe Leu Arg Ala Glu Ala Leu Leu Ala Glu Met Arg  
 50 55 60  
 Glu Ile Arg Gly Cys Leu Glu Gln Ser Leu Arg Thr Leu Val Pro Ser  
 65 70 75 80  
 Glu

&lt;210&gt;1220

&lt;211&gt;95

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1220

Met Met Lys Tyr Leu Pro Tyr Ile Ala Ile Thr Ala Cys Ile His Gly  
 1 5 10 15  
 Gly Ile Leu Leu Leu Val Phe Ala Ser Pro Leu Pro Lys Lys Arg Leu  
 20 25 30  
 Gln Pro Lys Ala Phe Gln Glu Lys Leu Val Thr Ile Gln Pro Lys Pro  
 35 40 45  
 Pro Val Pro Thr Pro Ser Val Val Val Asp Pro Ala Lys Thr Ile Arg  
 50 55 60  
 Pro Ser Val Leu Arg Ser His Lys Asn Lys Leu Asn Ala Ala Leu Leu  
 65 70 75 80  
 Lys Arg Thr Ser Arg Arg Leu Tyr Lys Asn Pro Phe Gln Lys Leu  
 85 90 95

&lt;210&gt;1221

&lt;211&gt;96

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1221

Leu Asn Lys Phe Lys Thr Tyr Leu Gln Thr Ala Leu Ile Ala Pro Phe  
 1 5 10 15  
 Phe Ser Phe Pro Ala Leu Ser Gly Ser Phe Ser Ser Ile Gln Ala Glu

20 25 30  
 Glu Ile Xaa Gln Gln Val Asn His Pro Gly Ala Glu Leu Ser Glu  
 35 40 45  
 Gly Ser Tyr Ile Pro Gly Leu Gln Thr Phe Arg Leu Gly Ile Lys Ile  
 50 55 60  
 Tyr Ser Phe Gln Arg Glu Pro Tyr Leu Leu Glu Glu Ser Arg Arg Asn  
 65 70 75 80  
 Trp Lys Ser Ser Gln Asn Phe Leu Ala Val Ala Glu Arg Phe Arg Gly  
 85 90 95

&lt;210&gt;1222

&lt;211&gt;76

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1222

Val Arg Ala Leu Phe Arg Ser Gly Tyr Lys Gly Arg Gln Gly Ile Tyr  
 1 5 10 15  
 Glu Phe Leu Arg Pro Asn Thr Leu Phe Arg Ser Glu Val Ala Ser Asn  
 20 25 30  
 Arg Pro Tyr His Ile Leu Arg Glu Thr Ala Glu Gln Asn Gly Phe Leu  
 35 40 45  
 Pro Ile Leu Glu His Gly Ile Ala Leu Ala Val Ser Gly Glu Thr Thr  
 50 55 60  
 Leu Ala Glu Val Leu Arg Val Thr Lys Arg Cys Asp  
 65 70 75

&lt;210&gt;1223

&lt;211&gt;185

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1223

Val Pro Thr Leu Ala Lys Ser Phe Tyr Ile Asn Ile Arg Asp Ser Arg  
 1 5 10 15  
 Phe Tyr Ser Trp Leu Cys Phe Ile Met Lys Glu Thr Tyr Tyr Arg Asp  
 20 25 30  
 Phe Leu His Glu Asn Tyr Leu Lys Asn Lys Lys Ser Met Phe Met Lys  
 35 40 45  
 Ile Tyr Lys Thr Ala Gly Glu Phe Phe Leu Ala Asn Ala Lys Trp Pro  
 50 55 60  
 Leu Val Pro Ala Gly Tyr Arg Arg Val Arg Gly Lys Asp Phe Val Leu  
 65 70 75 80  
 Ser Pro Leu Val Asp Leu Val Ile Leu Phe Pro Trp Val Thr Lys Asp  
 85 90 95  
 Ser Arg Tyr Ser Pro Cys Ser Met Thr Phe Thr Cys Ile Cys Arg Ser  
 100 105 110  
 Ile Val Glu Cys Ile Pro Val Val Ser Thr Leu Phe Gly Ile Gly Arg  
 115 120 125  
 Phe Cys Ala Val Trp Cys Val Glu Gly Phe Ser Gly Ser Thr Phe Asp  
 130 135 140  
 Lys Ile Tyr His Thr Ile Val Ala Val Leu Gly Ile Leu Gly Leu Gly  
 145 150 155 160  
 Ile Leu Thr Phe Ile Leu Arg Ile Ile Phe Ser Val Leu Met Leu Pro  
 165 170 175  
 Val Trp Phe Leu Phe Lys Cys Tyr Ser  
 180 185

&lt;210&gt;1224

&lt;211&gt;75

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1224

Met Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Thr Asp Arg Val His  
 1 5 10 15  
 Arg Ile Gly Gln Ser Arg Ser Val Ser Ser Tyr Lys Leu Val Thr Leu  
 20 25 30  
 Asn Thr Ile Glu Glu Lys Ile Leu Thr Leu Gln Asn Arg Lys Xaa Ser  
 35 40 45

Leu Val Lys Lys Val Ile Asn Ser Asp Asp Glu Val Val Ser Lys Leu  
 50 55 60  
 Thr Trp Glu Glu Val Leu Glu Leu Leu Gln Ile  
 65 70 75

&lt;210&gt;1225

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1225

Met Arg Asp Arg Leu Gly Ser Leu Ser Leu Ile Leu Lys Val Lys Ile  
 1 5 10 15  
 His Lys Tyr Leu Asp Thr Leu His Asn Gln Lys Arg Leu Ala Leu Thr  
 20 25 30  
 Val Ser Arg Asn Ile Gln Ala Thr Asn Lys Arg Ile Ala Asp Leu His  
 35 40 45  
 Leu Glu Arg Tyr Glu His Phe Ile Ser Arg Asp Asn Ile Lys His Tyr  
 50 55 60  
 Asp Ile Leu Leu Glu Tyr Leu Lys Thr Leu Gln Ser Ser Leu Tyr Lys  
 65 70 75 80  
 Gln Gln Ser Glu Ser Leu Arg Phe Leu Glu Ile His His Gln Gln Leu  
 85 90 95  
 Gln Glu Leu Ile Asn Arg Arg Lys Ile Ile Glu Lys Ile Lys Asn Asn  
 100 105 110  
 Lys Tyr Ser Lys Asp Gln Glu Ile Gly Thr  
 115 120

&lt;210&gt;1226

&lt;211&gt;178

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1226

Val Thr Thr Pro Gln Ser Pro Gly Ser Leu Ser Gln Ser His Leu Pro  
 1 5 10 15  
 His Pro His Asp Pro Trp Asp Thr Glu Pro Thr Ser Leu Xaa Glu Xaa  
 20 25 30  
 Pro Asn Asp Lys Ala Ser Gln Glu Leu His Ser Leu Val His Leu Phe  
 35 40 45  
 Arg Lys Leu Ser Ile His Leu Leu Ser Glu Val Glu Lys Thr Val Gln  
 50 55 60  
 Gln Leu Lys Pro Asp Leu Leu Glu Leu Ala Leu Leu Ile Cys Glu Lys  
 65 70 75 80  
 Phe Leu Tyr Lys Lys Leu Glu Asn Pro Gln Glu Leu Ala Leu Leu Leu  
 85 90 95  
 Ser Thr Ala Leu Gln Arg His Thr Thr Leu Arg Ser Leu Thr Pro Ile  
 100 105 110  
 Lys Val Phe Leu His Pro Glu Asp Leu Lys Thr Leu Thr Asp Trp Ile  
 115 120 125  
 Ser Thr His Glu Leu Pro Met Ile Lys His Ala Glu Phe Phe Pro Asp  
 130 135 140  
 Thr Ser Cys Arg Arg Ser Gly Phe Lys Ile Glu Thr Pro Asn Gly Ile  
 145 150 155 160  
 Leu Arg Gln Glu Ile Ser Glu Glu Leu Asp His Leu Leu Ser Val Leu  
 165 170 175

Thr Ala

&lt;210&gt;1227

&lt;211&gt;161

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1227

Leu Leu Leu Arg Tyr His Ala Lys Ala Glu Lys Pro Thr Leu Gln Leu  
 1 5 10 15  
 Thr Leu Asn Glu Asn Tyr Ile Ala His Leu Thr Lys Glu Glu Ser Glu  
 20 25 30  
 Lys Ile Val Ala His Thr Lys His Tyr Leu Leu Ser Asn Xaa Asp Asp

35 40 45  
 Ser Tyr Asp Ile Val Ile Glu Thr Leu Pro Phe Ala Arg Leu Gln Asn  
 50 55 60  
 Lys Lys Ser Phe Ser Ala Lys Val Leu Ile Gly Ser Met Ile Leu Val  
 65 70 75 80  
 Ile Ser Leu Met Ile Val Ala Leu Ala Ser Phe Tyr Leu Ala Arg His  
 85 90 95  
 Ala Tyr Glu Arg Val Ser Pro Glu Pro Arg Lys Ile Lys Arg Gly Ile  
 100 105 110  
 Asn Ile Ser Lys Leu Leu Glu Ile Ile Gln Lys Glu Ser Pro Glu Lys  
 115 120 125  
 Ile Ala Leu Ile Leu Ser Tyr Leu Asp Pro Lys Lys Ala Glu Ala Leu  
 130 135 140  
 Leu Asn Arg Leu Pro Glu Asp Leu Lys His Gln Val Leu Lys Tyr Lys  
 145 150 155 160  
 Leu

&lt;210&gt;1228

&lt;211&gt;75

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1228

Val Phe Phe Gln Asn Leu Ala Lys Lys Leu Thr Ala Leu Gly Ile Ser  
 1 5 10 15  
 Pro Leu Gly Cys Leu Leu Ile Gly Gly Val Val Ser Cys Ala Ile Leu  
 20 25 30  
 Phe Gly Arg Ser Ser Asn Pro Ser Leu Ala Pro Thr Gln Val Lys Thr  
 35 40 45  
 Glu Lys Thr Ser Gly Asn Trp Leu Lys Leu Thr Gln Met Gly Asn Pro  
 50 55 60  
 Lys Leu Ile Glu Ser Leu Thr Lys Lys Asp Ser  
 65 70 75

&lt;210&gt;1229

&lt;211&gt;100

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1229

Met Gly Tyr Val Phe Tyr Val Ile Ala Gly Ser Ile Phe Leu Gly Ile  
 1 5 10 15  
 Ser Leu Gly Ala Tyr Cys Gln Leu Tyr Tyr Ser Val Lys Ser Val Leu  
 20 25 30  
 Phe Ser Trp Tyr Leu Leu Thr Val Tyr Ala Leu Glu Lys Arg His Ala  
 35 40 45  
 Leu Leu Ala Leu Ser Gln Leu Val Gly Glu Glu Asp Ala Gln Ser Gln  
 50 55 60  
 Lys Glu Ile Asp Phe Leu Ser Gln Cys Asp Lys Leu Ser Trp Arg Ala  
 65 70 75 80  
 Phe Leu Lys Asn Ser Tyr Glu Ile Ile Pro Thr Phe Gln Arg Asp Gly  
 85 90 95  
 Arg Pro Ser Phe  
 100

&lt;210&gt;1230

&lt;211&gt;103

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1230

Val Thr Ser Ser Leu Gly Val Arg Ser Ser Lys Ile Ala Thr Arg Ser  
 1 5 10 15  
 Ser Gln His Phe Lys Glu Met Glu Asp Leu Leu Ser Glu Arg Val Gln  
 20 25 30  
 Gly Phe Leu Glu Ser Ile Glu Thr Ile Ala Glu His Asp Arg Ala Ile  
 35 40 45  
 Leu Cys Ile Glu Asn Phe Trp Ala Ser Lys Asn Leu Phe Asp Phe Glu  
 50 55 60

Ile Ala Ala Tyr Glu Glu Ala Val Glu Lys Tyr Leu Lys Leu Arg Gln  
 65 70 75 80  
 Arg Ala Pro Leu Arg Leu Ala Ser Lys Leu Phe Arg Phe Leu Asp Val  
 85 90 95  
 Pro Ser Ile Arg Phe Ser Ser  
 100

&lt;210&gt;1231

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1231

Ser Ile Ala Thr Gly Glu Thr Met Leu Tyr Phe Ile Glu Gln Leu Asn  
 1 5 10 15  
 Lys Leu Ser Thr Ser Phe Cys Val Phe Pro Met Ile Leu Leu Leu Gly  
 20 25 30  
 Gly Phe Leu Thr Trp Lys Leu Arg Gly Leu Gln Phe His Gly Leu Lys  
 35 40 45  
 Leu Gly Phe Asn Leu Met Leu Gln Asn Lys Leu Asp Asp Ser Ser Ser  
 50 55 60  
 Lys Ala Asn Glu Val Ser Ser Tyr Glu Ala Val Ala Gly Ile Leu Ala  
 65 70 75 80  
 Gly Asn Phe Gly Thr Gly Asn Ile Ala Gly Met Leu Ser Pro  
 85 90

&lt;210&gt;1232

&lt;211&gt;240

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1232

Val Pro Asn Arg His Val Asp Met Asn Ser Trp Trp Arg Ser Ala Cys  
 1 5 10 15  
 Tyr Pro Arg Ser Thr Phe Tyr Pro Leu Ser Asp Gly Asp Ser Thr Phe  
 20 25 30  
 His Arg Arg Ile Thr Lys Pro Asp Phe Arg Leu Cys Ser Thr Cys Lys  
 35 40 45  
 Ser Cys Ser Gln Pro Ile Leu Tyr Leu Tyr Ala Leu Val Ile Ala  
 50 55 60  
 Asn His Asp Glu Ile Ser Phe Gly Leu Leu Arg Tyr Phe Leu Gly Gly  
 65 70 75 80  
 Tyr Arg Pro Ser Lys Thr Ala Arg Leu Ala Met Ser Ile Leu Gln Ile  
 85 90 95  
 His Gly Val Met Leu Asp Ser Gln Leu Val Lys Thr Ser Ile Ser Thr  
 100 105 110  
 Met Thr Pro Thr Leu Leu Thr Lys Ser Val His Ser Leu Leu Ala Ile  
 115 120 125  
 Leu His Ile Thr Asn Gln Lys Ser Ile Pro Lys Tyr Ser Lys Gly Ser  
 130 135 140  
 Arg Gly Leu Phe Val Leu Leu Arg Val Asn Ser Ile Phe Thr Ala Thr  
 145 150 155 160  
 Thr Ile Ser Pro Ser Leu Ser Leu Arg Gln Cys Pro Asp Arg Tyr Thr  
 165 170 175  
 Ile Arg Ala Gly Arg Asn Leu Pro Asp Lys Glu Phe Arg Tyr Leu Ser  
 180 185 190  
 Thr Val Ile Val Thr Ala Ala Ile His Gln Gly Leu Gly Ser Met Leu  
 195 200 205  
 Ser Leu Arg Leu Thr Tyr Pro Phe Asn Leu Leu Ala Leu Gly Arg Arg  
 210 215 220  
 His Thr Ile Tyr Phe Pro Leu Glu Val Cys Ile Val Leu Cys Phe Cys  
 225 230 235 240

&lt;210&gt;1233

&lt;211&gt;133

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1233

Leu Asn Phe Val Ser Thr Leu Thr Gly Ser Asp Phe Tyr Ala Pro Val



1 5 10 15  
 Leu Glu Lys Leu Glu Glu Ala Phe Ala Asp Thr Thr Gly Gln Ala Ile  
 20 25 30  
 Leu Phe Ser Ser Ser Pro Asp Phe Ile Val His Pro Ile Ala Gln Gln  
 35 40 45  
 Leu Gly Ile Ser Ser Trp Tyr Ala Ser Cys Tyr Arg Asp Gln Ser Ala  
 50 55 60  
 Glu Gln Thr Ile Tyr Lys Lys Cys Leu Thr Gly Asp Lys Lys Ala Gln  
 65 70 75 80  
 Ile Leu Ser Tyr Ile Lys Lys Ile Asn Gln Ala Arg Ser His Thr Phe  
 85 90 95  
 Ser Asp His Ile Leu Asp Leu Pro Phe Leu Met Leu Gly Glu Glu Lys  
 100 105 110  
 Thr Val Val Arg Pro Gln Gly Arg Leu Lys Lys Met Ala Lys Lys Tyr  
 115 120 125  
 Tyr Trp Asn Ile Val  
 130  
 <210>1234  
 <211>118  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1234  
 Val Ile Leu Leu Gln Asn Ile Lys Arg Cys Ser Leu Lys Gln Leu Lys  
 1 5 10 15  
 Val Leu Ala Thr Leu Leu Leu Ser Leu Ser Leu Pro Thr Leu Glu Ala  
 20 25 30  
 Ala Glu Asn Arg Asp Ser Asp Ser Ile Val Trp His Leu Asp Tyr Gln  
 35 40 45  
 Glu Ala Leu Gln Lys Ser Lys Glu Ala Glu Leu Pro Leu Leu Val Ile  
 50 55 60  
 Phe Ser Gly Ser Asp Trp Asn Gly Pro Cys Met Lys Ile Arg Lys Glu  
 65 70 75 80  
 Val Leu Glu Ser Pro Glu Phe Ile Lys Arg Val Gln Gly Lys Phe Val  
 85 90 95  
 Cys Val Glu Val Glu Tyr Leu Lys His Arg Pro Gln Leu Lys Thr Phe  
 100 105 110  
 Val Ser Lys Ile Leu Leu  
 115  
 <210>1235  
 <211>87  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1235  
 Met Lys Ser Phe Lys Phe Leu Leu Pro Phe Leu Ser Val Ile Leu Cys  
 1 5 10 15  
 Cys Gly Asn Leu Leu Ser Ser Pro Arg Ser Arg Ala Ile Ser Val Thr  
 20 25 30  
 Glu Ser Ile Gly Met Ser Ala Val Lys Thr Leu Val Leu Ser Glu Lys  
 35 40 45  
 Ala His Glu Phe Leu Glu Gly Ile Gly Tyr Gly Val Gly Ala Ser Ser  
 50 55 60  
 Ile Leu Arg Asp Trp Gln Thr Gln Gln Trp Leu Glu Ile Glu Ser Leu  
 65 70 75 80  
 Leu Ala Gln Asn Glu Val Met  
 85  
 <210>1236  
 <211>141  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1236  
 Met Gln Tyr Phe Ser Pro Ala Lys Leu Asn Leu Phe Leu Lys Ile Trp  
 1 5 10 15  
 Gly Lys Arg Phe Asp Asn Phe His Glu Leu Thr Thr Leu Tyr Gln Ala  
 20 25 30

Ile Asp Phe Gly Asp Thr Leu Ser Leu Lys Asn Ser Met Lys Asp Ser  
 35 40 45  
 Leu Ser Ser Asn Val Asn Glu Leu Leu Ser Pro Ser Asn Leu Ile Trp  
 50 55 60  
 Lys Ser Leu Glu Ile Phe Arg Arg Glu Thr Gln Ile His Gln Pro Val  
 65 70 75 80  
 Ser Trp His Leu Asn Lys Ser Ile Pro Leu Gln Ser Gly Leu Gly Gly  
 85 90 95  
 Gly Ser Ser Asn Ala Ala Thr Ala Leu Tyr Ala Leu Asn Glu His Phe  
 100 105 110  
 Gln Thr His Ile Pro Ile Thr Thr Leu Gln Leu Trp Ala Arg Glu Ile  
 115 120 125  
 Gly Ser Asp Val Pro Phe Phe Phe Leu Gln Glu Gln His  
 130 135 140

&lt;210&gt;1237

&lt;211&gt;174

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1237

Leu Gly Ser Arg Asn Arg Lys Arg Cys Ser Phe Phe Phe Ser Ser Gly  
 1 5 10 15  
 Thr Ala Leu Gly Lys Gly Arg Gly Glu His Leu Phe Ser Ile Lys Lys  
 20 25 30  
 Leu Asn His Lys His Lys Tyr Val Leu Tyr Leu Asp His Gln Gly Ile  
 35 40 45  
 Pro Thr Glu Lys Ala Tyr Gln Ser Leu Leu Pro Gln Asp Tyr Ser Thr  
 50 55 60  
 Gly Asn His Asn Ala Cys Phe Tyr Gly Glu Asn Asp Leu Glu Lys Ser  
 65 70 75 80  
 Val Phe Arg Ile Arg Thr Asp Leu Lys Asn Lys Lys His Met Leu Glu  
 85 90 95  
 Arg Met Trp Ser Pro Phe Glu Ser His Val Leu Met Ser Gly Ser Gly  
 100 105 110  
 Ala Thr Leu Phe Val Cys Tyr Leu Glu Glu Leu Glu Gln Asp Ser Lys  
 115 120 125  
 Val Ser Ser Gln Ile His Ser Leu Ile Lys Gln Thr Gln Gly Ile Pro  
 130 135 140  
 Val Ser Arg Leu Tyr Arg Glu Pro His Trp Tyr Ser Leu Lys Gln Ser  
 145 150 155 160  
 Thr Tyr Lys Asn Ser Pro Leu Glu Cys Phe Gln Pro Gln Ile  
 165 170

&lt;210&gt;1238

&lt;211&gt;106

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1238

Met Gly Leu Tyr Asp Arg Asp Tyr Ile Gln Asp Ser Arg Val Gln Gly  
 1 5 10 15  
 Thr Phe Ala Ser Arg Val Tyr Gly Trp Met Thr Ala Gly Leu Ile Val  
 20 25 30  
 Thr Ser Cys Val Ala Leu Gly Leu Tyr Phe Ser Gly Leu Tyr Arg Ser  
 35 40 45  
 Leu Phe Ser Phe Trp Trp Val Trp Cys Phe Ala Thr Leu Gly Val Ser  
 50 55 60  
 Phe Phe Ile Asn Ser Lys Ile Gln Thr Leu Ser Val Val Gly Gln Val  
 65 70 75 80  
 Met Ala Tyr Ala Met Val Leu Ala Lys Gly Met Glu Ile Asp Cys Pro  
 85 90 95  
 Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 100 105

&lt;210&gt;1239

&lt;211&gt;217

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1239

Met Ser Asn Lys Val Leu Gly Gly Ser Leu Leu Ile Ala Gly Ser Ala  
 1 5 10 15  
 Ile Gly Ala Gly Val Leu Ala Val Pro Val Leu Thr Ala Lys Gly Gly  
 20 25 30  
 Phe Phe Pro Ala Thr Phe Leu Tyr Ile Val Ser Trp Leu Phe Ser Met  
 35 40 45  
 Ala Ser Gly Leu Cys Leu Leu Glu Val Met Thr Trp Met Lys Glu Ser  
 50 55 60  
 Lys Asn Pro Val Asn Met Leu Ser Met Ala Glu Ser Ile Leu Gly His  
 65 70 75 80  
 Val Gly Lys Ile Ser Ile Cys Leu Val Tyr Leu Phe Leu Phe Tyr Ser  
 85 90 95  
 Leu Leu Ile Ala Tyr Phe Cys Glu Gly Gly Asn Ile Leu Cys Arg Val  
 100 105 110  
 Phe Asn Cys Gln Asn Leu Gly Ile Ser Trp Ile Xaa Xaa Leu Gly Pro  
 115 120 125  
 Leu Gly Phe Ala Ile Leu Met Gly Pro Ile Ile Xaa Xaa Gly Thr Xaa  
 130 135 140  
 Xaa Ile Asp Tyr Cys Xaa Xaa Phe Phe Xaa Xaa Gly Leu Xaa Val Xaa  
 145 150 155 160  
 Phe Gly Ile Xaa Xaa Ala Leu Gly Phe Leu Lys Ile Gln Pro Ser Phe  
 165 170 175  
 Met Val Arg Ser Ser Met Val Asn Tyr Asn Lys Arg Ile Ser Cys Val  
 180 185 190  
 Phe Ser Leu Leu Phe Gly Phe Gln Ser Xaa Ile Pro Thr Leu Tyr Tyr  
 195 200 205  
 Tyr Met Asp Lys Lys Ser Trp Arg Cys  
 210 215

&lt;210&gt;1240

&lt;211&gt;115

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1240

Leu Val Ser Ser Phe Val Gly Val Ala Leu Gly Val Met Asp Phe Leu  
 1 5 10 15  
 Ala Asp Gly Leu Lys Trp Asn Lys Lys Ser His Pro Phe Ser Ile Phe  
 20 25 30  
 Phe Leu Thr Phe Ile Ile Pro Leu Ala Trp Ala Val Cys Tyr Pro Glu  
 35 40 45  
 Ile Val Leu Thr Cys Leu Lys Tyr Ala Gly Gly Phe Gly Ala Ala Val  
 50 55 60  
 Ile Ile Gly Val Phe Pro Thr Leu Ile Val Trp Lys Gly Arg Tyr Gly  
 65 70 75 80  
 Lys Gln His His Arg Glu Lys Gln Leu Val Pro Gly Gly Lys Phe Ala  
 85 90 95  
 Leu Phe Leu Met Phe Leu Leu Ile Val Ile Asn Val Val Ser Ile Tyr  
 100 105 110  
 His Glu Leu  
 115

&lt;210&gt;1241

&lt;211&gt;105

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1241

Leu Phe Pro Leu Val Leu Leu Ala Trp Val Ile Arg Tyr Gln Leu His  
 1 5 10 15  
 Ala Asn Phe His Cys Ser Val Val Pro Phe Pro Gly Phe Ser Val Asn  
 20 25 30  
 Gln Ala Tyr Lys Cys Ser Glu Ala Lys Ile Glu Glu Met Leu Asp Leu  
 35 40 45  
 Leu Asp Leu Glu Thr Leu Glu Trp Ser Ser Arg Cys Leu Arg Gln Asp  
 50 55 60  
 Met Thr Phe Ala Asn Arg Leu Glu Glu Glu Leu Ile Gln Glu Leu Arg



Leu Leu Leu Thr Ser Ala Trp His Thr Leu Lys Ala Ile Leu Gly Gly  
 50 55 60  
 Phe Phe Leu Ala Ile Thr Leu Ser Ile Val Leu Ala Thr Ile Met Leu  
 65 70 75 80  
 Ser Tyr Lys Ser Ala Lys Asp Leu Leu Gln Pro Leu Phe Ile Leu Leu  
 85 90 95  
 Gln Cys Thr Pro Met Phe Ala Leu Ala Pro Leu Ile Val Leu Trp Phe  
 100 105 110  
 Gly Trp Gly Ile Gly Ala Val Ile Val Pro Thr Ala Leu Thr Ile Phe  
 115 120 125  
 Phe Pro Leu Thr Leu Thr Ile Tyr Gln Gly Ile Leu Ser Thr Pro Glu  
 130 135 140  
 Glu Leu Ile Glu Gln Phe Val Leu Cys Gly Val Gln Asn Ser Asn Ser  
 145 150 155 160

&lt;210&gt;1245

&lt;211&gt;227

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1245

Met Leu Trp Gly Val Ser Met Arg Gln Ser Phe Asp Glu Leu Ser Gln  
 1 5 10 15  
 Asn Ala Phe Lys Asn Ile Phe Asn Lys Gln Arg Phe Cys Phe Ile Phe  
 20 25 30  
 Cys Ser Leu Cys Cys Phe Gly Phe Val Phe Ala Leu Phe Leu Lys Leu  
 35 40 45  
 Cys Ser Arg Leu Ala Pro Glu Ile Ser Leu Ser Thr Leu Gly Leu Gly  
 50 55 60  
 Ala Phe Phe Cys Ala Phe Ser Val Ile Cys Ala Ser Ala Ile Ile Val  
 65 70 75 80  
 Gln Phe Leu Leu His Lys Glu Ser Gln Gly Glu Thr Ser Lys Leu Cys  
 85 90 95  
 Cys Ala Ile Lys Asn Thr Trp Ser Ser Leu Trp Leu Ser Leu Leu Val  
 100 105 110  
 Ser Met Pro Phe Phe Ile Ala Met Val Ala Val Val Thr Val Ala Met  
 115 120 125  
 Leu Ser Ser Phe Leu Gly Ser Leu Pro Trp Val Gly Lys Leu Phe His  
 130 135 140  
 Thr Val Leu Ile Phe Ile Pro Tyr Leu Ser Ala Thr Ala Leu Ile Leu  
 145 150 155 160  
 Leu Phe Leu Gly Ser Phe Ser Cys Leu Phe Cys Ile Pro Val Leu  
 165 170 175  
 His Asn Gln Glu Ser Ile Asp Tyr Arg Lys Leu Pro Arg Val Phe Ser  
 180 185 190  
 Trp Glu Tyr Pro Ser Ala Val Tyr Arg Gly Gly Asp Cys Phe Gly Ser  
 195 200 205  
 Xaa Ser Pro Met Gln Leu Val Ser Phe Arg Phe Phe Leu Phe Asp Asp  
 210 215 220  
 Thr Ser Cys  
 225

&lt;210&gt;1246

&lt;211&gt;78

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1246

Val Val Ile Ala Leu Val Pro Leu Ala Leu Cys Ser Trp Leu Ala Leu  
 1 5 10 15  
 Asp Ser Phe Tyr Leu Met Thr His Leu Val Glu Ile Ala Asp Ile His  
 20 25 30  
 Thr Trp Ser Phe Leu Ala Gln Met Phe Val Leu Ile Val Pro Ile Ala  
 35 40 45  
 Leu Ile Leu Thr Pro Ala Val Ser Phe Phe Phe Asn Phe Ser Phe Ser  
 50 55 60  
 Phe Tyr Leu Ala Lys Gln Glu Glu Glu Lys Ala Leu Val Lys  
 65 70 75

&lt;210&gt;1247

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1247

Leu Arg Ala Phe Phe Pro Val Lys Ala Trp Arg Ser Pro Glu Asp Ile  
 1 5 10 15  
 Pro Glu Ala Pro Ser Pro Lys Gly Ile Gly Ser Lys Arg Ser Ile Val  
 20 25 30  
 Ala Val Pro Trp Glu Trp Arg Ser Arg Cys Gln Val Thr Glu Ser Pro  
 35 40 45  
 Ala Tyr Pro Ala Pro Lys Thr Ala Ile Arg Ile Lys Cys Thr Leu Asn  
 50 55 60  
 Gln Val Ser Leu His Arg Pro Cys Leu Glu Asn Lys Arg Ile Arg Asp  
 65 70 75 80  
 Lys Arg Thr Gly Gly Asn Leu Ser Asp Trp Glu Ile Lys Met  
 85 90

&lt;210&gt;1248

&lt;211&gt;86

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1248

Met Arg Ile Ala Val Leu Gly Ala Gly Tyr Ala Gly Leu Ser Val Thr  
 1 5 10 15  
 Trp His Leu Leu Leu His Ser Gln Gly Thr Ala Thr Ile Asp Leu Phe  
 20 25 30  
 Asp Pro Ile Pro Leu Gly Glu Gly Ala Ser Gly Met Ser Ser Gly Leu  
 35 40 45  
 Leu His Ala Phe Thr Gly Lys Lys Ala Leu Lys Pro Pro Leu Val Gly  
 50 55 60  
 Ser Arg Asn Gln Cys Tyr Thr Arg Val Asn His Xaa Ala Leu Val Lys  
 65 70 75 80  
 Pro Ser Thr Tyr Leu Leu  
 85

&lt;210&gt;1249

&lt;211&gt;232

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1249

Leu Pro Met Asn Thr Ser His Arg Lys Thr Leu Val Phe Ser Tyr Leu  
 1 5 10 15  
 Ser Ser Thr Phe Thr Leu Leu Leu Val Leu Ser Asn Leu Val Leu Ser  
 20 25 30  
 Ser Lys Leu Ile Pro Thr Thr Phe Phe Asn Phe Ile Ile Pro Gly Gly  
 35 40 45  
 Leu Ile Leu Tyr Pro Leu Thr Phe Leu Ile Ser Asp Val Val Asn Glu  
 50 55 60  
 Ile Phe Gly Pro Lys Lys Ala Arg Val Met Ile Phe Ser Ala Phe Ile  
 65 70 75 80  
 Ala Asn Leu Leu Ala Ser Ser Ile Val Gln Ile Phe Met Phe Phe Pro  
 85 90 95  
 Val Ala Ser Pro Glu Met Gln Thr Ala Trp His Cys Leu Phe Asp Leu  
 100 105 110  
 Ser Pro Leu Arg Phe Leu Ala Ser Leu Leu Ala Phe Ile Val Ser Gln  
 115 120 125  
 Gln Leu Asp Ile Val Leu Tyr Thr Phe Phe Lys Asn Arg Thr Pro Asn  
 130 135 140  
 Ser Ser Leu Trp Leu Arg Ser Asn Gly Ser Thr Trp Ile Ser Gln Xaa  
 145 150 155 160  
 Pro Asp Thr Phe Ile Val Asp Thr Cys Ile Leu Tyr Phe Gly Met Gly  
 165 170 175  
 Leu Ser Phe Pro Gln Thr Leu Asn Ile Met Phe Tyr Ser Tyr Ile Tyr  
 180 185 190  
 Lys Ile Thr Phe Cys Val Leu Thr Thr Pro Leu Phe Tyr Leu Ala Val

195 200 205  
 Asn Thr Ile Arg Lys Phe Leu Gly Met Pro Ser Thr Lys Ile Ala Asn  
 210 215 220  
 Thr Val Pro Leu Ile Asn Gln Pro  
 225 230  
 <210>1250  
 <211>103  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1250  
 Met Thr Pro Lys Ser Ile Gln Gln Leu His Leu Ile Lys Thr Ile Asp  
 1 5 10 15  
 Pro Val Arg Lys Ile Ser Pro Val Thr Thr Lys Lys Ser Ser Phe Phe  
 20 25 30  
 Arg Gln Ser Leu Leu Arg Phe Leu Glu Leu Phe Trp Met Phe Leu Tyr  
 35 40 45  
 Cys Ile Arg Ser Ile Arg Phe His Cys Val His Ile Ala Thr Phe Ile  
 50 55 60  
 Cys Arg Gly Leu Ile Leu Phe Leu Thr Thr Leu Phe Leu Ser Met Ile  
 65 70 75 80  
 Cys Ile Leu His Phe Ile Thr Leu Pro Trp Ile Cys Lys Glu Asp Pro  
 85 90 95  
 Arg Ile Ile Arg Lys Asn Lys  
 100  
 <210>1251  
 <211>79  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1251  
 Leu Asn Phe Ala Lys Ile Asp His Asn His Leu Tyr Leu Thr Cys Leu  
 1 5 10 15  
 Gly Asp Leu Gly Val Ala Cys Pro Ile Leu Ser Thr Asp Cys Leu Pro  
 20 25 30  
 Asn Tyr Ser Glu Lys Ala Ser His Glu Val Leu Val Tyr Ser Lys Phe  
 35 40 45  
 Arg Cys Ile Ser Gly Glu Pro Ser Arg Leu Ala Thr Ser Gly Asn Asp  
 50 55 60  
 Thr Tyr Tyr Ser Ile Val Ser Leu Pro Ile Gly Leu Arg Tyr Glu  
 65 70 75  
 <210>1252  
 <211>85  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1252  
 Met Val Glu Ile His His Lys Asp Pro Ser Leu Lys Lys Leu Phe Ala  
 1 5 10 15  
 Leu Gln Gln Ser Leu Glu Thr Leu Asn Ser Leu Ser Asp Ile Val Ala  
 20 25 30  
 Thr Tyr Glu Ala Met Phe Ser Leu Ile Tyr Glu Gly Leu Asn Lys Ala  
 35 40 45  
 Leu Arg Lys Asp Gln Leu Cys Tyr Leu Leu Ser Val Asn Ser Lys Gly  
 50 55 60  
 Glu Leu Leu Lys Ser Pro Ser Gly Asp Pro Ile Val Gln Thr Phe Pro  
 65 70 75 80  
 Ile His Pro His His  
 85  
 <210>1253  
 <211>75  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1253  
 Met Glu Glu Val Pro Phe Glu Asn Ala Met Gln Arg Leu Glu Glu Ile  
 1 5 10 15  
 Val Asp Leu Met Asn Gln Pro Thr Thr Ser Leu Asp Ala Ser Leu Ala

20 25 30  
 Leu Tyr Glu Glu Ala Asp Ala Leu Met Arg Ile Cys Glu Ser Arg Ile  
 35 40 45  
 Arg Gln Val Glu Gln Arg Val Arg Glu Leu Ala Glu Lys Arg His Glu  
 50 55 60  
 Ser Ser Leu Phe Glu Glu Gln Ala Val Val Arg  
 65 70 75  
 <210>1254  
 <211>126  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1254  
 Met Tyr Ile Ser Ser Ser Phe Ser Ser Ser Ala Lys Val Ser Ala Ile  
 1 5 10 15  
 Cys Leu Ala Ser Ile Cys Ser Lys Val Ser Ser Arg Phe Leu Ser Asn  
 20 25 30  
 Asn Ile Asn Pro Lys Thr Asn Arg Thr Thr Pro Arg Glu Ile Val Leu  
 35 40 45  
 Ile Pro Asn Pro Gln Thr Met Ser Ala Leu Asn Pro Glu Ile Thr Pro  
 50 55 60  
 Leu Ser Thr Ile Ala Pro Gln Thr Thr Arg Arg Met Pro Thr Thr Asn  
 65 70 75 80  
 Lys Val Ile Pro Arg Ala Arg Asp Leu Leu Ser Leu Gly Ile Thr Asn  
 85 90 95  
 Phe Val Ser Ser Gly Gly Val Gly Asp Thr Cys Arg Ile Ala Gly Ala  
 100 105 110  
 Ala Val Met Ile Glu Tyr Gln Asn His Lys Arg Asn Ile Asp  
 115 120 125  
 <210>1255  
 <211>81  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1255  
 Met Glu Ser Lys Lys Val Ser Lys Leu Ala Ser Asn Ser Thr Phe Phe  
 1 5 10 15  
 Leu Ala Ser Val Ser Cys Leu Gly Ser Thr Val Pro Pro Tyr Arg Ala  
 20 25 30  
 Leu Arg Ser Leu Thr Arg Val Ser Thr Ser Ser Cys Phe Phe Arg Lys  
 35 40 45  
 Asn Phe Val Leu Ala Ser Ser Arg Arg Ser Thr Lys Ser Asp Lys Ser  
 50 55 60  
 Phe Leu Phe Ala Ser Val Asp Ser Phe Glu Leu Ser Ser Arg Ser Phe  
 65 70 75 80  
 Ser  
 <210>1256  
 <211>80  
 <212>PRT  
 <213>Chlamydia pneumoniae  
 <400>1256  
 Leu Leu Gly Met Cys Thr Leu Leu Leu Ile Pro Lys Gln Leu Arg Leu  
 1 5 10 15  
 Leu Ile Leu Thr Lys Cys Leu Ser Ile Thr Leu Ser His Thr Leu Ile  
 20 25 30  
 His Thr Arg Leu Gln Gly Ser Lys Cys Leu Phe Lys Gly Arg Leu Arg  
 35 40 45  
 His Thr Ile Asn Met Pro Ile Lys Ser His Gly Tyr Leu Pro Tyr Val  
 50 55 60  
 Thr Ser Arg Ser His Lys Ala Ile His Asn Leu Thr Ser Arg Phe Leu  
 65 70 75 80  
 <210>1257  
 <211>87  
 <212>PRT  
 <213>Chlamydia pneumoniae



&lt;400&gt;1257

Gly Ser Thr Phe Ala Asn Leu Ser Leu His Leu Leu Tyr Cys Thr Lys  
 1 5 10 15  
 Ala Leu Val Asn Ala Cys Phe Ile Gly Trp Ser Gly Arg Ser Ala Ile  
 20 25 30  
 Arg Ser Ile Ile Ser Ile Ser Ser Thr Arg Gly Arg Val Ser Ser Ile  
 35 40 45  
 Ser Ser His Lys Thr Leu Arg Arg Phe Ala Ala Ser Glu Ser Met Val  
 50 55 60  
 Tyr Ser Ile Ser Ser Val Ala Ser Leu Ser Thr Pro Lys Ala Lys Val  
 65 70 75 80  
 Ser Ala Phe Asp Asn Leu Leu  
 85

&lt;210&gt;1258

&lt;211&gt;81

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1258

Met His Pro His Ser Lys Cys Arg Phe Leu Gly Phe Ser Cys Phe Lys  
 1 5 10 15  
 Lys Leu Ser Ile Ala Gly Thr Asn Val Leu Leu Ile Lys Glu Asp Phe  
 20 25 30  
 Pro Asp Pro Glu Thr Pro Val Thr Pro Ile Ser Arg Ala Asn Gly Arg  
 35 40 45  
 Arg Ile Glu Arg Phe Leu Arg Leu Trp Ile Val Ala Ser Val Ser Lys  
 50 55 60  
 Ser Gln Asp Val Gly Ala Ser Arg Asp Ser Gly Met Gly Met Val Ser  
 65 70 75 80  
 Ser

&lt;210&gt;1259

&lt;211&gt;107

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1259

Met Ile Ala Pro Ser Leu Pro Ala Leu Leu Ala Ile Cys Phe Asn Gly  
 1 5 10 15  
 Ala Val Asn Ala Phe Arg Ile Ile Arg Val Pro Ile Ala Ser Ser Ser  
 20 25 30  
 Phe Ala Ser Ile Gly Arg Lys Ala Ser Ser Val Gly Ile Gln Arg Thr  
 35 40 45  
 Lys Ala Val Pro Pro Pro Gly Arg Ile Pro Ser Ser Thr Ala Ala Met  
 50 55 60  
 Val Ala Cys Cys Ala Ser Ser Thr Leu Ser Phe Phe Ser Phe Ile Ser  
 65 70 75 80  
 Ile Ser Val Ala Ala Pro Thr Arg Ile Thr Ala Thr Pro Pro Glu Ser  
 85 90 95  
 Leu Ala Lys Arg Ser Trp Ser Phe Ser Leu Ser  
 100 105

&lt;210&gt;1260

&lt;211&gt;76

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1260

Leu Pro Pro Ala Leu Gln Val Leu Tyr Met Lys Ser Leu Asp Asn Ala  
 1 5 10 15  
 Asn Leu Glu Ile Leu His Lys Ile Phe Gln Val Gln Val Glu Ala Asn  
 20 25 30  
 Glu Leu Pro Leu Gln Met Leu His Glu Thr Thr Pro Lys Ala Leu Leu  
 35 40 45  
 Gln Gly His Ala Ala Phe Ser Asp Gln Asn Glu Leu Leu Glu Ile Ser  
 50 55 60  
 Tyr Thr Tyr His Lys Leu Thr Ser Tyr Lys Glu Ala  
 65 70 75

&lt;210&gt;1261

&lt;211&gt;76

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1261

```

Met Cys Asn Arg Cys Lys Asp Ser Ser Thr Ser Leu Val Phe Ser Thr
 1             5             10             15
Cys Leu Gly Thr His Lys Thr Glu Thr Pro Ser Phe Ile Asn Phe Cys
             20             25             30
Thr Thr Gly Ser His Phe Pro Ala Ser Leu Leu Cys Ile Glu Pro Arg
             35             40             45
Ile Thr Asn Phe Glu Ser Val Gly Asn Leu Lys Arg Ser Leu Gln Val
             50             55             60
Ser Leu Ser Lys Cys Ser Ala Val Cys Ala Ala Thr
             65             70             75

```

&lt;210&gt;1262

&lt;211&gt;80

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1262

```

Met Leu Asn His Gln Gln His Lys Val Val Ser Ile Ser Gln Phe His
 1             5             10             15
Gln Gln Arg Gln Leu Val His Lys Lys Asn Trp Arg Arg Gly Ser Thr
             20             25             30
Thr His Lys Glu Cys Ala Thr Asp Ala Lys Ile Leu Gln His Pro Trp
             35             40             45
Ser Phe Gln Arg Val Leu Ala Pro Ile Lys Leu Arg Pro Pro Leu Leu
             50             55             60
Leu Ile Ser Ala Leu Gln Glu Ala Ile Phe Leu His His Phe Tyr Ala
             65             70             75             80

```

&lt;210&gt;1263

&lt;211&gt;112

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1263

```

Met Ile Arg Leu Trp Ser Cys Ser Ser Ile Lys Ile Glu Thr Val Pro
 1             5             10             15
Tyr Ser Lys Glu Ile Ala Tyr Cys Arg Trp Tyr Ser Asn Thr Thr Leu
             20             25             30
Ser Tyr Trp Ile Leu Ile Arg Glu Lys Cys Arg Pro Thr Lys Lys Ser
             35             40             45
Ala Ser Ser Arg Phe Leu Thr Lys Asn Asn Asn Ile Val His His Met
             50             55             60
Ser Ser Gln Lys Leu Phe Ala Phe Gln Ala Lys Ile Phe Val Ala Phe
             65             70             75             80
Phe Phe Gln Lys Asn Ile Phe Tyr Gln Phe Phe Phe Phe Arg Met Thr
             85             90             95
Cys Lys Val Lys Arg Ser Ile Phe Gln Glu Glu Phe Cys Arg Pro Ile
             100             105             110

```

&lt;210&gt;1264

&lt;211&gt;148

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1264

```

Ser Gly Arg Ile Ile Ser Val Met Leu Ser Ala Pro Pro Cys Glu Leu
 1             5             10             15
His Ser Asp Leu Ile Asp Pro Asp Leu Phe Glu Phe Asn His Arg Leu
             20             25             30
Asn Ile Cys Ile Ser Ala Glu Val Arg Gly Arg Val Thr Thr His Thr
             35             40             45
Phe Arg Gly Asp Ser Cys Asn Met Ser Phe Asn Cys Ser Val Arg Gly
             50             55             60
Asn Val Ile Thr Ile Pro Arg Ile Ile Arg Ile Glu Ile Arg Ser Leu
             65             70             75             80

```

Thr Ser Ser Phe Ser Ile Ile Thr Lys Cys Lys Arg Ile Ser Ser Arg  
                     85                    90                    95  
 Leu Arg Ile Thr Asn Ile Ile Ala Tyr Trp Ser Leu Arg Tyr Val Cys  
                     100                    105                    110  
 Leu Arg Ile Asp Ile Lys Thr Val Arg Glu Cys Ser Ser Ile Lys Leu  
                     115                    120                    125  
 Arg Thr Phe Arg Arg His Ile Thr Leu His Asn Lys Phe Thr Trp Arg  
                     130                    135                    140

Ser Arg Gly Ile

145

<210>1265

<211>130

<212>PRT

<213>Chlamydia pneumoniae

<400>1265

Ser Phe Phe Ser Phe Arg Lys Val Pro Asn Phe Ser Asn Gln Pro Met  
   1                    5                    10                    15  
 Cys Phe Leu Ile Arg Ser Cys Trp Ser Ala Ser Ile Asn Ala Trp Arg  
                     20                    25                    30  
 Gly Asp Arg Phe Cys Asp Ser Ser Leu Ser Asn His Asp His Met Val  
                     35                    40                    45  
 Cys Asn Arg Asn Met Pro Ser Asn Ser Gly Leu Pro Ser Asn Asp Asp  
                     50                    55                    60  
 Met Phe Thr Asn Phe Cys Arg Thr Cys Asn Ala Cys Leu Gly Asn Asn  
                     65                    70                    75                    80  
 Asn Thr Met Leu Ser Asn Phe Tyr Val Met Ser Tyr Leu Tyr Leu Val  
                     85                    90                    95  
 Ile Tyr Phe Ser Ser Phe Met Asp His Gly Val Leu Glu Ser Thr Thr  
                     100                    105                    110  
 Ile Tyr Arg Ser Val Gly Ser Asp Phe Tyr Ile Ile Thr Tyr Asn His  
                     115                    120                    125

Ile Ala

130

<210>1266

<211>78

<212>PRT

<213>Chlamydia pneumoniae

<400>1266

Glu Ala Val Phe Val Ser Gly Lys Lys Asp Gly Val Arg Gly Met Ile  
   1                    5                    10                    15  
 Phe Val Pro Leu Ser Ile Leu Val Leu Ile Phe Leu Pro Leu Pro Gln  
                     20                    25                    30  
 Ile Leu Leu Asp Phe Gly Leu Cys Ile Ser Phe Ala Leu Ser Leu Leu  
                     35                    40                    45  
 Thr Val Cys Trp Val Phe Thr Leu Asn Ser Ser Asn Ser Ala Lys Phe  
                     50                    55                    60  
 Phe Leu His Phe Ser Tyr Ile Phe Ala Tyr Cys Gly Trp Asp  
                     65                    70                    75

<210>1267

<211>74

<212>PRT

<213>Chlamydia pneumoniae

<400>1267

Leu Cys Thr Asp Ser Thr Ser Ile Ser Cys Cys Ser Ile Ile Ile Glu  
   1                    5                    10                    15  
 Gly Cys Asn Ser Trp Val Val Phe Tyr Arg Thr Thr Asn Ala Ile Asp  
                     20                    25                    30  
 Ser Pro Ser Arg Gly Met Val Ser Arg Asp Val Arg Phe His Gly Lys  
                     35                    40                    45  
 Ile Ile Val Glu Asp His Arg Thr Gly Ile Leu Cys Lys Asn Ala Leu  
                     50                    55                    60  
 Leu Met Tyr Ser Tyr Cys Thr Thr Gln Thr  
                     65                    70

<210>1268

&lt;211&gt;90

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1268

```

Met Gly Ala Glu Ile Glu Ile Ser Gly Val Leu Asp Ser Glu Leu Ser
 1           5           10           15
Leu Val Leu Ala Pro Cys Leu Cys Ala His Pro Thr Lys Ala Phe Ile
           20           25           30
Asn Gly Glu Ser Ser Arg Gly Leu Pro Phe Leu Arg Gly Thr Ser Cys
           35           40           45
Gly Glu Pro Val Leu Ser Val Ser Ser Ile Ser Glu Gly Asp Pro Thr
           50           55           60
Asp Ile Glu Ser Ser Ser Glu Glu Val His Ser Ser Pro Arg His Val
           65           70           75           80
Gln Gln Arg Pro Thr Ala Ser Ala Ala Ala
           85           90

```

&lt;210&gt;1269

&lt;211&gt;184

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1269

```

Phe Phe Val Phe Thr His Val Trp Tyr Leu Ile Ser Arg Gly Tyr Phe
 1           5           10           15
Tyr Ser Leu Phe Ser Leu Gly Val Gly Ala Leu Ala Thr Leu Thr Leu
           20           25           30
Ala Thr Arg Ile Gly Arg Ser Pro Ile Leu Tyr Pro Phe Ala Asn Ser
           35           40           45
Ser Lys Ile Val Pro Ser Gly Thr Ser Glu Val Ser Ser Val Cys Thr
           50           55           60
Ala Ser Cys Arg Lys Gly Leu Asn Phe Trp Pro Ile Glu Glu Tyr Ser
           65           70           75           80
Ile Ile Pro Phe Ser Ser Lys Ile Cys Leu Asn Trp Leu Arg Ile Met
           85           90           95
Leu Asn Pro Arg Ala Gln Phe Phe Thr Ser Ser Asp Ile Cys Val Ala
           100           105           110
Asn Pro Arg Ala Phe Ser Met Leu Ser Met Gly Leu Arg Lys Ser Ile
           115           120           125
Lys Val Phe Ser Lys Ala Tyr Cys Ile Ser Ser Trp Arg Ser Phe Cys
           130           135           140
Lys Arg Phe Leu Glu Phe Ser Asp Ser Ala Arg Ala Met Arg Tyr Leu
           145           150           155           160
Ser Phe Phe Ser Phe Asn Ser Val Phe Arg Val Thr Ile Ser Cys Cys
           165           170           175
Lys Cys Ser Thr Ser Phe Ser Phe
           180

```

&lt;210&gt;1270

&lt;211&gt;98

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1270

```

Leu Ile Ser Val Glu Glu Thr Pro Glu Ser Ser Ile Phe Ala Phe Ser
 1           5           10           15
Ala Ala Ser Leu Ser Leu Cys Lys Ala Ile Leu Ser Leu Leu Arg Ser
           20           25           30
Met Pro Ser Cys Phe Leu Asn Ser Ser Ile Ile His Leu Ile Met Thr
           35           40           45
Ser Ser Lys Ser Ser Pro Pro Arg Arg Val Ser Pro Phe Val Asp Arg
           50           55           60
Thr Ser Lys Thr Pro Ser Pro Ile Ser Arg Met Glu Ile Ser Lys Val
           65           70           75           80
Pro Pro Pro Arg Ser Lys Thr Ala Ile Phe Leu Ser Pro Thr Leu Ser
           85           90           95
Ile Pro

```

&lt;210&gt;1271

&lt;211&gt;78

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1271

Phe Leu Lys Thr Met Thr Lys Gly Phe Ala Phe Cys Ser Ala Ser Phe  
 1 5 10 15  
 Pro Ile Ala Ile Ile Glu Asn Val Val Ser Lys Ser Val Glu Gly Val  
 20 25 30  
 Ser His Pro Glu Gly Glu Asn Ala Asn Pro Ser Leu Leu Ser Leu Val  
 35 40 45  
 Met Ala Ser Trp Thr Leu Gly Gly Thr Ser Thr Ser Ser Leu Asn Lys  
 50 55 60  
 Ala Leu Ala Lys Val Leu Ile Ser Ser Gly Asp Val Phe Pro  
 65 70 75

&lt;210&gt;1272

&lt;211&gt;122

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1272

Met Thr Thr Gly Ser Cys Ser Pro Ser Lys Ala Leu Phe Val Cys Ile  
 1 5 10 15  
 Asn Cys Ile Ala Phe Ile Glu Met Ser Thr Asn Thr Thr Glu Ala Ala  
 20 25 30  
 Pro Arg Leu Arg Ala Ser Lys Pro Ile Ala Pro Ile Pro Ala Lys Arg  
 35 40 45  
 Ser Lys Lys Ala Ala Pro Ser Ile Ser Ser Leu Gln Ile Leu Lys Asn  
 50 55 60  
 Ala Ser Phe Thr Lys Pro Glu Val Gly Arg Ile Cys Gly Leu Glu Asn  
 65 70 75 80  
 Val Phe Lys Asp Phe Pro Leu Tyr Leu Pro Ala Lys Ile Leu Thr Ser  
 85 90 95  
 Pro Leu Glu Glu Gln Ser Leu Arg Asn Gln Gln Pro Leu Val Cys Ser  
 100 105 110  
 Gly Ser Leu Gly Tyr Tyr Arg Ile His Leu  
 115 120

&lt;210&gt;1273

&lt;211&gt;112

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1273

Phe Thr Phe Phe Phe Leu Ala Gln Leu Glu Lys Gln Leu Pro His Leu  
 1 5 10 15  
 Val Leu Phe Phe Phe Phe Ser Ala Thr Ser Ser Leu Arg Ala Ser Phe  
 20 25 30  
 Ile His Ser Ser Leu Trp Ser Arg Val Phe Ser Ser Ser Phe Leu Arg  
 35 40 45  
 Phe Ala Lys Phe Thr Ser Ala Phe Ser Ser Ser Leu Glu Ala Ala Ser  
 50 55 60  
 Thr Thr Ser Phe Cys Leu Leu Thr Phe Ser Ser Ser Ser Glu Ser Cys  
 65 70 75 80  
 Thr Ala Thr Thr Leu Met Tyr Asp Phe Ile Cys Lys Thr Ala Ser Leu  
 85 90 95  
 Val Val Pro Ser Ser Asn Lys Ser Arg Ser Cys Trp Ile Phe Cys Ile  
 100 105 110

&lt;210&gt;1274

&lt;211&gt;82

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1274

Leu Ser Ala Lys Leu Met Lys Thr Ser Leu Gly Val Cys Val Gly Ile  
 1 5 10 15  
 Ala Gly Ile Ser Lys Gly Arg Cys Leu Ile Asn Ala Lys Ser Pro Phe  
 20 25 30

Ser Leu Lys Ile Ser Glu Arg Ser Glu Arg Glu Arg Val Trp Arg Ser  
                   35                  40                  45  
 Tyr Val Tyr Ser Val Asp Val Gly Pro Gly Val Phe Leu Met Met Thr  
           50                  55                  60  
 Ser Lys Arg Glu Arg Leu Phe Pro Arg Arg Ile Ala Val Thr Thr Pro  
       65                  70                  75                  80  
 Glu Thr

&lt;210&gt;1275

&lt;211&gt;134

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1275

Met Asn Ser Pro Thr Ile Lys Asp Pro Ser Leu Glu Thr Ala Cys Ala  
   1                  5                  10                  15  
 Asp Asp Leu Leu Ala Pro Gly Ile Leu Glu Ser Arg Cys Cys Ser Pro  
           20                  25                  30  
 Ser Phe Gln Tyr Thr Ala Leu Ala Ile Ser Ser Leu Pro Met Ala Ser  
           35                  40                  45  
 Pro Thr Ile Thr Glu Pro Ser Ser Glu Ala Ser Gln Ala Gln Glu Cys  
           50                  55                  60  
 Arg Ser Ser Gly Lys Leu Gly Arg Thr Thr Ile Pro Val Ser Ser His  
       65                  70                  75                  80  
 Phe Thr Ala Lys Phe Val Ser Val Ser Ser Leu Tyr Arg His Pro Thr  
                   85                  90                  95  
 Ile Val Phe Pro Ser Leu Glu Thr Pro Ser Ala Lys Asp Cys Ile Pro  
           100                  105                  110  
 Ser Glu Asn Ile Pro Arg Ser Thr Ser Ala Pro Phe Thr His Phe Thr  
           115                  120                  125  
 Ala Arg Gln Asp Gly Ser  
           130

&lt;210&gt;1276

&lt;211&gt;84

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1276

Met Arg Ser Trp Thr Arg Trp Thr Arg Cys Gly Ser Cys Cys Arg Cys  
   1                  5                  10                  15  
 Ser Gly Ser Trp Arg Cys Ser Arg Ser Cys Cys Arg Asn His Gly Ser  
           20                  25                  30  
 Asn Thr Asn Tyr Ser Ser Ser Cys Cys Pro Ser Gly Glu Thr Ser Cys  
           35                  40                  45  
 Tyr His Ser Cys Gln Thr Ser Asp His Arg Gly Tyr Lys Ser Gly Cys  
           50                  55                  60  
 Gln Ile Trp Asn Lys Ser Ile Tyr Gln Asn Phe Ser Gln Ser Asp Cys  
       65                  70                  75                  80  
 Gln Ser His Phe

&lt;210&gt;1277

&lt;211&gt;76

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1277

Met Arg Glu Phe Ser Cys Ile Lys Asp Arg Lys Asn Arg Cys Phe Arg  
   1                  5                  10                  15  
 Ala Ala Ala Val Lys Ile Met Cys Thr Pro Ser Arg Ser Ser Ala Arg  
           20                  25                  30  
 Thr Thr Arg Pro Lys Glu Val Lys Arg Thr Ser Leu Glu Tyr Ile  
           35                  40                  45  
 Gln Ser Ile Trp Asp Leu Gly Pro Leu Asp Val Tyr Ser Cys Phe Ser  
           50                  55                  60  
 Lys Glu Thr Ser Ser Glu Leu Tyr Ala Lys Arg Phe  
       65                  70                  75  
 <210>1278

&lt;211&gt;78

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1278

```

Met Met Ile Val Arg Cys Cys Phe Arg Ala Leu Leu Cys Phe Ser Met
 1             5             10             15
Cys Ser Arg Thr Ser Arg Pro Arg Ser Pro Ile Lys Ala Ile Thr Leu
             20             25             30
Ile Val Asp Phe Asp Pro Lys Ala Ile Ala Glu Ser Ser Glu Asp Phe
             35             40             45
Pro Leu Pro Gly Ser Glu Lys Thr Pro Ile Arg Cys Pro Phe Pro Lys
             50             55             60
Val Arg Asn Ala Ser Ile Ala Leu Ile Pro Val Gly Lys Ile
             65             70             75

```

&lt;210&gt;1279

&lt;211&gt;86

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1279

```

Met Arg Arg Ile Phe Pro Thr Ser Ile Leu Leu Ile Ala Thr Phe Cys
 1             5             10             15
Lys Leu Pro Ser Ser Lys Thr Ser Gln Pro Val Val Gly Ala Ser Cys
             20             25             30
Phe Lys Glu Thr Lys Val Leu Phe Ala Phe Pro Asp Thr Ile Cys Pro
             35             40             45
Asn Ala Ser Glu Ile Ala Asn Lys Thr Arg Ser Lys Ala Pro Ser Lys
             50             55             60
Ala Pro Pro Ile Lys Ile Glu Pro Lys Gly Ala Asp Val Ile Lys Ile
             65             70             75             80
Ser Met Phe Thr Thr Phe
                        85

```

&lt;210&gt;1280

&lt;211&gt;124

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1280

```

Val Lys Gly Val Leu Lys Arg Gln Arg Leu Ser Leu Thr Met Gly Gly
 1             5             10             15
Arg Ser Lys Leu Lys Arg Arg Ser Trp Leu Lys Ala Ala Gln Thr Thr
             20             25             30
Pro Val Val Cys Trp Arg Arg Asn Val Ile Phe Ser Thr Val Ile Phe
             35             40             45
Ser Pro Ala Ile Ile Arg Ser Pro Ser Ser Ser Leu Glu Ala Ser Ser
             50             55             60
Thr Thr Ile Thr Asn Phe Pro Ala Leu Lys Ser Ser Ile Ala Arg Ser
             65             70             75             80
Lys Glu Thr Lys Phe Ala Glu Pro Thr Ser Ser Arg Val Ser Ile Ile
             85             90             95
Asp Ser Leu Ala Leu Thr Asp Ser Asp Ala Lys His Ala Thr Leu Lys
             100             105             110
Ile Leu Ser Phe Gln Phe Leu Met Gly Ser Lys Thr
             115             120

```

&lt;210&gt;1281

&lt;211&gt;85

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1281

```

Ile Gln Arg Thr Leu Cys Leu Leu Phe Phe Lys Lys Phe Ile Leu Leu
 1             5             10             15
Ile Leu Val Arg Thr Leu Arg Phe Pro Ile Leu Thr Phe Leu Ser Trp
             20             25             30
Leu Asn Phe Arg Leu Lys Leu Ile Phe Ser Leu Ile Leu Tyr Gly Leu
             35             40             45
Ala Asn Val Ala Gln Leu Val Arg Ala Ser Asp Cys Gly Ser Glu Gly

```

50                      55                      60  
 Arg Gly Phe Lys Pro Arg Arg Ser Pro Ser Leu Ser Ser Leu Phe Leu  
 65                      70                      75                      80  
 Leu Phe Phe Leu Ile  
                                  85

&lt;210&gt;1282

&lt;211&gt;112

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1282

Val Leu Tyr Asn Pro Lys Ala Phe Ile Thr His Ala Ala Ser Leu Arg  
 1                      5                      10                      15  
 Gln Thr Phe Val His Cys Glu Arg Phe Ser Thr Ala Ala Ser Arg Arg  
                          20                      25                      30  
 Ser Leu Gly Ser Val Ser Val Pro Val Leu Ala Val Asn Leu Ser Ile  
                          35                      40                      45  
 Arg Leu Asp Val Ile Ala Leu Val Gly Phe Tyr Pro Thr Asn Lys Leu  
                          50                      55                      60  
 Ile Ser His Lys Leu Phe Leu Asn Arg Lys Val Arg Arg Ser Pro Ser  
 65                      70                      75                      80  
 Leu Ile Tyr Ile Arg Cys Leu Ile Thr Leu His Ser Val Leu Ala Ile  
                                  85                      90                      95  
 Val Ser Asn Arg Tyr Pro Gln Val Glu Gly Arg Leu Ser Met Tyr Tyr  
                          100                      105                      110

&lt;210&gt;1283

&lt;211&gt;77

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1283

Leu Glu Ser Gly Leu Pro Arg Phe Arg Leu Gly Phe Thr Cys Leu Ala  
 1                      5                      10                      15  
 Leu Leu Arg Tyr Arg Leu Ala Ser Phe Val Phe Ser Phe Thr Gly Leu  
                          20                      25                      30  
 Ser Pro Cys Ile Val Gln Leu Ser Arg Ser Ile Gln Leu Lys Leu Lys  
                          35                      40                      45  
 Ile Pro Cys Tyr Arg Pro Tyr Asn Pro Ile Leu Lys Ile Trp Phe Arg  
                          50                      55                      60  
 Leu Phe Pro Phe Arg Ser Pro Leu His Arg Glu Ser Leu  
 65                      70                      75

&lt;210&gt;1284

&lt;211&gt;85

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1284

Met Ile Tyr Gln Asn Gly Ile Gly Val Trp Asn Ile Asn Pro Val Phe  
 1                      5                      10                      15  
 Tyr Gln Cys Ser Ser Asn Glu Asp Val Gly Phe Leu Ile Phe Glu Phe  
                          20                      25                      30  
 Arg Lys Asp Ile Arg Glu Val Leu Ser Ser His Leu Thr Met Ser Tyr  
                          35                      40                      45  
 Ala Asn Thr Ser Leu Arg Asn Gln Ile Ala Asn Gly Leu Ser Lys Ser  
                          50                      55                      60  
 Ile Asp Ala Leu Asn Pro Ile Met Asn Asp Ile Gly Leu Ser Ser Ser  
 65                      70                      75                      80  
 Lys Glu Leu Val Pro  
                                  85

&lt;210&gt;1285

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1285

Val Lys Leu Lys Leu Phe Ser Val Ile Ala Cys Ile Thr Phe Gln Lys  
 1                      5                      10                      15  
 Arg Asp Thr Leu Cys Ser Ile Tyr Thr Ile Gly Asp Phe Leu Gln Ile



20 25 30  
 Gln Ser Ile Asp Ser Ile Trp Val Met Asp Gln Asn Asn Leu Phe Phe  
 35 40 45  
 Tyr Lys Pro Trp Lys Lys Gly Lys Ser His Lys Asn Asn Cys Ile Leu  
 50 55 60  
 Gln Gly Phe Leu Gly Ile Asn Gly Phe Cys Leu His Glu Glu Ser Leu  
 65 70 75 80  
 Ser Cys Pro Arg Cys Ala Arg Thr Tyr His Trp Ile Phe Arg  
 85 90

&lt;210&gt;1286

&lt;211&gt;74

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1286

Met Gln Gln Ser Val Arg Lys Leu Phe Gly Thr Asp Gly Val Arg Gly  
 1 5 10 15  
 Arg Ala Asn Phe Glu Pro Met Thr Val Glu Thr Thr Val Leu Leu Gly  
 20 25 30  
 Lys Ala Val Ala Arg Val Leu Arg Glu Gly Arg Ser Gly Lys His Arg  
 35 40 45  
 Val Val Val Gly Lys Asp Thr Arg Leu Ser Gly Tyr Met Phe Glu Asn  
 50 55 60  
 Ala Leu Ile Ala Gly Ser Ile Leu Trp Gly  
 65 70

&lt;210&gt;1287

&lt;211&gt;88

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1287

Val His Phe Ser Asn Ser Ser Pro Phe Asn Val Trp Thr Leu Trp Leu  
 1 5 10 15  
 Ala Ala Cys Cys Thr Leu Ile Ala Arg Asn His Asn Thr Leu Ile Asn  
 20 25 30  
 Phe Gln Ile Leu Ile Leu Ser Trp Leu Leu Ile Thr Leu Ala Thr Phe  
 35 40 45  
 Ser Leu Gln Ile Phe Cys Lys Gly Asn Lys Val Leu Leu Ala Thr Gln  
 50 55 60  
 Thr Val Leu Gly Leu Phe Val Thr Ile Val Gly Thr Gln Leu Leu Val  
 65 70 75 80  
 Ser Gly Leu Gln Gln Ala Phe Leu  
 85

&lt;210&gt;1288

&lt;211&gt;119

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1288

Met Phe Arg Arg Lys Leu Ser Ile Leu Phe Gln Leu Ser Leu Thr Ser  
 1 5 10 15  
 Ser Met Val Arg Val Thr Ser Ser Cys Leu Ile Leu Lys Thr Ser Phe  
 20 25 30  
 Leu Tyr Ser Ala Thr Ala Arg Thr Ala Leu Ser Asp Asn Ser Cys Thr  
 35 40 45  
 Leu Glu Ala Ala Ser Val Ser Cys Asp Arg Glu Val Lys Thr Phe Pro  
 50 55 60  
 Ile Pro Leu Lys Lys Val Phe Ala Val Ala Ser Leu Asn Leu Pro Glu  
 65 70 75 80  
 Ile Leu Trp Thr Asn Pro Lys Met Leu Ser Pro Glu Ile Ser Pro Thr  
 85 90 95  
 Ile Gly Ala Ile Ala Pro Lys Ile Pro Asn Val Ala Val Ala Ile Pro  
 100 105 110  
 Ser Gln Arg Ala Tyr Leu Ala  
 115

&lt;210&gt;1289

&lt;211&gt;126

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1289

```

Met Val Ile Ile Phe Arg Leu Ser Ser Ser Leu Phe Ile Gly Arg Cys
 1           5           10           15
Phe Ser Ser Gln Ser Gln Asn Phe Ser Phe Ser Lys His Leu Ile Thr
           20           25           30
Arg Glu Ile Ser Pro Ala Lys Lys Pro Ala Lys Ala Lys Ile Pro Pro
           35           40           45
Pro Leu Lys Ile Ala Thr Met Pro Ile Pro Ile Glu Thr Asn Gly Ala
           50           55           60
Ser Gln Pro Ile Met Ser Glu Arg Asp Pro His Asn Leu Ser Arg Phe
           65           70           75           80
Ser Phe Ser Met Leu Thr Leu Ile Val Ser Ile Leu Phe Ser Cys Arg
           85           90           95
Ala Ser Ser Ser Arg Cys Val Asp Ser Thr Glu Ser Leu Trp His Pro
           100          105          110
Tyr Glu Glu Lys Ser Glu Arg Ile Pro Cys Phe Val Ser Arg
           115          120          125

```

&lt;210&gt;1290

&lt;211&gt;94

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1290

```

Arg Asp Tyr Val Gly His Pro Met Gly Ile Tyr Arg Asn Arg Arg Cys
 1           5           10           15
Arg Gly Asp Val Trp Thr Ser Lys Lys Ser Ser Leu Cys Arg Ala Ser
           20           25           30
Tyr Ser Leu Arg Ile Phe Arg Leu Pro Asn Asn Leu His Leu Ile Phe
           35           40           45
Phe Ile Thr Phe Trp Leu Ala Leu Pro Thr Ser Thr Ser Glu His Pro
           50           55           60
Gln Ser Leu Tyr Ser Trp Cys Pro Arg His Pro Arg Arg Glu Met Gly
           65           70           75           80
Arg Ser Ala His Glu Cys Arg Pro Asp Tyr Cys Cys Phe Ile
           85           90

```

&lt;210&gt;1291

&lt;211&gt;98

&lt;212&gt;PRT

&lt;213&gt;Chlamydia pneumoniae

&lt;400&gt;1291

```

Met Gly Phe Cys Asn Phe Val Ile Tyr Pro Cys Arg Glu Glu Phe Asn
 1           5           10           15
Ile Phe Cys Cys Pro Ser Ala Asn Lys Leu Ser Ile Phe Ile Phe Thr
           20           25           30
Pro Ala Asn Ala Asp Ser Gly Gly Asp Arg Met Gly Ser Val Arg Glu
           35           40           45
Ser Ser Thr Thr Thr Arg His Asp Tyr Phe Lys Asp Ser Ala Val Phe
           50           55           60
Glu Arg Phe Tyr Thr Gly Ile Tyr Arg Asn Asp Ile Pro Lys Glu Leu
           65           70           75           80
Phe Arg Lys Tyr Arg Cys Ile Arg Asp Asp Ile Lys Ile Phe Asp Phe
           85           90           95
Cys Leu

```

&lt;210&gt;1292

&lt;211&gt;20

&lt;212&gt;DNA

&lt;400&gt;1292

tgaccacttg gttgtaggga 20

&lt;210&gt;1293

&lt;211&gt;20

&lt;212&gt;DNA

&lt;400&gt;1293

ggagttctcc tttggagtta 20  
<210>1294  
<211>20  
<212>DNA  
<400>1294  
cgcttagtcc atcggtttt 20  
<210>1295  
<211>20  
<212>DNA  
<400>1295  
cgaacacctg aacttgctct 20  
<210>1296  
<211>20  
<212>DNA  
<400>1296  
tctgagagcg ttgaagcaga 20  
<210>1297  
<211>20  
<212>DNA  
<400>1297  
taggagcata gaccgcaagc 20  
<210>1298  
<211>20  
<212>DNA  
<400>1298  
ggaaggattc actgcacgta 20  
<210>1299  
<211>20  
<212>DNA  
<400>1299  
ggctcactccg agcgtcgtca 20  
<210>1300  
<211>20  
<212>DNA  
<400>1300  
gcatgcagga catctaccta 20  
<210>1301  
<211>20  
<212>DNA  
<400>1301  
ccacgaatct cttggggaaa 20  
<210>1302  
<211>20  
<212>DNA  
<400>1302  
ggctcggatc gttgttttct 20  
<210>1303  
<211>20  
<212>DNA  
<400>1303  
ctgaaacccc gatcataggt 20  
<210>1304  
<211>20  
<212>DNA  
<400>1304  
gcgggttatt tcttattgga 20  
<210>1305  
<211>20  
<212>DNA  
<400>1305  
cttgggttgg atggagatag 20  
<210>1306  
<211>20  
<212>DNA

<400>1306  
 gtggagtcgt agaagtgcaa 20  
 <210>1307  
 <211>20  
 <212>DNA  
 <400>1307  
 ggggaagaaa tgccgcaaaa 20  
 <210>1308  
 <211>20  
 <212>DNA  
 <400>1308  
 ccaagaagca cagggtttac 20  
 <210>1309  
 <211>20  
 <212>DNA  
 <400>1309  
 catgggtctg ttcgcattca 20  
 <210>1310  
 <211>20  
 <212>DNA  
 <400>1310  
 cactctgccca ctcttccgta 20  
 <210>1311  
 <211>20  
 <212>DNA  
 <400>1311  
 cagacgcagc accaaagaaa 20  
 <210>1312  
 <211>20  
 <212>DNA  
 <400>1312  
 cgcttttctc ctaagtgatg 20  
 <210>1313  
 <211>20  
 <212>DNA  
 <400>1313  
 ggggcatgaa ctttttaggc 20  
 <210>1314  
 <211>20  
 <212>DNA  
 <400>1314  
 ctgaagagct tatccaggag 20  
 <210>1315  
 <211>20  
 <212>DNA  
 <400>1315  
 catgagcgga gatttaggtt 20  
 <210>1316  
 <211>20  
 <212>DNA  
 <400>1316  
 cccgcgtttg aaataggaga 20  
 <210>1317  
 <211>20  
 <212>DNA  
 <400>1317  
 agtcccacgt tcaatgcaca 20  
 <210>1318  
 <211>20  
 <212>DNA  
 <400>1318  
 gggctagaat tttctgtcac 20  
 <210>1319  
 <211>20

```

<212>DNA
<400>1319
aagaaagcta cggcagtgcg      20
<210>1320
<211>20
<212>DNA
<400>1320
ggacgagctt accgtttttg      20
<210>1321
<211>20
<212>DNA
<400>1321
gaccttgcca gaacttcctt      20
<210>1322
<211>20
<212>DNA
<400>1322
gagcgcttcg aagaggttcc      20
<210>1323
<211>20
<212>DNA
<400>1323
gggaccatac tcttttctgg      20
<210>1324
<211>20
<212>DNA
<400>1324
cccaatctcg tttggctgat      20
<210>1325
<211>20
<212>DNA
<400>1325
ggtcacgggc tagaagagaa      20
<210>1326
<211>20
<212>DNA
<400>1326
cgagcggatc gattaaagag      20
<210>1327
<211>20
<212>DNA
<400>1327
ccaactgttc aagggacgac      20
<210>1328
<211>20
<212>DNA
<400>1328
cgagtcaaag gcttctaacc      20
<210>1329
<211>20
<212>DNA
<400>1329
cctaagtacg aagatcgagg      20
<210>1330
<211>20
<212>DNA
<400>1330
gagcggatcc aagagtttga      20
<210>1331
<211>20
<212>DNA
<400>1331
gggtcgattt cttctccatc      20
<210>1332

```

```

<211>20
<212>DNA
<400>1332
cagcgaagtgt cagcatttga      20
<210>1333
<211>20
<212>DNA
<400>1333
caggaagtgt tcgcatgttt      20
<210>1334
<211>20
<212>DNA
<400>1334
cgtgatctta ggcaactctt      20
<210>1335
<211>20
<212>DNA
<400>1335
gtgcgtagc gaaaacaacc      20
<210>1336
<211>20
<212>DNA
<400>1336
gcacagtaga tcctaagcag      20
<210>1337
<211>20
<212>DNA
<400>1337
caactgcgag agcggatcca      20
<210>1338
<211>20
<212>DNA
<400>1338
cctcttagct gaggatcttc      20
<210>1339
<211>20
<212>DNA
<400>1339
gttactttct ggagaaaggc      20
<210>1340
<211>20
<212>DNA
<400>1340
gctgcagctg gagatctaaa      20
<210>1341
<211>20
<212>DNA
<400>1341
cgacagtga cgttggaatc      20
<210>1342
<211>20
<212>DNA
<400>1342
ctgcgcaagg acatacgata      20
<210>1343
<211>20
<212>DNA
<400>1343
ggtggactag tcagatagaa      20
<210>1344
<211>20
<212>DNA
<400>1344
cgatgctatt tttccatggc      20

```

```

<210>1345
<211>20
<212>DNA
<400>1345
ggaggtgcta tcgcgattgc      20
<210>1346
<211>20
<212>DNA
<400>1346
gaacaggcac agcaatcaca      20
<210>1347
<211>20
<212>DNA
<400>1347
cggtttctct caggatgcaa      20
<210>1348
<211>20
<212>DNA
<400>1348
gtatcggctc tttagtcacct      20
<210>1349
<211>20
<212>DNA
<400>1349
cctagtagag gttgagtga      20
<210>1350
<211>20
<212>DNA
<400>1350
agctccatac atcgaaggga      20
<210>1351
<211>20
<212>DNA
<400>1351
tcgaactggc ttccggagga      20
<210>1352
<211>20
<212>DNA
<400>1352
ctgcagatct cggcaatatc      20
<210>1353
<211>20
<212>DNA
<400>1353
cggaggaact ctctattacc      20
<210>1354
<211>20
<212>DNA
<400>1354
gccctctctt tgtcttgctt      20
<210>1355
<211>20
<212>DNA
<400>1355
gaggggcaat tgcgattcta      20
<210>1356
<211>20
<212>DNA
<400>1356
cgtatcaatg aggtcagtgc      20
<210>1357
<211>20
<212>DNA
<400>1357

```

gcgggttcctg tagggataaa	20
<210>1358	
<211>20	
<212>DNA	
<400>1358	
gctcttcact caaggagggg	20
<210>1359	
<211>20	
<212>DNA	
<400>1359	
gttaagggaa gctggggaaa	20
<210>1360	
<211>20	
<212>DNA	
<400>1360	
gagacctcac ctggatctat	20
<210>1361	
<211>20	
<212>DNA	
<400>1361	
ggggaatcag gtcactaaa	20
<210>1362	
<211>20	
<212>DNA	
<400>1362	
caggctttga cccacagtat	20
<210>1363	
<211>20	
<212>DNA	
<400>1363	
gacacaggag gttcattctc	20
<210>1364	
<211>20	
<212>DNA	
<400>1364	
tctgctcttc aagacctcgg	20
<210>1365	
<211>20	
<212>DNA	
<400>1365	
gaaggtaacg aacggctcta	20
<210>1366	
<211>20	
<212>DNA	
<400>1366	
gcggatctga ggagtggatg	20
<210>1367	
<211>20	
<212>DNA	
<400>1367	
cggaggtaga gatatatccc	20
<210>1368	
<211>20	
<212>DNA	
<400>1368	
ggcgaatgta gctcagaaac	20
<210>1369	
<211>20	
<212>DNA	
<400>1369	
ggatggggtc tttgggttttc	20
<210>1370	
<211>20	
<212>DNA	



<400>1370  
cctctgtcgt gagagacaaa 20  
<210>1371  
<211>20  
<212>DNA  
<400>1371  
tcgggttggtg gagagcaacc 20  
<210>1372  
<211>20  
<212>DNA  
<400>1372  
cgcaggatcc ccactttttt 20  
<210>1373  
<211>20  
<212>DNA  
<400>1373  
caaacgtcat aagcgccaca 20  
<210>1374  
<211>20  
<212>DNA  
<400>1374  
gtatggcatt cgatgtcacg 20  
<210>1375  
<211>20  
<212>DNA  
<400>1375  
gacctgcagt atagtctacc 20  
<210>1376  
<211>20  
<212>DNA  
<400>1376  
aggagcgagg ttaccacgtt 20  
<210>1377  
<211>20  
<212>DNA  
<400>1377  
cccaatccat tgttcccgat 20  
<210>1378  
<211>20  
<212>DNA  
<400>1378  
ccttgattgc gtgttcgtgt 20  
<210>1379  
<211>20  
<212>DNA  
<400>1379  
aagagctttg ccctgttctc 20  
<210>1380  
<211>20  
<212>DNA  
<400>1380  
gcttgtttga tcggttgagg 20  
<210>1381  
<211>20  
<212>DNA  
<400>1381  
gctttaggaa ggctagcttc 20  
<210>1382  
<211>20  
<212>DNA  
<400>1382  
gatagatcaa cacgtacgtc 20  
<210>1383  
<211>20

<212>DNA  
<400>1383  
ggtggaggag atgaagaatc 20  
<210>1384  
<211>20  
<212>DNA  
<400>1384  
gggtaaaaag agggagcgat 20  
<210>1385  
<211>20  
<212>DNA  
<400>1385  
ccctaagtag gtctgcagat 20  
<210>1386  
<211>20  
<212>DNA  
<400>1386  
cccgttcctc gcctgaaata 20  
<210>1387  
<211>20  
<212>DNA  
<400>1387  
ctccatgata actcgcacca 20  
<210>1388  
<211>20  
<212>DNA  
<400>1388  
ctccagaaac tcctgtgatg 20  
<210>1389  
<211>20  
<212>DNA  
<400>1389  
ggtatatattcc gccgaagaag 20  
<210>1390  
<211>20  
<212>DNA  
<400>1390  
gacgcatgta cttctataag 20  
<210>1391  
<211>20  
<212>DNA  
<400>1391  
gagacgactt cgctaaaacc 20  
<210>1392  
<211>20  
<212>DNA  
<400>1392  
ggtaatgcat gcccagtgtt 20  
<210>1393  
<211>20  
<212>DNA  
<400>1393  
tggtgaagga gcttgaccaa 20  
<210>1394  
<211>20  
<212>DNA  
<400>1394  
gttcatggga aaggctcgtgg 20  
<210>1395  
<211>20  
<212>DNA  
<400>1395  
cgggtccagat cttggaattg 20  
<210>1396

<211>20  
<212>DNA  
<400>1396  
gaccttgcca gcttgggtcg 20  
<210>1397  
<211>20  
<212>DNA  
<400>1397  
gctgctaaat cccatcgctt 20  
<210>1398  
<211>20  
<212>DNA  
<400>1398  
gttttgtggc tttggcagtg 20  
<210>1399  
<211>20  
<212>DNA  
<400>1399  
actttcctaa gaagcgtagc 20  
<210>1400  
<211>20  
<212>DNA  
<400>1400  
gaggaatggc gcaggagtta 20  
<210>1401  
<211>20  
<212>DNA  
<400>1401  
gcagtgaaaa cggaatccag 20  
<210>1402  
<211>20  
<212>DNA  
<400>1402  
gcgtggggat tgtagggata 20  
<210>1403  
<211>20  
<212>DNA  
<400>1403  
ggccggggat caatcagcta 20  
<210>1404  
<211>20  
<212>DNA  
<400>1404  
gaataagatg caggcggaag 20  
<210>1405  
<211>20  
<212>DNA  
<400>1405  
gggagacgtt tgtgcgtaaa 20  
<210>1406  
<211>20  
<212>DNA  
<400>1406  
cgtcctgcag gtgttattgt 20  
<210>1407  
<211>20  
<212>DNA  
<400>1407  
caaggggtgt agagaaagga 20  
<210>1408  
<211>20  
<212>DNA  
<400>1408  
gaagacaaac cttgtcctgg 20

```

<210>1409
<211>20
<212>DNA
<400>1409
cgtactaggg attgagcata      20
<210>1410
<211>20
<212>DNA
<400>1410
gagtgtctga cgtttctgag      20
<210>1411
<211>20
<212>DNA
<400>1411
ggaccgccat tacgagaaat      20
<210>1412
<211>20
<212>DNA
<400>1412
gagttgaact cctgccttga      20
<210>1413
<211>20
<212>DNA
<400>1413
atcagatcga agagctccag      20
<210>1414
<211>20
<212>DNA
<400>1414
ggtctaagca cgtaggttgt      20
<210>1415
<211>20
<212>DNA
<400>1415
gggatggcct taggtaaagt      20
<210>1416
<211>20
<212>DNA
<400>1416
ctgagagctg aacttgcttg      20
<210>1417
<211>20
<212>DNA
<400>1417
ctttggaaca tcgcaaagcg      20
<210>1418
<211>20
<212>DNA
<400>1418
cttggtaggg ttgtagagtc      20
<210>1419
<211>20
<212>DNA
<400>1419
gagttgaact cctgccttga      20
<210>1420
<211>20
<212>DNA
<400>1420
ggcatgttta tagtgtggcg      20
<210>1421
<211>20
<212>DNA
<400>1421

```

atgtgacagg tgctacccca 20  
<210>1422  
<211>20  
<212>DNA  
<400>1422  
gagaatcaga ggcaagtcca 20  
<210>1423  
<211>20  
<212>DNA  
<400>1423  
gaaggcttcc ttagtgagca 20  
<210>1424  
<211>20  
<212>DNA  
<400>1424  
cagcgagttg cagcatttga 20  
<210>1425  
<211>20  
<212>DNA  
<400>1425  
tcgcatgttt aggaccgctg 20  
<210>1426  
<211>20  
<212>DNA  
<400>1426  
ttcctgaggc cccagaagag 20  
<210>1427  
<211>20  
<212>DNA  
<400>1427  
gcatgttttag gaccgctgaa 20  
<210>1428  
<211>20  
<212>DNA  
<400>1428  
ccataactctc tgatgcagcg 20  
<210>1429  
<211>20  
<212>DNA  
<400>1429  
ggctctttaga gaaaccgagt 20  
<210>1430  
<211>20  
<212>DNA  
<400>1430  
ctcggcaacg agttcaagaa 20  
<210>1431  
<211>20  
<212>DNA  
<400>1431  
ggatatccag cacgtgctct 20  
<210>1432  
<211>20  
<212>DNA  
<400>1432  
gttgtggctc aagaaggaca 20  
<210>1433  
<211>20  
<212>DNA  
<400>1433  
gcgtgtgaaa gaagctgaag 20  
<210>1434  
<211>20  
<212>DNA

<400>1434  
cagctgaagg ctttcatttg 20  
<210>1435  
<211>20  
<212>DNA  
<400>1435  
gcggagttgt gtgggtattt 20  
<210>1436  
<211>20  
<212>DNA  
<400>1436  
gcaacaaagg cgaaatggca 20  
<210>1437  
<211>20  
<212>DNA  
<400>1437  
cctatctatc ttacccaccg 20  
<210>1438  
<211>20  
<212>DNA  
<400>1438  
gggaagcatc atcctactat 20  
<210>1439  
<211>20  
<212>DNA  
<400>1439  
gtgcagatag cctctattgc 20  
<210>1440  
<211>20  
<212>DNA  
<400>1440  
ggcatcgacg ccatcagtga 20  
<210>1441  
<211>20  
<212>DNA  
<400>1441  
gtggcgtttg atttccagca 20  
<210>1442  
<211>20  
<212>DNA  
<400>1442  
gattttgtca cgtggccgat 20  
<210>1443  
<211>20  
<212>DNA  
<400>1443  
ggagatagcc taagttagcc 20  
<210>1444  
<211>20  
<212>DNA  
<400>1444  
cgaacaaccc ctctccaag 20  
<210>1445  
<211>20  
<212>DNA  
<400>1445  
ggggttttga gaagaaaacc 20  
<210>1446  
<211>20  
<212>DNA  
<400>1446  
gagcagtagc tccacattga 20  
<210>1447  
<211>20

```

<212>DNA
<400>1447
cttaaactcg cagctttcgc      20
<210>1448
<211>20
<212>DNA
<400>1448
ccaaggacag catctcctaa      20
<210>1449
<211>20
<212>DNA
<400>1449
acaggggtca gagtaacaga      20
<210>1450
<211>20
<212>DNA
<400>1450
ccccgcttgc tttcaatact      20
<210>1451
<211>20
<212>DNA
<400>1451
cagagtttag cgtgggggta      20
<210>1452
<211>20
<212>DNA
<400>1452
gagcgcgtta ccgataaaga      20
<210>1453
<211>20
<212>DNA
<400>1453
cggctttgag tgatcaagtg      20
<210>1454
<211>20
<212>DNA
<400>1454
aaactccctc tgcttggcgt      20
<210>1455
<211>20
<212>DNA
<400>1455
agagattggt gccgcctgta      20
<210>1456
<211>20
<212>DNA
<400>1456
ccccgaaggc ttcaaaaatc      20
<210>1457
<211>20
<212>DNA
<400>1457
cagggaaata ccaagtagag      20
<210>1458
<211>20
<212>DNA
<400>1458
gcgggaaaag taaagctcct      20
<210>1459
<211>20
<212>DNA
<400>1459
ccctcaggaa cagaacctaa      20
<210>1460

```

```

<211>20
<212>DNA
<400>1460
ctcggagcgg tttggcttta      20
<210>1461
<211>20
<212>DNA
<400>1461
gagtacttgc tttcctagca      20
<210>1462
<211>20
<212>DNA
<400>1462
tgctataggc atccatacgc      20
<210>1463
<211>20
<212>DNA
<400>1463
tccctctgct tggcgtggat      20
<210>1464
<211>20
<212>DNA
<400>1464
ggctctagat ggaaaacctg      20
<210>1465
<211>20
<212>DNA
<400>1465
gcgcacgtat gcaggaatct      20
<210>1466
<211>20
<212>DNA
<400>1466
caccctacac ttgacctatg      20
<210>1467
<211>20
<212>DNA
<400>1467
gaatgggagt cccaaactca      20
<210>1468
<211>20
<212>DNA
<400>1468
tttgggcgag tccgttcgta      20
<210>1469
<211>20
<212>DNA
<400>1469
gagagagaaa aagcaacctc      20
<210>1470
<211>20
<212>DNA
<400>1470
gcctcaggaa taggattctc      20
<210>1471
<211>20
<212>DNA
<400>1471
ggagtcgtag acctaaggta      20
<210>1472
<211>20
<212>DNA
<400>1472
gataccgaaa tgcccctgta      20

```



<210>1473  
 <211>20  
 <212>DNA  
 <400>1473  
 aggctgcatc cggattctat 20  
 <210>1474  
 <211>20  
 <212>DNA  
 <400>1474  
 gttgcctgat gtaacctcag 20  
 <210>1475  
 <211>20  
 <212>DNA  
 <400>1475  
 gtgacagggg attggacgac 20  
 <210>1476  
 <211>20  
 <212>DNA  
 <400>1476  
 ctcaagatca attttggggc 20  
 <210>1477  
 <211>20  
 <212>DNA  
 <400>1477  
 gccccccctt aatatcagta 20  
 <210>1478  
 <211>20  
 <212>DNA  
 <400>1478  
 caataggttg tgaaaggaga 20  
 <210>1479  
 <211>20  
 <212>DNA  
 <400>1479  
 ctgattgtca ctctgggatg 20  
 <210>1480  
 <211>20  
 <212>DNA  
 <400>1480  
 gacgggtcac ttatacgcat 20  
 <210>1481  
 <211>20  
 <212>DNA  
 <400>1481  
 gttactatgc tcgtctagcc 20  
 <210>1482  
 <211>20  
 <212>DNA  
 <400>1482  
 gtaggtgcgt gactgattag 20  
 <210>1483  
 <211>20  
 <212>DNA  
 <400>1483  
 ccgccaccag gatattttga 20  
 <210>1484  
 <211>20  
 <212>DNA  
 <400>1484  
 ggcgattcct gaagacacta 20  
 <210>1485  
 <211>20  
 <212>DNA  
 <400>1485

ggctctctcc gactgtctat 20  
 <210>1486  
 <211>20  
 <212>DNA  
 <400>1486  
 gggttgtcta cagacatcgt 20  
 <210>1487  
 <211>20  
 <212>DNA  
 <400>1487  
 cgcattgtaca gagattctcc 20  
 <210>1488  
 <211>20  
 <212>DNA  
 <400>1488  
 gctcattgga acagttgctc 20  
 <210>1489  
 <211>20  
 <212>DNA  
 <400>1489  
 cgatctagaa gagctcagtc 20  
 <210>1490  
 <211>20  
 <212>DNA  
 <400>1490  
 ccttcgcacc cgtagattta 20  
 <210>1491  
 <211>20  
 <212>DNA  
 <400>1491  
 cgcaagggttt tgtgaaaggg 20  
 <210>1492  
 <211>20  
 <212>DNA  
 <400>1492  
 ttatcggcac ggtttccgaa 20  
 <210>1493  
 <211>20  
 <212>DNA  
 <400>1493  
 attacacgcg cgctatcagg 20  
 <210>1494  
 <211>20  
 <212>DNA  
 <400>1494  
 agcctccagt ctctcttcta 20  
 <210>1495  
 <211>20  
 <212>DNA  
 <400>1495  
 cgtggttctg ctttgaaagc 20  
 <210>1496  
 <211>20  
 <212>DNA  
 <400>1496  
 gaccgcgcag gcgtatgtaa 20  
 <210>1497  
 <211>20  
 <212>DNA  
 <400>1497  
 ccttcgcacc cgtagattta 20  
 <210>1498  
 <211>20  
 <212>DNA

<400>1498  
 ggatggacaa tgcgtctctg 20  
 <210>1499  
 <211>20  
 <212>DNA  
 <400>1499  
 gtacagcagg tatagtcgag 20  
 <210>1500  
 <211>20  
 <212>DNA  
 <400>1500  
 gtcggttaggg aagtaactgg 20  
 <210>1501  
 <211>20  
 <212>DNA  
 <400>1501  
 aggtgctgct ggagtcaata 20  
 <210>1502  
 <211>20  
 <212>DNA  
 <400>1502  
 ggctctagaa gcatatgggg 20  
 <210>1503  
 <211>20  
 <212>DNA  
 <400>1503  
 catgacagcc gatgttgaag 20  
 <210>1504  
 <211>20  
 <212>DNA  
 <400>1504  
 tattactggc ggtttgcctc 20  
 <210>1505  
 <211>20  
 <212>DNA  
 <400>1505  
 agcctgtggc tattccttcg 20  
 <210>1506  
 <211>20  
 <212>DNA  
 <400>1506  
 cagatgcagc ttgttgtagc 20  
 <210>1507  
 <211>20  
 <212>DNA  
 <400>1507  
 gtagcaagca taacccttg 20  
 <210>1508  
 <211>20  
 <212>DNA  
 <400>1508  
 gctgctggat gagctaaaga 20  
 <210>1509  
 <211>20  
 <212>DNA  
 <400>1509  
 gggtgagggg atctctacag 20  
 <210>1510  
 <211>20  
 <212>DNA  
 <400>1510  
 cgtcagtttg tagcactatg 20  
 <210>1511  
 <211>20

<212>DNA  
 <400>1511  
 caacgtggag atagtgtgat 20  
 <210>1512  
 <211>20  
 <212>DNA  
 <400>1512  
 ggatctagaa gaaggcctac 20  
 <210>1513  
 <211>20  
 <212>DNA  
 <400>1513  
 ggaaggtatt cgagctgttg 20  
 <210>1514  
 <211>20  
 <212>DNA  
 <400>1514  
 catgtgagtc ctagagctgt 20  
 <210>1515  
 <211>20  
 <212>DNA  
 <400>1515  
 cccttggtgt tgcaaaggca 20  
 <210>1516  
 <211>20  
 <212>DNA  
 <400>1516  
 cagggcgttt tggatgacta 20  
 <210>1517  
 <211>20  
 <212>DNA  
 <400>1517  
 gagagcgagg gttttttctc 20  
 <210>1518  
 <211>20  
 <212>DNA  
 <400>1518  
 tcgccagatg ggactagata 20  
 <210>1519  
 <211>20  
 <212>DNA  
 <400>1519  
 gttcctcagc tcttcttgag 20  
 <210>1520  
 <211>20  
 <212>DNA  
 <400>1520  
 cctgtggact gttattgtcc 20  
 <210>1521  
 <211>20  
 <212>DNA  
 <400>1521  
 gattccgtgc aagagtcttg 20  
 <210>1522  
 <211>20  
 <212>DNA  
 <400>1522  
 gtctttatgc ggattcccgt 20  
 <210>1523  
 <211>20  
 <212>DNA  
 <400>1523  
 cccgagagtc ttcgatctat 20  
 <210>1524

<211>20  
<212>DNA  
<400>1524  
aagtcacggc cgaagtctcg 20  
<210>1525  
<211>20  
<212>DNA  
<400>1525  
cctgtggact gttattgtcc 20  
<210>1526  
<211>20  
<212>DNA  
<400>1526  
ggaggagtga ttcacggact 20  
<210>1527  
<211>20  
<212>DNA  
<400>1527  
catcacggat gtaggtcaag 20  
<210>1528  
<211>20  
<212>DNA  
<400>1528  
gagtcgcttc acatgcagta 20  
<210>1529  
<211>20  
<212>DNA  
<400>1529  
gtctccgagg tccttacttt 20  
<210>1530  
<211>20  
<212>DNA  
<400>1530  
ccgttgcggt atgtagcggg 20  
<210>1531  
<211>20  
<212>DNA  
<400>1531  
gcttttgtgc tcttcttctc 20  
<210>1532  
<211>20  
<212>DNA  
<400>1532  
tgatactata cgcctgggga 20  
<210>1533  
<211>20  
<212>DNA  
<400>1533  
acactgggat cgcagtgtct 20  
<210>1534  
<211>20  
<212>DNA  
<400>1534  
gatcgcatatt tccctgcttc 20  
<210>1535  
<211>20  
<212>DNA  
<400>1535  
gacggtcaga gaattccaag 20  
<210>1536  
<211>20  
<212>DNA  
<400>1536  
gaacgatttc ctcggagtta 20

<210>1537  
<211>20  
<212>DNA  
<400>1537  
cagagactcc tgtaactccg 20  
<210>1538  
<211>20  
<212>DNA  
<400>1538  
gcatagaaca gggcattctc 20  
<210>1539  
<211>20  
<212>DNA  
<400>1539  
gagaagagca aggtgcgaaa 20  
<210>1540  
<211>20  
<212>DNA  
<400>1540  
gctaagtttg tgagggctgt 20  
<210>1541  
<211>20  
<212>DNA  
<400>1541  
gcaacgcaga tgctagaatc 20  
<210>1542  
<211>20  
<212>DNA  
<400>1542  
gctaagtttg tgagggctgt 20  
<210>1543  
<211>20  
<212>DNA  
<400>1543  
cacgagctga agtctctgat 20  
<210>1544  
<211>20  
<212>DNA  
<400>1544  
cagaagctcc aagcactcca 20  
<210>1545  
<211>20  
<212>DNA  
<400>1545  
ccgtgactcc aagcacttct 20  
<210>1546  
<211>20  
<212>DNA  
<400>1546  
cggaggtctt gaacggtatt 20  
<210>1547  
<211>20  
<212>DNA  
<400>1547  
caaaggcgat tccaggatag 20  
<210>1548  
<211>20  
<212>DNA  
<400>1548  
ctcgggtgcc ccagaaaaat 20  
<210>1549  
<211>20  
<212>DNA  
<400>1549

ccgtctgctg taaaaagtgc	20
<210>1550	
<211>20	
<212>DNA	
<400>1550	
tgggaagaca accttgggta	20
<210>1551	
<211>20	
<212>DNA	
<400>1551	
ggaaagctgc gtcgtatcat	20
<210>1552	
<211>20	
<212>DNA	
<400>1552	
ggccttcctt tcatcattac	20
<210>1553	
<211>20	
<212>DNA	
<400>1553	
ggagctcata tgagtgcctt	20
<210>1554	
<211>20	
<212>DNA	
<400>1554	
tcgtctaacc gttggttgaa	20
<210>1555	
<211>20	
<212>DNA	
<400>1555	
tagttgccag tgcgtttgct	20
<210>1556	
<211>20	
<212>DNA	
<400>1556	
cagcataggg ttttgattgc	20
<210>1557	
<211>20	
<212>DNA	
<400>1557	
ttgctgcata ctggcccaga	20
<210>1558	
<211>20	
<212>DNA	
<400>1558	
cctcactccc catgaaatca	20
<210>1559	
<211>20	
<212>DNA	
<400>1559	
tctggtctgg gtaaaagcgt	20
<210>1560	
<211>20	
<212>DNA	
<400>1560	
cgcgtagatc ccagaagaaa	20
<210>1561	
<211>20	
<212>DNA	
<400>1561	
gcagagatga atgggggaat	20
<210>1562	
<211>20	
<212>DNA	

<400>1562  
ctggtggcca tgggaacggc 20  
<210>1563  
<211>20  
<212>DNA  
<400>1563  
catctatgat ccagaagccc 20  
<210>1564  
<211>20  
<212>DNA  
<400>1564  
ccaacgccct ccgcatgcaa 20  
<210>1565  
<211>20  
<212>DNA  
<400>1565  
gtatccatct catgcggaact 20  
<210>1566  
<211>20  
<212>DNA  
<400>1566  
ctgaccgcat cgcattaaga 20  
<210>1567  
<211>20  
<212>DNA  
<400>1567  
ctgtagatgc tcacggaagt 20  
<210>1568  
<211>20  
<212>DNA  
<400>1568  
gcggaggata tgacgacttt 20  
<210>1569  
<211>20  
<212>DNA  
<400>1569  
ggacatgcaa cgcaaattga 20  
<210>1570  
<211>20  
<212>DNA  
<400>1570  
gttctttgag accctcgact 20  
<210>1571  
<211>20  
<212>DNA  
<400>1571  
cgcacatcct tgagcaacaa 20  
<210>1572  
<211>20  
<212>DNA  
<400>1572  
cactacctgc tgctaaagga 20  
<210>1573  
<211>20  
<212>DNA  
<400>1573  
ggtcttccca tgcaacgttt 20  
<210>1574  
<211>20  
<212>DNA  
<400>1574  
cttaaagccc ggattcgtga 20  
<210>1575  
<211>20



```

<212>DNA
<400>1575
ggagctggag ataaaggaag      20
<210>1576
<211>20
<212>DNA
<400>1576
gtatcgccca agaattgcct      20
<210>1577
<211>20
<212>DNA
<400>1577
caagcccgag aatgggtttt      20
<210>1578
<211>20
<212>DNA
<400>1578
aagaacggag gcgattatcc      20
<210>1579
<211>20
<212>DNA
<400>1579
gcgaagccct gtatattctc      20
<210>1580
<211>20
<212>DNA
<400>1580
ggtacgatcc acatagctct      20
<210>1581
<211>20
<212>DNA
<400>1581
gccgtcgcaa atgaaaatgc      20
<210>1582
<211>20
<212>DNA
<400>1582
gctgctgctt cgcatttgat      20
<210>1583
<211>20
<212>DNA
<400>1583
gctctcttgg atgccgatgt      20
<210>1584
<211>20
<212>DNA
<400>1584
cgagaagttc aagctgagaa      20
<210>1585
<211>20
<212>DNA
<400>1585
gtagctatgg ggcaagatgt      20
<210>1586
<211>20
<212>DNA
<400>1586
ggtgaaggca tggaaaagag      20
<210>1587
<211>20
<212>DNA
<400>1587
gaggcgatta tcctgtccat      20
<210>1588

```

<211>20  
<212>DNA  
<400>1588  
cccatgacat tccttgtaag 20  
<210>1589  
<211>20  
<212>DNA  
<400>1589  
gatggtccat tgcaaacgag 20  
<210>1590  
<211>20  
<212>DNA  
<400>1590  
ctcggatgcc tagtgtatct 20  
<210>1591  
<211>20  
<212>DNA  
<400>1591  
gagcaaagtg agcgtagaac 20  
<210>1592  
<211>20  
<212>DNA  
<400>1592  
gcctagtga ctacgcgatt 20  
<210>1593  
<211>20  
<212>DNA  
<400>1593  
gcatgcgaag aggacttttg 20  
<210>1594  
<211>20  
<212>DNA  
<400>1594  
ggatacgatg tatgctaggg 20  
<210>1595  
<211>20  
<212>DNA  
<400>1595  
gctagcagct gcaaatcagt 20  
<210>1596  
<211>20  
<212>DNA  
<400>1596  
cgtttagcgg cttttcctgt 20  
<210>1597  
<211>20  
<212>DNA  
<400>1597  
cgggtgtagag tatgtccagt 20  
<210>1598  
<211>20  
<212>DNA  
<400>1598  
aaactgggat agggattgcc 20  
<210>1599  
<211>20  
<212>DNA  
<400>1599  
gagttcccct tcatttaccc 20  
<210>1600  
<211>20  
<212>DNA  
<400>1600  
ctgctgcaga agatgctttg 20

## WO 99/27105

```

<210>1601
<211>20
<212>DNA
<400>1601
ccgcagattt tctccataga      20
<210>1602
<211>20
<212>DNA
<400>1602
cggtgtcgat gacagctact     20
<210>1603
<211>20
<212>DNA
<400>1603
ccttaggatt gggctgtggt     20
<210>1604
<211>20
<212>DNA
<400>1604
cgctttctga agctgagtct     20
<210>1605
<211>20
<212>DNA
<400>1605
gcgcaagagg aggttacaaa     20
<210>1606
<211>20
<212>DNA
<400>1606
gtttgttgcg tcagtggaag     20
<210>1607
<211>20
<212>DNA
<400>1607
cttgcattctt tgacgcgtga     20
<210>1608
<211>20
<212>DNA
<400>1608
gtagtgcgaa accgcctttt     20
<210>1609
<211>20
<212>DNA
<400>1609
gaagatgcaa gtgaacggct     20
<210>1610
<211>20
<212>DNA
<400>1610
cttccgaaga gaactaggca     20
<210>1611
<211>20
<212>DNA
<400>1611
gaggaagagg agcatcatct     20
<210>1612
<211>20
<212>DNA
<400>1612
ccccagtata ggcaggcaac     20
<210>1613
<211>20
<212>DNA
<400>1613

```

gcaatgagca agagcttagg 20  
<210>1614  
<211>20  
<212>DNA  
<400>1614  
agcctgcgag catagtgtct 20  
<210>1615  
<211>20  
<212>DNA  
<400>1615  
ctttttacggg atccggtcta 20  
<210>1616  
<211>20  
<212>DNA  
<400>1616  
cagcagttga gcgggttttt 20  
<210>1617  
<211>20  
<212>DNA  
<400>1617  
gtagtgaggg tgttttctct 20  
<210>1618  
<211>20  
<212>DNA  
<400>1618  
cttcacaagc tgcggttcta 20  
<210>1619  
<211>20  
<212>DNA  
<400>1619  
tcgaactcgg tgataagctg 20  
<210>1620  
<211>20  
<212>DNA  
<400>1620  
cgctacttga gacaaaggga 20  
<210>1621  
<211>20  
<212>DNA  
<400>1621  
cttcctgtgt taaggctatc 20  
<210>1622  
<211>20  
<212>DNA  
<400>1622  
atctccttgg aagacgtagc 20  
<210>1623  
<211>20  
<212>DNA  
<400>1623  
agcacggtaa ggggattcag 20  
<210>1624  
<211>20  
<212>DNA  
<400>1624  
acttgctgag aatgatgtgc 20  
<210>1625  
<211>20  
<212>DNA  
<400>1625  
cggaacagct tttactccct 20  
<210>1626  
<211>20  
<212>DNA

<400>1626  
 cggtttagata gccattgctc 20  
 <210>1627  
 <211>20  
 <212>DNA  
 <400>1627  
 cgctacttga gacaaaggga 20  
 <210>1628  
 <211>20  
 <212>DNA  
 <400>1628  
 gagegccccat gttttcatgt 20  
 <210>1629  
 <211>20  
 <212>DNA  
 <400>1629  
 cgtaggggaa tatggtgaag 20  
 <210>1630  
 <211>20  
 <212>DNA  
 <400>1630  
 ggtaagatga ttcctccacg 20  
 <210>1631  
 <211>20  
 <212>DNA  
 <400>1631  
 gagacctcat ggaaaattgt 20  
 <210>1632  
 <211>20  
 <212>DNA  
 <400>1632  
 gggagaacga tcttttccag 20  
 <210>1633  
 <211>20  
 <212>DNA  
 <400>1633  
 gtggcttctt cttcttcctt 20  
 <210>1634  
 <211>20  
 <212>DNA  
 <400>1634  
 ggggttgtaat tcggcgtatc 20  
 <210>1635  
 <211>20  
 <212>DNA  
 <400>1635  
 gggatgttat gttggaatag 20  
 <210>1636  
 <211>20  
 <212>DNA  
 <400>1636  
 cgtccgtgag tatctaggaa 20  
 <210>1637  
 <211>20  
 <212>DNA  
 <400>1637  
 gtggtaggca atgagttgga 20  
 <210>1638  
 <211>20  
 <212>DNA  
 <400>1638  
 gagatttcaa atcccagggt 20  
 <210>1639  
 <211>20

<212>DNA  
 <400>1639  
 gaaaccatcc gcagatgaga 20  
 <210>1640  
 <211>20  
 <212>DNA  
 <400>1640  
 cacttggata tcgaaacctg 20  
 <210>1641  
 <211>20  
 <212>DNA  
 <400>1641  
 ccttgagatc ggatttcctc 20  
 <210>1642  
 <211>20  
 <212>DNA  
 <400>1642  
 ggtaggagtt gggggaaaaa 20  
 <210>1643  
 <211>20  
 <212>DNA  
 <400>1643  
 cgaagcgttt gcagagttct 20  
 <210>1644  
 <211>20  
 <212>DNA  
 <400>1644  
 gggtaggaac ggatcttttg 20  
 <210>1645  
 <211>20  
 <212>DNA  
 <400>1645  
 ggctagaaaa agccgtgagt 20  
 <210>1646  
 <211>20  
 <212>DNA  
 <400>1646  
 gatgccactc tatagtcacg 20  
 <210>1647  
 <211>20  
 <212>DNA  
 <400>1647  
 ccacagcgct actactatgt 20  
 <210>1648  
 <211>20  
 <212>DNA  
 <400>1648  
 cttgctttct aaggctttgc 20  
 <210>1649  
 <211>20  
 <212>DNA  
 <400>1649  
 gggtgtaggg aaaactgcta 20  
 <210>1650  
 <211>20  
 <212>DNA  
 <400>1650  
 caggaagact gccagaagtt 20  
 <210>1651  
 <211>20  
 <212>DNA  
 <400>1651  
 acagaggggg ctttgaatgc 20  
 <210>1652

## WO 99/27105

<211>20  
 <212>DNA  
 <400>1652  
 catatccaaa gtggctcctc 20  
 <210>1653  
 <211>20  
 <212>DNA  
 <400>1653  
 cccgccctttt aaaacgtttg 20  
 <210>1654  
 <211>20  
 <212>DNA  
 <400>1654  
 tctccaagag cgtcaacgcc 20  
 <210>1655  
 <211>20  
 <212>DNA  
 <400>1655  
 cgtggctttt ctcctgaaga 20  
 <210>1656  
 <211>20  
 <212>DNA  
 <400>1656  
 agcgtcaacg ccatcttgcc 20  
 <210>1657  
 <211>20  
 <212>DNA  
 <400>1657  
 cgtggctttt ctcctgaaga 20  
 <210>1658  
 <211>20  
 <212>DNA  
 <400>1658  
 gcaggagaag ccggtcgcgg 20  
 <210>1659  
 <211>20  
 <212>DNA  
 <400>1659  
 ggtgcgtact cctgaagaaa 20  
 <210>1660  
 <211>20  
 <212>DNA  
 <400>1660  
 cctgtgacga acgaacagtt 20  
 <210>1661  
 <211>20  
 <212>DNA  
 <400>1661  
 agcatggggg accaatggct 20  
 <210>1662  
 <211>20  
 <212>DNA  
 <400>1662  
 gtgccaaagat tggatatgggt 20  
 <210>1663  
 <211>20  
 <212>DNA  
 <400>1663  
 gtggtgttgc aggagaagcc 20  
 <210>1664  
 <211>20  
 <212>DNA  
 <400>1664  
 ctgctatccg gaattgtggg 20

<210>1665  
<211>20  
<212>DNA  
<400>1665  
catcgtata atcctggggc 20  
<210>1666  
<211>20  
<212>DNA  
<400>1666  
ggcgaagaaa gctatagacc 20  
<210>1667  
<211>20  
<212>DNA  
<400>1667  
ggtggagagg tgattccaaa 20  
<210>1668  
<211>20  
<212>DNA  
<400>1668  
gcagaaagaa ctggtgggtc 20  
<210>1669  
<211>20  
<212>DNA  
<400>1669  
ctaagagcaa ggagtttgag 20  
<210>1670  
<211>20  
<212>DNA  
<400>1670  
gccaaaatga gacctgtagg 20  
<210>1671  
<211>20  
<212>DNA  
<400>1671  
ggacgactta aggaatcaag 20  
<210>1672  
<211>20  
<212>DNA  
<400>1672  
gaagccccta tagctactga 20  
<210>1673  
<211>20  
<212>DNA  
<400>1673  
gagtattaga gaggctacct 20  
<210>1674  
<211>20  
<212>DNA  
<400>1674  
gtctgggcaa gaagctaaag 20  
<210>1675  
<211>20  
<212>DNA  
<400>1675  
caattggagc ccatacactc 20  
<210>1676  
<211>20  
<212>DNA  
<400>1676  
ggaacgtgga tctcaacttg 20  
<210>1677  
<211>20  
<212>DNA  
<400>1677



gcccttatag ctactgaaaa 20  
 <210>1678  
 <211>20  
 <212>DNA  
 <400>1678  
 agcagcatgg cctcaaatag 20  
 <210>1679  
 <211>20  
 <212>DNA  
 <400>1679  
 ctccgctatg ggattttcgt 20  
 <210>1680  
 <211>20  
 <212>DNA  
 <400>1680  
 aaagtacgtc ctgatgcctt 20  
 <210>1681  
 <211>20  
 <212>DNA  
 <400>1681  
 tgggaaaccc accagggatt 20  
 <210>1682  
 <211>20  
 <212>DNA  
 <400>1682  
 ccaggttcct cactaagaac 20  
 <210>1683  
 <211>20  
 <212>DNA  
 <400>1683  
 ggtggcaagc caagtgttta 20  
 <210>1684  
 <211>20  
 <212>DNA  
 <400>1684  
 acgaagcttg ccaattaggg 20  
 <210>1685  
 <211>20  
 <212>DNA  
 <400>1685  
 gggtgcacat tccttatggg 20  
 <210>1686  
 <211>20  
 <212>DNA  
 <400>1686  
 ccggtttcga gcttaaagag 20  
 <210>1687  
 <211>20  
 <212>DNA  
 <400>1687  
 aggtgggttag agcagcagaa 20  
 <210>1688  
 <211>20  
 <212>DNA  
 <400>1688  
 ttcgggcaga tgcctggaga 20  
 <210>1689  
 <211>20  
 <212>DNA  
 <400>1689  
 gattgtggag ttgcagctct 20  
 <210>1690  
 <211>20  
 <212>DNA

<400>1690  
cctcctgata gtaaaacccc 20  
<210>1691  
<211>20  
<212>DNA  
<400>1691  
ccagttctttt aggcgtgtct 20  
<210>1692  
<211>20  
<212>DNA  
<400>1692  
ggtgcgctgc tcatgctttt 20  
<210>1693  
<211>20  
<212>DNA  
<400>1693  
caagcagctc ttctgtagca 20  
<210>1694  
<211>20  
<212>DNA  
<400>1694  
gaggggcaaa ttggaaacct 20  
<210>1695  
<211>20  
<212>DNA  
<400>1695  
taagaggcct gctgccccat 20  
<210>1696  
<211>20  
<212>DNA  
<400>1696  
gcacatactg aggagctctt 20  
<210>1697  
<211>20  
<212>DNA  
<400>1697  
gggagacgaa gtttcttgga 20  
<210>1698  
<211>20  
<212>DNA  
<400>1698  
gttcgccgat tttccacct 20  
<210>1699  
<211>20  
<212>DNA  
<400>1699  
gcgagccttt cttggtctat 20  
<210>1700  
<211>20  
<212>DNA  
<400>1700  
gggctaattc taggaagcgt 20  
<210>1701  
<211>20  
<212>DNA  
<400>1701  
gggttgatag gaatcttccc 20  
<210>1702  
<211>20  
<212>DNA  
<400>1702  
gtcagtgtgt gtctatagag 20  
<210>1703  
<211>20

<212>DNA  
 <400>1703  
 ggaataggca catactgagg 20  
 <210>1704  
 <211>20  
 <212>DNA  
 <400>1704  
 agtgggtgcg ggagtcactc 20  
 <210>1705  
 <211>20  
 <212>DNA  
 <400>1705  
 ccaaggtgta tctacatctg 20  
 <210>1706  
 <211>20  
 <212>DNA  
 <400>1706  
 cggttgacgc taaacgttct 20  
 <210>1707  
 <211>20  
 <212>DNA  
 <400>1707  
 ggggggatttg gtttgatct 20  
 <210>1708  
 <211>20  
 <212>DNA  
 <400>1708  
 caaagccgtc cttctcatct 20  
 <210>1709  
 <211>20  
 <212>DNA  
 <400>1709  
 gattcgctat gctcaaggtc 20  
 <210>1710  
 <211>20  
 <212>DNA  
 <400>1710  
 ggtctttcct cttgtttcca 20  
 <210>1711  
 <211>20  
 <212>DNA  
 <400>1711  
 ccgtccttgt cttgcttttt 20  
 <210>1712  
 <211>20  
 <212>DNA  
 <400>1712  
 gcgattgtat tgagtcgtgg 20  
 <210>1713  
 <211>20  
 <212>DNA  
 <400>1713  
 ccattgtttt tggaaccag 20  
 <210>1714  
 <211>20  
 <212>DNA  
 <400>1714  
 caggatctaa atgtggagcc 20  
 <210>1715  
 <211>20  
 <212>DNA  
 <400>1715  
 cattgaacag cttcttgggc 20  
 <210>1716

<211>20  
 <212>DNA  
 <400>1716  
 gcgtcaactc caatctcagc 20  
 <210>1717  
 <211>20  
 <212>DNA  
 <400>1717  
 cgagtctttg atttaccct 20  
 <210>1718  
 <211>20  
 <212>DNA  
 <400>1718  
 gcttcttcca tgtatgctac 20  
 <210>1719  
 <211>20  
 <212>DNA  
 <400>1719  
 acgtaagggc tcgactaact 20  
 <210>1720  
 <211>20  
 <212>DNA  
 <400>1720  
 ccggaaatac gctaaagtcc 20  
 <210>1721  
 <211>20  
 <212>DNA  
 <400>1721  
 gatggatggg cgtatatcca 20  
 <210>1722  
 <211>20  
 <212>DNA  
 <400>1722  
 ctctcaagcc gaagaaagag 20  
 <210>1723  
 <211>20  
 <212>DNA  
 <400>1723  
 ccatgccgcg gtacctttta 20  
 <210>1724  
 <211>20  
 <212>DNA  
 <400>1724  
 gcaatcacct cttgaagcag 20  
 <210>1725  
 <211>20  
 <212>DNA  
 <400>1725  
 gcatgagctg tgtcaatgac 20  
 <210>1726  
 <211>20  
 <212>DNA  
 <400>1726  
 ccgttctgga gacgagatac 20  
 <210>1727  
 <211>20  
 <212>DNA  
 <400>1727  
 tgaacttgct ctcgacccca 20  
 <210>1728  
 <211>20  
 <212>DNA  
 <400>1728  
 gaccctgccg ttaccctagc 20

<210>1729  
<211>20  
<212>DNA  
<400>1729  
ctgtagctgc agcaagttct 20  
<210>1730  
<211>20  
<212>DNA  
<400>1730  
cggctcttacc agctatatgg 20  
<210>1731  
<211>20  
<212>DNA  
<400>1731  
ggcccaaaac cagtccaaat 20  
<210>1732  
<211>20  
<212>DNA  
<400>1732  
gccggagaga tctaaaagca 20  
<210>1733  
<211>20  
<212>DNA  
<400>1733  
acctcgggtga ggtaggata 20  
<210>1734  
<211>20  
<212>DNA  
<400>1734  
gggcttgac agctttttct 20  
<210>1735  
<211>20  
<212>DNA  
<400>1735  
gactcttcat cagtcttagc 20  
<210>1736  
<211>20  
<212>DNA  
<400>1736  
cagctcctgt gatctcacag 20  
<210>1737  
<211>20  
<212>DNA  
<400>1737  
caacaaccct tggaacctca 20  
<210>1738  
<211>20  
<212>DNA  
<400>1738  
ttaggggtccg ttgggatagg 20  
<210>1739  
<211>20  
<212>DNA  
<400>1739  
gggcttgac agctttttct 20  
<210>1740  
<211>20  
<212>DNA  
<400>1740  
gacagtcaca cctgccttta 20  
<210>1741  
<211>20  
<212>DNA  
<400>1741

gacctggaga tggtgagaaa 20  
<210>1742  
<211>20  
<212>DNA  
<400>1742  
ggactactac cataatacag 20  
<210>1743  
<211>20  
<212>DNA  
<400>1743  
caggatcccc attggtaatc 20  
<210>1744  
<211>20  
<212>DNA  
<400>1744  
ggactactac cataatacag 20  
<210>1745  
<211>20  
<212>DNA  
<400>1745  
caggatcccc attggtaatc 20  
<210>1746  
<211>20  
<212>DNA  
<400>1746  
caaccatctt caccgtaga 20  
<210>1747  
<211>20  
<212>DNA  
<400>1747  
ccgcttgaac cccacatttt 20  
<210>1748  
<211>20  
<212>DNA  
<400>1748  
gcgatcggta aactctcatc 20  
<210>1749  
<211>20  
<212>DNA  
<400>1749  
ggactactac cataatacag 20  
<210>1750  
<211>20  
<212>DNA  
<400>1750  
cctctccttt cactttcctc 20  
<210>1751  
<211>20  
<212>DNA  
<400>1751  
cgactccagg tattcctaca 20  
<210>1752  
<211>20  
<212>DNA  
<400>1752  
ggtgaggtct ctcaatgtct 20  
<210>1753  
<211>20  
<212>DNA  
<400>1753  
cactagaacc ctacctatgc 20  
<210>1754  
<211>20  
<212>DNA

<400>1754  
cctgatgtca gtatttccgc 20  
<210>1755  
<211>20  
<212>DNA  
<400>1755  
ggcagaaaac ctttgtcgaa 20  
<210>1756  
<211>20  
<212>DNA  
<400>1756  
ccatgtctgg agcatggaaa 20  
<210>1757  
<211>20  
<212>DNA  
<400>1757  
ttcacttatg gcgccctcgt 20  
<210>1758  
<211>20  
<212>DNA  
<400>1758  
gttcctctgg agacttgaac 20  
<210>1759  
<211>20  
<212>DNA  
<400>1759  
cagcattgtc ttgggattcc 20  
<210>1760  
<211>20  
<212>DNA  
<400>1760  
gcttacgcta gaatcgctct 20  
<210>1761  
<211>20  
<212>DNA  
<400>1761  
ccatgtctgg agcatggaaa 20  
<210>1762  
<211>20  
<212>DNA  
<400>1762  
ggacaaacaa tgcttgcagg 20  
<210>1763  
<211>20  
<212>DNA  
<400>1763  
taatccccctc ttagcagggg 20  
<210>1764  
<211>20  
<212>DNA  
<400>1764  
gtggatgggt gcaatttcct 20  
<210>1765  
<211>20  
<212>DNA  
<400>1765  
ccttcccttg ggaaaaatct 20  
<210>1766  
<211>20  
<212>DNA  
<400>1766  
ccgcggataa cagtcacata 20  
<210>1767  
<211>20

<212>DNA  
<400>1767  
aggtagggttc cgtgggtcata 20  
<210>1768  
<211>20  
<212>DNA  
<400>1768  
gccaacgaga tacagacgac 20  
<210>1769  
<211>20  
<212>DNA  
<400>1769  
ggacaaacaa tgcttgacagg 20  
<210>1770  
<211>20  
<212>DNA  
<400>1770  
gcctgcacta ctattgcaca 20  
<210>1771  
<211>20  
<212>DNA  
<400>1771  
gcccagcaca aataagatac 20  
<210>1772  
<211>20  
<212>DNA  
<400>1772  
ggacttccgt tatgctaagg 20  
<210>1773  
<211>20  
<212>DNA  
<400>1773  
gctctcctgc tccagagata 20  
<210>1774  
<211>20  
<212>DNA  
<400>1774  
ccctatcacc tccaagattc 20  
<210>1775  
<211>20  
<212>DNA  
<400>1775  
cgctatccct attgtcggaa 20  
<210>1776  
<211>20  
<212>DNA  
<400>1776  
gagacctttc ttcaccagta 20  
<210>1777  
<211>20  
<212>DNA  
<400>1777  
ctatcccgaa cggaaaagac 20  
<210>1778  
<211>20  
<212>DNA  
<400>1778  
ggccacacag atctcaaaaa 20  
<210>1779  
<211>20  
<212>DNA  
<400>1779  
cttctggagc tgtagatctc 20  
<210>1780



<211>20  
 <212>DNA  
 <400>1780  
 caggaacctt tgctatcgaa 20  
 <210>1781  
 <211>20  
 <212>DNA  
 <400>1781  
 tatcccagac gcctccacag 20  
 <210>1782  
 <211>20  
 <212>DNA  
 <400>1782  
 ccctagctcc catcatatct 20  
 <210>1783  
 <211>20  
 <212>DNA  
 <400>1783  
 ctaggccaca cagatctcaa 20  
 <210>1784  
 <211>20  
 <212>DNA  
 <400>1784  
 cacaagctca agtccttagg 20  
 <210>1785  
 <211>20  
 <212>DNA  
 <400>1785  
 actcccgact ctcgcacttg 20  
 <210>1786  
 <211>20  
 <212>DNA  
 <400>1786  
 ccgtccaatc tagggttaga 20  
 <210>1787  
 <211>20  
 <212>DNA  
 <400>1787  
 gtctcgaaga gggatctcat 20  
 <210>1788  
 <211>20  
 <212>DNA  
 <400>1788  
 cccctcagct attgctaaag 20  
 <210>1789  
 <211>20  
 <212>DNA  
 <400>1789  
 cgctcaacca atccctaatac 20  
 <210>1790  
 <211>20  
 <212>DNA  
 <400>1790  
 ccttttgacgg aggacttggt 20  
 <210>1791  
 <211>20  
 <212>DNA  
 <400>1791  
 tggaggggact cgtacacaaa 20  
 <210>1792  
 <211>20  
 <212>DNA  
 <400>1792  
 aaagcctttg acggaggact 20

<210>1793  
<211>20  
<212>DNA  
<400>1793  
tcttttgagg gactcgtaca 20  
<210>1794  
<211>20  
<212>DNA  
<400>1794  
gcgctatgtt cctcactgct 20  
<210>1795  
<211>20  
<212>DNA  
<400>1795  
gcatgggcta ccaaattcttc 20  
<210>1796  
<211>20  
<212>DNA  
<400>1796  
gccttctgtc ataagctctc 20  
<210>1797  
<211>20  
<212>DNA  
<400>1797  
aggagccggg aaaattccta 20  
<210>1798  
<211>20  
<212>DNA  
<400>1798  
gccatgacga atcaaaggga 20  
<210>1799  
<211>20  
<212>DNA  
<400>1799  
cttttagcctt gggatgatgc 20  
<210>1800  
<211>20  
<212>DNA  
<400>1800  
gtttgtggta tcgcccttga 20  
<210>1801  
<211>20  
<212>DNA  
<400>1801  
ggaggcttca actgtatagg 20  
<210>1802  
<211>20  
<212>DNA  
<400>1802  
aaatttgtcc tggcccagcc 20  
<210>1803  
<211>20  
<212>DNA  
<400>1803  
gggcaattcc cgtagtgaaa 20  
<210>1804  
<211>20  
<212>DNA  
<400>1804  
acctcttctg ttgtatctgg 20  
<210>1805  
<211>20  
<212>DNA  
<400>1805

## WO 99/27105

cggtacgaat gccacgccat 20  
 <210>1806  
 <211>20  
 <212>DNA  
 <400>1806  
 ccctcaactc tcgaaaacag 20  
 <210>1807  
 <211>20  
 <212>DNA  
 <400>1807  
 cttgtcggct tctggtcttt 20  
 <210>1808  
 <211>20  
 <212>DNA  
 <400>1808  
 agacctatgc aaagtatggg 20  
 <210>1809  
 <211>20  
 <212>DNA  
 <400>1809  
 gtgcagaaaa cccacgaatc 20  
 <210>1810  
 <211>20  
 <212>DNA  
 <400>1810  
 ctcttggtcc gaagagaaaag 20  
 <210>1811  
 <211>20  
 <212>DNA  
 <400>1811  
 cgacagctct cagagagatt 20  
 <210>1812  
 <211>20  
 <212>DNA  
 <400>1812  
 ggagaacacc caagacaatc 20  
 <210>1813  
 <211>20  
 <212>DNA  
 <400>1813  
 cctgagcttt cacatcaagc 20  
 <210>1814  
 <211>20  
 <212>DNA  
 <400>1814  
 gtgcgtgcct tgttctagat 20  
 <210>1815  
 <211>20  
 <212>DNA  
 <400>1815  
 ggacgctcat agtcttcctt 20  
 <210>1816  
 <211>20  
 <212>DNA  
 <400>1816  
 gtagcctctc tggtcacttt 20  
 <210>1817  
 <211>20  
 <212>DNA  
 <400>1817  
 gagggcccca gatattcttt 20  
 <210>1818  
 <211>20  
 <212>DNA

<400>1818  
caggaggaag ctacatttgc 20  
<210>1819  
<211>20  
<212>DNA  
<400>1819  
ccgctatcct cagcttttct 20  
<210>1820  
<211>20  
<212>DNA  
<400>1820  
cgatattcag agaaacgccc 20  
<210>1821  
<211>20  
<212>DNA  
<400>1821  
ccctgaatgc gcttctatca 20  
<210>1822  
<211>20  
<212>DNA  
<400>1822  
cattgtcttc cctcccacaa 20  
<210>1823  
<211>20  
<212>DNA  
<400>1823  
tcttcttcat ccaggcccag 20  
<210>1824  
<211>20  
<212>DNA  
<400>1824  
caagcagttc tccaagctct 20  
<210>1825  
<211>20  
<212>DNA  
<400>1825  
ggcatacctg agacaccttt 20  
<210>1826  
<211>20  
<212>DNA  
<400>1826  
tggttcggtg gtaaagctgc 20  
<210>1827  
<211>20  
<212>DNA  
<400>1827  
gatcaccagc taaagactgc 20  
<210>1828  
<211>20  
<212>DNA  
<400>1828  
cgactttaca gcacactctc 20  
<210>1829  
<211>20  
<212>DNA  
<400>1829  
ggtgcatctg aaaaccaaac 20  
<210>1830  
<211>20  
<212>DNA  
<400>1830  
gacgactcta tagcgtttgg 20  
<210>1831  
<211>20

## WO 99/27105

<212>DNA  
 <400>1831  
 ctccctgtgga gaatgaagtc 20  
 <210>1832  
 <211>20  
 <212>DNA  
 <400>1832  
 cccttttagca atctgggtcca 20  
 <210>1833  
 <211>20  
 <212>DNA  
 <400>1833  
 tgggtgcgtat ggaaccaaatt 20  
 <210>1834  
 <211>20  
 <212>DNA  
 <400>1834  
 aagccttagga ctgcctgagg 20  
 <210>1835  
 <211>20  
 <212>DNA  
 <400>1835  
 gcttagggat tctcatcctc 20  
 <210>1836  
 <211>20  
 <212>DNA  
 <400>1836  
 gcttgcagct gacgaatatg 20  
 <210>1837  
 <211>20  
 <212>DNA  
 <400>1837  
 cattctggga gctatcccta 20  
 <210>1838  
 <211>20  
 <212>DNA  
 <400>1838  
 cagaacaaga aggctcctca 20  
 <210>1839  
 <211>20  
 <212>DNA  
 <400>1839  
 ctcggcctcg gaatagtaag 20  
 <210>1840  
 <211>20  
 <212>DNA  
 <400>1840  
 cctataacac cgcaaattctc 20  
 <210>1841  
 <211>20  
 <212>DNA  
 <400>1841  
 ccgaagcagc cttcttcaat 20  
 <210>1842  
 <211>20  
 <212>DNA  
 <400>1842  
 actgcttcca gcttgggaat 20  
 <210>1843  
 <211>20  
 <212>DNA  
 <400>1843  
 gactcgggat ttagctctt 20  
 <210>1844

```

<211>20
<212>DNA
<400>1844
ccgtggtcctt tgcttacgat      20
<210>1845
<211>20
<212>DNA
<400>1845
gcatccctgg aatttcttgc      20
<210>1846
<211>20
<212>DNA
<400>1846
gggccttcct acctttccta      20
<210>1847
<211>20
<212>DNA
<400>1847
gcttgcagct gacgaatatg      20
<210>1848
<211>20
<212>DNA
<400>1848
gccaggggaag aatcacatca      20
<210>1849
<211>20
<212>DNA
<400>1849
cgcagtgcac agaactagga      20
<210>1850
<211>20
<212>DNA
<400>1850
gaacttgga cctcgacatt      20
<210>1851
<211>20
<212>DNA
<400>1851
gggccacttt gcgctatatt      20
<210>1852
<211>20
<212>DNA
<400>1852
caaatcggga gtctcaagat      20
<210>1853
<211>20
<212>DNA
<400>1853
gtgacaagaa gcaccgtctt      20
<210>1854
<211>20
<212>DNA
<400>1854
ccagggatag ggtgaaaagc      20
<210>1855
<211>20
<212>DNA
<400>1855
cactcttgag caaggtatcc      20
<210>1856
<211>20
<212>DNA
<400>1856
gcaaccccag tatatctcca      20

```

<210>1857  
<211>20  
<212>DNA  
<400>1857  
gagtaacccc aggtaaagca 20  
<210>1858  
<211>20  
<212>DNA  
<400>1858  
ccgccatcgc tatgaagtaa 20  
<210>1859  
<211>20  
<212>DNA  
<400>1859  
gcagtgatga cttctcctac 20  
<210>1860  
<211>20  
<212>DNA  
<400>1860  
cagtacaagc ggaacgtatg 20  
<210>1861  
<211>20  
<212>DNA  
<400>1861  
ggaggagttg tctcctcttt 20  
<210>1862  
<211>20  
<212>DNA  
<400>1862  
tcgggatatg gtacagaacc 20  
<210>1863  
<211>20  
<212>DNA  
<400>1863  
atggaactct ctcaatgcga 20  
<210>1864  
<211>20  
<212>DNA  
<400>1864  
ccagaagcat acgagcgttt 20  
<210>1865  
<211>20  
<212>DNA  
<400>1865  
caagccatgt ctaagccatc 20  
<210>1866  
<211>20  
<212>DNA  
<400>1866  
gaccttaacc tttccttgcg 20  
<210>1867  
<211>20  
<212>DNA  
<400>1867  
gatttccaac agcgcctctt 20  
<210>1868  
<211>20  
<212>DNA  
<400>1868  
cctccttgaa ctaactgagc 20  
<210>1869  
<211>20  
<212>DNA  
<400>1869

ggcataggat ctgcggcaa 20  
 <210>1870  
 <211>20  
 <212>DNA  
 <400>1870  
 gcagctcgat ggaagacatt 20  
 <210>1871  
 <211>20  
 <212>DNA  
 <400>1871  
 gccgaagaat gttcacgttg 20  
 <210>1872  
 <211>20  
 <212>DNA  
 <400>1872  
 cttcaactct cgagactgat 20  
 <210>1873  
 <211>20  
 <212>DNA  
 <400>1873  
 cggggagcat tttatgtagc 20  
 <210>1874  
 <211>20  
 <212>DNA  
 <400>1874  
 cctcatgaaa cagagtctcg 20  
 <210>1875  
 <211>20  
 <212>DNA  
 <400>1875  
 ggaggaaaat gaccttgtgg 20  
 <210>1876  
 <211>20  
 <212>DNA  
 <400>1876  
 cttcaactct cgagactgat 20  
 <210>1877  
 <211>20  
 <212>DNA  
 <400>1877  
 cggggagcat tttatgtagc 20  
 <210>1878  
 <211>20  
 <212>DNA  
 <400>1878  
 gaagaagagt ttccttggtc 20  
 <210>1879  
 <211>20  
 <212>DNA  
 <400>1879  
 gctcctaaaa cgatcgctga 20  
 <210>1880  
 <211>20  
 <212>DNA  
 <400>1880  
 cctcgggcta ggaatacttt 20  
 <210>1881  
 <211>20  
 <212>DNA  
 <400>1881  
 acctgcagct cgatggaaga 20  
 <210>1882  
 <211>20  
 <212>DNA



## WO 99/27105

<400>1882  
 ccgccataaa agggtagaga 20  
 <210>1883  
 <211>20  
 <212>DNA  
 <400>1883  
 gcacgctata cacagaagca 20  
 <210>1884  
 <211>20  
 <212>DNA  
 <400>1884  
 ccccatgtcg tacgaaaagt 20  
 <210>1885  
 <211>20  
 <212>DNA  
 <400>1885  
 gtaggcccga acacaatagc 20  
 <210>1886  
 <211>20  
 <212>DNA  
 <400>1886  
 gacgataccc cggaaatcat 20  
 <210>1887  
 <211>20  
 <212>DNA  
 <400>1887  
 ctgccaatg aagaatcggg 20  
 <210>1888  
 <211>20  
 <212>DNA  
 <400>1888  
 gctgcagatc aatatgcgga 20  
 <210>1889  
 <211>20  
 <212>DNA  
 <400>1889  
 tacacgaggg cagaggcctt 20  
 <210>1890  
 <211>20  
 <212>DNA  
 <400>1890  
 ccaccgtca cacgaataat 20  
 <210>1891  
 <211>20  
 <212>DNA  
 <400>1891  
 ccccatgtcg tacgaaaagt 20  
 <210>1892  
 <211>20  
 <212>DNA  
 <400>1892  
 gtcttactag agagggcgat 20  
 <210>1893  
 <211>20  
 <212>DNA  
 <400>1893  
 gggaagctat gtagggtttc 20  
 <210>1894  
 <211>20  
 <212>DNA  
 <400>1894  
 cctgcatgca gtgataacga 20  
 <210>1895  
 <211>20

```

<212>DNA
<400>1895
gtggaggggaa aaaagtggag      20
<210>1896
<211>20
<212>DNA
<400>1896
gacaaagccg atatgctggt      20
<210>1897
<211>20
<212>DNA
<400>1897
cctagaaacg ctgcagatca      20
<210>1898
<211>20
<212>DNA
<400>1898
cttccccttc ctggaatcaa      20
<210>1899
<211>20
<212>DNA
<400>1899
cgagtccgta ctttgtcttc      20
<210>1900
<211>20
<212>DNA
<400>1900
cagaagctca ttgggggaaaa      20
<210>1901
<211>20
<212>DNA
<400>1901
tttgctgccc tcctagatca      20
<210>1902
<211>20
<212>DNA
<400>1902
ccagaacacg tcgacatagc      20
<210>1903
<211>20
<212>DNA
<400>1903
cttccccttc ctggaatcaa      20
<210>1904
<211>20
<212>DNA
<400>1904
cggaaagatc gttctggcat      20
<210>1905
<211>20
<212>DNA
<400>1905
gcaggttacg agtctactaa      20
<210>1906
<211>20
<212>DNA
<400>1906
gcagacacat tacccttcac      20
<210>1907
<211>20
<212>DNA
<400>1907
cccggcagca gaactccctg      20
<210>1908

```

<211>20  
<212>DNA  
<400>1908  
caccatctac agttgagtct 20  
<210>1909  
<211>20  
<212>DNA  
<400>1909  
gtcctccatc tgcataca 20  
<210>1910  
<211>20  
<212>DNA  
<400>1910  
gctattggtg cttgtaggtc 20  
<210>1911  
<211>20  
<212>DNA  
<400>1911  
catggagaag tcgtggtatc 20  
<210>1912  
<211>20  
<212>DNA  
<400>1912  
atccgcccc gacagtaa 20  
<210>1913  
<211>20  
<212>DNA  
<400>1913  
cctgaagtta atccagttgc 20  
<210>1914  
<211>20  
<212>DNA  
<400>1914  
ctgtgatctc cattgcgaac 20  
<210>1915  
<211>20  
<212>DNA  
<400>1915  
cgtaagaaat agaagccaag 20  
<210>1916  
<211>20  
<212>DNA  
<400>1916  
tggctggatt tgaaccaacg 20  
<210>1917  
<211>20  
<212>DNA  
<400>1917  
actagtccta tgctctctg 20  
<210>1918  
<211>20  
<212>DNA  
<400>1918  
gtgatectct tccacacaag 20  
<210>1919  
<211>20  
<212>DNA  
<400>1919  
ccgcgctgtg atctccattg 20  
<210>1920  
<211>20  
<212>DNA  
<400>1920  
gctaaggaaa acgcttcgca 20

<210>1921  
<211>20  
<212>DNA  
<400>1921  
ccatctactg ttgaatcgag 20  
<210>1922  
<211>20  
<212>DNA  
<400>1922  
cccctagtct ttggtatcag 20  
<210>1923  
<211>20  
<212>DNA  
<400>1923  
gtgatcctct tccacacaag 20  
<210>1924  
<211>20  
<212>DNA  
<400>1924  
gctaggccat attctcatgg 20  
<210>1925  
<211>20  
<212>DNA  
<400>1925  
catgggtcat ccaaatacaca 20  
<210>1926  
<211>20  
<212>DNA  
<400>1926  
ctgacgctaa agagctctct 20  
<210>1927  
<211>20  
<212>DNA  
<400>1927  
ctcttgtctc aaccctttcc 20  
<210>1928  
<211>20  
<212>DNA  
<400>1928  
gccaagacaa caagctgatt 20  
<210>1929  
<211>20  
<212>DNA  
<400>1929  
cggagaacct agaaaccttc 20  
<210>1930  
<211>20  
<212>DNA  
<400>1930  
caattcgccct aacaccagag 20  
<210>1931  
<211>20  
<212>DNA  
<400>1931  
caggaacact acgcaatcct 20  
<210>1932  
<211>20  
<212>DNA  
<400>1932  
ctctttgttg ggggattggc 20  
<210>1933  
<211>20  
<212>DNA  
<400>1933

cgtatagagg gtagttcttg	20
<210>1934	
<211>20	
<212>DNA	
<400>1934	
gggattggca gggttgcgga	20
<210>1935	
<211>20	
<212>DNA	
<400>1935	
gggtagttct tgtgcatcag	20
<210>1936	
<211>20	
<212>DNA	
<400>1936	
gactccctga aactgaagag	20
<210>1937	
<211>20	
<212>DNA	
<400>1937	
aggttcccta ggactcagcg	20
<210>1938	
<211>20	
<212>DNA	
<400>1938	
gaggatccgt tctcttcttc	20
<210>1939	
<211>20	
<212>DNA	
<400>1939	
ctctcctgga ttaagcgttc	20
<210>1940	
<211>20	
<212>DNA	
<400>1940	
gggaacaagg gccatcaaaa	20
<210>1941	
<211>20	
<212>DNA	
<400>1941	
gtagcagtac atctacctgg	20
<210>1942	
<211>20	
<212>DNA	
<400>1942	
ccgcacaaaa ccgcttatac	20
<210>1943	
<211>20	
<212>DNA	
<400>1943	
gactcttgct tctcctttga	20
<210>1944	
<211>20	
<212>DNA	
<400>1944	
gccacggtta tgaagacgaa	20
<210>1945	
<211>20	
<212>DNA	
<400>1945	
atagcacaca cctgctgacg	20
<210>1946	
<211>20	
<212>DNA	

<400>1946  
gtcttccctt tccttctgga 20  
<210>1947  
<211>20  
<212>DNA  
<400>1947  
gctcctggga aaagttgagc 20  
<210>1948  
<211>20  
<212>DNA  
<400>1948  
gagcacgtga tccaagaaac 20  
<210>1949  
<211>20  
<212>DNA  
<400>1949  
ggttacggat cacttgctga 20  
<210>1950  
<211>20  
<212>DNA  
<400>1950  
ccagaggtat cccacaaat 20  
<210>1951  
<211>20  
<212>DNA  
<400>1951  
cgactgggtc tcagtcacaa 20  
<210>1952  
<211>20  
<212>DNA  
<400>1952  
acaatacccc cgtcctctaa 20  
<210>1953  
<211>20  
<212>DNA  
<400>1953  
gctatagtta cagcttgggg 20  
<210>1954  
<211>20  
<212>DNA  
<400>1954  
gaacttgaga tcctcccctt 20  
<210>1955  
<211>20  
<212>DNA  
<400>1955  
tccacgtcag catctgtcat 20  
<210>1956  
<211>20  
<212>DNA  
<400>1956  
cctcagcata agtgctacta 20  
<210>1957  
<211>20  
<212>DNA  
<400>1957  
ctccttggcg tgtaggaata 20  
<210>1958  
<211>20  
<212>DNA  
<400>1958  
gctcgattc gtcataaga 20  
<210>1959  
<211>20

```

<212>DNA
<400>1959
cagtaatagc ggatgcatcg      20
<210>1960
<211>20
<212>DNA
<400>1960
aatcgcaa at ggaatcgcg      20
<210>1961
<211>20
<212>DNA
<400>1961
ggataaggct tatctggaga      20
<210>1962
<211>20
<212>DNA
<400>1962
gacgaacttc ttggtgacga      20
<210>1963
<211>20
<212>DNA
<400>1963
ccccagaaa tctcctagaa      20
<210>1964
<211>20
<212>DNA
<400>1964
gtaggcctaa ttaactcggg      20
<210>1965
<211>20
<212>DNA
<400>1965
catcgatctc atgcgacact      20
<210>1966
<211>20
<212>DNA
<400>1966
gcctctattc tgtaccagga      20
<210>1967
<211>20
<212>DNA
<400>1967
ctacctatgg aacactgagc      20
<210>1968
<211>20
<212>DNA
<400>1968
gagctcgcaa aagctgtggt      20
<210>1969
<211>20
<212>DNA
<400>1969
aagcggctag aacagcagtg      20
<210>1970
<211>20
<212>DNA
<400>1970
ggtcgagtgt ttcttcggat      20
<210>1971
<211>20
<212>DNA
<400>1971
gtatcctgcc gtggttagctt      20
<210>1972

```

<211>20  
 <212>DNA  
 <400>1972  
 gagcagaccg atagagggat 20  
 <210>1973  
 <211>20  
 <212>DNA  
 <400>1973  
 ccatagcaat agtgattccg 20  
 <210>1974  
 <211>20  
 <212>DNA  
 <400>1974  
 atgacaccct accaaagcga 20  
 <210>1975  
 <211>20  
 <212>DNA  
 <400>1975  
 aggggggtgat tttcgaaagc 20  
 <210>1976  
 <211>20  
 <212>DNA  
 <400>1976  
 ccgcgaagca gaatctgtat 20  
 <210>1977  
 <211>20  
 <212>DNA  
 <400>1977  
 cgactcaaga aacgaggaag 20  
 <210>1978  
 <211>20  
 <212>DNA  
 <400>1978  
 gaaggtgttc ttaccacta 20  
 <210>1979  
 <211>20  
 <212>DNA  
 <400>1979  
 gcaagcttac ctaaacacac 20  
 <210>1980  
 <211>20  
 <212>DNA  
 <400>1980  
 cagaaacgga cagggtatca 20  
 <210>1981  
 <211>20  
 <212>DNA  
 <400>1981  
 gcctgatata cagaagcact 20  
 <210>1982  
 <211>20  
 <212>DNA  
 <400>1982  
 ataggaaatg cgggcgtacc 20  
 <210>1983  
 <211>20  
 <212>DNA  
 <400>1983  
 gcaagagggt ccaacaaact 20  
 <210>1984  
 <211>20  
 <212>DNA  
 <400>1984  
 ctcttccagg agccgttcaa 20



## WO 99/27105

<210>1985  
 <211>20  
 <212>DNA  
 <400>1985  
 gggaaagatg ccttaggact 20  
 <210>1986  
 <211>20  
 <212>DNA  
 <400>1986  
 gcagtgggtct ttaggactca 20  
 <210>1987  
 <211>20  
 <212>DNA  
 <400>1987  
 cctcgcccaa ggtttttattg 20  
 <210>1988  
 <211>20  
 <212>DNA  
 <400>1988  
 ggaagtactg aaggatctgt 20  
 <210>1989  
 <211>20  
 <212>DNA  
 <400>1989  
 cgccagtttt tcatctcgac 20  
 <210>1990  
 <211>20  
 <212>DNA  
 <400>1990  
 cgtcttgcct caagtagctt 20  
 <210>1991  
 <211>20  
 <212>DNA  
 <400>1991  
 agcaatggag ctctaacagc 20  
 <210>1992  
 <211>20  
 <212>DNA  
 <400>1992  
 cggtttcctt ttgaaactct 20  
 <210>1993  
 <211>20  
 <212>DNA  
 <400>1993  
 tgaaggcggtt acctacgctc 20  
 <210>1994  
 <211>20  
 <212>DNA  
 <400>1994  
 ccgcatgcta gttcttagca 20  
 <210>1995  
 <211>20  
 <212>DNA  
 <400>1995  
 agtatcttcc cccatcctgc 20  
 <210>1996  
 <211>20  
 <212>DNA  
 <400>1996  
 cttcttttgg atccactcct 20  
 <210>1997  
 <211>20  
 <212>DNA  
 <400>1997

gactacgaca atgctcgcac 20  
<210>1998  
<211>20  
<212>DNA  
<400>1998  
cgcaatcttt cactccacca 20  
<210>1999  
<211>20  
<212>DNA  
<400>1999  
gcgatccaga ctttccaatc 20  
<210>2000  
<211>20  
<212>DNA  
<400>2000  
ggccgcagta tttccatact 20  
<210>2001  
<211>20  
<212>DNA  
<400>2001  
ctagggacaa agagaaagag 20  
<210>2002  
<211>20  
<212>DNA  
<400>2002  
ctggccgact ctcccctatg 20  
<210>2003  
<211>20  
<212>DNA  
<400>2003  
cagcttttagc agcagcatag 20  
<210>2004  
<211>20  
<212>DNA  
<400>2004  
gctatagctt tctctgcagc 20  
<210>2005  
<211>20  
<212>DNA  
<400>2005  
ccacccaagc ctgttaaact 20  
<210>2006  
<211>20  
<212>DNA  
<400>2006  
gagttatttg agcgacaagg 20  
<210>2007  
<211>20  
<212>DNA  
<400>2007  
acatatggc tcccttggtc 20  
<210>2008  
<211>20  
<212>DNA  
<400>2008  
cccttcgctc caaccgagac 20  
<210>2009  
<211>20  
<212>DNA  
<400>2009  
ggaaatcaag tcgttctctga 20  
<210>2010  
<211>20  
<212>DNA

<400>2010  
 gcgtaccagt ctcagtacta 20  
 <210>2011  
 <211>20  
 <212>DNA  
 <400>2011  
 gaggttttgc caaaacgcct 20  
 <210>2012  
 <211>20  
 <212>DNA  
 <400>2012  
 acctctccag gcatttatgg 20  
 <210>2013  
 <211>20  
 <212>DNA  
 <400>2013  
 gagactacag ttcggggata 20  
 <210>2014  
 <211>20  
 <212>DNA  
 <400>2014  
 ccgtctatcg aatccacgta 20  
 <210>2015  
 <211>20  
 <212>DNA  
 <400>2015  
 gcaacatgcc cacctaaaga 20  
 <210>2016  
 <211>20  
 <212>DNA  
 <400>2016  
 ccgatttcga gggcattcta 20  
 <210>2017  
 <211>20  
 <212>DNA  
 <400>2017  
 gtccgcaata gttgcatgac 20  
 <210>2018  
 <211>20  
 <212>DNA  
 <400>2018  
 atgactggag ggaagttttc 20  
 <210>2019  
 <211>20  
 <212>DNA  
 <400>2019  
 cccctcccaa acctatagaa 20  
 <210>2020  
 <211>20  
 <212>DNA  
 <400>2020  
 cggtacgaaa aacttcacgc 20  
 <210>2021  
 <211>20  
 <212>DNA  
 <400>2021  
 cgtccatgtg atgtaatcct 20  
 <210>2022  
 <211>20  
 <212>DNA  
 <400>2022  
 caggccactt tgcctaattgt 20  
 <210>2023  
 <211>20

<212>DNA  
 <400>2023  
 cgggcccgcgct tcctgtatta 20  
 <210>2024  
 <211>20  
 <212>DNA  
 <400>2024  
 taacaagctg ccagtctccc 20  
 <210>2025  
 <211>20  
 <212>DNA  
 <400>2025  
 agactccaag tcagccaaga 20  
 <210>2026  
 <211>20  
 <212>DNA  
 <400>2026  
 gctcttggtc ttgacggaga 20  
 <210>2027  
 <211>20  
 <212>DNA  
 <400>2027  
 gcctgcgccc tattatagaa 20  
 <210>2028  
 <211>20  
 <212>DNA  
 <400>2028  
 gcccgtttca tagagtcaac 20  
 <210>2029  
 <211>20  
 <212>DNA  
 <400>2029  
 tgctcagcca tagaaactcg 20  
 <210>2030  
 <211>20  
 <212>DNA  
 <400>2030  
 ccttaggaat cggccattgt 20  
 <210>2031  
 <211>20  
 <212>DNA  
 <400>2031  
 ggcaaaggaa cggatcaatg 20  
 <210>2032  
 <211>20  
 <212>DNA  
 <400>2032  
 gaacacgaat gggcttattg 20  
 <210>2033  
 <211>20  
 <212>DNA  
 <400>2033  
 gcccgtttca tagagtcaac 20  
 <210>2034  
 <211>20  
 <212>DNA  
 <400>2034  
 cagctagcgt ctgttctgaa 20  
 <210>2035  
 <211>20  
 <212>DNA  
 <400>2035  
 cgaggctcct cgtaataaga 20  
 <210>2036

<211>20  
 <212>DNA  
 <400>2036  
 cgaccaagta actgattccc 20  
 <210>2037  
 <211>20  
 <212>DNA  
 <400>2037  
 gcaaggtctc atatccagga 20  
 <210>2038  
 <211>20  
 <212>DNA  
 <400>2038  
 gcgtagctgg cttttggaaa 20  
 <210>2039  
 <211>20  
 <212>DNA  
 <400>2039  
 gggatatagga aagaactcgg 20  
 <210>2040  
 <211>20  
 <212>DNA  
 <400>2040  
 cagctgagtc tatcttctga 20  
 <210>2041  
 <211>20  
 <212>DNA  
 <400>2041  
 ggaatatagt cgcttcctga 20  
 <210>2042  
 <211>20  
 <212>DNA  
 <400>2042  
 ccttcatttg caggtcgctt 20  
 <210>2043  
 <211>20  
 <212>DNA  
 <400>2043  
 ccaacacgaa ctgcgtagtt 20  
 <210>2044  
 <211>20  
 <212>DNA  
 <400>2044  
 gcgccaaatc ctgtttctct 20  
 <210>2045  
 <211>20  
 <212>DNA  
 <400>2045  
 gccttctctt tagtccttcg 20  
 <210>2046  
 <211>20  
 <212>DNA  
 <400>2046  
 ctgacaagcc ctttgcaaaa 20  
 <210>2047  
 <211>20  
 <212>DNA  
 <400>2047  
 gacgagaatt tatgggggtgc 20  
 <210>2048  
 <211>20  
 <212>DNA  
 <400>2048  
 tctgaaaatg gtggagcgga 20

<210>2049  
<211>20  
<212>DNA  
<400>2049  
ccttcctacc tggatcacao 20  
<210>2050  
<211>20  
<212>DNA  
<400>2050  
cgagctcgaa gtacaacgta 20  
<210>2051  
<211>20  
<212>DNA  
<400>2051  
ccctacggag ctttcattga 20  
<210>2052  
<211>20  
<212>DNA  
<400>2052  
cgatcctttc ttcgtcgtga 20  
<210>2053  
<211>20  
<212>DNA  
<400>2053  
gatccttgag caagtcagca 20  
<210>2054  
<211>20  
<212>DNA  
<400>2054  
gatgaagggt ctgctgagat 20  
<210>2055  
<211>20  
<212>DNA  
<400>2055  
gctgaacctt aaagcgtcgt 20  
<210>2056  
<211>20  
<212>DNA  
<400>2056  
gcactctgca cgtgtttatg 20  
<210>2057  
<211>20  
<212>DNA  
<400>2057  
cgtcaaagat ctggcaacag 20  
<210>2058  
<211>20  
<212>DNA  
<400>2058  
cagttcaagt tcacttgcag 20  
<210>2059  
<211>20  
<212>DNA  
<400>2059  
cgcaaaaaca ggagaaggtc 20  
<210>2060  
<211>20  
<212>DNA  
<400>2060  
ctacctgtca ggggtgttatg 20  
<210>2061  
<211>20  
<212>DNA  
<400>2061

gtcaaagaag ttcgcaaagg	20
<210>2062	
<211>20	
<212>DNA	
<400>2062	
gcagcagcga ctaatctatg	20
<210>2063	
<211>20	
<212>DNA	
<400>2063	
gactatggat cttgcagtag	20
<210>2064	
<211>20	
<212>DNA	
<400>2064	
cgattgaagt tttccctacc	20
<210>2065	
<211>20	
<212>DNA	
<400>2065	
gactgggttag gtgtccttac	20
<210>2066	
<211>20	
<212>DNA	
<400>2066	
tttggatgat gggcgttgtc	20
<210>2067	
<211>20	
<212>DNA	
<400>2067	
cgtgtgtaac gtctggatca	20
<210>2068	
<211>20	
<212>DNA	
<400>2068	
gcaggttctt accttgctct	20
<210>2069	
<211>20	
<212>DNA	
<400>2069	
caatttcgtc agcagaacac	20
<210>2070	
<211>20	
<212>DNA	
<400>2070	
gaagctggaa aggctgagaa	20
<210>2071	
<211>20	
<212>DNA	
<400>2071	
gctggtatga ttgatgccac	20
<210>2072	
<211>20	
<212>DNA	
<400>2072	
tccgcaatct cataggagac	20
<210>2073	
<211>20	
<212>DNA	
<400>2073	
ggcattcatg ttcgcacaga	20
<210>2074	
<211>20	
<212>DNA	

<400>2074  
 ctctgtaaat ggctcgttcc 20  
 <210>2075  
 <211>20  
 <212>DNA  
 <400>2075  
 ccattgcaaa agcttacgga 20  
 <210>2076  
 <211>20  
 <212>DNA  
 <400>2076  
 ccttccttag aagaactcgc 20  
 <210>2077  
 <211>20  
 <212>DNA  
 <400>2077  
 ccatgtccct gtgcaaataag 20  
 <210>2078  
 <211>20  
 <212>DNA  
 <400>2078  
 cgccgtgggtt atagctatac 20  
 <210>2079  
 <211>20  
 <212>DNA  
 <400>2079  
 cctgaccttc atgttttggg 20  
 <210>2080  
 <211>20  
 <212>DNA  
 <400>2080  
 tcccttcggtt atcgatgccc 20  
 <210>2081  
 <211>20  
 <212>DNA  
 <400>2081  
 acaggaaaga gacctcgccg 20  
 <210>2082  
 <211>20  
 <212>DNA  
 <400>2082  
 ggtctaaagg aagattctcc 20  
 <210>2083  
 <211>20  
 <212>DNA  
 <400>2083  
 cagtctccaa catgacttcc 20  
 <210>2084  
 <211>20  
 <212>DNA  
 <400>2084  
 cttgcttttg tccgagtagc 20  
 <210>2085  
 <211>20  
 <212>DNA  
 <400>2085  
 cttcccatg gatatcaggg 20  
 <210>2086  
 <211>20  
 <212>DNA  
 <400>2086  
 ctcttcttag gcttcccat 20  
 <210>2087  
 <211>20



```

<212>DNA
<400>2087
gttcctccct ggaaacgatg      20
<210>2088
<211>20
<212>DNA
<400>2088
agccgccttg gtcattgtga      20
<210>2089
<211>20
<212>DNA
<400>2089
tctatcatgc cttcgttgcc      20
<210>2090
<211>20
<212>DNA
<400>2090
cggaaaacct cccagaaatc      20
<210>2091
<211>20
<212>DNA
<400>2091
gccacctgaa actgccataa      20
<210>2092
<211>20
<212>DNA
<400>2092
gcagcaggta cgatcttaga      20
<210>2093
<211>20
<212>DNA
<400>2093
taagggactg gtactcgctc      20
<210>2094
<211>20
<212>DNA
<400>2094
cccccataat tggggacaaa      20
<210>2095
<211>20
<212>DNA
<400>2095
atgtggacgg gcttcaccct      20
<210>2096
<211>20
<212>DNA
<400>2096
gagaggcgta gcccttcata      20
<210>2097
<211>20
<212>DNA
<400>2097
gccctcatga tgcaaaagca      20
<210>2098
<211>20
<212>DNA
<400>2098
ggaaaggtaa gcatggctgt      20
<210>2099
<211>20
<212>DNA
<400>2099
gaagcagcag gtacgatctt      20
<210>2100

```

<211>20  
<212>DNA  
<400>2100  
ccttcggatc ttcccatttc 20  
<210>2101  
<211>20  
<212>DNA  
<400>2101  
gaggaatcaa agtcatgccc 20  
<210>2102  
<211>20  
<212>DNA  
<400>2102  
ctgggtcaga ctctgattac 20  
<210>2103  
<211>20  
<212>DNA  
<400>2103  
cgctatttcc attccctcca 20  
<210>2104  
<211>20  
<212>DNA  
<400>2104  
gggggattaa aggaaacctc 20  
<210>2105  
<211>20  
<212>DNA  
<400>2105  
ctgacggaaa gcgttttagca 20  
<210>2106  
<211>20  
<212>DNA  
<400>2106  
ccacacgagt catacctaca 20  
<210>2107  
<211>20  
<212>DNA  
<400>2107  
ctcactggct cctaaactca 20  
<210>2108  
<211>20  
<212>DNA  
<400>2108  
ctgatacgaa catagcctcc 20  
<210>2109  
<211>20  
<212>DNA  
<400>2109  
ccacacgagt catacctaca 20  
<210>2110  
<211>20  
<212>DNA  
<400>2110  
gctaacggag caaactcctg 20  
<210>2111  
<211>20  
<212>DNA  
<400>2111  
ccctagggtg acgagaaaag 20  
<210>2112  
<211>20  
<212>DNA  
<400>2112  
ggacagtatg agagacagca 20

<210>2113  
 <211>20  
 <212>DNA  
 <400>2113  
 gagtggcagg cataaacctt 20  
 <210>2114  
 <211>20  
 <212>DNA  
 <400>2114  
 atttgtcgat accaccacca 20  
 <210>2115  
 <211>20  
 <212>DNA  
 <400>2115  
 cgcaagtcga ggaattgtca 20  
 <210>2116  
 <211>20  
 <212>DNA  
 <400>2116  
 cagcacaccc aaacaacaca 20  
 <210>2117  
 <211>20  
 <212>DNA  
 <400>2117  
 gaccaagcca taagactcct 20  
 <210>2118  
 <211>20  
 <212>DNA  
 <400>2118  
 atgcgctgac gcaccttctt 20  
 <210>2119  
 <211>20  
 <212>DNA  
 <400>2119  
 cccaaagcca ttagacttcc 20  
 <210>2120  
 <211>20  
 <212>DNA  
 <400>2120  
 tttactttac gatttttatg 20  
 <210>2121  
 <211>20  
 <212>DNA  
 <400>2121  
 cagtagggcc acaacaaatc 20  
 <210>2122  
 <211>20  
 <212>DNA  
 <400>2122  
 gctgtaagct ctcccaacct 20  
 <210>2123  
 <211>20  
 <212>DNA  
 <400>2123  
 cccctcctaa ttcttctgtg 20  
 <210>2124  
 <211>20  
 <212>DNA  
 <400>2124  
 ggagctatga ccccttatct 20  
 <210>2125  
 <211>20  
 <212>DNA  
 <400>2125

agaatcgga accccacgca 20  
 <210>2126  
 <211>20  
 <212>DNA  
 <400>2126  
 cgagtgtct tgttcagaag 20  
 <210>2127  
 <211>20  
 <212>DNA  
 <400>2127  
 ctcttggtta ttgcctatgg 20  
 <210>2128  
 <211>20  
 <212>DNA  
 <400>2128  
 aggggctcgc ccttttttta 20  
 <210>2129  
 <211>20  
 <212>DNA  
 <400>2129  
 gggtgtcga gctatacaga 20  
 <210>2130  
 <211>20  
 <212>DNA  
 <400>2130  
 ccgtcgtcag tcaaccaata 20  
 <210>2131  
 <211>20  
 <212>DNA  
 <400>2131  
 ggaacaggct cagatgattc 20  
 <210>2132  
 <211>20  
 <212>DNA  
 <400>2132  
 gctctctctt acccttcaga 20  
 <210>2133  
 <211>20  
 <212>DNA  
 <400>2133  
 ccctctcttc aagaggatga 20  
 <210>2134  
 <211>20  
 <212>DNA  
 <400>2134  
 cccgtgtttt gttggtttgc 20  
 <210>2135  
 <211>20  
 <212>DNA  
 <400>2135  
 taaaacgatc cgtcgtcagt 20  
 <210>2136  
 <211>20  
 <212>DNA  
 <400>2136  
 ctagccactc tggaactcta 20  
 <210>2137  
 <211>20  
 <212>DNA  
 <400>2137  
 gtcattgtca tagccaactc 20  
 <210>2138  
 <211>20  
 <212>DNA

<400>2138  
 gcaaagtgtt atggcggaga 20  
 <210>2139  
 <211>20  
 <212>DNA  
 <400>2139  
 cactctggaa ctctacctca 20  
 <210>2140  
 <211>20  
 <212>DNA  
 <400>2140  
 ggaaagggga actccagaat 20  
 <210>2141  
 <211>20  
 <212>DNA  
 <400>2141  
 cccttacgtt ggcattatgg 20  
 <210>2142  
 <211>20  
 <212>DNA  
 <400>2142  
 ctttcgtggg ctctccaatg 20  
 <210>2143  
 <211>20  
 <212>DNA  
 <400>2143  
 cccctcaaga atatctgagc 20  
 <210>2144  
 <211>20  
 <212>DNA  
 <400>2144  
 ggattccaaa cctgcggtaa 20  
 <210>2145  
 <211>20  
 <212>DNA  
 <400>2145  
 ccggatcttt caatgctagg 20  
 <210>2146  
 <211>20  
 <212>DNA  
 <400>2146  
 caaggcacca cctatctaac 20  
 <210>2147  
 <211>20  
 <212>DNA  
 <400>2147  
 aagaacagca gggacggccc 20  
 <210>2148  
 <211>20  
 <212>DNA  
 <400>2148  
 ggcatccctg aaatcaaacg 20  
 <210>2149  
 <211>20  
 <212>DNA  
 <400>2149  
 cgtctgtaca cgcctatcaa 20  
 <210>2150  
 <211>20  
 <212>DNA  
 <400>2150  
 gagaatccct gccttttctc 20  
 <210>2151  
 <211>20

<212>DNA  
 <400>2151  
 cagtagaagt tccaaacctc 20  
 <210>2152  
 <211>20  
 <212>DNA  
 <400>2152  
 ggtggctgtg tcaaagttac 20  
 <210>2153  
 <211>20  
 <212>DNA  
 <400>2153  
 ttctctaaca aggaggcgag 20  
 <210>2154  
 <211>20  
 <212>DNA  
 <400>2154  
 gtctccacca acctacagta 20  
 <210>2155  
 <211>20  
 <212>DNA  
 <400>2155  
 aataagagtg gctgcagcac 20  
 <210>2156  
 <211>20  
 <212>DNA  
 <400>2156  
 caagatcttt ccatgacgca 20  
 <210>2157  
 <211>20  
 <212>DNA  
 <400>2157  
 cagcttggtt agcgcggttg 20  
 <210>2158  
 <211>20  
 <212>DNA  
 <400>2158  
 gggtagaatc gttccccata 20  
 <210>2159  
 <211>20  
 <212>DNA  
 <400>2159  
 ccctctgcat tactcacaga 20  
 <210>2160  
 <211>20  
 <212>DNA  
 <400>2160  
 ctggactctc caagatccta 20  
 <210>2161  
 <211>20  
 <212>DNA  
 <400>2161  
 gtacagtaga ttcgcgaacg 20  
 <210>2162  
 <211>20  
 <212>DNA  
 <400>2162  
 ccgtacgtag tgggtaaattg 20  
 <210>2163  
 <211>20  
 <212>DNA  
 <400>2163  
 ctgccattgc agtccttgct 20  
 <210>2164

```

<211>20
<212>DNA
<400>2164
ccgccccgtt tcgatctaac 20
<210>2165
<211>20
<212>DNA
<400>2165
cctgaaaacc tcaggaagag 20
<210>2166
<211>20
<212>DNA
<400>2166
cccctgggta agcaaaagag 20
<210>2167
<211>20
<212>DNA
<400>2167
ctcccgagaa ggaggggggaa 20
<210>2168
<211>20
<212>DNA
<400>2168
gaacaactgc tgaacagcag 20
<210>2169
<211>20
<212>DNA
<400>2169
tatgtcggaa agcgtccgtg 20
<210>2170
<211>20
<212>DNA
<400>2170
gttccttacg aatcgtcctc 20
<210>2171
<211>20
<212>DNA
<400>2171
caggctaaca cagatatgcc 20
<210>2172
<211>20
<212>DNA
<400>2172
cctaccagga cttaagatcg 20
<210>2173
<211>20
<212>DNA
<400>2173
gggattcggt ctacgaacac 20
<210>2174
<211>20
<212>DNA
<400>2174
cccaatctca caggccaaca 20
<210>2175
<211>20
<212>DNA
<400>2175
ggaatggtag cctcagcaat 20
<210>2176
<211>20
<212>DNA
<400>2176
gaggaagcag atgcactttc 20

```

<210>2177  
<211>20  
<212>DNA  
<400>2177  
ccatcaagtg ccttgccctat 20  
<210>2178  
<211>20  
<212>DNA  
<400>2178  
cttgatcata ccgggaaacc 20  
<210>2179  
<211>20  
<212>DNA  
<400>2179  
tattccttcca cactcacccct 20  
<210>2180  
<211>20  
<212>DNA  
<400>2180  
ccaaaatccc cacttgcggg 20  
<210>2181  
<211>20  
<212>DNA  
<400>2181  
ctgtcaccgt aggtactatg 20  
<210>2182  
<211>20  
<212>DNA  
<400>2182  
ccccccctac aggaacaaca 20  
<210>2183  
<211>20  
<212>DNA  
<400>2183  
cgaagcttta ggcttccctc 20  
<210>2184  
<211>20  
<212>DNA  
<400>2184  
ccgagctgat acccttcaaa 20  
<210>2185  
<211>20  
<212>DNA  
<400>2185  
gcaccattag caaaatcccc 20  
<210>2186  
<211>20  
<212>DNA  
<400>2186  
ggcaccaaga agaaatccga 20  
<210>2187  
<211>20  
<212>DNA  
<400>2187  
agagtctcgc gatccaaaga 20  
<210>2188  
<211>20  
<212>DNA  
<400>2188  
gcgatgcac cccatagaaa 20  
<210>2189  
<211>20  
<212>DNA  
<400>2189



ttctagctga gatgagcctc	20
<210>2190	
<211>20	
<212>DNA	
<400>2190	
taaataagaca gggccgtctc	20
<210>2191	
<211>20	
<212>DNA	
<400>2191	
ggggcaagcg ttgaaatttg	20
<210>2192	
<211>20	
<212>DNA	
<400>2192	
ctgacaatga taccggggat	20
<210>2193	
<211>20	
<212>DNA	
<400>2193	
ggcgtaatac ggacttcaca	20
<210>2194	
<211>20	
<212>DNA	
<400>2194	
gtgctgtcat caacgctcta	20
<210>2195	
<211>20	
<212>DNA	
<400>2195	
ttcggactcc tgatgctccg	20
<210>2196	
<211>20	
<212>DNA	
<400>2196	
ccgtgtttta cgataggctc	20
<210>2197	
<211>20	
<212>DNA	
<400>2197	
cggaatctct ctctagactg	20
<210>2198	
<211>20	
<212>DNA	
<400>2198	
cgcctgggaa aagtcatcaa	20
<210>2199	
<211>20	
<212>DNA	
<400>2199	
tgttggtggt gaagatcgag	20
<210>2200	
<211>20	
<212>DNA	
<400>2200	
cgcctgggaa aagtcatcaa	20
<210>2201	
<211>20	
<212>DNA	
<400>2201	
ttggggatag aggttccggt	20
<210>2202	
<211>20	
<212>DNA	

<400>2202  
 ccgcaacttt ttttagcaggc 20  
 <210>2203  
 <211>20  
 <212>DNA  
 <400>2203  
 ctgaaaaagc ctgcacagga 20  
 <210>2204  
 <211>20  
 <212>DNA  
 <400>2204  
 ggctgacgcc tctaaaagat 20  
 <210>2205  
 <211>20  
 <212>DNA  
 <400>2205  
 gatccctctt caatactacg 20  
 <210>2206  
 <211>20  
 <212>DNA  
 <400>2206  
 gcctaagagg acaatgcggt 20  
 <210>2207  
 <211>20  
 <212>DNA  
 <400>2207  
 gccatgcttt ctcgtagctg 20  
 <210>2208  
 <211>20  
 <212>DNA  
 <400>2208  
 ccagaggctt gagcatgaaa 20  
 <210>2209  
 <211>20  
 <212>DNA  
 <400>2209  
 cgctctctta gctgtagtct 20  
 <210>2210  
 <211>20  
 <212>DNA  
 <400>2210  
 cgctcttcag gatctgcccc 20  
 <210>2211  
 <211>20  
 <212>DNA  
 <400>2211  
 cgaacaccaa aacctgaagc 20  
 <210>2212  
 <211>20  
 <212>DNA  
 <400>2212  
 ggtgaagaga gaactcacca 20  
 <210>2213  
 <211>20  
 <212>DNA  
 <400>2213  
 ggtctaaacc tccagagtca 20  
 <210>2214  
 <211>20  
 <212>DNA  
 <400>2214  
 cgccctggaa atttcttagc 20  
 <210>2215  
 <211>20

## WO 99/27105

<212>DNA  
 <400>2215  
 gacatgaggg aatctccttg 20  
 <210>2216  
 <211>20  
 <212>DNA  
 <400>2216  
 ggccttgaat cgctgtgtct 20  
 <210>2217  
 <211>20  
 <212>DNA  
 <400>2217  
 ttatgcctct gatccttgcg 20  
 <210>2218  
 <211>20  
 <212>DNA  
 <400>2218  
 cctacctgaa gttctcccta 20  
 <210>2219  
 <211>20  
 <212>DNA  
 <400>2219  
 gcaagcagat agagcttctt 20  
 <210>2220  
 <211>20  
 <212>DNA  
 <400>2220  
 ccgcctatct cgagaattca 20  
 <210>2221  
 <211>20  
 <212>DNA  
 <400>2221  
 ctgagaatcc tgagatactc 20  
 <210>2222  
 <211>20  
 <212>DNA  
 <400>2222  
 ggagttacgt acagaagagc 20  
 <210>2223  
 <211>20  
 <212>DNA  
 <400>2223  
 gaggagcgga ctaaaatctc 20  
 <210>2224  
 <211>20  
 <212>DNA  
 <400>2224  
 cacctcagga gctgatgtta 20  
 <210>2225  
 <211>20  
 <212>DNA  
 <400>2225  
 agatggccct aaatgccgat 20  
 <210>2226  
 <211>20  
 <212>DNA  
 <400>2226  
 cctggcaact ctgcataaaa 20  
 <210>2227  
 <211>20  
 <212>DNA  
 <400>2227  
 ccgtagcccc tcttattctt 20  
 <210>2228

<211>20  
<212>DNA  
<400>2228  
gaggacacgg ccctgaaacg 20  
<210>2229  
<211>20  
<212>DNA  
<400>2229  
ccagattacg ctcctttcac 20  
<210>2230  
<211>20  
<212>DNA  
<400>2230  
cgaagaactg cctatgcaaa 20  
<210>2231  
<211>20  
<212>DNA  
<400>2231  
aagcagagag gcgattcccc 20  
<210>2232  
<211>20  
<212>DNA  
<400>2232  
gtctgtacgt gttcgcgttt 20  
<210>2233  
<211>20  
<212>DNA  
<400>2233  
catcgcctcc acgagtattg 20  
<210>2234  
<211>20  
<212>DNA  
<400>2234  
gggttggttta acctcacctc 20  
<210>2235  
<211>20  
<212>DNA  
<400>2235  
gttagctctt agtggttgcg 20  
<210>2236  
<211>20  
<212>DNA  
<400>2236  
gccctctcgt tctaacagaa 20  
<210>2237  
<211>20  
<212>DNA  
<400>2237  
gagacggtct ctttgcttgt 20  
<210>2238  
<211>20  
<212>DNA  
<400>2238  
cccaatccct ccataaactt 20  
<210>2239  
<211>20  
<212>DNA  
<400>2239  
gtggatcatc atcatcccag 20  
<210>2240  
<211>20  
<212>DNA  
<400>2240  
ttctcaaaac atcgtgcagc 20

<210>2241  
<211>20  
<212>DNA  
<400>2241  
atgacgtacc ggcaatacga 20  
<210>2242  
<211>20  
<212>DNA  
<400>2242  
cgactacgga cctaaagaac 20  
<210>2243  
<211>20  
<212>DNA  
<400>2243  
cctcgtgaaa ttcctgacac 20  
<210>2244  
<211>20  
<212>DNA  
<400>2244  
cacacaactc gccgcatccg 20  
<210>2245  
<211>20  
<212>DNA  
<400>2245  
cgcgtttgct gtagcataac 20  
<210>2246  
<211>20  
<212>DNA  
<400>2246  
ggattcgtca aacaacctcc 20  
<210>2247  
<211>20  
<212>DNA  
<400>2247  
gctcggcact tacttcaaga 20  
<210>2248  
<211>20  
<212>DNA  
<400>2248  
caggaccttt agcaagccga 20  
<210>2249  
<211>20  
<212>DNA  
<400>2249  
aaaccatcca cacaactcgc 20  
<210>2250  
<211>20  
<212>DNA  
<400>2250  
agcacaccct agaagggtat 20  
<210>2251  
<211>20  
<212>DNA  
<400>2251  
ggcggattca tgctaaagat 20  
<210>2252  
<211>20  
<212>DNA  
<400>2252  
ccctaacgcc gaaaacttct 20  
<210>2253  
<211>20  
<212>DNA  
<400>2253

tggatacggg	gggggcatga	20
<210>2254		
<211>20		
<212>DNA		
<400>2254		
cagctcgttt	actccatctc	20
<210>2255		
<211>20		
<212>DNA		
<400>2255		
ggtgcggaac	tcatcacaat	20
<210>2256		
<211>20		
<212>DNA		
<400>2256		
gagctctaga	tgacgtagtg	20
<210>2257		
<211>20		
<212>DNA		
<400>2257		
gagccgctca	tacacctttt	20
<210>2258		
<211>20		
<212>DNA		
<400>2258		
gggcagactt	tggagagcta	20
<210>2259		
<211>20		
<212>DNA		
<400>2259		
ccctaacgcc	gaaaacttct	20
<210>2260		
<211>20		
<212>DNA		
<400>2260		
ctctgggttac	ctctccagta	20
<210>2261		
<211>20		
<212>DNA		
<400>2261		
ggctcttcaa	gagcaacaag	20
<210>2262		
<211>20		
<212>DNA		
<400>2262		
ggcatcagag	actgtaagtg	20
<210>2263		
<211>20		
<212>DNA		
<400>2263		
gctaatagcc	tcacaagcag	20
<210>2264		
<211>20		
<212>DNA		
<400>2264		
ggctacaaaa	gcggatgaag	20
<210>2265		
<211>20		
<212>DNA		
<400>2265		
ggcatcagag	actgtaagtg	20
<210>2266		
<211>20		
<212>DNA		

```

<400>2266
cccaaggagt caaatccgaa      20
<210>2267
<211>20
<212>DNA
<400>2267
cagcacatcc cctcatgatg      20
<210>2268
<211>20
<212>DNA
<400>2268
cttatcttgg cacgcataga      20
<210>2269
<211>20
<212>DNA
<400>2269
catggaagct gcttcgctat      20
<210>2270
<211>20
<212>DNA
<400>2270
gcgcaatcac tataaaccat      20
<210>2271
<211>20
<212>DNA
<400>2271
tttcgtgtgg aagaagttcc      20
<210>2272
<211>20
<212>DNA
<400>2272
gaggtttata acccatccgc      20
<210>2273
<211>20
<212>DNA
<400>2273
gaagcggcta caaaagcgga      20
<210>2274
<211>20
<212>DNA
<400>2274
acacagcctt acctccccct      20
<210>2275
<211>20
<212>DNA
<400>2275
accgtcaaag caagagacag      20
<210>2276
<211>20
<212>DNA
<400>2276
atatcgacag cgaaaggctg      20
<210>2277
<211>20
<212>DNA
<400>2277
ccgtctcatc aagactttgg      20
<210>2278
<211>20
<212>DNA
<400>2278
cgggaagagc tgctatttcc      20
<210>2279
<211>20

```

```

<212>DNA
<400>2279
agaggagtgt gcggtcagca      20
<210>2280
<211>20
<212>DNA
<400>2280
cgcacgttcg gacataagaa      20
<210>2281
<211>20
<212>DNA
<400>2281
ctggatcaca ggattgatcg      20
<210>2282
<211>20
<212>DNA
<400>2282
ctcactcgag ggaagttttc      20
<210>2283
<211>20
<212>DNA
<400>2283
tgccccttcg aaaaggatca      20
<210>2284
<211>20
<212>DNA
<400>2284
cctaacgaaa ccaacgatcc      20
<210>2285
<211>20
<212>DNA
<400>2285
gggaaaacgc caagaagagc      20
<210>2286
<211>20
<212>DNA
<400>2286
gggaaactca cgctctaaag      20
<210>2287
<211>20
<212>DNA
<400>2287
ctgggggagat gatgagttag      20
<210>2288
<211>20
<212>DNA
<400>2288
ctcctacgta ttgacggaac      20
<210>2289
<211>20
<212>DNA
<400>2289
gcgtttacct gcggaggaag      20
<210>2290
<211>20
<212>DNA
<400>2290
ggctacatag acgtgttttcg      20
<210>2291
<211>20
<212>DNA
<400>2291
tggccgctcc tacaaccctt      20
<210>2292

```



<211>20  
 <212>DNA  
 <400>2292  
 cggaggactt gcttttgggtt 20  
 <210>2293  
 <211>20  
 <212>DNA  
 <400>2293  
 tccctccaac gatagtttgc 20  
 <210>2294  
 <211>20  
 <212>DNA  
 <400>2294  
 ggcaagagca attctatggg 20  
 <210>2295  
 <211>20  
 <212>DNA  
 <400>2295  
 cctatccttt gggaaggact 20  
 <210>2296  
 <211>20  
 <212>DNA  
 <400>2296  
 ggctgggtct tacttggtcat 20  
 <210>2297  
 <211>20  
 <212>DNA  
 <400>2297  
 cagttcgatt ctgcctatgc 20  
 <210>2298  
 <211>20  
 <212>DNA  
 <400>2298  
 ggccctcattg ctatggcttt 20  
 <210>2299  
 <211>20  
 <212>DNA  
 <400>2299  
 ctctgagggtt tcctatcctg 20  
 <210>2300  
 <211>20  
 <212>DNA  
 <400>2300  
 cagagtctca gttgagaacc 20  
 <210>2301  
 <211>20  
 <212>DNA  
 <400>2301  
 gaaactccag gtttaggagc 20  
 <210>2302  
 <211>20  
 <212>DNA  
 <400>2302  
 ggactagctg gatccataga 20  
 <210>2303  
 <211>20  
 <212>DNA  
 <400>2303  
 ctcctgacag tgtgagaatg 20  
 <210>2304  
 <211>20  
 <212>DNA  
 <400>2304  
 caccttctgg agcttcgtta 20

<210>2305  
 <211>20  
 <212>DNA  
 <400>2305  
 gaactcctta tgggggtttcg 20  
 <210>2306  
 <211>20  
 <212>DNA  
 <400>2306  
 gctatactcc ttagggagtc 20  
 <210>2307  
 <211>20  
 <212>DNA  
 <400>2307  
 cggggaacgt acttaggtaa 20  
 <210>2308  
 <211>20  
 <212>DNA  
 <400>2308  
 ggagaagagc tcttttgcac 20  
 <210>2309  
 <211>20  
 <212>DNA  
 <400>2309  
 gctttcatgc gctaccttag 20  
 <210>2310  
 <211>20  
 <212>DNA  
 <400>2310  
 agagaatcgt ccccaaccca 20  
 <210>2311  
 <211>20  
 <212>DNA  
 <400>2311  
 cccctgttc tataaagcgt 20  
 <210>2312  
 <211>20  
 <212>DNA  
 <400>2312  
 gataccgttt cccatagagc 20  
 <210>2313  
 <211>20  
 <212>DNA  
 <400>2313  
 gctctgctta ggaacttgct 20  
 <210>2314  
 <211>20  
 <212>DNA  
 <400>2314  
 cctggagtgc acataaactc 20  
 <210>2315  
 <211>20  
 <212>DNA  
 <400>2315  
 cggactcaga gatctctaaa 20  
 <210>2316  
 <211>20  
 <212>DNA  
 <400>2316  
 agcgttcggc ctctgtcat 20  
 <210>2317  
 <211>20  
 <212>DNA  
 <400>2317

WO 99/27105

atttgctgcg gtactccaac	20
<210>2318	
<211>20	
<212>DNA	
<400>2318	
gccgctgaag attttcctga	20
<210>2319	
<211>20	
<212>DNA	
<400>2319	
cgacttctgg agattcgata	20
<210>2320	
<211>20	
<212>DNA	
<400>2320	
tcccagactc tgtgatttcc	20
<210>2321	
<211>20	
<212>DNA	
<400>2321	
ccaagagagg ttcgtaagga	20
<210>2322	
<211>20	
<212>DNA	
<400>2322	
cgctatcctc ttcccaattc	20
<210>2323	
<211>20	
<212>DNA	
<400>2323	
gctcacagaa gctgaaagtg	20
<210>2324	
<211>20	
<212>DNA	
<400>2324	
cagcagctcc atacgacagt	20
<210>2325	
<211>20	
<212>DNA	
<400>2325	
gcttgaagtc ccatatggac	20
<210>2326	
<211>20	
<212>DNA	
<400>2326	
cagaaacagc cgaaacggaa	20
<210>2327	
<211>20	
<212>DNA	
<400>2327	
ccctgatgtt gccctacaat	20
<210>2328	
<211>20	
<212>DNA	
<400>2328	
ctctgctcag gtacaatacc	20
<210>2329	
<211>20	
<212>DNA	
<400>2329	
aggaaacgag cgaacactct	20
<210>2330	
<211>20	
<212>DNA	

<400>2330  
 cgggttggtct attgggaatg 20  
 <210>2331  
 <211>20  
 <212>DNA  
 <400>2331  
 gggagaagat tcgacctgaa 20  
 <210>2332  
 <211>20  
 <212>DNA  
 <400>2332  
 ccctctcata agcgagtctt 20  
 <210>2333  
 <211>20  
 <212>DNA  
 <400>2333  
 gcgaaaaagg aatcgatcca 20  
 <210>2334  
 <211>20  
 <212>DNA  
 <400>2334  
 cagccaagcg tggtaaaacg 20  
 <210>2335  
 <211>20  
 <212>DNA  
 <400>2335  
 tcgctgcatt tgcgggacac 20  
 <210>2336  
 <211>20  
 <212>DNA  
 <400>2336  
 ctgctatcgt cgttcctatc 20  
 <210>2337  
 <211>20  
 <212>DNA  
 <400>2337  
 ctggctatat aggtgcggat 20  
 <210>2338  
 <211>20  
 <212>DNA  
 <400>2338  
 ctcccctacc cttaagcatt 20  
 <210>2339  
 <211>20  
 <212>DNA  
 <400>2339  
 ggtcttagga gctcttaagg 20  
 <210>2340  
 <211>20  
 <212>DNA  
 <400>2340  
 cattcagcca actctttggc 20  
 <210>2341  
 <211>20  
 <212>DNA  
 <400>2341  
 gcccagagtaa ttcttcagca 20  
 <210>2342  
 <211>20  
 <212>DNA  
 <400>2342  
 gcaaactgtg gaactcgtaa 20  
 <210>2343  
 <211>20

```

<212>DNA
<400>2343
cttagaggct attgatgggg      20
<210>2344
<211>20
<212>DNA
<400>2344
tgaaaccac tacgggtatc      20
<210>2345
<211>20
<212>DNA
<400>2345
agggtatcag agggggaggg      20
<210>2346
<211>20
<212>DNA
<400>2346
agcgatgcta actggatggc      20
<210>2347
<211>20
<212>DNA
<400>2347
acagcactga caactgttcg      20
<210>2348
<211>20
<212>DNA
<400>2348
gaagtacgaa gttcttcacg      20
<210>2349
<211>20
<212>DNA
<400>2349
gctggaggtc ctactctatt      20
<210>2350
<211>20
<212>DNA
<400>2350
agctgcttat gagcttcgtg      20
<210>2351
<211>20
<212>DNA
<400>2351
ggagagactc ctactcttac      20
<210>2352
<211>20
<212>DNA
<400>2352
gacgaggaga agtcgaaaga      20
<210>2353
<211>20
<212>DNA
<400>2353
ctcttggtgg agacatcact      20
<210>2354
<211>20
<212>DNA
<400>2354
cgagagtgac accacgttta      20
<210>2355
<211>20
<212>DNA
<400>2355
ggatctctct tctcgatgg      20
<210>2356

```

<211>20  
 <212>DNA  
 <400>2356  
 gcaactctaa tctttgcagc 20  
 <210>2357  
 <211>20  
 <212>DNA  
 <400>2357  
 cgtggaaaac tacaggaacg 20  
 <210>2358  
 <211>20  
 <212>DNA  
 <400>2358  
 gccgtattag cagtaatcgg 20  
 <210>2359  
 <211>20  
 <212>DNA  
 <400>2359  
 ccgtctctgc aactctaadc 20  
 <210>2360  
 <211>20  
 <212>DNA  
 <400>2360  
 gcgctcgatt tattcccttc 20  
 <210>2361  
 <211>20  
 <212>DNA  
 <400>2361  
 cttcacccct ataggcaaag 20  
 <210>2362  
 <211>20  
 <212>DNA  
 <400>2362  
 cctgtgttag tacttccgtc 20  
 <210>2363  
 <211>20  
 <212>DNA  
 <400>2363  
 tgcacctccg atagcatatc 20  
 <210>2364  
 <211>20  
 <212>DNA  
 <400>2364  
 ccctagttct tctagggagt 20  
 <210>2365  
 <211>20  
 <212>DNA  
 <400>2365  
 ctctggaggc tttacagagt 20  
 <210>2366  
 <211>20  
 <212>DNA  
 <400>2366  
 aggtccctct atgcacacat 20  
 <210>2367  
 <211>20  
 <212>DNA  
 <400>2367  
 gatgttggtta ccaaactccg 20  
 <210>2368  
 <211>20  
 <212>DNA  
 <400>2368  
 cgaggcacia gcatcacaat 20

<210>2369  
<211>20  
<212>DNA  
<400>2369  
cggcgccata tctacccaca 20  
<210>2370  
<211>20  
<212>DNA  
<400>2370  
gagccctcta tggcaaaaag 20  
<210>2371  
<211>20  
<212>DNA  
<400>2371  
ctccaggaac cactctgctc 20  
<210>2372  
<211>20  
<212>DNA  
<400>2372  
cgtcacaatc ctgattgcga 20  
<210>2373  
<211>20  
<212>DNA  
<400>2373  
gcgctatcta tgctaacgga 20  
<210>2374  
<211>20  
<212>DNA  
<400>2374  
ccttattagg gaagggcctt 20  
<210>2375  
<211>20  
<212>DNA  
<400>2375  
ccaagtttgc cactctagga 20  
<210>2376  
<211>20  
<212>DNA  
<400>2376  
aggagcctct gctctccaac 20  
<210>2377  
<211>20  
<212>DNA  
<400>2377  
ctcgctttaa gaaacggtgc 20  
<210>2378  
<211>20  
<212>DNA  
<400>2378  
ctcctagcgc aaatactctc 20  
<210>2379  
<211>20  
<212>DNA  
<400>2379  
gaggcatgcc tctttctttc 20  
<210>2380  
<211>20  
<212>DNA  
<400>2380  
ccccctctct caagtctatt 20  
<210>2381  
<211>20  
<212>DNA  
<400>2381

cgttccaagg aaacatgctc 20  
 <210>2382  
 <211>20  
 <212>DNA  
 <400>2382  
 cgacaactac gtctttctcc 20  
 <210>2383  
 <211>20  
 <212>DNA  
 <400>2383  
 ctttcgggca gctttatgga 20  
 <210>2384  
 <211>20  
 <212>DNA  
 <400>2384  
 gcctgtaaag cagagtatcc 20  
 <210>2385  
 <211>20  
 <212>DNA  
 <400>2385  
 aggagtgctc ctaactgctc 20  
 <210>2386  
 <211>20  
 <212>DNA  
 <400>2386  
 ggagacctga gaaaggttgt 20  
 <210>2387  
 <211>20  
 <212>DNA  
 <400>2387  
 gcggattgca gcatctaaag 20  
 <210>2388  
 <211>20  
 <212>DNA  
 <400>2388  
 cgaacggtag aaatccaaga 20  
 <210>2389  
 <211>20  
 <212>DNA  
 <400>2389  
 cgaacggaat ctccagatcg 20  
 <210>2390  
 <211>20  
 <212>DNA  
 <400>2390  
 ctctgagatc ccaaaatccc 20  
 <210>2391  
 <211>20  
 <212>DNA  
 <400>2391  
 cgatctccaa agaactgacg 20  
 <210>2392  
 <211>20  
 <212>DNA  
 <400>2392  
 ccctgacagg gaattctgaa 20  
 <210>2393  
 <211>20  
 <212>DNA  
 <400>2393  
 tgcgtttcat tcgcgagact 20  
 <210>2394  
 <211>20  
 <212>DNA



<400>2394  
catctgccaa gttcttcgct 20  
<210>2395  
<211>20  
<212>DNA  
<400>2395  
taaccactcc atcccatga 20  
<210>2396  
<211>20  
<212>DNA  
<400>2396  
cgtgggatac ctaagagaaa 20  
<210>2397  
<211>20  
<212>DNA  
<400>2397  
cggcctgttt aattacagcg 20  
<210>2398  
<211>20  
<212>DNA  
<400>2398  
cctgttggat taccgcattg 20  
<210>2399  
<211>20  
<212>DNA  
<400>2399  
gggacaatcc ttcttcaga 20  
<210>2400  
<211>20  
<212>DNA  
<400>2400  
gagaaccaag aggacgtgta 20  
<210>2401  
<211>20  
<212>DNA  
<400>2401  
ttgagctgag tcacaagctg 20  
<210>2402  
<211>20  
<212>DNA  
<400>2402  
cctgctgaga tattctgagg 20  
<210>2403  
<211>20  
<212>DNA  
<400>2403  
tccacgtctc tgacggactg 20  
<210>2404  
<211>20  
<212>DNA  
<400>2404  
cggatgtgca gattttctac 20  
<210>2405  
<211>20  
<212>DNA  
<400>2405  
gaagtcgaac cctaagctgt 20  
<210>2406  
<211>20  
<212>DNA  
<400>2406  
gcaaagagct tgatcctctg 20  
<210>2407  
<211>20

<212>DNA  
 <400>2407  
 gattcgcctg cgtaatcagt 20  
 <210>2408  
 <211>20  
 <212>DNA  
 <400>2408  
 cctagtcttg ctcacagaaa 20  
 <210>2409  
 <211>20  
 <212>DNA  
 <400>2409  
 gggaggcata ttttctaccc 20  
 <210>2410  
 <211>20  
 <212>DNA  
 <400>2410  
 ggatgactcc tgcagtgtat 20  
 <210>2411  
 <211>20  
 <212>DNA  
 <400>2411  
 atcctccata cagaaacgcc 20  
 <210>2412  
 <211>20  
 <212>DNA  
 <400>2412  
 ctcgacatct acgcaccatc 20  
 <210>2413  
 <211>20  
 <212>DNA  
 <400>2413  
 ccatagacga taaccctgga 20  
 <210>2414  
 <211>20  
 <212>DNA  
 <400>2414  
 ggggctatac atgcactaga 20  
 <210>2415  
 <211>20  
 <212>DNA  
 <400>2415  
 cgatccctac gacagtatag 20  
 <210>2416  
 <211>20  
 <212>DNA  
 <400>2416  
 cgcagcatta atcaggacga 20  
 <210>2417  
 <211>20  
 <212>DNA  
 <400>2417  
 caaatcgggtg tcacgtact 20  
 <210>2418  
 <211>20  
 <212>DNA  
 <400>2418  
 tcacgacact actcatcagc 20  
 <210>2419  
 <211>20  
 <212>DNA  
 <400>2419  
 gccctaggag tcattatctc 20  
 <210>2420

```

<211>20
<212>DNA
<400>2420
ggaacaacct caaacactgc      20
<210>2421
<211>20
<212>DNA
<400>2421
cctcgatcac cagaattcca      20
<210>2422
<211>20
<212>DNA
<400>2422
cctcatcaac gacgacacat      20
<210>2423
<211>20
<212>DNA
<400>2423
caggaattgc agccttcgat      20
<210>2424
<211>20
<212>DNA
<400>2424
ctccgattcc tgatgccata      20
<210>2425
<211>20
<212>DNA
<400>2425
agggggaacg gctcatatct      20
<210>2426
<211>20
<212>DNA
<400>2426
cgatcgactt ctatccccat      20
<210>2427
<211>20
<212>DNA
<400>2427
gcctgacctc tcctgtaaaa      20
<210>2428
<211>20
<212>DNA
<400>2428
acgagacccc cataccctcc      20
<210>2429
<211>20
<212>DNA
<400>2429
ggatacgatc tctaaagccc      20
<210>2430
<211>20
<212>DNA
<400>2430
gccaccaact gccataattg      20
<210>2431
<211>20
<212>DNA
<400>2431
gccgaagaag agctctgaga      20
<210>2432
<211>20
<212>DNA
<400>2432
ggaatttggt actggcgaga      20

```

<210>2433  
<211>20  
<212>DNA  
<400>2433  
atcttgagcc gcctacgcca 20  
<210>2434  
<211>20  
<212>DNA  
<400>2434  
ggataagaaa aagagccccg 20  
<210>2435  
<211>20  
<212>DNA  
<400>2435  
caaaccctaa gcgaccctt 20  
<210>2436  
<211>20  
<212>DNA  
<400>2436  
cagaagtcac tgcaagcccc 20  
<210>2437  
<211>20  
<212>DNA  
<400>2437  
ggtcacttca tgacgactgt 20  
<210>2438  
<211>20  
<212>DNA  
<400>2438  
caggacctct tggtaacct 20  
<210>2439  
<211>20  
<212>DNA  
<400>2439  
gggcaacatg aatcaagcgg 20  
<210>2440  
<211>20  
<212>DNA  
<400>2440  
gtggaagctg aggggtgtttt 20  
<210>2441  
<211>20  
<212>DNA  
<400>2441  
ctgggccacc tgttcaatca 20  
<210>2442  
<211>20  
<212>DNA  
<400>2442  
cgggatttcc tgtgcctaaa 20  
<210>2443  
<211>20  
<212>DNA  
<400>2443  
ggaagaggag agagcaaacg 20  
<210>2444  
<211>20  
<212>DNA  
<400>2444  
gtacgggtag gccttgaaat 20  
<210>2445  
<211>20  
<212>DNA  
<400>2445

cacggctgga aaagatttcc 20  
<210>2446  
<211>20  
<212>DNA  
<400>2446  
cgacctgtgg gaaaatgaca 20  
<210>2447  
<211>20  
<212>DNA  
<400>2447  
atcccgcaat caaaggggct 20  
<210>2448  
<211>20  
<212>DNA  
<400>2448  
cctgagcatc cacatactca 20  
<210>2449  
<211>20  
<212>DNA  
<400>2449  
gcagaggaac cctgactcat 20  
<210>2450  
<211>20  
<212>DNA  
<400>2450  
gcccgcctaa taacaagaat 20  
<210>2451  
<211>20  
<212>DNA  
<400>2451  
tgtgcttcat agcgggcgac 20  
<210>2452  
<211>20  
<212>DNA  
<400>2452  
gcgctctata cgctaaattc 20  
<210>2453  
<211>20  
<212>DNA  
<400>2453  
ctcagcacag ttatatcccc 20  
<210>2454  
<211>20  
<212>DNA  
<400>2454  
tgacggggtg atttcttctc 20  
<210>2455  
<211>20  
<212>DNA  
<400>2455  
ggaacagagg ttgccataag 20  
<210>2456  
<211>20  
<212>DNA  
<400>2456  
ggctaacgac gtcgctgcta 20  
<210>2457  
<211>20  
<212>DNA  
<400>2457  
gcagaaatgg ctgaactcct 20  
<210>2458  
<211>20  
<212>DNA

<400>2458  
ctctcttatac gacctgctct 20  
<210>2459  
<211>20  
<212>DNA  
<400>2459  
cttttaggaat ggggtggaacg 20  
<210>2460  
<211>20  
<212>DNA  
<400>2460  
gtgatggaga taacgtccag 20  
<210>2461  
<211>20  
<212>DNA  
<400>2461  
taacagccaa ttggaagaac 20  
<210>2462  
<211>20  
<212>DNA  
<400>2462  
agcttcctac caatctcacg 20  
<210>2463  
<211>20  
<212>DNA  
<400>2463  
gacaacacac tgacaggcta 20  
<210>2464  
<211>20  
<212>DNA  
<400>2464  
cctatgccct cttctgaaac 20  
<210>2465  
<211>20  
<212>DNA  
<400>2465  
ctacgggtgct gagcttaaag 20  
<210>2466  
<211>20  
<212>DNA  
<400>2466  
cgatcatgag ctaactctgg 20  
<210>2467  
<211>20  
<212>DNA  
<400>2467  
ctctcgcgat cttctacctt 20  
<210>2468  
<211>20  
<212>DNA  
<400>2468  
gatacccatc ggcaattcca 20  
<210>2469  
<211>20  
<212>DNA  
<400>2469  
ctctgagctt acgctcttca 20  
<210>2470  
<211>20  
<212>DNA  
<400>2470  
cctccattgt aaccagagag 20  
<210>2471  
<211>20

<212>DNA  
<400>2471  
ttccacgcct ctcgacgttc 20  
<210>2472  
<211>20  
<212>DNA  
<400>2472  
cgaaggagag gtcctcattg 20  
<210>2473  
<211>20  
<212>DNA  
<400>2473  
cgggtcacgga aggatttttcg 20  
<210>2474  
<211>20  
<212>DNA  
<400>2474  
cctaccacac aagaatctgg 20  
<210>2475  
<211>20  
<212>DNA  
<400>2475  
gcacgttggc aactttctct 20  
<210>2476  
<211>20  
<212>DNA  
<400>2476  
cttcctaatac ggacctgtag 20  
<210>2477  
<211>20  
<212>DNA  
<400>2477  
cgctagtctt agaagcgcaa 20  
<210>2478  
<211>20  
<212>DNA  
<400>2478  
gctgtcttca tcgtaaagac 20  
<210>2479  
<211>20  
<212>DNA  
<400>2479  
cctaatacgct ggggattatg 20  
<210>2480  
<211>20  
<212>DNA  
<400>2480  
tctggagaag gattcctacc 20  
<210>2481  
<211>20  
<212>DNA  
<400>2481  
cgggttcacga atgaattggc 20  
<210>2482  
<211>20  
<212>DNA  
<400>2482  
acctcccgcc atctctttat 20  
<210>2483  
<211>20  
<212>DNA  
<400>2483  
gctgtcttca tcgtaaagac 20  
<210>2484

```

<211>20
<212>DNA
<400>2484
gcctgtagcg tggattacaa      20
<210>2485
<211>20
<212>DNA
<400>2485
gtttcgcaag gagaatccag      20
<210>2486
<211>20
<212>DNA
<400>2486
gctgtgagtt aggctatacg      20
<210>2487
<211>20
<212>DNA
<400>2487
ctaggtctac aggatcctgt      20
<210>2488
<211>20
<212>DNA
<400>2488
gcgccgtcat tgcgaacaat      20
<210>2489
<211>20
<212>DNA
<400>2489
gcgattgtca ccttaggaac      20
<210>2490
<211>20
<212>DNA
<400>2490
ctgacgacat agtactacaa      20
<210>2491
<211>20
<212>DNA
<400>2491
gggaaaggat tgtaccgaga      20
<210>2492
<211>20
<212>DNA
<400>2492
gatcgagatg aaagactcgg      20
<210>2493
<211>20
<212>DNA
<400>2493
ttacctcttc tggattcggg      20
<210>2494
<211>20
<212>DNA
<400>2494
cgagatggct agatccaaag      20
<210>2495
<211>20
<212>DNA
<400>2495
ctcttgacga tcaatcactg      20
<210>2496
<211>20
<212>DNA
<400>2496
gagctttagg tatcctaggc      20

```



```

<210>2497
<211>20
<212>DNA
<400>2497
cccttgtcgt aaaactctcc 20
<210>2498
<211>20
<212>DNA
<400>2498
gccctcggat tcaacatgat 20
<210>2499
<211>20
<212>DNA
<400>2499
gtatctcaag agcttgcgga 20
<210>2500
<211>20
<212>DNA
<400>2500
gtcccatggc caaagataac 20
<210>2501
<211>20
<212>DNA
<400>2501
cccacctgaa aatgaggaac 20
<210>2502
<211>20
<212>DNA
<400>2502
cagtacgaag cctccttcaa 20
<210>2503
<211>20
<212>DNA
<400>2503
ctcctgcgta tctgttatgg 20
<210>2504
<211>20
<212>DNA
<400>2504
cgcacttaca aaatcggcga 20
<210>2505
<211>20
<212>DNA
<400>2505
ggtggagacg actttgatga 20
<210>2506
<211>20
<212>DNA
<400>2506
tccgtagcgt cattcgaagc 20
<210>2507
<211>20
<212>DNA
<400>2507
catcgtagtt ctccaaggag 20
<210>2508
<211>20
<212>DNA
<400>2508
ggttcattgc agcagcagaa 20
<210>2509
<211>20
<212>DNA
<400>2509

```

ggctttgaat ttgagactgc 20  
<210>2510  
<211>20  
<212>DNA  
<400>2510  
gtcccatgga gatttctcct 20  
<210>2511  
<211>20  
<212>DNA  
<400>2511  
gagacttcga cgatgccatc 20  
<210>2512  
<211>20  
<212>DNA  
<400>2512  
cacaggttta cctaagaccc 20  
<210>2513  
<211>20  
<212>DNA  
<400>2513  
gctcttcag aatctatccc 20  
<210>2514  
<211>20  
<212>DNA  
<400>2514  
gatcccgctt atcctcatgt 20  
<210>2515  
<211>20  
<212>DNA  
<400>2515  
ccacgcctac aactacagaa 20  
<210>2516  
<211>20  
<212>DNA  
<400>2516  
gcacagaacg aaatgtcgga 20  
<210>2517  
<211>20  
<212>DNA  
<400>2517  
cgcagagcga aaagtcctaa 20  
<210>2518  
<211>20  
<212>DNA  
<400>2518  
gagtcctact gcaaagctac 20  
<210>2519  
<211>20  
<212>DNA  
<400>2519  
ggttcttacg ctcttagagc 20  
<210>2520  
<211>20  
<212>DNA  
<400>2520  
gtttactctc ccctacgaac 20  
<210>2521  
<211>20  
<212>DNA  
<400>2521  
ccctaaacca acgcttcttc 20  
<210>2522  
<211>20  
<212>DNA

<400>2522  
ccctaagttc agtgacccta 20  
<210>2523  
<211>20  
<212>DNA  
<400>2523  
gtcctgacta cagtcccaaa 20  
<210>2524  
<211>20  
<212>DNA  
<400>2524  
atcaggccag ggtcatgcca 20  
<210>2525  
<211>20  
<212>DNA  
<400>2525  
gagaacctca tctcgaggga 20  
<210>2526  
<211>20  
<212>DNA  
<400>2526  
cggggtggta tgatcttaca 20  
<210>2527  
<211>20  
<212>DNA  
<400>2527  
cagggtcact caggcagaca 20  
<210>2528  
<211>20  
<212>DNA  
<400>2528  
ccgacgccta tagctatctc 20  
<210>2529  
<211>20  
<212>DNA  
<400>2529  
gagtacgatc ctcagatcca 20  
<210>2530  
<211>20  
<212>DNA  
<400>2530  
gcggggcccag cctcctcata 20  
<210>2531  
<211>20  
<212>DNA  
<400>2531  
cgaagcgta tattgccgca 20  
<210>2532  
<211>20  
<212>DNA  
<400>2532  
cgcagctcag tagtgatgac 20  
<210>2533  
<211>20  
<212>DNA  
<400>2533  
ggcttagact cgaattccga 20  
<210>2534  
<211>20  
<212>DNA  
<400>2534  
gtcggcatt ctcttcta 20  
<210>2535  
<211>20

<212>DNA  
<400>2535  
agtagggaag tcacagagcc 20  
<210>2536  
<211>20  
<212>DNA  
<400>2536  
gctaagtgag caatcgaca 20  
<210>2537  
<211>20  
<212>DNA  
<400>2537  
gaactagacg tgtgctcaac 20  
<210>2538  
<211>20  
<212>DNA  
<400>2538  
cctgcgtcca cagatcccc 20  
<210>2539  
<211>20  
<212>DNA  
<400>2539  
cagcctgagg gacttttgta 20  
<210>2540  
<211>20  
<212>DNA  
<400>2540  
caacgaaacc accgcaacca 20  
<210>2541  
<211>20  
<212>DNA  
<400>2541  
gtcgcctcta catagacatc 20  
<210>2542  
<211>20  
<212>DNA  
<400>2542  
caactgtaag agctttcgcc 20  
<210>2543  
<211>20  
<212>DNA  
<400>2543  
caccatcatg tggttgtctg 20  
<210>2544  
<211>20  
<212>DNA  
<400>2544  
taccaccata gctattgggc 20  
<210>2545  
<211>20  
<212>DNA  
<400>2545  
gccatatcta cccacaagac 20  
<210>2546  
<211>20  
<212>DNA  
<400>2546  
ggaagtgttc ttacaggaac 20  
<210>2547  
<211>20  
<212>DNA  
<400>2547  
gcaagacctg tgatcagaga 20  
<210>2548

```

<211>20
<212>DNA
<400>2548
gtaggagcca ttaaggtgac 20
<210>2549
<211>20
<212>DNA
<400>2549
ccctaagttc aaggtagcga 20
<210>2550
<211>20
<212>DNA
<400>2550
gcgtgaggaa cctcatctga 20
<210>2551
<211>20
<212>DNA
<400>2551
gcaacagaaa acactccgct 20
<210>2552
<211>20
<212>DNA
<400>2552
ggagaaaaga acagagcacg 20
<210>2553
<211>20
<212>DNA
<400>2553
cgccttatgc gcgtaaagaa 20
<210>2554
<211>20
<212>DNA
<400>2554
gaagcaacct cgtctccctc 20
<210>2555
<211>20
<212>DNA
<400>2555
ggaagaacag ctacaggact 20
<210>2556
<211>20
<212>DNA
<400>2556
ggccgacact tttaatgcc 20
<210>2557
<211>20
<212>DNA
<400>2557
gccaaaggcct ttgcaatact 20
<210>2558
<211>20
<212>DNA
<400>2558
gagtgtggaa ggaaaccggt 20
<210>2559
<211>20
<212>DNA
<400>2559
ctcagcggac actcccaaact 20
<210>2560
<211>20
<212>DNA
<400>2560
gccaaagtcg agtctaagca 20

```

<210>2561  
 <211>20  
 <212>DNA  
 <400>2561  
 ctaaggtaac cccgacaaac 20  
 <210>2562  
 <211>20  
 <212>DNA  
 <400>2562  
 gcacatcaga aaatgcgacc 20  
 <210>2563  
 <211>20  
 <212>DNA  
 <400>2563  
 gactggcttt tatagccacg 20  
 <210>2564  
 <211>20  
 <212>DNA  
 <400>2564  
 cccaccccat ttaacaacag 20  
 <210>2565  
 <211>20  
 <212>DNA  
 <400>2565  
 gcgcaccaca ttaggattgt 20  
 <210>2566  
 <211>20  
 <212>DNA  
 <400>2566  
 ggtcaagacc aagttcatgc 20  
 <210>2567  
 <211>20  
 <212>DNA  
 <400>2567  
 agaaggcaag gctcccacac 20  
 <210>2568  
 <211>20  
 <212>DNA  
 <400>2568  
 cgacaccttt gatcggacta 20  
 <210>2569  
 <211>20  
 <212>DNA  
 <400>2569  
 atgggtcaca cgagctccac 20  
 <210>2570  
 <211>20  
 <212>DNA  
 <400>2570  
 ctataggaaa cgtcggggat 20  
 <210>2571  
 <211>20  
 <212>DNA  
 <400>2571  
 ctcaggaatc aatcccacag 20  
 <210>2572  
 <211>20  
 <212>DNA  
 <400>2572  
 gagccctact cctttgcttt 20  
 <210>2573  
 <211>20  
 <212>DNA  
 <400>2573

ggagaagaaa ttcctctcgc 20  
 <210>2574  
 <211>20  
 <212>DNA  
 <400>2574  
 gcgaagttgc tagctaagaa 20  
 <210>2575  
 <211>20  
 <212>DNA  
 <400>2575  
 tattttttgc ctccgcaggc 20  
 <210>2576  
 <211>20  
 <212>DNA  
 <400>2576  
 ccttcgctga caaccaagaa 20  
 <210>2577  
 <211>20  
 <212>DNA  
 <400>2577  
 ctacttcctg gttggaaga 20  
 <210>2578  
 <211>20  
 <212>DNA  
 <400>2578  
 cctctaggga aagaagctct 20  
 <210>2579  
 <211>20  
 <212>DNA  
 <400>2579  
 tctattcaca gtggggcgat 20  
 <210>2580  
 <211>20  
 <212>DNA  
 <400>2580  
 ttgctgtagg tggcatcact 20  
 <210>2581  
 <211>20  
 <212>DNA  
 <400>2581  
 caagtcagca cctcgtaacat 20  
 <210>2582  
 <211>20  
 <212>DNA  
 <400>2582  
 cgaaccacg gtacgcgtta 20  
 <210>2583  
 <211>20  
 <212>DNA  
 <400>2583  
 ggaaaccaca gccactacaa 20  
 <210>2584  
 <211>20  
 <212>DNA  
 <400>2584  
 ggcagatcgt ttccacatgc 20  
 <210>2585  
 <211>20  
 <212>DNA  
 <400>2585  
 ggcttcggct ataggatcctt 20  
 <210>2586  
 <211>20  
 <212>DNA

<400>2586  
ccgacgacaa acattgatcc 20  
<210>2587  
<211>20  
<212>DNA  
<400>2587  
gcattagctt ggcgtgagat 20  
<210>2588  
<211>20  
<212>DNA  
<400>2588  
ccgtgattca tttcccttc 20  
<210>2589  
<211>20  
<212>DNA  
<400>2589  
gagggatccg gtttgtattc 20  
<210>2590  
<211>20  
<212>DNA  
<400>2590  
gaggtacacg gctttaaac 20  
<210>2591  
<211>20  
<212>DNA  
<400>2591  
caaggagtta cgacaaggag 20  
<210>2592  
<211>20  
<212>DNA  
<400>2592  
ttgccaccat tgccctcgta 20  
<210>2593  
<211>20  
<212>DNA  
<400>2593  
ccgacgacaa acattgatcc 20  
<210>2594  
<211>20  
<212>DNA  
<400>2594  
gttgctcagg aacaacagag 20  
<210>2595  
<211>20  
<212>DNA  
<400>2595  
ttaggagcct ccgtagctgg 20  
<210>2596  
<211>20  
<212>DNA  
<400>2596  
tgccagagc cgggatcgaa 20  
<210>2597  
<211>20  
<212>DNA  
<400>2597  
ggaatttgca tcgcctactg 20  
<210>2598  
<211>20  
<212>DNA  
<400>2598  
gggatttatc ttgaggaggc 20  
<210>2599  
<211>20



```

<212>DNA
<400>2599
gttctaactc tacctgacgg      20
<210>2600
<211>20
<212>DNA
<400>2600
gagcaaaactc cgaagcgttt    20
<210>2601
<211>20
<212>DNA
<400>2601
gccccttgtc ctttcttatg     20
<210>2602
<211>20
<212>DNA
<400>2602
gaacgtgttc ggagacctct     20
<210>2603
<211>20
<212>DNA
<400>2603
cgaagcaact tcccctagta     20
<210>2604
<211>20
<212>DNA
<400>2604
caagacgttt gtgagtacga     20
<210>2605
<211>20
<212>DNA
<400>2605
ccatctgagc tatctagcca     20
<210>2606
<211>20
<212>DNA
<400>2606
cagcaaaata gtctgctccc     20
<210>2607
<211>20
<212>DNA
<400>2607
cctgcaggaa gtgctaacat     20
<210>2608
<211>20
<212>DNA
<400>2608
gttgcagcag aggtaatcgt     20
<210>2609
<211>20
<212>DNA
<400>2609
ccctgatcga atcctttcag     20
<210>2610
<211>20
<212>DNA
<400>2610
cgacgggaac gaacttctaa     20
<210>2611
<211>20
<212>DNA
<400>2611
cccaggttcg ttaggttcta     20
<210>2612

```

<211>20  
<212>DNA  
<400>2612  
gggaacgtat cctgcttgaa 20  
<210>2613  
<211>20  
<212>DNA  
<400>2613  
ggcaaccact tgacaatcac 20  
<210>2614  
<211>20  
<212>DNA  
<400>2614  
ggcaacaaag tcctcattcg 20  
<210>2615  
<211>20  
<212>DNA  
<400>2615  
gccgatgttt ctaattgcac 20  
<210>2616  
<211>20  
<212>DNA  
<400>2616  
ccccttttca ggagcgtatt 20  
<210>2617  
<211>20  
<212>DNA  
<400>2617  
gtgccgcctt gacatataca 20  
<210>2618  
<211>20  
<212>DNA  
<400>2618  
gtgagcaaag gctttctgag 20  
<210>2619  
<211>20  
<212>DNA  
<400>2619  
caacctcgca aagcttcttt 20  
<210>2620  
<211>20  
<212>DNA  
<400>2620  
cgttctccta gtgtagttcc 20  
<210>2621  
<211>20  
<212>DNA  
<400>2621  
ggcatgtgtg gaattggtgt 20  
<210>2622  
<211>20  
<212>DNA  
<400>2622  
gccatactcg ttagcgcaag 20  
<210>2623  
<211>20  
<212>DNA  
<400>2623  
gacataccgt tctcctagtg 20  
<210>2624  
<211>20  
<212>DNA  
<400>2624  
ccctcgtcaa taaagcgcat 20

<210>2625  
<211>20  
<212>DNA  
<400>2625  
cttcttttgag ggcagaactc 20  
<210>2626  
<211>20  
<212>DNA  
<400>2626  
cttcataccc tgaaaacggc 20  
<210>2627  
<211>20  
<212>DNA  
<400>2627  
cgaggggggaa atgaaattat 20  
<210>2628  
<211>20  
<212>DNA  
<400>2628  
cgccagggac gtttttctaa 20  
<210>2629  
<211>20  
<212>DNA  
<400>2629  
cataacctga gtcgcggtaa 20  
<210>2630  
<211>20  
<212>DNA  
<400>2630  
gtgacgaccc tcattctagaa 20  
<210>2631  
<211>20  
<212>DNA  
<400>2631  
gcttgagtga tcgaaaccca 20  
<210>2632  
<211>20  
<212>DNA  
<400>2632  
ggctcgacag atggctgtat 20  
<210>2633  
<211>20  
<212>DNA  
<400>2633  
gcgtgttggt cccttgcaat 20  
<210>2634  
<211>20  
<212>DNA  
<400>2634  
aggcacagcc ctctttccct 20  
<210>2635  
<211>20  
<212>DNA  
<400>2635  
cgcatTTgag caacatcgct 20  
<210>2636  
<211>20  
<212>DNA  
<400>2636  
caaagccaaa gcaaacacgc 20  
<210>2637  
<211>20  
<212>DNA  
<400>2637

gacgtagaaa gacccctggca	20
<210>2638	
<211>20	
<212>DNA	
<400>2638	
cgtcatgagt aagccgagta	20
<210>2639	
<211>20	
<212>DNA	
<400>2639	
cacatggagt cttgcagact	20
<210>2640	
<211>20	
<212>DNA	
<400>2640	
ctgacgacct ttcagaatct	20
<210>2641	
<211>20	
<212>DNA	
<400>2641	
agtgcacag gaactccaag	20
<210>2642	
<211>20	
<212>DNA	
<400>2642	
tgcgagttac ttcccgatgc	20
<210>2643	
<211>20	
<212>DNA	
<400>2643	
ctgaaatgga tatgcgagga	20
<210>2644	
<211>20	
<212>DNA	
<400>2644	
ctcagcttgg caactgtgta	20
<210>2645	
<211>20	
<212>DNA	
<400>2645	
cacacacacg tcaggtcatt	20
<210>2646	
<211>20	
<212>DNA	
<400>2646	
ggtattggta tgatggctgc	20
<210>2647	
<211>20	
<212>DNA	
<400>2647	
ccggtgcata cggtgattta	20
<210>2648	
<211>20	
<212>DNA	
<400>2648	
ggctaaagac tttggagagg	20
<210>2649	
<211>20	
<212>DNA	
<400>2649	
gttccgatca tccctgtcta	20
<210>2650	
<211>20	
<212>DNA	

## WO 99/27105

```

<400>2650
ggagattcaa gaacctgctg      20
<210>2651
<211>20
<212>DNA
<400>2651
cacatgtgtg tccatgagtg      20
<210>2652
<211>20
<212>DNA
<400>2652
cgttcccctt tggcatcaaa      20
<210>2653
<211>20
<212>DNA
<400>2653
acgtaaagct ccgagagctt      20
<210>2654
<211>20
<212>DNA
<400>2654
ggagaaacaa gcagagctga      20
<210>2655
<211>20
<212>DNA
<400>2655
gagcttgctt acccaatttg      20
<210>2656
<211>20
<212>DNA
<400>2656
cgatacagat ccatccggtc      20
<210>2657
<211>20
<212>DNA
<400>2657
caagcagctt agttgcagca      20
<210>2658
<211>20
<212>DNA
<400>2658
cagggactgg aacacagaat      20
<210>2659
<211>20
<212>DNA
<400>2659
gcactctttt tctaccctcc      20
<210>2660
<211>20
<212>DNA
<400>2660
cccatgacca tacagtcac      20
<210>2661
<211>20
<212>DNA
<400>2661
accctctgca tggcgtcgtg      20
<210>2662
<211>20
<212>DNA
<400>2662
gtaaacgcag tgcaccttga      20
<210>2663
<211>20

```

```

<212>DNA
<400>2663
cgacaacatc tgaatacggc      20
<210>2664
<211>20
<212>DNA
<400>2664
ctccagcaac attcccattg      20
<210>2665
<211>20
<212>DNA
<400>2665
ggcatgttgc tacaatctcc      20
<210>2666
<211>20
<212>DNA
<400>2666
gagatcccca agcaatttcc      20
<210>2667
<211>20
<212>DNA
<400>2667
ctactagacg caagggaaga      20
<210>2668
<211>20
<212>DNA
<400>2668
caaggacttc ctagagcttc      20
<210>2669
<211>20
<212>DNA
<400>2669
gtaaacgcag tgcaccttga      20
<210>2670
<211>20
<212>DNA
<400>2670
gttcgctggt gacttaggct      20
<210>2671
<211>20
<212>DNA
<400>2671
ctccagcaac attcccattg      20
<210>2672
<211>20
<212>DNA
<400>2672
ctgcaacaat accctggaga      20
<210>2673
<211>20
<212>DNA
<400>2673
caagagttct tgtctgctc      20
<210>2674
<211>20
<212>DNA
<400>2674
gcactctgga ccgagacaat      20
<210>2675
<211>20
<212>DNA
<400>2675
cacctttact aggagtcacc      20
<210>2676

```

WO 99/27105

```

<211>20
<212>DNA
<400>2676
ggcatctctt ggagagttag      20
<210>2677
<211>20
<212>DNA
<400>2677
ggccgaagtt tgctcgaaaa      20
<210>2678
<211>20
<212>DNA
<400>2678
cgaacgatct ataccctgga      20
<210>2679
<211>20
<212>DNA
<400>2679
ccataagaga gttcctgaga      20
<210>2680
<211>20
<212>DNA
<400>2680
ctcggctcgc atacagaaat      20
<210>2681
<211>20
<212>DNA
<400>2681
ccctctattt gcaaacgcga      20
<210>2682
<211>20
<212>DNA
<400>2682
gaagggcctt ttccttgcta      20
<210>2683
<211>20
<212>DNA
<400>2683
cgaacgatct ataccctgga      20
<210>2684
<211>20
<212>DNA
<400>2684
ggacaagctc ttcactccat      20
<210>2685
<211>20
<212>DNA
<400>2685
ccgaaggggt tctctatgat      20
<210>2686
<211>20
<212>DNA
<400>2686
acgagttcgc ggatcttctt      20
<210>2687
<211>20
<212>DNA
<400>2687
ccgatcaccg gcataattct      20
<210>2688
<211>20
<212>DNA
<400>2688
ccagtaagtc tcagatcctc      20

```

<210>1409  
<211>20  
<212>DNA  
<400>1409  
cgtactaggg attgagcata 20  
<210>1410  
<211>20  
<212>DNA  
<400>1410  
gagtgtctga cgtttctgag 20  
<210>1411  
<211>20  
<212>DNA  
<400>1411  
ggaccgccat tacgagaaat 20  
<210>1412  
<211>20  
<212>DNA  
<400>1412  
gagttgaact cctgccttga 20  
<210>1413  
<211>20  
<212>DNA  
<400>1413  
atcagatcga agagctccag 20  
<210>1414  
<211>20  
<212>DNA  
<400>1414  
ggtctaagca cgtaggttgt 20  
<210>1415  
<211>20  
<212>DNA  
<400>1415  
gggatggcct taggtaaagt 20  
<210>1416  
<211>20  
<212>DNA  
<400>1416  
ctgagagctg aacttgcttg 20  
<210>1417  
<211>20  
<212>DNA  
<400>1417  
ctttggaaca tcgcaaagcg 20  
<210>1418  
<211>20  
<212>DNA  
<400>1418  
cttggtaggg ttgtagagtc 20  
<210>1419  
<211>20  
<212>DNA  
<400>1419  
gagttgaact cctgccttga 20  
<210>1420  
<211>20  
<212>DNA  
<400>1420  
ggcatgttta tagtgtggcg 20  
<210>1421  
<211>20  
<212>DNA  
<400>1421



atgtgacagg tgctacccca 20  
 <210>1422  
 <211>20  
 <212>DNA  
 <400>1422  
 gagaatcaga ggcaagtcca 20  
 <210>1423  
 <211>20  
 <212>DNA  
 <400>1423  
 gaaggcttcc ttagtgagca 20  
 <210>1424  
 <211>20  
 <212>DNA  
 <400>1424  
 cagcgagttg cagcatttga 20  
 <210>1425  
 <211>20  
 <212>DNA  
 <400>1425  
 tcgcatgttt aggaccgctg 20  
 <210>1426  
 <211>20  
 <212>DNA  
 <400>1426  
 ttcctgaggc cccagaagag 20  
 <210>1427  
 <211>20  
 <212>DNA  
 <400>1427  
 gcatgttttag gaccgctgaa 20  
 <210>1428  
 <211>20  
 <212>DNA  
 <400>1428  
 ccataactctc tgatgcagcg 20  
 <210>1429  
 <211>20  
 <212>DNA  
 <400>1429  
 ggctctttaga gaaaccgagt 20  
 <210>1430  
 <211>20  
 <212>DNA  
 <400>1430  
 ctcggcaacg agttcaagaa 20  
 <210>1431  
 <211>20  
 <212>DNA  
 <400>1431  
 ggatatccag cacgtgctct 20  
 <210>1432  
 <211>20  
 <212>DNA  
 <400>1432  
 gttgtggctc aagaaggaca 20  
 <210>1433  
 <211>20  
 <212>DNA  
 <400>1433  
 gcgtgtgaaa gaagctgaag 20  
 <210>1434  
 <211>20  
 <212>DNA

<400>2714  
 gtgatcttag ggcgagtggt 20  
 <210>2715  
 <211>20  
 <212>DNA  
 <400>2715  
 gcatcttggtc gactctttgc 20  
 <210>2716  
 <211>20  
 <212>DNA  
 <400>2716  
 gggataagga gcaaagactc 20  
 <210>2717  
 <211>20  
 <212>DNA  
 <400>2717  
 gccacccttc gatctgttta 20  
 <210>2718  
 <211>20  
 <212>DNA  
 <400>2718  
 caagaggggt tcgcagtaaa 20  
 <210>2719  
 <211>20  
 <212>DNA  
 <400>2719  
 cgctcttctt ttcttcttct 20  
 <210>2720  
 <211>20  
 <212>DNA  
 <400>2720  
 cgcaagacag aatgctggaa 20  
 <210>2721  
 <211>20  
 <212>DNA  
 <400>2721  
 ccgtatgccca atctgtcttg 20  
 <210>2722  
 <211>20  
 <212>DNA  
 <400>2722  
 ccactgcgca actatgtcaa 20  
 <210>2723  
 <211>20  
 <212>DNA  
 <400>2723  
 cgtcggcatg tattctagga 20  
 <210>2724  
 <211>20  
 <212>DNA  
 <400>2724  
 gtcccacagc cagtaaacad 20  
 <210>2725  
 <211>20  
 <212>DNA  
 <400>2725  
 ggctccacaa acaaagagga 20  
 <210>2726  
 <211>20  
 <212>DNA  
 <400>2726  
 caggaagttg ttctccgagt 20  
 <210>2727  
 <211>20

<212>DNA  
 <400>2727  
 cctattctgt tacgggaagc 20  
 <210>2728  
 <211>20  
 <212>DNA  
 <400>2728  
 gatggtatcc tatccagggg 20  
 <210>2729  
 <211>20  
 <212>DNA  
 <400>2729  
 ggaacatggt ggtagaggct 20  
 <210>2730  
 <211>20  
 <212>DNA  
 <400>2730  
 ggcgatcttc agaagaaagc 20  
 <210>2731  
 <211>20  
 <212>DNA  
 <400>2731  
 ggatgtttcc cgaaacaatc 20  
 <210>2732  
 <211>20  
 <212>DNA  
 <400>2732  
 ccttttgccc tcccctccac 20  
 <210>2733  
 <211>20  
 <212>DNA  
 <400>2733  
 tggggggtag tgtgtcatca 20  
 <210>2734  
 <211>20  
 <212>DNA  
 <400>2734  
 tctggagaac ttctggagag 20  
 <210>2735  
 <211>20  
 <212>DNA  
 <400>2735  
 gtcaggaatg tgcgtgcctt 20  
 <210>2736  
 <211>20  
 <212>DNA  
 <400>2736  
 gtgggaactt atagtgaggc 20  
 <210>2737  
 <211>20  
 <212>DNA  
 <400>2737  
 ctccgagata catgactcgt 20  
 <210>2738  
 <211>20  
 <212>DNA  
 <400>2738  
 ctcaaagacg acctgagact 20  
 <210>2739  
 <211>20  
 <212>DNA  
 <400>2739  
 cctggagtaa ataacccttc 20  
 <210>2740

<211>20  
<212>DNA  
<400>2740  
gaatggcttc cagaccttgt 20  
<210>2741  
<211>20  
<212>DNA  
<400>2741  
ctttataaag cagtcccgtg 20  
<210>2742  
<211>20  
<212>DNA  
<400>2742  
cgcctgacgg ctttgtttat 20  
<210>2743  
<211>20  
<212>DNA  
<400>2743  
gcctgttgtc catacacgat 20  
<210>2744  
<211>20  
<212>DNA  
<400>2744  
gaggaagcta tgagtgcgaa 20  
<210>2745  
<211>20  
<212>DNA  
<400>2745  
ccctgtgtca aagctaaacc 20  
<210>2746  
<211>20  
<212>DNA  
<400>2746  
ccttcccaac tttatggcgt 20  
<210>2747  
<211>20  
<212>DNA  
<400>2747  
caggcaagct aacgaaggta 20  
<210>2748  
<211>20  
<212>DNA  
<400>2748  
ctctcctcct cattcgaaag 20  
<210>2749  
<211>20  
<212>DNA  
<400>2749  
tagtccccag aacaacatcg 20  
<210>2750  
<211>20  
<212>DNA  
<400>2750  
cgtctgcatc ctattgaacc 20  
<210>2751  
<211>20  
<212>DNA  
<400>2751  
tcgaaccctc ggtacccttt 20  
<210>2752  
<211>20  
<212>DNA  
<400>2752  
ggttctcaat gcctccttag 20

<210>2753  
 <211>20  
 <212>DNA  
 <400>2753  
 cgcaatgcga atcagagtca 20  
 <210>2754  
 <211>20  
 <212>DNA  
 <400>2754  
 ctactacctg ccaattcctc 20  
 <210>2755  
 <211>20  
 <212>DNA  
 <400>2755  
 ggtgtgattt ctggagtcac 20  
 <210>2756  
 <211>20  
 <212>DNA  
 <400>2756  
 ggacgctctc tatgcacaaa 20  
 <210>2757  
 <211>20  
 <212>DNA  
 <400>2757  
 gggctgcata cccaagagat 20  
 <210>2758  
 <211>20  
 <212>DNA  
 <400>2758  
 aaacactctc gctcttctcg 20  
 <210>2759  
 <211>20  
 <212>DNA  
 <400>2759  
 gcactatctc gtcctgaagt 20  
 <210>2760  
 <211>20  
 <212>DNA  
 <400>2760  
 tagcgctggt ccactgcaat 20  
 <210>2761  
 <211>20  
 <212>DNA  
 <400>2761  
 gtccactact tcctaatacc 20  
 <210>2762  
 <211>20  
 <212>DNA  
 <400>2762  
 tccctagtgt ctaccattcc 20  
 <210>2763  
 <211>20  
 <212>DNA  
 <400>2763  
 gcccaacggt ctgtaatagc 20  
 <210>2764  
 <211>20  
 <212>DNA  
 <400>2764  
 aacctcatag tctccggcag 20  
 <210>2765  
 <211>20  
 <212>DNA  
 <400>2765

ggcatagcca tacctttctc	20
<210>2766	
<211>20	
<212>DNA	
<400>2766	
cgtccatgtg tagagtcgaa	20
<210>2767	
<211>20	
<212>DNA	
<400>2767	
gacagtctgt tcagagaagc	20
<210>2768	
<211>20	
<212>DNA	
<400>2768	
accataagcc gtccaatagc	20
<210>2769	
<211>20	
<212>DNA	
<400>2769	
ccgcagaagt aactactgga	20
<210>2770	
<211>20	
<212>DNA	
<400>2770	
cttcaaagtc cccttcttgc	20
<210>2771	
<211>20	
<212>DNA	
<400>2771	
gtcttcgata ggaacccgaa	20
<210>2772	
<211>20	
<212>DNA	
<400>2772	
gcctgtcata gcaaacgaga	20
<210>2773	
<211>20	
<212>DNA	
<400>2773	
gcagtagcag catgaactgt	20
<210>2774	
<211>20	
<212>DNA	
<400>2774	
ggcagcaaag gctgaagatt	20
<210>2775	
<211>20	
<212>DNA	
<400>2775	
cgaggacttc tactgaagag	20
<210>2776	
<211>20	
<212>DNA	
<400>2776	
gagttcagtc gtcctacttc	20
<210>2777	
<211>20	
<212>DNA	
<400>2777	
tgtcggcgta gttcttttagc	20
<210>2778	
<211>20	
<212>DNA	

<400>2778  
 gcaaaagcgc ctccagaaaa 20  
 <210>2779  
 <211>20  
 <212>DNA  
 <400>2779  
 gctccagtac ccttcaaaca 20  
 <210>2780  
 <211>20  
 <212>DNA  
 <400>2780  
 cggctaaacg tcctgtagta 20  
 <210>2781  
 <211>20  
 <212>DNA  
 <400>2781  
 ctcgataaga atggatggcg 20  
 <210>2782  
 <211>20  
 <212>DNA  
 <400>2782  
 caactcgatc aagttgaagg 20  
 <210>2783  
 <211>20  
 <212>DNA  
 <400>2783  
 ggatttttct cactccctcg 20  
 <210>2784  
 <211>20  
 <212>DNA  
 <400>2784  
 ctcgcaaagc tcttcgtctt 20  
 <210>2785  
 <211>20  
 <212>DNA  
 <400>2785  
 ggatagaatt ccaagggcga 20  
 <210>2786  
 <211>20  
 <212>DNA  
 <400>2786  
 gcatacagct aggtctatcg 20  
 <210>2787  
 <211>20  
 <212>DNA  
 <400>2787  
 gcaaaagcgc ctccagaaaa 20  
 <210>2788  
 <211>20  
 <212>DNA  
 <400>2788  
 gatacccgtt tcagttggtg 20  
 <210>2789  
 <211>20  
 <212>DNA  
 <400>2789  
 cggctaaacg tcctgtagta 20  
 <210>2790  
 <211>20  
 <212>DNA  
 <400>2790  
 ccggcaatag aatttcgagc 20  
 <210>2791  
 <211>20

```

<212>DNA
<400>2791
gcatctgtga gttcattggc      20
<210>2792
<211>20
<212>DNA
<400>2792
cgaacgttta caccttcgac      20
<210>2793
<211>20
<212>DNA
<400>2793
ggctttgtag gggaaccttt      20
<210>2794
<211>20
<212>DNA
<400>2794
cgtgtgcgca cgatcacagc      20
<210>2795
<211>20
<212>DNA
<400>2795
ccaactgctt atcaagccct      20
<210>2796
<211>20
<212>DNA
<400>2796
cactagccat ggactttacc      20
<210>2797
<211>20
<212>DNA
<400>2797
cataactccc tgagaagtgg      20
<210>2798
<211>20
<212>DNA
<400>2798
catacgagtt tctgcaggct      20
<210>2799
<211>20
<212>DNA
<400>2799
atattcaatc cctgggtgcg      20
<210>2800
<211>20
<212>DNA
<400>2800
cggtttggat ggtcacttca      20
<210>2801
<211>20
<212>DNA
<400>2801
cgaacgttta caccttcgac      20
<210>2802
<211>20
<212>DNA
<400>2802
ctcgaacttc ggtaacgctt      20
<210>2803
<211>20
<212>DNA
<400>2803
cagctttgat aacgtctccc      20
<210>2804

```



```

<211>20
<212>DNA
<400>2804
cctttcttca caggatggct      20
<210>2805
<211>20
<212>DNA
<400>2805
cttttagttc agtgtgagcg      20
<210>2806
<211>20
<212>DNA
<400>2806
gccacgatga cggcaggata      20
<210>2807
<211>20
<212>DNA
<400>2807
gaagaggagt tctctccaag      20
<210>2808
<211>20
<212>DNA
<400>2808
ggcgggttga ggttttacat      20
<210>2809
<211>20
<212>DNA
<400>2809
cagatcaact tcagcgcctt      20
<210>2810
<211>20
<212>DNA
<400>2810
cgggaattac ccgtaccttt      20
<210>2811
<211>20
<212>DNA
<400>2811
cccaccatag tttctgaaac      20
<210>2812
<211>20
<212>DNA
<400>2812
gagaccgcat aaacttatcc      20
<210>2813
<211>20
<212>DNA
<400>2813
ctcttccacc agaactcttc      20
<210>2814
<211>20
<212>DNA
<400>2814
gctttcctct tggaggaaca      20
<210>2815
<211>20
<212>DNA
<400>2815
gcgcaactca ccacgcgttg      20
<210>2816
<211>20
<212>DNA
<400>2816
gttgccccta caaactttgc      20

```

<210>2817  
<211>20  
<212>DNA  
<400>2817  
ctgctacttc aacttcgcct 20  
<210>2818  
<211>20  
<212>DNA  
<400>2818  
gctccatagg caaccacaat 20  
<210>2819  
<211>20  
<212>DNA  
<400>2819  
cagaggggga agatttttac 20  
<210>2820  
<211>20  
<212>DNA  
<400>2820  
gcgaactctc gaatttcgca 20  
<210>2821  
<211>20  
<212>DNA  
<400>2821  
cagaaaccgc cttacttagc 20  
<210>2822  
<211>20  
<212>DNA  
<400>2822  
gcttgggcca aagcttctaa 20  
<210>2823  
<211>20  
<212>DNA  
<400>2823  
acagtcccgg gggctccata 20  
<210>2824  
<211>20  
<212>DNA  
<400>2824  
cgtactgggt catcggcaaa 20  
<210>2825  
<211>20  
<212>DNA  
<400>2825  
gcatccatac ggatgacagt 20  
<210>2826  
<211>20  
<212>DNA  
<400>2826  
cgattacagc actacccta 20  
<210>2827  
<211>20  
<212>DNA  
<400>2827  
cgcttacttg ggctttgaca 20  
<210>2828  
<211>20  
<212>DNA  
<400>2828  
gatccgagag catccaagaa 20  
<210>2829  
<211>20  
<212>DNA  
<400>2829

catcagaggg aaaagctgct	20
<210>2830	
<211>20	
<212>DNA	
<400>2830	
ggctaaacga tcgagcaaac	20
<210>2831	
<211>20	
<212>DNA	
<400>2831	
gggtaatctc cacaataccc	20
<210>2832	
<211>20	
<212>DNA	
<400>2832	
cgaacagcgg caatttcaat	20
<210>2833	
<211>20	
<212>DNA	
<400>2833	
gaagagtggag cacccataac	20
<210>2834	
<211>20	
<212>DNA	
<400>2834	
ggcacaaccg cttaggttca	20
<210>2835	
<211>20	
<212>DNA	
<400>2835	
gtccttagag gtaatgaggg	20
<210>2836	
<211>20	
<212>DNA	
<400>2836	
cagagccgag aattatggtg	20
<210>2837	
<211>20	
<212>DNA	
<400>2837	
cgatgattcc catcataggg	20
<210>2838	
<211>20	
<212>DNA	
<400>2838	
cggatgctca ctcctatctt	20
<210>2839	
<211>20	
<212>DNA	
<400>2839	
cgaaagtaaa gcgaacagcg	20
<210>2840	
<211>20	
<212>DNA	
<400>2840	
gcctgaagat ggcaaggaaa	20
<210>2841	
<211>20	
<212>DNA	
<400>2841	
aggacatcgt cttcttctgc	20
<210>2842	
<211>20	
<212>DNA	

<400>2842  
 cttgcgtaat tggcgtgcta 20  
 <210>2843  
 <211>20  
 <212>DNA  
 <400>2843  
 acaggacgaa ggcttagagc 20  
 <210>2844  
 <211>20  
 <212>DNA  
 <400>2844  
 agacgtggac atactttccc 20  
 <210>2845  
 <211>20  
 <212>DNA  
 <400>2845  
 ccaacttctg tacttcagcc 20  
 <210>2846  
 <211>20  
 <212>DNA  
 <400>2846  
 gcatgcgcct cccaaagtta 20  
 <210>2847  
 <211>20  
 <212>DNA  
 <400>2847  
 cccatcctgc caattgaaca 20  
 <210>2848  
 <211>20  
 <212>DNA  
 <400>2848  
 gcgagctatc cactagagaa 20  
 <210>2849  
 <211>20  
 <212>DNA  
 <400>2849  
 ggccccgtgt tcaagaaaag 20  
 <210>2850  
 <211>20  
 <212>DNA  
 <400>2850  
 cagcagcaga actctctcat 20  
 <210>2851  
 <211>20  
 <212>DNA  
 <400>2851  
 cctgcctaag cctaagtcac 20  
 <210>2852  
 <211>20  
 <212>DNA  
 <400>2852  
 cctggctcac ggacattagt 20  
 <210>2853  
 <211>20  
 <212>DNA  
 <400>2853  
 tacaggggtt catgctgctg 20  
 <210>2854  
 <211>20  
 <212>DNA  
 <400>2854  
 tcagcagcaa gccgcataat 20  
 <210>2855  
 <211>20

<212>DNA  
<400>2855  
gagagagatc atcatgggtcc 20  
<210>2856  
<211>20  
<212>DNA  
<400>2856  
cctagggaca tcttgcgtaa 20  
<210>2857  
<211>20  
<212>DNA  
<400>2857  
gaagtttgct gtccttcgtg 20  
<210>2858  
<211>20  
<212>DNA  
<400>2858  
gcaagctaag aaagagcctc 20  
<210>2859  
<211>20  
<212>DNA  
<400>2859  
gacgacgcgt atttcgtttg 20  
<210>2860  
<211>20  
<212>DNA  
<400>2860  
ggagataaga ctcacaggca 20  
<210>2861  
<211>20  
<212>DNA  
<400>2861  
caaaaggagg cactctcgaa 20  
<210>2862  
<211>20  
<212>DNA  
<400>2862  
ctcccataga ggagacttag 20  
<210>2863  
<211>20  
<212>DNA  
<400>2863  
gagaagcaac aaaagcagca 20  
<210>2864  
<211>20  
<212>DNA  
<400>2864  
gtcagtgtta gcatcagtgc 20  
<210>2865  
<211>20  
<212>DNA  
<400>2865  
gtcgattaga gggcttccca 20  
<210>2866  
<211>20  
<212>DNA  
<400>2866  
gggataatcc ccatcactta 20  
<210>2867  
<211>20  
<212>DNA  
<400>2867  
caggaacgag ccaaatagca 20  
<210>2868

<211>20  
<212>DNA  
<400>2868  
cgatccttag accccaaaga 20  
<210>2869  
<211>20  
<212>DNA  
<400>2869  
cgggtatttaa cgagccgcta 20  
<210>2870  
<211>20  
<212>DNA  
<400>2870  
gtggtactta gagcttttct 20  
<210>2871  
<211>20  
<212>DNA  
<400>2871  
gttagggaaa tgccctgaga 20  
<210>2872  
<211>20  
<212>DNA  
<400>2872  
ctgaggcgtg ctcttctgac 20  
<210>2873  
<211>20  
<212>DNA  
<400>2873  
ctcctcggcc tgttcttctc 20  
<210>2874  
<211>20  
<212>DNA  
<400>2874  
ccgcgagctt catattctac 20  
<210>2875  
<211>20  
<212>DNA  
<400>2875  
gctggttccc aataagagag 20  
<210>2876  
<211>20  
<212>DNA  
<400>2876  
gaaggattga ttccattgc 20  
<210>2877  
<211>20  
<212>DNA  
<400>2877  
gagagccttt tggagacttc 20  
<210>2878  
<211>20  
<212>DNA  
<400>2878  
gaggagtccct ctggtgaaaa 20  
<210>2879  
<211>20  
<212>DNA  
<400>2879  
ctgggtctaa tgtaggtcct 20  
<210>2880  
<211>20  
<212>DNA  
<400>2880  
ggtcgcccta aatgactcat 20

<210>2881  
<211>20  
<212>DNA  
<400>2881  
tgccggacgt tttgcattag 20  
<210>2882  
<211>20  
<212>DNA  
<400>2882  
ggtcgccccta aatgactcat 20  
<210>2883  
<211>20  
<212>DNA  
<400>2883  
tgcgttgccg gacgttttgc 20  
<210>2884  
<211>20  
<212>DNA  
<400>2884  
gctcgagata tcggcatgaa 20  
<210>2885  
<211>20  
<212>DNA  
<400>2885  
aggcatcgca ctgcgaatac 20  
<210>2886  
<211>20  
<212>DNA  
<400>2886  
cccagaggca atcataggat 20  
<210>2887  
<211>20  
<212>DNA  
<400>2887  
gctttcacat cgctaggcaa 20  
<210>2888  
<211>20  
<212>DNA  
<400>2888  
ccccaaatga actttcaagc 20  
<210>2889  
<211>20  
<212>DNA  
<400>2889  
gaggcacatg atgtcctaag 20  
<210>2890  
<211>20  
<212>DNA  
<400>2890  
ctcatcccta tacccgagat 20  
<210>2891  
<211>20  
<212>DNA  
<400>2891  
ggggagagaa tccagctaat 20  
<210>2892  
<211>20  
<212>DNA  
<400>2892  
cactgagtgt cccatggctg 20  
<210>2893  
<211>20  
<212>DNA  
<400>2893

gcatctcttaa accccgtgtt 20  
 <210>2894  
 <211>20  
 <212>DNA  
 <400>2894  
 gcttttcctgg atcgtcttag 20  
 <210>2895  
 <211>20  
 <212>DNA  
 <400>2895  
 gacgtgctcg tgctctatgc 20  
 <210>2896  
 <211>20  
 <212>DNA  
 <400>2896  
 gtcttctttg ctcgcagaca 20  
 <210>2897  
 <211>20  
 <212>DNA  
 <400>2897  
 gtactagcaa cggtaaggga 20  
 <210>2898  
 <211>20  
 <212>DNA  
 <400>2898  
 cgcattgtata gcgatggaga 20  
 <210>2899  
 <211>20  
 <212>DNA  
 <400>2899  
 ggaaagccaa gcttccaact 20  
 <210>2900  
 <211>20  
 <212>DNA  
 <400>2900  
 gcagatcact acccctattc 20  
 <210>2901  
 <211>20  
 <212>DNA  
 <400>2901  
 ctcaagtcaca atatctcctg 20  
 <210>2902  
 <211>20  
 <212>DNA  
 <400>2902  
 catcccaaag ctgaacgtct 20  
 <210>2903  
 <211>20  
 <212>DNA  
 <400>2903  
 gagcctacta cgcaggactc 20  
 <210>2904  
 <211>20  
 <212>DNA  
 <400>2904  
 tccgtgacgt tcctagagga 20  
 <210>2905  
 <211>20  
 <212>DNA  
 <400>2905  
 cccctaaagt aatcacaggg 20  
 <210>2906  
 <211>20  
 <212>DNA



<400>2906  
ctgggataac gaaggttcgt 20  
<210>2907  
<211>20  
<212>DNA  
<400>2907  
cctaagccta aaactccagc 20  
<210>2908  
<211>20  
<212>DNA  
<400>2908  
cgctcttctg gcaacataga 20  
<210>2909  
<211>20  
<212>DNA  
<400>2909  
gagtcgttgc agctgaatct 20  
<210>2910  
<211>20  
<212>DNA  
<400>2910  
cttgaaagac gaacctaccc 20  
<210>2911  
<211>20  
<212>DNA  
<400>2911  
tcttgattcg cacgacggcg 20  
<210>2912  
<211>20  
<212>DNA  
<400>2912  
ggagactctt ccagtctcta 20  
<210>2913  
<211>20  
<212>DNA  
<400>2913  
cgcatagccg ccatacctcca 20  
<210>2914  
<211>20  
<212>DNA  
<400>2914  
cgccccctct tcataaggaa 20  
<210>2915  
<211>20  
<212>DNA  
<400>2915  
cccagcacat gattcgttga 20  
<210>2916  
<211>20  
<212>DNA  
<400>2916  
caagggaaca aaggaggaag 20  
<210>2917  
<211>20  
<212>DNA  
<400>2917  
ccagtcttaa gcacctctac 20  
<210>2918  
<211>20  
<212>DNA  
<400>2918  
cttggttgaa atatgcggt 20  
<210>2919  
<211>20

```

<212>DNA
<400>2919
ggattaagat atgcccctct 20
<210>2920
<211>20
<212>DNA
<400>2920
cccctacttc acatcacatc 20
<210>2921
<211>20
<212>DNA
<400>2921
cggtcgtttc atgctatgga 20
<210>2922
<211>20
<212>DNA
<400>2922
cccctgtaat gatgactctc 20
<210>2923
<211>20
<212>DNA
<400>2923
actggatccg ctgctgcaaa 20
<210>2924
<211>20
<212>DNA
<400>2924
gttcctgctg aagctattgc 20
<210>2925
<211>20
<212>DNA
<400>2925
cacttactgc agaagctcgt 20
<210>2926
<211>20
<212>DNA
<400>2926
gcatgtagac ggtgtctatg 20
<210>2927
<211>20
<212>DNA
<400>2927
cgttggctag gcggaatggt 20
<210>2928
<211>20
<212>DNA
<400>2928
ggttcgaatc cccttggggt 20
<210>2929
<211>20
<212>DNA
<400>2929
cgaactcaga gcagtgacta 20
<210>2930
<211>20
<212>DNA
<400>2930
ggctgccacc aatgttatac 20
<210>2931
<211>20
<212>DNA
<400>2931
ggctaagcaa actagacgag 20
<210>2932

```

<211>20  
<212>DNA  
<400>2932  
tgcccaaagc cgggatcgaa 20  
<210>2933  
<211>20  
<212>DNA  
<400>2933  
cattttattcg tcttggcccc 20  
<210>2934  
<211>20  
<212>DNA  
<400>2934  
gccagagtac caagaacatc 20  
<210>2935  
<211>20  
<212>DNA  
<400>2935  
gccaaacttga gctgaaagag 20  
<210>2936  
<211>20  
<212>DNA  
<400>2936  
ccgctttgtc aatcgctctt 20  
<210>2937  
<211>20  
<212>DNA  
<400>2937  
gatccttcat cagcttccca 20  
<210>2938  
<211>20  
<212>DNA  
<400>2938  
cctggagtggt ttttcttggt 20  
<210>2939  
<211>20  
<212>DNA  
<400>2939  
cctgagccat gattctagga 20  
<210>2940  
<211>20  
<212>DNA  
<400>2940  
ggctctgtgc ttccttaaga 20  
<210>2941  
<211>20  
<212>DNA  
<400>2941  
ggttggacgt ctttctctgt 20  
<210>2942  
<211>20  
<212>DNA  
<400>2942  
acgccgaatt ctttcgtagc 20  
<210>2943  
<211>20  
<212>DNA  
<400>2943  
ggactgtaac ctaaccacag 20  
<210>2944  
<211>20  
<212>DNA  
<400>2944  
gctcttcctc tttggatcct 20

<210>2945  
 <211>20  
 <212>DNA  
 <400>2945  
 gagggggaag gagaaaaaac 20  
 <210>2946  
 <211>20  
 <212>DNA  
 <400>2946  
 gcttggttgta ccttcgtcca 20  
 <210>2947  
 <211>20  
 <212>DNA  
 <400>2947  
 cgctttcttc gggttcagga 20  
 <210>2948  
 <211>20  
 <212>DNA  
 <400>2948  
 cctaaaggag agagaaaggc 20  
 <210>2949  
 <211>20  
 <212>DNA  
 <400>2949  
 gcgttctcag caaggcaaaa 20  
 <210>2950  
 <211>20  
 <212>DNA  
 <400>2950  
 ctgcatcatt gccatcggat 20  
 <210>2951  
 <211>20  
 <212>DNA  
 <400>2951  
 cgttcagctt ctttctctcg 20  
 <210>2952  
 <211>20  
 <212>DNA  
 <400>2952  
 ggcgttcttc agcatcgaaa 20  
 <210>2953  
 <211>20  
 <212>DNA  
 <400>2953  
 tcctgctacc aagacggtat 20  
 <210>2954  
 <211>20  
 <212>DNA  
 <400>2954  
 gatggttgac accgattcca 20  
 <210>2955  
 <211>20  
 <212>DNA  
 <400>2955  
 cgacgattgg tcagaagtag 20  
 <210>2956  
 <211>20  
 <212>DNA  
 <400>2956  
 cgactgttgt tgcccaaaag 20  
 <210>2957  
 <211>20  
 <212>DNA  
 <400>2957

```

ggggtgcacg aaaaatagga      20
<210>2958
<211>20
<212>DNA
<400>2958
actatagtat cagcgggggc      20
<210>2959
<211>20
<212>DNA
<400>2959
cttgatgcaa gacgatgagc      20
<210>2960
<211>20
<212>DNA
<400>2960
cggcactgtc agaatcttct      20
<210>2961
<211>20
<212>DNA
<400>2961
catagccgt ctagcatctt      20
<210>2962
<211>20
<212>DNA
<400>2962
ggatcgctac gccatttaca      20
<210>2963
<211>20
<212>DNA
<400>2963
gaagatggcc tgcaattgct      20
<210>2964
<211>20
<212>DNA
<400>2964
tgcagaaaca gcattgagcg      20
<210>2965
<211>20
<212>DNA
<400>2965
cccgtcatta ccgacagtaa      20
<210>2966
<211>20
<212>DNA
<400>2966
gagttccaag gattctgtcc      20
<210>2967
<211>20
<212>DNA
<400>2967
gtatcagcag atggaggcaa      20
<210>2968
<211>20
<212>DNA
<400>2968
cctgataccta gtatcttccc      20
<210>2969
<211>20
<212>DNA
<400>2969
ccttctttgg tgcattgcag      20
<210>2970
<211>20
<212>DNA

```

<400>2970  
gggaatacac agattcggtc 20  
<210>2971  
<211>20  
<212>DNA  
<400>2971  
tccttccctt ccttttagagc 20  
<210>2972  
<211>20  
<212>DNA  
<400>2972  
ggcgttacag caatttgga 20  
<210>2973  
<211>20  
<212>DNA  
<400>2973  
gcaggcctat gttttgcagt 20  
<210>2974  
<211>20  
<212>DNA  
<400>2974  
gtgtacctga gtacatgacg 20  
<210>2975  
<211>20  
<212>DNA  
<400>2975  
cactcttgcc tctttagaa 20  
<210>2976  
<211>20  
<212>DNA  
<400>2976  
tgcttgtcaa actgccatcg 20  
<210>2977  
<211>20  
<212>DNA  
<400>2977  
cgactcagtc ctttagctcg 20  
<210>2978  
<211>20  
<212>DNA  
<400>2978  
ccagaaaccc ggcaattttg 20  
<210>2979  
<211>20  
<212>DNA  
<400>2979  
catggacact taggagagag 20  
<210>2980  
<211>20  
<212>DNA  
<400>2980  
cgagcaaagg aaatccctca 20  
<210>2981  
<211>20  
<212>DNA  
<400>2981  
ctttaagggtt gctggcctgt 20  
<210>2982  
<211>20  
<212>DNA  
<400>2982  
gctctatcta cagaaagcgg 20  
<210>2983  
<211>20

<212>DNA  
 <400>2983  
 actgcaaaaa cgcggcaggc 20  
 <210>2984  
 <211>20  
 <212>DNA  
 <400>2984  
 caccgcgcatc tcagggcata 20  
 <210>2985  
 <211>20  
 <212>DNA  
 <400>2985  
 gaggatatgc gttccctctt 20  
 <210>2986  
 <211>20  
 <212>DNA  
 <400>2986  
 cgaatgtaga tcctctcgtc 20  
 <210>2987  
 <211>20  
 <212>DNA  
 <400>2987  
 gaattccacc tccttacctg 20  
 <210>2988  
 <211>20  
 <212>DNA  
 <400>2988  
 aagcaagcgt cttcatagc 20  
 <210>2989  
 <211>20  
 <212>DNA  
 <400>2989  
 cccacctgg gatcaattat 20  
 <210>2990  
 <211>20  
 <212>DNA  
 <400>2990  
 gagaccttca gggaaaccta 20  
 <210>2991  
 <211>20  
 <212>DNA  
 <400>2991  
 atacctcacc cggatctcag 20  
 <210>2992  
 <211>20  
 <212>DNA  
 <400>2992  
 ggcaaaaatc ctgtagatcc 20  
 <210>2993  
 <211>20  
 <212>DNA  
 <400>2993  
 gatatccagg gtagcgcttt 20  
 <210>2994  
 <211>20  
 <212>DNA  
 <400>2994  
 gattccctgt gtctttgtgc 20  
 <210>2995  
 <211>20  
 <212>DNA  
 <400>2995  
 ttcgctcccc cagcacctac 20  
 <210>2996

```

<211>20
<212>DNA
<400>2996
gctaatagaga ctgtcttttg 20
<210>2997
<211>20
<212>DNA
<400>2997
ccctctgata caaaacttcg 20
<210>2998
<211>20
<212>DNA
<400>2998
gaacatctcc taagctgctg 20
<210>2999
<211>20
<212>DNA
<400>2999
gaatgaacac cctcagcact 20
<210>3000
<211>20
<212>DNA
<400>3000
gacatctcca agagttctgc 20
<210>3001
<211>20
<212>DNA
<400>3001
gttggttggtg gttcatgggt 20
<210>3002
<211>20
<212>DNA
<400>3002
gcttccgcac tcttatttgc 20
<210>3003
<211>20
<212>DNA
<400>3003
caaaggcctt accaaagcac 20
<210>3004
<211>20
<212>DNA
<400>3004
gcgtttctac aaaaccccgt 20
<210>3005
<211>20
<212>DNA
<400>3005
ggactactgg gttatcttgc 20
<210>3006
<211>20
<212>DNA
<400>3006
ctctcatgat cttctcgctg 20
<210>3007
<211>20
<212>DNA
<400>3007
gcttgggcga accaaaactt 20
<210>3008
<211>20
<212>DNA
<400>3008
cgatacctgt cagcagcttt 20

```



<210>3009  
<211>20  
<212>DNA  
<400>3009  
gcatcacgtg ttgtctttgc 20  
<210>3010  
<211>20  
<212>DNA  
<400>3010  
cccgaagcaa tccagtagat 20  
<210>3011  
<211>20  
<212>DNA  
<400>3011  
tgaagcaaag cgccgtttac 20  
<210>3012  
<211>20  
<212>DNA  
<400>3012  
cgagccatgt atttcagtcc 20  
<210>3013  
<211>20  
<212>DNA  
<400>3013  
cgatacctgt cagcagcttt 20  
<210>3014  
<211>20  
<212>DNA  
<400>3014  
ggatgttggtg gtgaagagtg 20  
<210>3015  
<211>20  
<212>DNA  
<400>3015  
cttggagagg gctatatagg 20  
<210>3016  
<211>20  
<212>DNA  
<400>3016  
caaaatgcgg gtcctttgag 20  
<210>3017  
<211>20  
<212>DNA  
<400>3017  
gctcaagggtg cggagtaaaa 20  
<210>3018  
<211>20  
<212>DNA  
<400>3018  
gattgtggtg tgacatgcca 20  
<210>3019  
<211>20  
<212>DNA  
<400>3019  
ggggcttgga caatctcatt 20  
<210>3020  
<211>20  
<212>DNA  
<400>3020  
ccacgtctcc tcaagatttc 20  
<210>3021  
<211>20  
<212>DNA  
<400>3021

caagaaatcc cagtgcgagt	20
<210>3022	
<211>20	
<212>DNA	
<400>3022	
ctgatgtctt cgcaacccat	20
<210>3023	
<211>20	
<212>DNA	
<400>3023	
ccacgtctcc tcaagatttc	20
<210>3024	
<211>20	
<212>DNA	
<400>3024	
ccttgtgctg cctttactgt	20
<210>3025	
<211>20	
<212>DNA	
<400>3025	
cctacctctc tgctttcttc	20
<210>3026	
<211>20	
<212>DNA	
<400>3026	
tcactcttct aaaggtctcg	20
<210>3027	
<211>20	
<212>DNA	
<400>3027	
tcagccggct tctttaccca	20
<210>3028	
<211>20	
<212>DNA	
<400>3028	
gagagacaaa ctccgattac	20
<210>3029	
<211>20	
<212>DNA	
<400>3029	
gtcgatctcc aagagtatct	20
<210>3030	
<211>20	
<212>DNA	
<400>3030	
tctaaagaag ccaccctctc	20
<210>3031	
<211>20	
<212>DNA	
<400>3031	
ccaccaactt cttcacctga	20
<210>3032	
<211>20	
<212>DNA	
<400>3032	
tcgggacgct tatctgcaaa	20
<210>3033	
<211>20	
<212>DNA	
<400>3033	
ccccatctaa tcctgttgct	20
<210>3034	
<211>20	
<212>DNA	

<400>3034  
gaacgacggt atccacaatc 20  
<210>3035  
<211>20  
<212>DNA  
<400>3035  
atcggcatcc caaggtccta 20  
<210>3036  
<211>20  
<212>DNA  
<400>3036  
ccgttcttct tgcgatgagt 20  
<210>3037  
<211>20  
<212>DNA  
<400>3037  
ccaccaagta gtggtgtaac 20  
<210>3038  
<211>20  
<212>DNA  
<400>3038  
gggttttttag aggtttgtgg 20  
<210>3039  
<211>20  
<212>DNA  
<400>3039  
cgcagattgg ccttcttcta 20  
<210>3040  
<211>20  
<212>DNA  
<400>3040  
ctgtgatctt ttggccttga 20  
<210>3041  
<211>20  
<212>DNA  
<400>3041  
cacttgctgg tactgcacta 20  
<210>3042  
<211>20  
<212>DNA  
<400>3042  
ctgacgtccg atgtatttgc 20  
<210>3043  
<211>20  
<212>DNA  
<400>3043  
gccgatgaga attcctgtag 20  
<210>3044  
<211>20  
<212>DNA  
<400>3044  
gattggcggt gctgaattcc 20  
<210>3045  
<211>20  
<212>DNA  
<400>3045  
gggaagatgt ccgttcagtt 20  
<210>3046  
<211>20  
<212>DNA  
<400>3046  
ctacagctaa agctgagtcc 20  
<210>3047  
<211>20

<212>DNA  
 <400>3047  
 ggagatgtct tcttcaccga 20  
 <210>3048  
 <211>20  
 <212>DNA  
 <400>3048  
 caccagactc tacagtacca 20  
 <210>3049  
 <211>20  
 <212>DNA  
 <400>3049  
 gaaccaacga cctaagtctc 20  
 <210>3050  
 <211>20  
 <212>DNA  
 <400>3050  
 gcgaagataa actgagatcc 20  
 <210>3051  
 <211>20  
 <212>DNA  
 <400>3051  
 gtgttcttga cctcgggttag 20  
 <210>3052  
 <211>20  
 <212>DNA  
 <400>3052  
 agacgcagaa ggcattagca 20  
 <210>3053  
 <211>20  
 <212>DNA  
 <400>3053  
 gagatcctca gtaacaaaca 20  
 <210>3054  
 <211>20  
 <212>DNA  
 <400>3054  
 ttcaggagta tgcgtaccgt 20  
 <210>3055  
 <211>20  
 <212>DNA  
 <400>3055  
 cgattcttct tagccggagt 20  
 <210>3056  
 <211>20  
 <212>DNA  
 <400>3056  
 gggagtgaat acgatgaggt 20  
 <210>3057  
 <211>20  
 <212>DNA  
 <400>3057  
 cagctgggtct tgaggtttac 20  
 <210>3058  
 <211>20  
 <212>DNA  
 <400>3058  
 ggagcttcct aaagcatgtc 20  
 <210>3059  
 <211>20  
 <212>DNA  
 <400>3059  
 cggctctctgt atacgatacg 20  
 <210>3060

## WO 99/27105

<211>20  
 <212>DNA  
 <400>3060  
 ctccagacaa gacaagaact 20  
 <210>3061  
 <211>20  
 <212>DNA  
 <400>3061  
 ccccttcaag atctcatagg 20  
 <210>3062  
 <211>20  
 <212>DNA  
 <400>3062  
 ggatggagga tcttcattcc 20  
 <210>3063  
 <211>20  
 <212>DNA  
 <400>3063  
 caccagaaaa cccttcagtt 20  
 <210>3064  
 <211>20  
 <212>DNA  
 <400>3064  
 gccttcttga tggcaaacct 20  
 <210>3065  
 <211>20  
 <212>DNA  
 <400>3065  
 cggggtattg tgcagaagat 20  
 <210>3066  
 <211>20  
 <212>DNA  
 <400>3066  
 ccgacaagct ttcagatgct 20  
 <210>3067  
 <211>20  
 <212>DNA  
 <400>3067  
 ctctaaggct agaaatcccc 20  
 <210>3068  
 <211>20  
 <212>DNA  
 <400>3068  
 ctgcgcaatc tttggctact 20  
 <210>3069  
 <211>20  
 <212>DNA  
 <400>3069  
 gagagggtag tgaaagttcc 20  
 <210>3070  
 <211>20  
 <212>DNA  
 <400>3070  
 gcagtcgtcg tgttttctca 20  
 <210>3071  
 <211>20  
 <212>DNA  
 <400>3071  
 ccaagtttcg tatgtggttg 20  
 <210>3072  
 <211>20  
 <212>DNA  
 <400>3072  
 ggtcgtgctt tgaagatgac 20

<210>3073  
<211>20  
<212>DNA  
<400>3073  
cgtcgatttt gcactcaagg 20  
<210>3074  
<211>20  
<212>DNA  
<400>3074  
cctgatgctg ttttgcaagg 20  
<210>3075  
<211>20  
<212>DNA  
<400>3075  
cgagtgcata atgttgctgc 20  
<210>3076  
<211>20  
<212>DNA  
<400>3076  
ggggtggaag gttttagatg 20  
<210>3077  
<211>20  
<212>DNA  
<400>3077  
cgttggtctg aaggaaagtt 20  
<210>3078  
<211>20  
<212>DNA  
<400>3078  
gagctagggt acatttctgg 20  
<210>3079  
<211>20  
<212>DNA  
<400>3079  
cggagccttg ttcttgtaag 20  
<210>3080  
<211>20  
<212>DNA  
<400>3080  
ccataaatgg gactcatggc 20  
<210>3081  
<211>20  
<212>DNA  
<400>3081  
gcactagaat acaaggacct 20  
<210>3082  
<211>20  
<212>DNA  
<400>3082  
cgtaattgct tgcaagaggc 20  
<210>3083  
<211>20  
<212>DNA  
<400>3083  
cgaggggata agaacaggat 20  
<210>3084  
<211>20  
<212>DNA  
<400>3084  
gcctatatct ttgcttcttg 20  
<210>3085  
<211>20  
<212>DNA  
<400>3085

cagacgagct ggtgatttga 20  
 <210>3086  
 <211>20  
 <212>DNA  
 <400>3086  
 cctaccgttg catgtccgca 20  
 <210>3087  
 <211>20  
 <212>DNA  
 <400>3087  
 ctaggacggg aagtatactc 20  
 <210>3088  
 <211>20  
 <212>DNA  
 <400>3088  
 ctaatttccg cggctaaggt 20  
 <210>3089  
 <211>20  
 <212>DNA  
 <400>3089  
 ggaagcacag tttgtgggaa 20  
 <210>3090  
 <211>20  
 <212>DNA  
 <400>3090  
 ggtctatatg aaggctagca 20  
 <210>3091  
 <211>20  
 <212>DNA  
 <400>3091  
 ctgtaggacg taaccgttga 20  
 <210>3092  
 <211>20  
 <212>DNA  
 <400>3092  
 cgattgtgca tggcgcagag 20  
 <210>3093  
 <211>20  
 <212>DNA  
 <400>3093  
 cgggctttct cttcagagtt 20  
 <210>3094  
 <211>20  
 <212>DNA  
 <400>3094  
 ggtccaggag tctgattcaa 20  
 <210>3095  
 <211>20  
 <212>DNA  
 <400>3095  
 ctaggacacg aaacgtggaa 20  
 <210>3096  
 <211>20  
 <212>DNA  
 <400>3096  
 ggcgcgatgc cttggttaat 20  
 <210>3097  
 <211>20  
 <212>DNA  
 <400>3097  
 aactcagtaa gtggcgattg 20  
 <210>3098  
 <211>20  
 <212>DNA

<400>3098  
ggagctgttt acagatgcca 20  
<210>3099  
<211>20  
<212>DNA  
<400>3099  
gtatccaagg cttgttggca 20  
<210>3100  
<211>20  
<212>DNA  
<400>3100  
gaagctccca tgaatgaagg 20  
<210>3101  
<211>20  
<212>DNA  
<400>3101  
ctgcgaagta gagcgtcttc 20  
<210>3102  
<211>20  
<212>DNA  
<400>3102  
ggggaagttt atagtcagga 20  
<210>3103  
<211>20  
<212>DNA  
<400>3103  
gcttttccgc gtcactttga 20  
<210>3104  
<211>20  
<212>DNA  
<400>3104  
agcatatcgc acaaagagcg 20  
<210>3105  
<211>20  
<212>DNA  
<400>3105  
gcctttgctc tgtgagaaac 20  
<210>3106  
<211>20  
<212>DNA  
<400>3106  
gcgttggtga ttgaggactc 20  
<210>3107  
<211>20  
<212>DNA  
<400>3107  
cacgtcgatc ttccatatgc 20  
<210>3108  
<211>20  
<212>DNA  
<400>3108  
ctttcagagg agttttcctg 20  
<210>3109  
<211>20  
<212>DNA  
<400>3109  
ggagatggtc taccagcaat 20  
<210>3110  
<211>20  
<212>DNA  
<400>3110  
ggactgctga catctccaag 20  
<210>3111  
<211>20



```

<212>DNA
<400>3111
gcgacaagtc gttttggaag      20
<210>3112
<211>20
<212>DNA
<400>3112
ggtttctggg tttgctgctg      20
<210>3113
<211>20
<212>DNA
<400>3113
tgcgatcccc tcattgtaac      20
<210>3114
<211>20
<212>DNA
<400>3114
ctgcaacttg gcttgacttg      20
<210>3115
<211>20
<212>DNA
<400>3115
cctacggaat tgcacgcatt      20
<210>3116
<211>20
<212>DNA
<400>3116
gcgagctgag gtatttctgt      20
<210>3117
<211>20
<212>DNA
<400>3117
ctgggtttgc tgctgtccat      20
<210>3118
<211>20
<212>DNA
<400>3118
attgggctgt agatggccag      20
<210>3119
<211>20
<212>DNA
<400>3119
cgcaagggtc tcttcacctt      20
<210>3120
<211>20
<212>DNA
<400>3120
tttgtggctg cgtagtacag      20
<210>3121
<211>20
<212>DNA
<400>3121
ctggcaatgc aagtaaagcc      20
<210>3122
<211>20
<212>DNA
<400>3122
ccaggagcaa gagctataga      20
<210>3123
<211>20
<212>DNA
<400>3123
cctgaagtta gtgagaacgg      20
<210>3124

```

```

<211>20
<212>DNA
<400>3124
gatcggatgc tcgttcaaag      20
<210>3125
<211>20
<212>DNA
<400>3125
acggccgtct ttgttcgata      20
<210>3126
<211>20
<212>DNA
<400>3126
gtccaagtac acacagaaag      20
<210>3127
<211>20
<212>DNA
<400>3127
ctagcgatgc gaagcaaaag      20
<210>3128
<211>20
<212>DNA
<400>3128
gagagaagtg taccatggaa      20
<210>3129
<211>20
<212>DNA
<400>3129
gggatagagc gttaggattc      20
<210>3130
<211>20
<212>DNA
<400>3130
gcagcatatg ctgccctttt      20
<210>3131
<211>20
<212>DNA
<400>3131
gaggaagagg gcactacatt      20
<210>3132
<211>20
<212>DNA
<400>3132
ccgttgccaa tgtaaaaggg      20
<210>3133
<211>20
<212>DNA
<400>3133
gcaaacctag gagggaggtt      20
<210>3134
<211>20
<212>DNA
<400>3134
gtgatgcctt gggatcacta      20
<210>3135
<211>20
<212>DNA
<400>3135
cacaagcatt cgtagggtgga      20
<210>3136
<211>20
<212>DNA
<400>3136
gcgattacta agggagctct      20

```

<210>3137  
<211>20  
<212>DNA  
<400>3137  
gtcggagagg aactcctatt 20  
<210>3138  
<211>20  
<212>DNA  
<400>3138  
gcaatttccc aagcgcgtta 20  
<210>3139  
<211>20  
<212>DNA  
<400>3139  
ggacgtgctt gcggcattat 20  
<210>3140  
<211>20  
<212>DNA  
<400>3140  
ccgtagtacg gtaggcttta 20  
<210>3141  
<211>20  
<212>DNA  
<400>3141  
gagagtggga tccttcttct 20  
<210>3142  
<211>20  
<212>DNA  
<400>3142  
gcagaaggag atgcatagga 20  
<210>3143  
<211>20  
<212>DNA  
<400>3143  
tcgatttccc cattgtcagc 20  
<210>3144  
<211>20  
<212>DNA  
<400>3144  
ggaacgtctt tcctctagtg 20  
<210>3145  
<211>20  
<212>DNA  
<400>3145  
cctgtggacg gcatcagcag 20  
<210>3146  
<211>20  
<212>DNA  
<400>3146  
ccgtagaaac ggcaaatacag 20  
<210>3147  
<211>20  
<212>DNA  
<400>3147  
caccacctac agtaatggca 20  
<210>3148  
<211>20  
<212>DNA  
<400>3148  
gggtctatgg agagcacgat 20  
<210>3149  
<211>20  
<212>DNA  
<400>3149

```

ggctccctaa gagaatgcaa      20
<210>3150
<211>20
<212>DNA
<400>3150
gcagttggca cgcatttatg      20
<210>3151
<211>20
<212>DNA
<400>3151
gatcccttgg agttcttgag      20
<210>3152
<211>20
<212>DNA
<400>3152
agggcatttg cggaaatgcg      20
<210>3153
<211>20
<212>DNA
<400>3153
cggagggaat caagtgagtc      20
<210>3154
<211>20
<212>DNA
<400>3154
ccttaacagg cacactaagc      20
<210>3155
<211>20
<212>DNA
<400>3155
gtttaagcag atccgaaacc      20
<210>3156
<211>20
<212>DNA
<400>3156
cgttgggtgg tcagatacta      20
<210>3157
<211>20
<212>DNA
<400>3157
gggactttag gaggaactac      20
<210>3158
<211>20
<212>DNA
<400>3158
aagaagctcg agtggttcgac      20
<210>3159
<211>20
<212>DNA
<400>3159
ccgttcccaa gttcatggaa      20
<210>3160
<211>20
<212>DNA
<400>3160
acagatgggtg aataccgtgc      20
<210>3161
<211>20
<212>DNA
<400>3161
ggcagtagaa ttgtaggagc      20
<210>3162
<211>20
<212>DNA

```

## WO 99/27105

<400>3162  
 gctgccatat tttcctctcg 20  
 <210>3163  
 <211>20  
 <212>DNA  
 <400>3163  
 gatccgaggc cttggtatatt 20  
 <210>3164  
 <211>20  
 <212>DNA  
 <400>3164  
 ggaccatcca taagctactc 20  
 <210>3165  
 <211>20  
 <212>DNA  
 <400>3165  
 ggttatgaag gtggcaatgc 20  
 <210>3166  
 <211>20  
 <212>DNA  
 <400>3166  
 tggatatcgg caatgacagc 20  
 <210>3167  
 <211>20  
 <212>DNA  
 <400>3167  
 tcgacaatcc ccgcgattat 20  
 <210>3168  
 <211>20  
 <212>DNA  
 <400>3168  
 gtttctgaga cagccgcaaa 20  
 <210>3169  
 <211>20  
 <212>DNA  
 <400>3169  
 cagccatttg cgcaacttga 20  
 <210>3170  
 <211>20  
 <212>DNA  
 <400>3170  
 gctgagcagc tagcgttttg 20  
 <210>3171  
 <211>20  
 <212>DNA  
 <400>3171  
 ctgatactgc tctgcttctt 20  
 <210>3172  
 <211>20  
 <212>DNA  
 <400>3172  
 cctacactta gccaatcagc 20  
 <210>3173  
 <211>20  
 <212>DNA  
 <400>3173  
 gaggggaaac ggaatccata 20  
 <210>3174  
 <211>20  
 <212>DNA  
 <400>3174  
 ctgaggagca agttcttgtg 20  
 <210>3175  
 <211>20

<212>DNA  
<400>3175  
ctgtcaggat attcctaggg 20  
<210>3176  
<211>20  
<212>DNA  
<400>3176  
gctgggtaag atcagggttct 20  
<210>3177  
<211>20  
<212>DNA  
<400>3177  
ccttgacgat agcgtgcttt 20  
<210>3178  
<211>20  
<212>DNA  
<400>3178  
gcaccaagat gaagggttgt 20  
<210>3179  
<211>20  
<212>DNA  
<400>3179  
gcaggtattc tgcacatcag 20  
<210>3180  
<211>20  
<212>DNA  
<400>3180  
acacaacagc aaggctgtca 20  
<210>3181  
<211>20  
<212>DNA  
<400>3181  
cgtccgctat tgaagtgcct 20  
<210>3182  
<211>20  
<212>DNA  
<400>3182  
gctcacgaat caactctgtc 20  
<210>3183  
<211>20  
<212>DNA  
<400>3183  
ggcagattct gtaagccaac 20  
<210>3184  
<211>20  
<212>DNA  
<400>3184  
ctgctgtagt accttcgagt 20  
<210>3185  
<211>20  
<212>DNA  
<400>3185  
gctgtttaca gcgatggtct 20  
<210>3186  
<211>20  
<212>DNA  
<400>3186  
gctacaacct gtacgcaaaa 20  
<210>3187  
<211>20  
<212>DNA  
<400>3187  
catcgtegat ttgcagtgtg 20  
<210>3188

<211>20  
<212>DNA  
<400>3188  
gtttgtgttt gagagtccgc 20  
<210>3189  
<211>20  
<212>DNA  
<400>3189  
ggtcccgttt ttttgcttcc 20  
<210>3190  
<211>20  
<212>DNA  
<400>3190  
gctaccgaag ttgaggattt 20  
<210>3191  
<211>20  
<212>DNA  
<400>3191  
cgaggcggtt ttgttggtat 20  
<210>3192  
<211>20  
<212>DNA  
<400>3192  
agcaccagca atagtggcat 20  
<210>3193  
<211>20  
<212>DNA  
<400>3193  
agctgatgct tgatgggttcg 20  
<210>3194  
<211>20  
<212>DNA  
<400>3194  
gagccgcgat gatgctatta 20  
<210>3195  
<211>20  
<212>DNA  
<400>3195  
gctaccgaag ttgaggattt 20  
<210>3196  
<211>20  
<212>DNA  
<400>3196  
gggcttgctc atcgatctaa 20  
<210>3197  
<211>20  
<212>DNA  
<400>3197  
agaaaccgcg atcatcacag 20  
<210>3198  
<211>20  
<212>DNA  
<400>3198  
tgctattggc agcaaggggc 20  
<210>3199  
<211>20  
<212>DNA  
<400>3199  
cttccgtagg tacgggatgg 20  
<210>3200  
<211>20  
<212>DNA  
<400>3200  
ggaagtcagg tgaaactgga 20

<210>3201  
<211>20  
<212>DNA  
<400>3201  
ccacacgtca aggacagaaa 20  
<210>3202  
<211>20  
<212>DNA  
<400>3202  
ggaaagctta ggggggattc 20  
<210>3203  
<211>20  
<212>DNA  
<400>3203  
gcgatgtgca agaagaagag 20  
<210>3204  
<211>20  
<212>DNA  
<400>3204  
ggaaaggtaa caggacctct 20  
<210>3205  
<211>20  
<212>DNA  
<400>3205  
gccttttagag tgcttcacag 20  
<210>3206  
<211>20  
<212>DNA  
<400>3206  
catcagacag tctcacggag 20  
<210>3207  
<211>20  
<212>DNA  
<400>3207  
ggagcagacg attatgaggg 20  
<210>3208  
<211>20  
<212>DNA  
<400>3208  
gctccatacg aatgacgcta 20  
<210>3209  
<211>20  
<212>DNA  
<400>3209  
ccgtatcgag gtgctgttat 20  
<210>3210  
<211>20  
<212>DNA  
<400>3210  
gcgtgcattg tttcgttccg 20  
<210>3211  
<211>20  
<212>DNA  
<400>3211  
gcgagtcctt ctgtagttac 20  
<210>3212  
<211>20  
<212>DNA  
<400>3212  
aatcgaaggc ctcgacttgg 20  
<210>3213  
<211>20  
<212>DNA  
<400>3213



agaatccgct accgcattga 20  
 <210>3214  
 <211>20  
 <212>DNA  
 <400>3214  
 cgaggcagta tccataaagg 20  
 <210>3215  
 <211>20  
 <212>DNA  
 <400>3215  
 cgatatcctt atggtcggag 20  
 <210>3216  
 <211>20  
 <212>DNA  
 <400>3216  
 ccacaggtct tttgaggaag 20  
 <210>3217  
 <211>20  
 <212>DNA  
 <400>3217  
 gcgtgcattg tttcggtccg 20  
 <210>3218  
 <211>20  
 <212>DNA  
 <400>3218  
 cggtacgagc ttctctccat 20  
 <210>3219  
 <211>20  
 <212>DNA  
 <400>3219  
 ctccaaggggt gtctgcaaaa 20  
 <210>3220  
 <211>20  
 <212>DNA  
 <400>3220  
 cgcaccgact tccgcctgga 20  
 <210>3221  
 <211>20  
 <212>DNA  
 <400>3221  
 cttggtgtaa agagggtagg 20  
 <210>3222  
 <211>20  
 <212>DNA  
 <400>3222  
 tcgatgtcgc tgcccttcaa 20  
 <210>3223  
 <211>20  
 <212>DNA  
 <400>3223  
 ggggtctcga cgtaaactta 20  
 <210>3224  
 <211>20  
 <212>DNA  
 <400>3224  
 gccctccttt cctcaacttt 20  
 <210>3225  
 <211>20  
 <212>DNA  
 <400>3225  
 cgaggagcct ggatcattat 20  
 <210>3226  
 <211>20  
 <212>DNA

<400>3226  
 ccgccaagac ttttggaag 20  
 <210>3227  
 <211>20  
 <212>DNA  
 <400>3227  
 caaactctca gtcgctactg 20  
 <210>3228  
 <211>20  
 <212>DNA  
 <400>3228  
 ccctccagag atcattaagg 20  
 <210>3229  
 <211>20  
 <212>DNA  
 <400>3229  
 cgatacgatt tgctcccctt 20  
 <210>3230  
 <211>20  
 <212>DNA  
 <400>3230  
 tgatcataag cccttggagc 20  
 <210>3231  
 <211>20  
 <212>DNA  
 <400>3231  
 cctccaaaga atcgctctca 20  
 <210>3232  
 <211>20  
 <212>DNA  
 <400>3232  
 tcatcagcat tcagtggggg 20  
 <210>3233  
 <211>20  
 <212>DNA  
 <400>3233  
 gagcctaggg gattagagta 20  
 <210>3234  
 <211>20  
 <212>DNA  
 <400>3234  
 cgtggatgat gaagtctcag 20  
 <210>3235  
 <211>20  
 <212>DNA  
 <400>3235  
 gagacagagc tggcacatct 20  
 <210>3236  
 <211>20  
 <212>DNA  
 <400>3236  
 cagctctttg gcatcaagga 20  
 <210>3237  
 <211>20  
 <212>DNA  
 <400>3237  
 gccggaggat gttgaaagat 20  
 <210>3238  
 <211>20  
 <212>DNA  
 <400>3238  
 ctctggcaac cacgctaata 20  
 <210>3239  
 <211>20

<212>DNA  
<400>3239  
ccgtggggaa catcacataa 20  
<210>3240  
<211>20  
<212>DNA  
<400>3240  
cttggcttcc aaggcattct 20  
<210>3241  
<211>20  
<212>DNA  
<400>3241  
cgagggacag gagttttcat 20  
<210>3242  
<211>20  
<212>DNA  
<400>3242  
aagctctcta cctttgttgc 20  
<210>3243  
<211>20  
<212>DNA  
<400>3243  
gcttatgaac gaactgtcgt 20  
<210>3244  
<211>20  
<212>DNA  
<400>3244  
ccttgcagca tgacattcac 20  
<210>3245  
<211>20  
<212>DNA  
<400>3245  
cgggatgagg agattcaaca 20  
<210>3246  
<211>20  
<212>DNA  
<400>3246  
ggccggcttt ggatagttat 20  
<210>3247  
<211>20  
<212>DNA  
<400>3247  
gagttagggg taggacgtta 20  
<210>3248  
<211>20  
<212>DNA  
<400>3248  
cgagagcaag gtaggtggca 20  
<210>3249  
<211>20  
<212>DNA  
<400>3249  
gcggggtatc tacgtgttcg 20  
<210>3250  
<211>20  
<212>DNA  
<400>3250  
cgagcttttt agggaggact 20  
<210>3251  
<211>20  
<212>DNA  
<400>3251  
gaagatcgca aggatgacag 20  
<210>3252

```

<211>20
<212>DNA
<400>3252
gcaaacgttc cctcggtaaa      20
<210>3253
<211>20
<212>DNA
<400>3253
cgctgacaaa gcaatgcgct      20
<210>3254
<211>20
<212>DNA
<400>3254
cctgagtgga catgggttaca     20
<210>3255
<211>20
<212>DNA
<400>3255
cctatgacat aagctccgag      20
<210>3256
<211>20
<212>DNA
<400>3256
ggatgcgctc ttcaagtgt      20
<210>3257
<211>20
<212>DNA
<400>3257
gaccaatagc caccaagaca      20
<210>3258
<211>20
<212>DNA
<400>3258
cgtctatccg acagaggatt      20
<210>3259
<211>20
<212>DNA
<400>3259
gaagaggacc ctgtgcttat      20
<210>3260
<211>20
<212>DNA
<400>3260
gcaacgtatt ctacagaacc      20
<210>3261
<211>20
<212>DNA
<400>3261
gagcgtcaga gggaagataa      20
<210>3262
<211>20
<212>DNA
<400>3262
caggacaact gcaagaagca      20
<210>3263
<211>20
<212>DNA
<400>3263
ggaggtaaac acgctgcttt      20
<210>3264
<211>20
<212>DNA
<400>3264
cagctccgaa gaacatagca      20

```

<210>3265  
<211>20  
<212>DNA  
<400>3265  
cgcgagttcc aacttaggaa 20  
<210>3266  
<211>20  
<212>DNA  
<400>3266  
ctgggtatagc ttccctggag 20  
<210>3267  
<211>20  
<212>DNA  
<400>3267  
catcctgtcg aaagatggct 20  
<210>3268  
<211>20  
<212>DNA  
<400>3268  
cagagagtcg tacaacagca 20  
<210>3269  
<211>20  
<212>DNA  
<400>3269  
ggacaaaagg tagagttacg 20  
<210>3270  
<211>20  
<212>DNA  
<400>3270  
cggcaacgct ctctatttag 20  
<210>3271  
<211>20  
<212>DNA  
<400>3271  
gagggtttttc cagcctcttg 20  
<210>3272  
<211>20  
<212>DNA  
<400>3272  
gacgttcgca gattttgcga 20  
<210>3273  
<211>20  
<212>DNA  
<400>3273  
ggacgttacc ttgtgtatcc 20  
<210>3274  
<211>20  
<212>DNA  
<400>3274  
ggtctccctg gtctgtattt 20  
<210>3275  
<211>20  
<212>DNA  
<400>3275  
ctccatcaag ctatcgaagc 20  
<210>3276  
<211>20  
<212>DNA  
<400>3276  
gagttgtccc ctcttgagaa 20  
<210>3277  
<211>20  
<212>DNA  
<400>3277

```

gggtccattc tgaccaaact 20
<210>3278
<211>20
<212>DNA
<400>3278
caatactgat gacgtctggg 20
<210>3279
<211>20
<212>DNA
<400>3279
gctcttcatt gagaagaccg 20
<210>3280
<211>20
<212>DNA
<400>3280
gtaggttctg taaggatggc 20
<210>3281
<211>20
<212>DNA
<400>3281
cagcttcctt agcgccggtg 20
<210>3282
<211>20
<212>DNA
<400>3282
aggggtaagc accctgagat 20
<210>3283
<211>20
<212>DNA
<400>3283
tactgttgcg gcttcctcac 20
<210>3284
<211>20
<212>DNA
<400>3284
ctttcgcaga agttaccacc 20
<210>3285
<211>20
<212>DNA
<400>3285
ctaatagccgg ggcttccttta 20
<210>3286
<211>20
<212>DNA
<400>3286
ccacggcccg tatectcgac 20
<210>3287
<211>20
<212>DNA
<400>3287
gcctgatatc ctgcattacg 20
<210>3288
<211>20
<212>DNA
<400>3288
ccaacagttc tgctttgcga 20
<210>3289
<211>20
<212>DNA
<400>3289
ccagtttttg cttgcttggc 20
<210>3290
<211>20
<212>DNA

```

<400>3290  
 cgagacttcg attacagcgt 20  
 <210>3291  
 <211>20  
 <212>DNA  
 <400>3291  
 gcgacatcgt aatcagcagc 20  
 <210>3292  
 <211>20  
 <212>DNA  
 <400>3292  
 aaaagcgggt gatgaggctt 20  
 <210>3293  
 <211>20  
 <212>DNA  
 <400>3293  
 catcatacgg ctatggggaa 20  
 <210>3294  
 <211>20  
 <212>DNA  
 <400>3294  
 ggccataaga ctgtggtctt 20  
 <210>3295  
 <211>20  
 <212>DNA  
 <400>3295  
 cgttccttta gtcgtttgcg 20  
 <210>3296  
 <211>20  
 <212>DNA  
 <400>3296  
 ctgctgtaga gaatcaagcg 20  
 <210>3297  
 <211>20  
 <212>DNA  
 <400>3297  
 agcagcatct ttggctttgc 20  
 <210>3298  
 <211>20  
 <212>DNA  
 <400>3298  
 ggggcgcttt aattaaggga 20  
 <210>3299  
 <211>20  
 <212>DNA  
 <400>3299  
 ctcggaatgc aaaatcgggtg 20  
 <210>3300  
 <211>20  
 <212>DNA  
 <400>3300  
 agggacttcg gggaagtttt 20  
 <210>3301  
 <211>20  
 <212>DNA  
 <400>3301  
 gggtccacca agaacagact 20  
 <210>3302  
 <211>20  
 <212>DNA  
 <400>3302  
 ggcttgaatc ttgacctaca 20  
 <210>3303  
 <211>20

<212>DNA  
 <400>3303  
 ggctgaacct attcagcaga 20  
 <210>3304  
 <211>20  
 <212>DNA  
 <400>3304  
 gggcaaaatg gaattacccc 20  
 <210>3305  
 <211>20  
 <212>DNA  
 <400>3305  
 cgcccaagtt caaacctcaa 20  
 <210>3306  
 <211>20  
 <212>DNA  
 <400>3306  
 cttgtcgatg gtaagggtgga 20  
 <210>3307  
 <211>20  
 <212>DNA  
 <400>3307  
 caaactatag aggatgctgc 20  
 <210>3308  
 <211>20  
 <212>DNA  
 <400>3308  
 gggagaagat acaatcccga 20  
 <210>3309  
 <211>20  
 <212>DNA  
 <400>3309  
 ggggtacggaa cttgccatta 20  
 <210>3310  
 <211>20  
 <212>DNA  
 <400>3310  
 ggaggtcact ccttctacaa 20  
 <210>3311  
 <211>20  
 <212>DNA  
 <400>3311  
 ccaacggcct tctacactat 20  
 <210>3312  
 <211>20  
 <212>DNA  
 <400>3312  
 gagggcaaatg acggttatcgg 20  
 <210>3313  
 <211>20  
 <212>DNA  
 <400>3313  
 acctgcaagg ccatttagag 20  
 <210>3314  
 <211>20  
 <212>DNA  
 <400>3314  
 agagtgtaac ggagataggg 20  
 <210>3315  
 <211>20  
 <212>DNA  
 <400>3315  
 gaagagggtg acctgcaagt 20  
 <210>3316



```

<211>20
<212>DNA
<400>3316
cgaagagatt cgctctgttg      20
<210>3317
<211>20
<212>DNA
<400>3317
gcatgatttc actgaggagg      20
<210>3318
<211>20
<212>DNA
<400>3318
gtgtaacgga gatagggaca      20
<210>3319
<211>20
<212>DNA
<400>3319
gaagagggtg acctgcaagt      20
<210>3320
<211>20
<212>DNA
<400>3320
ggtcggggtt tagctgttgt      20
<210>3321
<211>20
<212>DNA
<400>3321
ctggagttgt tggatgatgga      20
<210>3322
<211>20
<212>DNA
<400>3322
ccctaagttg tcagataggg      20
<210>3323
<211>20
<212>DNA
<400>3323
ccatcgggat aaagagtcca      20
<210>3324
<211>20
<212>DNA
<400>3324
ctatggcatt gttgccatcg      20
<210>3325
<211>20
<212>DNA
<400>3325
ggaaggactt ctgttccaag      20
<210>3326
<211>20
<212>DNA
<400>3326
gggattagat aagggtgacc      20
<210>3327
<211>20
<212>DNA
<400>3327
ggagattgtg gtgttgtcac      20
<210>3328
<211>20
<212>DNA
<400>3328
gattttctac aagggtgcc      20

```

<210>3329  
<211>20  
<212>DNA  
<400>3329  
ctatggcatt gttgccatcg 20  
<210>3330  
<211>20  
<212>DNA  
<400>3330  
ggaatgtcta cccatccaga 20  
<210>3331  
<211>20  
<212>DNA  
<400>3331  
tgacgcagtt gcccatcagt 20  
<210>3332  
<211>20  
<212>DNA  
<400>3332  
tcgtcgtgag tgaagggaaa 20  
<210>3333  
<211>20  
<212>DNA  
<400>3333  
gagttagagg agctcttcct 20  
<210>3334  
<211>20  
<212>DNA  
<400>3334  
cctgcaatag atagagccct 20  
<210>3335  
<211>20  
<212>DNA  
<400>3335  
ttccgagtcc ttgatggcga 20  
<210>3336  
<211>20  
<212>DNA  
<400>3336  
caggacatcg ttaggccatt 20  
<210>3337  
<211>20  
<212>DNA  
<400>3337  
ctgtagatcc tcgacatctc 20  
<210>3338  
<211>20  
<212>DNA  
<400>3338  
gctacgagat catcccaaca 20  
<210>3339  
<211>20  
<212>DNA  
<400>3339  
cccgtcaga aggaggaata 20  
<210>3340  
<211>20  
<212>DNA  
<400>3340  
tgttgcagtc gccactgatg 20  
<210>3341  
<211>20  
<212>DNA  
<400>3341

aaagegtcat gcgttgctcg 20  
 <210>3342  
 <211>20  
 <212>DNA  
 <400>3342  
 gataccgatc tgcaggaagc 20  
 <210>3343  
 <211>20  
 <212>DNA  
 <400>3343  
 gtgttcgtgg agggaaatttc 20  
 <210>3344  
 <211>20  
 <212>DNA  
 <400>3344  
 caggagtgcc agcaagaaaa 20  
 <210>3345  
 <211>20  
 <212>DNA  
 <400>3345  
 catgatgtgc gggctgctac 20  
 <210>3346  
 <211>20  
 <212>DNA  
 <400>3346  
 agcgcacgat tcgtaggaat 20  
 <210>3347  
 <211>20  
 <212>DNA  
 <400>3347  
 tctacccgac ctacaaaagc 20  
 <210>3348  
 <211>20  
 <212>DNA  
 <400>3348  
 tctacccctt gcgttttagc 20  
 <210>3349  
 <211>20  
 <212>DNA  
 <400>3349  
 gaacacgtag cgacctgtta 20  
 <210>3350  
 <211>20  
 <212>DNA  
 <400>3350  
 cctatgattc ttggggacca 20  
 <210>3351  
 <211>20  
 <212>DNA  
 <400>3351  
 caacttgagc tctgtcagca 20  
 <210>3352  
 <211>20  
 <212>DNA  
 <400>3352  
 ggaatatggc ataggagcac 20  
 <210>3353  
 <211>20  
 <212>DNA  
 <400>3353  
 caaggaatcg ccatgctacg 20  
 <210>3354  
 <211>20  
 <212>DNA

```

<400>3354
gcaggtattg gtgctctctc 20
<210>3355
<211>20
<212>DNA
<400>3355
gagtggatct tcacaaggct 20
<210>3356
<211>20
<212>DNA
<400>3356
cctcttctct atcacgttgc 20
<210>3357
<211>20
<212>DNA
<400>3357
ccatgctgta acaatcgggt 20
<210>3358
<211>20
<212>DNA
<400>3358
ttgccgcatt tgcctccacc 20
<210>3359
<211>20
<212>DNA
<400>3359
ctgggaagac cacgaaatgt 20
<210>3360
<211>20
<212>DNA
<400>3360
cgcaacagga gagacaatgt 20
<210>3361
<211>20
<212>DNA
<400>3361
gagaggttcc ctcaaacct 20
<210>3362
<211>20
<212>DNA
<400>3362
ccaggaagac gagcaaatct 20
<210>3363
<211>20
<212>DNA
<400>3363
ccatattttg cgggttaact 20
<210>3364
<211>20
<212>DNA
<400>3364
gaaatcttcg ctgtgcaagg 20
<210>3365
<211>20
<212>DNA
<400>3365
ggccgtgatt ggatttggaa 20
<210>3366
<211>20
<212>DNA
<400>3366
ggagctggag gacataatag 20
<210>3367
<211>20

```

WO 99/27105

```

<212>DNA
<400>3367
gctggctcct atttaggttc      20
<210>3368
<211>20
<212>DNA
<400>3368
caatgggagt gttatacgcc      20
<210>3369
<211>20
<212>DNA
<400>3369
tcattcctct agggggtggt      20
<210>3370
<211>20
<212>DNA
<400>3370
ggagtcgaag atagcgcaat      20
<210>3371
<211>20
<212>DNA
<400>3371
ggatctacag catcatgagg      20
<210>3372
<211>20
<212>DNA
<400>3372
tggcgcaagg ctttcaagaa      20
<210>3373
<211>20
<212>DNA
<400>3373
gctgatgact gggatgaagt      20
<210>3374
<211>20
<212>DNA
<400>3374
agagtaagtc gttgccaagc      20
<210>3375
<211>20
<212>DNA
<400>3375
taccgaaagg agtgctggag      20
<210>3376
<211>20
<212>DNA
<400>3376
gcgtgggata tatcaacgga      20
<210>3377
<211>20
<212>DNA
<400>3377
ctttcggttaa ggaactcggc      20
<210>3378
<211>20
<212>DNA
<400>3378
ctagcctcct cagcaatttc      20
<210>3379
<211>20
<212>DNA
<400>3379
ggaactgata gtgtggcgca      20
<210>3380

```

<211>20  
 <212>DNA  
 <400>3380  
 agacctcgaa gagatccctc 20  
 <210>3381  
 <211>20  
 <212>DNA  
 <400>3381  
 gtatatggtg tgacgcctgc 20  
 <210>3382  
 <211>20  
 <212>DNA  
 <400>3382  
 atctcaccat cttgtcgggtg 20  
 <210>3383  
 <211>20  
 <212>DNA  
 <400>3383  
 ccgaactcag aagttaagcc 20  
 <210>3384  
 <211>20  
 <212>DNA  
 <400>3384  
 cacctgcaag aatcacgcca 20  
 <210>3385  
 <211>20  
 <212>DNA  
 <400>3385  
 gcttcttcgg aatcaatggg 20  
 <210>3386  
 <211>20  
 <212>DNA  
 <400>3386  
 gttcgggacg ccataagata 20  
 <210>3387  
 <211>20  
 <212>DNA  
 <400>3387  
 ggattcgtag ggctaattgac 20  
 <210>3388  
 <211>20  
 <212>DNA  
 <400>3388  
 gacaacaatt cacaaggacc 20  
 <210>3389  
 <211>20  
 <212>DNA  
 <400>3389  
 cacctgcaag aatcacgcca 20  
 <210>3390  
 <211>20  
 <212>DNA  
 <400>3390  
 tgttgaatac ataggcatat 20  
 <210>3391  
 <211>20  
 <212>DNA  
 <400>3391  
 gcgcactctt gaaactgtgt 20  
 <210>3392  
 <211>20  
 <212>DNA  
 <400>3392  
 ggcaactttt ctcaggcagt 20

<210>3393  
 <211>20  
 <212>DNA  
 <400>3393  
 gggattgtga ctatggagtg 20  
 <210>3394  
 <211>20  
 <212>DNA  
 <400>3394  
 cctcgggtgtg taaatcacag 20  
 <210>3395  
 <211>20  
 <212>DNA  
 <400>3395  
 gaattggcaa aagagctggg 20  
 <210>3396  
 <211>20  
 <212>DNA  
 <400>3396  
 ggggtgaggaa tccttttaggt 20  
 <210>3397  
 <211>20  
 <212>DNA  
 <400>3397  
 gcctctgtgc caaggtctct 20  
 <210>3398  
 <211>20  
 <212>DNA  
 <400>3398  
 cctatggtct caacgacaag 20  
 <210>3399  
 <211>20  
 <212>DNA  
 <400>3399  
 ggtgtgggtta cacaagcttc 20  
 <210>3400  
 <211>20  
 <212>DNA  
 <400>3400  
 ggtcacagca aaaccatcca 20  
 <210>3401  
 <211>20  
 <212>DNA  
 <400>3401  
 acgtgcacat cagcttatgg 20  
 <210>3402  
 <211>20  
 <212>DNA  
 <400>3402  
 cccacagcat ctatgttcac 20  
 <210>3403  
 <211>20  
 <212>DNA  
 <400>3403  
 ggagtcgcag atactgtaag 20  
 <210>3404  
 <211>20  
 <212>DNA  
 <400>3404  
 cgtcagagac tcgagatagt 20  
 <210>3405  
 <211>20  
 <212>DNA  
 <400>3405

```

gccagcatct cgcgaaatta 20
<210>3406
<211>20
<212>DNA
<400>3406
gcatctgcta atgaggggaac 20
<210>3407
<211>20
<212>DNA
<400>3407
cccacagcat ctatgttcac 20
<210>3408
<211>20
<212>DNA
<400>3408
gctgcaccac tatcatcggg 20
<210>3409
<211>20
<212>DNA
<400>3409
tttgctgcaa ggaatgccgt 20
<210>3410
<211>20
<212>DNA
<400>3410
ggtggcggtt agcatagaat 20
<210>3411
<211>20
<212>DNA
<400>3411
cacgaaccac atcgctatac 20
<210>3412
<211>20
<212>DNA
<400>3412
cccttgttgg gagctttttg 20
<210>3413
<211>20
<212>DNA
<400>3413
ccttgccatt ataggagagt 20
<210>3414
<211>20
<212>DNA
<400>3414
gacacacgct ctcctttgta 20
<210>3415
<211>20
<212>DNA
<400>3415
ggctggatga agttcgtggt 20
<210>3416
<211>20
<212>DNA
<400>3416
gttgctgtag agcctcctat 20
<210>3417
<211>20
<212>DNA
<400>3417
cgacaagcat tgcccacact 20
<210>3418
<211>20
<212>DNA

```



<400>3418  
 acagtgcgta atatggaagc 20  
 <210>3419  
 <211>20  
 <212>DNA  
 <400>3419  
 cgtgtctcta tagaagcagg 20  
 <210>3420  
 <211>20  
 <212>DNA  
 <400>3420  
 gggattgaca gggagaacat 20  
 <210>3421  
 <211>20  
 <212>DNA  
 <400>3421  
 gacacacgct ctcctttgta 20  
 <210>3422  
 <211>20  
 <212>DNA  
 <400>3422  
 gcgagaagtg cgcataattc 20  
 <210>3423  
 <211>20  
 <212>DNA  
 <400>3423  
 gcataggacg tgggttactt 20  
 <210>3424  
 <211>20  
 <212>DNA  
 <400>3424  
 cagcttctcg aggagatatg 20  
 <210>3425  
 <211>20  
 <212>DNA  
 <400>3425  
 cctgaagctt ttctccctgc 20  
 <210>3426  
 <211>20  
 <212>DNA  
 <400>3426  
 cctgctaggg agctgcgctg 20  
 <210>3427  
 <211>20  
 <212>DNA  
 <400>3427  
 ccaaggagat agctttggtc 20  
 <210>3428  
 <211>20  
 <212>DNA  
 <400>3428  
 tccctgcctt agcttctgta 20  
 <210>3429  
 <211>20  
 <212>DNA  
 <400>3429  
 ctctgggtgt tcctgtaatg 20  
 <210>3430  
 <211>20  
 <212>DNA  
 <400>3430  
 gtctcaagat gtcagcaacg 20  
 <210>3431  
 <211>20

<212>DNA  
 <400>3431  
 gcgggatctg tcattctaca 20  
 <210>3432  
 <211>20  
 <212>DNA  
 <400>3432  
 gtgcttttgtt tacggaggggt 20  
 <210>3433  
 <211>20  
 <212>DNA  
 <400>3433  
 gctcttatgg ctgtagggaa 20  
 <210>3434  
 <211>20  
 <212>DNA  
 <400>3434  
 ggagcttatg gacatcagga 20  
 <210>3435  
 <211>20  
 <212>DNA  
 <400>3435  
 gatctaagca gtcccttagc 20  
 <210>3436  
 <211>20  
 <212>DNA  
 <400>3436  
 gacagcagct agccccatttt 20  
 <210>3437  
 <211>20  
 <212>DNA  
 <400>3437  
 gctcagaaag atccctccta 20  
 <210>3438  
 <211>20  
 <212>DNA  
 <400>3438  
 ctgctgcgac acgaatttct 20  
 <210>3439  
 <211>20  
 <212>DNA  
 <400>3439  
 cgggagttca tcgacgtcta 20  
 <210>3440  
 <211>20  
 <212>DNA  
 <400>3440  
 cctccgaagg gaaagatgta 20  
 <210>3441  
 <211>20  
 <212>DNA  
 <400>3441  
 gggaaatctt gcgaacacga 20  
 <210>3442  
 <211>20  
 <212>DNA  
 <400>3442  
 ggttcctaataa gggagaagga 20  
 <210>3443  
 <211>20  
 <212>DNA  
 <400>3443  
 ctgtgggtgct agtgggttta 20  
 <210>3444

<211>20  
 <212>DNA  
 <400>3444  
 cagtgcctag tgttcaagag 20  
 <210>3445  
 <211>20  
 <212>DNA  
 <400>3445  
 cgaacaggca ttcactaaag 20  
 <210>3446  
 <211>20  
 <212>DNA  
 <400>3446  
 gggaaaaccc ttcagcattc 20  
 <210>3447  
 <211>20  
 <212>DNA  
 <400>3447  
 cgctctcgat tacaggactt 20  
 <210>3448  
 <211>20  
 <212>DNA  
 <400>3448  
 ggctttctgt agaacgcaca 20  
 <210>3449  
 <211>20  
 <212>DNA  
 <400>3449  
 ccaggtctga acaggaatgt 20  
 <210>3450  
 <211>20  
 <212>DNA  
 <400>3450  
 gctgaggtct cttctcttct 20  
 <210>3451  
 <211>20  
 <212>DNA  
 <400>3451  
 gcccaaagct aaaatgcggt 20  
 <210>3452  
 <211>20  
 <212>DNA  
 <400>3452  
 gctcttgaag aattggatgc 20  
 <210>3453  
 <211>20  
 <212>DNA  
 <400>3453  
 ggctttctgt agaacgcaca 20  
 <210>3454  
 <211>20  
 <212>DNA  
 <400>3454  
 gtctgcagaa cagacgatct 20  
 <210>3455  
 <211>20  
 <212>DNA  
 <400>3455  
 ctcaaggctc agacttaagg 20  
 <210>3456  
 <211>20  
 <212>DNA  
 <400>3456  
 ggtagtgtga atgtgcatgt 20

<210>3457  
<211>20  
<212>DNA  
<400>3457  
gatctccgca aggaactgat 20  
<210>3458  
<211>20  
<212>DNA  
<400>3458  
agctgctgga ggtgttgaag 20  
<210>3459  
<211>20  
<212>DNA  
<400>3459  
ctcttctggt ccctgtgatg 20  
<210>3460  
<211>20  
<212>DNA  
<400>3460  
cgttcgcaaa gaagtcacct 20  
<210>3461  
<211>20  
<212>DNA  
<400>3461  
cgagtatcct aaagctgggt 20  
<210>3462  
<211>20  
<212>DNA  
<400>3462  
ggactcataa ttatcctggg 20  
<210>3463  
<211>20  
<212>DNA  
<400>3463  
caaatatggc cccagcactt 20  
<210>3464  
<211>20  
<212>DNA  
<400>3464  
gggaattctt tatgggtcccg 20  
<210>3465  
<211>20  
<212>DNA  
<400>3465  
gctgcagaga gagaattggt 20  
<210>3466  
<211>20  
<212>DNA  
<400>3466  
aaccaaacgg tgctcgcttc 20  
<210>3467  
<211>20  
<212>DNA  
<400>3467  
gctcaggcct aattgacttt 20  
<210>3468  
<211>20  
<212>DNA  
<400>3468  
cgagaacagg gaaagaggaa 20  
<210>3469  
<211>20  
<212>DNA  
<400>3469

cgtgggaacg tgattcgtaa 20  
 <210>3470  
 <211>20  
 <212>DNA  
 <400>3470  
 gggataaggt aaggctgtgt 20  
 <210>3471  
 <211>20  
 <212>DNA  
 <400>3471  
 ggtaaagaga gtaagcgctc 20  
 <210>3472  
 <211>20  
 <212>DNA  
 <400>3472  
 cgcacggaag caagtcttta 20  
 <210>3473  
 <211>20  
 <212>DNA  
 <400>3473  
 caaaagcagt ccctctaacc 20  
 <210>3474  
 <211>20  
 <212>DNA  
 <400>3474  
 cccaagagga gcaaagtagt 20  
 <210>3475  
 <211>20  
 <212>DNA  
 <400>3475  
 gcattaaggc gtgatggagt 20  
 <210>3476  
 <211>20  
 <212>DNA  
 <400>3476  
 ggagagatgc aagtgttgga 20  
 <210>3477  
 <211>20  
 <212>DNA  
 <400>3477  
 ggtatgatat ccccgacgat 20  
 <210>3478  
 <211>20  
 <212>DNA  
 <400>3478  
 cccgaactgg tcttcataga 20  
 <210>3479  
 <211>20  
 <212>DNA  
 <400>3479  
 cgcttggtgc tcgaagatag 20  
 <210>3480  
 <211>20  
 <212>DNA  
 <400>3480  
 cgctaagggga aggaacagaa 20  
 <210>3481  
 <211>20  
 <212>DNA  
 <400>3481  
 gggacttcta cagctttctc 20  
 <210>3482  
 <211>20  
 <212>DNA

<400>3482  
 cttggcgtgt gttgacgaaa 20  
 <210>3483  
 <211>20  
 <212>DNA  
 <400>3483  
 gttccatcac tgccatcagt 20  
 <210>3484  
 <211>20  
 <212>DNA  
 <400>3484  
 cactcggttc tgacttttgta 20  
 <210>3485  
 <211>20  
 <212>DNA  
 <400>3485  
 ctgggtcttt gaaagaggga 20  
 <210>3486  
 <211>20  
 <212>DNA  
 <400>3486  
 gagtgatcaa caacagtgga 20  
 <210>3487  
 <211>20  
 <212>DNA  
 <400>3487  
 caacgcggtt tttcgaggaa 20  
 <210>3488  
 <211>20  
 <212>DNA  
 <400>3488  
 gaactcttgg agcaacagca 20  
 <210>3489  
 <211>20  
 <212>DNA  
 <400>3489  
 cgcattcctga atcttgcata 20  
 <210>3490  
 <211>20  
 <212>DNA  
 <400>3490  
 gagttgcgta cgataatggc 20  
 <210>3491  
 <211>20  
 <212>DNA  
 <400>3491  
 gtgaagctgc tatgagtagg 20  
 <210>3492  
 <211>20  
 <212>DNA  
 <400>3492  
 cttcggccta tcctaacaaa 20  
 <210>3493  
 <211>20  
 <212>DNA  
 <400>3493  
 cgcatttgta gagegcttcg 20  
 <210>3494  
 <211>20  
 <212>DNA  
 <400>3494  
 gccgagaaca gagattctga 20  
 <210>3495  
 <211>20

<212>DNA  
<400>3495  
ttaggccctg acttagagtc 20  
<210>3496  
<211>20  
<212>DNA  
<400>3496  
cgtagccctg atagagtttc 20  
<210>3497  
<211>20  
<212>DNA  
<400>3497  
cctcagattg ggcgatttca 20  
<210>3498  
<211>20  
<212>DNA  
<400>3498  
cgagagatga cagtctggta 20  
<210>3499  
<211>20  
<212>DNA  
<400>3499  
gtagcgaagt tcaacgtttt 20  
<210>3500  
<211>20  
<212>DNA  
<400>3500  
ccgaccttcg taaaatcgtg 20  
<210>3501  
<211>20  
<212>DNA  
<400>3501  
gcagagcttc ctttgcttgt 20  
<210>3502  
<211>20  
<212>DNA  
<400>3502  
cgctagagaa atagggcacg 20  
<210>3503  
<211>20  
<212>DNA  
<400>3503  
ctttgaagct gtcctaacg 20  
<210>3504  
<211>20  
<212>DNA  
<400>3504  
cgtgtcgaag tgaacgtaga 20  
<210>3505  
<211>20  
<212>DNA  
<400>3505  
tccgtttcac agtgtcttcc 20  
<210>3506  
<211>20  
<212>DNA  
<400>3506  
tcgagagtcc cctttctcat 20  
<210>3507  
<211>20  
<212>DNA  
<400>3507  
cgtgtcgaag tgaacgtaga 20  
<210>3508

```

<211>20
<212>DNA
<400>3508
gcagtgcaat taaggaggct      20
<210>3509
<211>20
<212>DNA
<400>3509
ggtagtaatt cgcagcttgc     20
<210>3510
<211>20
<212>DNA
<400>3510
ccaaggcaat tctcggtagt     20
<210>3511
<211>20
<212>DNA
<400>3511
gagccaaaat ctcagtgcgt     20
<210>3512
<211>20
<212>DNA
<400>3512
cgtcacatca acagtgaagc     20
<210>3513
<211>20
<212>DNA
<400>3513
ctttggtcat cagtcgttcg     20
<210>3514
<211>20
<212>DNA
<400>3514
ctcattcctt aaccagctc     20
<210>3515
<211>20
<212>DNA
<400>3515
catccagaaa gaaaagctgc     20
<210>3516
<211>20
<212>DNA
<400>3516
atcggcgacc tgttctctat     20
<210>3517
<211>20
<212>DNA
<400>3517
agcgagacac gctttgcagt     20
<210>3518
<211>20
<212>DNA
<400>3518
cgccaagggc tttaatgtcg     20
<210>3519
<211>20
<212>DNA
<400>3519
cctactcttc gacagtgatg     20
<210>3520
<211>20
<212>DNA
<400>3520
actccagaag gacctggtga     20

```



<210>3521  
<211>20  
<212>DNA  
<400>3521  
gcaatgcaaa cctctctctc 20  
<210>3522  
<211>20  
<212>DNA  
<400>3522  
cgggcttttaa aatgacctgg 20  
<210>3523  
<211>20  
<212>DNA  
<400>3523  
gccgacacta agtcagcttt 20  
<210>3524  
<211>20  
<212>DNA  
<400>3524  
gagcaagagg gttctcgata 20  
<210>3525  
<211>20  
<212>DNA  
<400>3525  
aactagccaa cgtatagggc 20  
<210>3526  
<211>20  
<212>DNA  
<400>3526  
caagggctag tgggaaacta 20  
<210>3527  
<211>20  
<212>DNA  
<400>3527  
gccactctac atagctatcc 20  
<210>3528  
<211>20  
<212>DNA  
<400>3528  
ccagagtcct tttcttctcc 20  
<210>3529  
<211>20  
<212>DNA  
<400>3529  
tgcaagggct agtgggaaac 20  
<210>3530  
<211>20  
<212>DNA  
<400>3530  
ctcgtagaag atcgctctgt 20  
<210>3531  
<211>20  
<212>DNA  
<400>3531  
cagcataagt tagcctggct 20  
<210>3532  
<211>20  
<212>DNA  
<400>3532  
cccctcgaag aggtgttgag 20  
<210>3533  
<211>20  
<212>DNA  
<400>3533

tgcggtactac aataccctcg	20
<210>3534	
<211>20	
<212>DNA	
<400>3534	
ggcataacta attacggcgg	20
<210>3535	
<211>20	
<212>DNA	
<400>3535	
gggagaagta cttccacatc	20
<210>3536	
<211>20	
<212>DNA	
<400>3536	
gaacacagaa ggaagcgttt	20
<210>3537	
<211>20	
<212>DNA	
<400>3537	
gtaaggcagc ggtttttggt	20
<210>3538	
<211>20	
<212>DNA	
<400>3538	
cggatctgta accattgcag	20
<210>3539	
<211>20	
<212>DNA	
<400>3539	
gccctatctt ctacgggtctt	20
<210>3540	
<211>20	
<212>DNA	
<400>3540	
gcatgaagga tagtttgagc	20
<210>3541	
<211>20	
<212>DNA	
<400>3541	
cctaggcatg ggtatgcaaa	20
<210>3542	
<211>20	
<212>DNA	
<400>3542	
cgtatacggga cagacttgaa	20
<210>3543	
<211>20	
<212>DNA	
<400>3543	
taccgagtgg tgttcgaaat	20
<210>3544	
<211>20	
<212>DNA	
<400>3544	
gtcgtttcat ctgctttagg	20
<210>3545	
<211>20	
<212>DNA	
<400>3545	
gactcttaga gcagattctg	20
<210>3546	
<211>20	
<212>DNA	

<400>3546  
 ccctagtctc caatatccca 20  
 <210>3547  
 <211>20  
 <212>DNA  
 <400>3547  
 cccacagaaa aggcatacca 20  
 <210>3548  
 <211>20  
 <212>DNA  
 <400>3548  
 ggcaaacgct tggaattcag 20  
 <210>3549  
 <211>20  
 <212>DNA  
 <400>3549  
 ggatacagga tttccatggc 20  
 <210>3550  
 <211>20  
 <212>DNA  
 <400>3550  
 cttaaggcgg tgtaggttta 20  
 <210>3551  
 <211>20  
 <212>DNA  
 <400>3551  
 ggaatcccgt gttcctgaat 20  
 <210>3552  
 <211>20  
 <212>DNA  
 <400>3552  
 ccatgacttt ccttgtgcct 20  
 <210>3553  
 <211>20  
 <212>DNA  
 <400>3553  
 gtctggatgat ttgcaaggag 20  
 <210>3554  
 <211>20  
 <212>DNA  
 <400>3554  
 ggggaataat ccctttgagt 20  
 <210>3555  
 <211>20  
 <212>DNA  
 <400>3555  
 gcgagcagca tcgtatttca 20  
 <210>3556  
 <211>20  
 <212>DNA  
 <400>3556  
 gcacgtgcta agattcctct 20  
 <210>3557  
 <211>20  
 <212>DNA  
 <400>3557  
 ctcgctgtac ggcaaatcaa 20  
 <210>3558  
 <211>20  
 <212>DNA  
 <400>3558  
 gctctgtagt ctgtggtctt 20  
 <210>3559  
 <211>20

```

<212>DNA
<400>3559
gccttttgagc tgacgaactt      20
<210>3560
<211>20
<212>DNA
<400>3560
gtaaggggacc tgtctcttttg    20
<210>3561
<211>20
<212>DNA
<400>3561
cgcaaacagc cgcttctttaa    20
<210>3562
<211>20
<212>DNA
<400>3562
cgaggataaaa tcggcgaagt     20
<210>3563
<211>20
<212>DNA
<400>3563
tcgtatccac agtgggttcct    20
<210>3564
<211>20
<212>DNA
<400>3564
gaaatcggtc gagaggaagt     20
<210>3565
<211>20
<212>DNA
<400>3565
ggcgtgtttg acacgcattt     20
<210>3566
<211>20
<212>DNA
<400>3566
gtgcgtgtag aagtgaaaag     20
<210>3567
<211>20
<212>DNA
<400>3567
gtggctccta ttgaagagag     20
<210>3568
<211>20
<212>DNA
<400>3568
ctcagatttg acagcccaaa     20
<210>3569
<211>20
<212>DNA
<400>3569
ggaaacgctt accgaccaaaa    20
<210>3570
<211>20
<212>DNA
<400>3570
tgctcatcca catgtggatg     20
<210>3571
<211>20
<212>DNA
<400>3571
cccggtagag agctcttaaa     20
<210>3572

```

<211>20  
<212>DNA  
<400>3572  
ctgataccct agctgctttg 20  
<210>3573  
<211>20  
<212>DNA  
<400>3573  
gattgttcta gactgcgctc 20  
<210>3574  
<211>20  
<212>DNA  
<400>3574  
gacctcgcaa tcctatgatg 20  
<210>3575  
<211>20  
<212>DNA  
<400>3575  
ggctcttgcg gatgttattg 20  
<210>3576  
<211>20  
<212>DNA  
<400>3576  
cggggccgcc gtgattatcg 20  
<210>3577  
<211>20  
<212>DNA  
<400>3577  
cgacgtccct acataggtaa 20  
<210>3578  
<211>20  
<212>DNA  
<400>3578  
cgctaggcgt gtctttcttt 20  
<210>3579  
<211>20  
<212>DNA  
<400>3579  
gctgccctca aactcaaaga 20  
<210>3580  
<211>20  
<212>DNA  
<400>3580  
ggtgcgttcc tcaatggtta 20  
<210>3581  
<211>20  
<212>DNA  
<400>3581  
ggccctctag gttttgctat 20  
<210>3582  
<211>20  
<212>DNA  
<400>3582  
tgggggattc ggggccgccg 20  
<210>3583  
<211>20  
<212>DNA  
<400>3583  
gctgtagaag ctctcaagca 20  
<210>3584  
<211>20  
<212>DNA  
<400>3584  
gactctagtc tttgctgtgg 20

<210>3585  
<211>20  
<212>DNA  
<400>3585  
gtagttgggc aagtgatggc 20  
<210>3586  
<211>20  
<212>DNA  
<400>3586  
ttagtccgac gtaatcgtgc 20  
<210>3587  
<211>20  
<212>DNA  
<400>3587  
gcccatcggt cttgagcatt 20  
<210>3588  
<211>20  
<212>DNA  
<400>3588  
gatgagagcg tgaaagtgct 20  
<210>3589  
<211>20  
<212>DNA  
<400>3589  
catcttcagg aaaccgagac 20  
<210>3590  
<211>20  
<212>DNA  
<400>3590  
ctttccttac acacgacttt 20  
<210>3591  
<211>20  
<212>DNA  
<400>3591  
gaggggtgagc tacttgtect 20  
<210>3592  
<211>20  
<212>DNA  
<400>3592  
gctgcgttgg gaaaacattc 20  
<210>3593  
<211>20  
<212>DNA  
<400>3593  
gatatatcca cctgccggga 20  
<210>3594  
<211>20  
<212>DNA  
<400>3594  
cactatgcgt ggtaaccaag 20  
<210>3595  
<211>20  
<212>DNA  
<400>3595  
cccaggattt tcggtaaacc 20  
<210>3596  
<211>20  
<212>DNA  
<400>3596  
cccgcggtag aatataggat 20  
<210>3597  
<211>20  
<212>DNA  
<400>3597

cagaagctat ccgttgcgaa 20  
 <210>3598  
 <211>20  
 <212>DNA  
 <400>3598  
 cgcagtagaa gagaggatct 20  
 <210>3599  
 <211>20  
 <212>DNA  
 <400>3599  
 cgtttgactc attggcttcc 20  
 <210>3600  
 <211>20  
 <212>DNA  
 <400>3600  
 cgtgggcctt atgaaaatcc 20  
 <210>3601  
 <211>20  
 <212>DNA  
 <400>3601  
 cggactctct tgcattacag 20  
 <210>3602  
 <211>20  
 <212>DNA  
 <400>3602  
 tcaggaattg ctctgtgtca 20  
 <210>3603  
 <211>20  
 <212>DNA  
 <400>3603  
 caaaagctct ggggataagg 20  
 <210>3604  
 <211>20  
 <212>DNA  
 <400>3604  
 gctcttctgc agcgtgaata 20  
 <210>3605  
 <211>20  
 <212>DNA  
 <400>3605  
 cagattccct tctcaaggag 20  
 <210>3606  
 <211>20  
 <212>DNA  
 <400>3606  
 cgcagatata gaggggaagc 20  
 <210>3607  
 <211>20  
 <212>DNA  
 <400>3607  
 cgctgcttgc taaaaactcg 20  
 <210>3608  
 <211>20  
 <212>DNA  
 <400>3608  
 cgtgcttccg tagcgtttta 20  
 <210>3609  
 <211>20  
 <212>DNA  
 <400>3609  
 cgtacctttg caaaagcggc 20  
 <210>3610  
 <211>20  
 <212>DNA

<400>3610  
gctagacgat tgctgaaatc 20  
<210>3611  
<211>20  
<212>DNA  
<400>3611  
ggaattctat aacaggggcg 20  
<210>3612  
<211>20  
<212>DNA  
<400>3612  
caggaaacca tgacaattcc 20  
<210>3613  
<211>20  
<212>DNA  
<400>3613  
gacgatggag ctctttacct 20  
<210>3614  
<211>20  
<212>DNA  
<400>3614  
cccgagtggg ttatagagtg 20  
<210>3615  
<211>20  
<212>DNA  
<400>3615  
gcagctctca agaccccaat 20  
<210>3616  
<211>20  
<212>DNA  
<400>3616  
gagcgaaacc atggatctga 20  
<210>3617  
<211>20  
<212>DNA  
<400>3617  
agagctgtgg ggttgggggt 20  
<210>3618  
<211>20  
<212>DNA  
<400>3618  
gctccaagaa tggaaacacc 20  
<210>3619  
<211>20  
<212>DNA  
<400>3619  
aaacgcggca ttcagcctcg 20  
<210>3620  
<211>20  
<212>DNA  
<400>3620  
ggctatcttc cgaaaggga 20  
<210>3621  
<211>20  
<212>DNA  
<400>3621  
ggacttgatg aaggcgaagt 20  
<210>3622  
<211>20  
<212>DNA  
<400>3622  
cacatagtgt cgagagccta 20  
<210>3623  
<211>20



WO 99/27105

```

<212>DNA
<400>3623
aggccttggg cagttcatta 20
<210>3624
<211>20
<212>DNA
<400>3624
ccatcaaaac cacggtcac 20
<210>3625
<211>20
<212>DNA
<400>3625
tggtaatggg gattgggtag 20
<210>3626
<211>20
<212>DNA
<400>3626
gctaaggagt tgtgagaaag 20
<210>3627
<211>20
<212>DNA
<400>3627
gtcagagcaa gaaagaagtg 20
<210>3628
<211>20
<212>DNA
<400>3628
ggaaaagtct catgcccaag 20
<210>3629
<211>20
<212>DNA
<400>3629
ggaacaaagc tctccttcag 20
<210>3630
<211>20
<212>DNA
<400>3630
aggggatttc cgtagccttt 20
<210>3631
<211>20
<212>DNA
<400>3631
caggtcctcc aatgcggaaa 20
<210>3632
<211>20
<212>DNA
<400>3632
gaactttgtg gctaagagcc 20
<210>3633
<211>20
<212>DNA
<400>3633
gcatgttccg tggtagagaa 20
<210>3634
<211>20
<212>DNA
<400>3634
gggaagcggt ttgggatgaa 20
<210>3635
<211>20
<212>DNA
<400>3635
gccttttcag gtttcatagt 20
<210>3636

```

<211>20  
 <212>DNA  
 <400>3636  
 aacaagctga ggcattgagga 20  
 <210>3637  
 <211>20  
 <212>DNA  
 <400>3637  
 gggaagaagc ctcttttcacc 20  
 <210>3638  
 <211>20  
 <212>DNA  
 <400>3638  
 ggcaacaatt tcctgtagag 20  
 <210>3639  
 <211>20  
 <212>DNA  
 <400>3639  
 gtgaccgttg gtgttctact 20  
 <210>3640  
 <211>20  
 <212>DNA  
 <400>3640  
 gcaactttgc gcatgaggaa 20  
 <210>3641  
 <211>20  
 <212>DNA  
 <400>3641  
 aaggatcatg ccagcatacg 20  
 <210>3642  
 <211>20  
 <212>DNA  
 <400>3642  
 ccaaggaaga cactctacct 20  
 <210>3643  
 <211>20  
 <212>DNA  
 <400>3643  
 gggaggagaa cgttttttctc 20  
 <210>3644  
 <211>20  
 <212>DNA  
 <400>3644  
 cttcttcttg ccacaactgt 20  
 <210>3645  
 <211>20  
 <212>DNA  
 <400>3645  
 gagaatgctt ctagatgcgg 20  
 <210>3646  
 <211>20  
 <212>DNA  
 <400>3646  
 caaagacatc ggatgtctcc 20  
 <210>3647  
 <211>20  
 <212>DNA  
 <400>3647  
 ccttgcttcg cttgggaaag 20  
 <210>3648  
 <211>20  
 <212>DNA  
 <400>3648  
 cgtttggttg ataccgtcct 20

## WO 99/27105

```

<210>3649
<211>20
<212>DNA
<400>3649
gagaagggag ggaagaagta 20
<210>3650
<211>20
<212>DNA
<400>3650
gcgctctctc aagagaacta 20
<210>3651
<211>20
<212>DNA
<400>3651
gcaggaagag gatatacagc 20
<210>3652
<211>20
<212>DNA
<400>3652
ggagcccagg aattccaaaa 20
<210>3653
<211>20
<212>DNA
<400>3653
agctccgtta gcttgacgag 20
<210>3654
<211>20
<212>DNA
<400>3654
ggggagggtta atgagctctt 20
<210>3655
<211>20
<212>DNA
<400>3655
gtggaaaggt ctgagattgc 20
<210>3656
<211>20
<212>DNA
<400>3656
gggcaatgat ggagagggtta 20
<210>3657
<211>20
<212>DNA
<400>3657
ggaggcagag catctaata 20
<210>3658
<211>20
<212>DNA
<400>3658
gtagactccc tagttgtggt 20
<210>3659
<211>20
<212>DNA
<400>3659
aatcaccctc atggaggctt 20
<210>3660
<211>20
<212>DNA
<400>3660
gctgaaacga gttgtgtgga 20
<210>3661
<211>20
<212>DNA
<400>3661

```

gtgaggattg ctggttgatg 20  
<210>3662  
<211>20  
<212>DNA  
<400>3662  
gcccttttga gatgctttgc 20  
<210>3663  
<211>20  
<212>DNA  
<400>3663  
gtacgtgctt agcaaacgtc 20  
<210>3664  
<211>20  
<212>DNA  
<400>3664  
ctggagaatc gaacaggaca 20  
<210>3665  
<211>20  
<212>DNA  
<400>3665  
gagaagcagc gttgttctga 20  
<210>3666  
<211>20  
<212>DNA  
<400>3666  
gatggtgtag cgctaggata 20  
<210>3667  
<211>20  
<212>DNA  
<400>3667  
gggtctacaa cgccttcttt 20  
<210>3668  
<211>20  
<212>DNA  
<400>3668  
gagaaagcat ttcacgggca 20  
<210>3669  
<211>20  
<212>DNA  
<400>3669  
gctgtaattt ggcaggcggt 20  
<210>3670  
<211>20  
<212>DNA  
<400>3670  
aggtgatttg gaagaggctg 20  
<210>3671  
<211>20  
<212>DNA  
<400>3671  
ggatcaccgg ttgttggttc 20  
<210>3672  
<211>20  
<212>DNA  
<400>3672  
ggtgtgccaa gcagatgtta 20  
<210>3673  
<211>20  
<212>DNA  
<400>3673  
cgagtccgta aagagcaaac 20  
<210>3674  
<211>20  
<212>DNA

<400>3674  
 cgaaagcagc actgaaagca 20  
 <210>3675  
 <211>20  
 <212>DNA  
 <400>3675  
 ggctacccat tctcctgcaa 20  
 <210>3676  
 <211>20  
 <212>DNA  
 <400>3676  
 tgccgatggg aggaatatcg 20  
 <210>3677  
 <211>20  
 <212>DNA  
 <400>3677  
 cagtcaattg cgtcactgct 20  
 <210>3678  
 <211>20  
 <212>DNA  
 <400>3678  
 tgcccaaggg actttcacga 20  
 <210>3679  
 <211>20  
 <212>DNA  
 <400>3679  
 cgaaagcagc actgaaagca 20  
 <210>3680  
 <211>20  
 <212>DNA  
 <400>3680  
 gggctcgaga aagtagactt 20  
 <210>3681  
 <211>20  
 <212>DNA  
 <400>3681  
 gacttactgt cccaagtcca 20  
 <210>3682  
 <211>20  
 <212>DNA  
 <400>3682  
 ctgattacgt tgaggcagtg 20  
 <210>3683  
 <211>20  
 <212>DNA  
 <400>3683  
 ccagttatatt cggcggattg 20  
 <210>3684  
 <211>20  
 <212>DNA  
 <400>3684  
 cgaattccaa tcgtcttcgc 20  
 <210>3685  
 <211>20  
 <212>DNA  
 <400>3685  
 ccggggtaaa ttcacagtct 20  
 <210>3686  
 <211>20  
 <212>DNA  
 <400>3686  
 ctctcttcag gattcgcggtt 20  
 <210>3687  
 <211>20

```

<212>DNA
<400>3687
cttgtggaga ttttagcgctt    20
<210>3688
<211>20
<212>DNA
<400>3688
gtgctgctag aataggacct    20
<210>3689
<211>20
<212>DNA
<400>3689
tcttcgcgaa gtggctttga    20
<210>3690
<211>20
<212>DNA
<400>3690
cagtgtttgt gtcaaagcac    20
<210>3691
<211>20
<212>DNA
<400>3691
cttctcgttc agagagggtta    20
<210>3692
<211>20
<212>DNA
<400>3692
atgggtgata ggaggctcag    20
<210>3693
<211>20
<212>DNA
<400>3693
gtgctgctag aataggacct    20
<210>3694
<211>20
<212>DNA
<400>3694
cagcgaaaaa cggatgatgct    20
<210>3695
<211>20
<212>DNA
<400>3695
ggaggagtcg atatggattg    20
<210>3696
<211>20
<212>DNA
<400>3696
cctcagcgac tgcctctaca    20
<210>3697
<211>20
<212>DNA
<400>3697
gcttgtgctg ctttggctat    20
<210>3698
<211>20
<212>DNA
<400>3698
gcgggtttaga gggaaagaga    20
<210>3699
<211>20
<212>DNA
<400>3699
ccataggcat gcaaagcttg    20
<210>3700

```

<211>20  
<212>DNA  
<400>3700  
agcctacgcg ctaacgtagt 20  
<210>3701  
<211>20  
<212>DNA  
<400>3701  
ttgcggaggt aaggatctct 20  
<210>3702  
<211>20  
<212>DNA  
<400>3702  
ggctgtgcct ttatcagagg 20  
<210>3703  
<211>20  
<212>DNA  
<400>3703  
cattaggggc gtaggttgta 20  
<210>3704  
<211>20  
<212>DNA  
<400>3704  
gtctacctca gagagaggtt 20  
<210>3705  
<211>20  
<212>DNA  
<400>3705  
gctaacgtag tctctgcttc 20  
<210>3706  
<211>20  
<212>DNA  
<400>3706  
gtccctaagg gacctcttta 20  
<210>3707  
<211>20  
<212>DNA  
<400>3707  
gctgcacgt tgttaacgct 20  
<210>3708  
<211>20  
<212>DNA  
<400>3708  
ggccgcttta aatacagcag 20  
<210>3709  
<211>20  
<212>DNA  
<400>3709  
cggctgattc tctctacgat 20  
<210>3710  
<211>20  
<212>DNA  
<400>3710  
gtcctaaaag tgacgagtgg 20  
<210>3711  
<211>20  
<212>DNA  
<400>3711  
gagacgcaac ggctgttttt 20  
<210>3712  
<211>20  
<212>DNA  
<400>3712  
gtcactgtag ctatgctctc 20

<210>3713  
<211>20  
<212>DNA  
<400>3713  
ctcagaatgg acgggctctt 20  
<210>3714  
<211>20  
<212>DNA  
<400>3714  
gtgggtgattg ctttggttcc 20  
<210>3715  
<211>20  
<212>DNA  
<400>3715  
gtctggcatc cgtccgggtcc 20  
<210>3716  
<211>20  
<212>DNA  
<400>3716  
gaccatactg ggaatggaga 20  
<210>3717  
<211>20  
<212>DNA  
<400>3717  
gttcctgact tcacacaagc 20  
<210>3718  
<211>20  
<212>DNA  
<400>3718  
aggcgtcagc caatccctga 20  
<210>3719  
<211>20  
<212>DNA  
<400>3719  
gcatagcatg ctcgctcatc 20  
<210>3720  
<211>20  
<212>DNA  
<400>3720  
ctcctaaaac ggctatacgc 20  
<210>3721  
<211>20  
<212>DNA  
<400>3721  
caggaaaaag ctagcgtgtc 20  
<210>3722  
<211>20  
<212>DNA  
<400>3722  
gggacgtatt gtagagagga 20  
<210>3723  
<211>20  
<212>DNA  
<400>3723  
cgtcagccaa tccctgaata 20  
<210>3724  
<211>20  
<212>DNA  
<400>3724  
cacaggtatc tacaggaacg 20  
<210>3725  
<211>20  
<212>DNA  
<400>3725



cataagccgt ggggaaggat 20  
 <210>3726  
 <211>20  
 <212>DNA  
 <400>3726  
 cagactcata acgtcgtagc 20  
 <210>3727  
 <211>20  
 <212>DNA  
 <400>3727  
 ccgtgatgct gagcatagta 20  
 <210>3728  
 <211>20  
 <212>DNA  
 <400>3728  
 ccgtagaaga aggcatagtg 20  
 <210>3729  
 <211>20  
 <212>DNA  
 <400>3729  
 tagctggttc agcatttttcg 20  
 <210>3730  
 <211>20  
 <212>DNA  
 <400>3730  
 tctcctcctt gaagaagcgt 20  
 <210>3731  
 <211>20  
 <212>DNA  
 <400>3731  
 ggattctcag agacaagacc 20  
 <210>3732  
 <211>20  
 <212>DNA  
 <400>3732  
 gggttcaagt tttgctaggg 20  
 <210>3733  
 <211>20  
 <212>DNA  
 <400>3733  
 ggggtgaagtt cctgagcttt 20  
 <210>3734  
 <211>20  
 <212>DNA  
 <400>3734  
 cccccctcca attccaataa 20  
 <210>3735  
 <211>20  
 <212>DNA  
 <400>3735  
 gcacctacaa tggcaatgtg 20  
 <210>3736  
 <211>20  
 <212>DNA  
 <400>3736  
 gtgcctgtgg tctttccttt 20  
 <210>3737  
 <211>20  
 <212>DNA  
 <400>3737  
 cacgacctag atgctctatc 20  
 <210>3738  
 <211>20  
 <212>DNA

<400>3738  
 gtgaatacga ctatcgccag 20  
 <210>3739  
 <211>20  
 <212>DNA  
 <400>3739  
 tgttaggttc tccaggagga 20  
 <210>3740  
 <211>20  
 <212>DNA  
 <400>3740  
 cctagtttga atcgctcggt 20  
 <210>3741  
 <211>20  
 <212>DNA  
 <400>3741  
 cagagataag catccgcat 20  
 <210>3742  
 <211>20  
 <212>DNA  
 <400>3742  
 gggattgccc acaatttcca 20  
 <210>3743  
 <211>20  
 <212>DNA  
 <400>3743  
 cggtagagcc ttctactgtt 20  
 <210>3744  
 <211>20  
 <212>DNA  
 <400>3744  
 gggagagaag tctctgagat 20  
 <210>3745  
 <211>20  
 <212>DNA  
 <400>3745  
 gcactgctgt agttgcttac 20  
 <210>3746  
 <211>20  
 <212>DNA  
 <400>3746  
 cgagtttcga tacgagctct 20  
 <210>3747  
 <211>20  
 <212>DNA  
 <400>3747  
 tagaagctcc catctgcttg 20  
 <210>3748  
 <211>20  
 <212>DNA  
 <400>3748  
 ggcgcacaaa tatgactctc 20  
 <210>3749  
 <211>20  
 <212>DNA  
 <400>3749  
 gtaagtaagc ctcccagaag 20  
 <210>3750  
 <211>20  
 <212>DNA  
 <400>3750  
 gttcttctat acgctgacag 20  
 <210>3751  
 <211>20

<212>DNA  
<400>3751  
gctgagtcca acaaaatggc 20  
<210>3752  
<211>20  
<212>DNA  
<400>3752  
gcggatgtct tctaatgacc 20  
<210>3753  
<211>20  
<212>DNA  
<400>3753  
gatggctccc tgaaacacaa 20  
<210>3754  
<211>20  
<212>DNA  
<400>3754  
gaggttggcg ataaaagctg 20  
<210>3755  
<211>20  
<212>DNA  
<400>3755  
gcaagcctaa gtttgctgtg 20  
<210>3756  
<211>20  
<212>DNA  
<400>3756  
aaccgtgagg aaaggagtcg 20  
<210>3757  
<211>20  
<212>DNA  
<400>3757  
tttgcccttt ccacaacgtc 20  
<210>3758  
<211>20  
<212>DNA  
<400>3758  
catcgatagg accatcggtt 20  
<210>3759  
<211>20  
<212>DNA  
<400>3759  
gcaaagtacc tcaaaaccag 20  
<210>3760  
<211>20  
<212>DNA  
<400>3760  
attccccaat acctaccaac 20  
<210>3761  
<211>20  
<212>DNA  
<400>3761  
ggagcaacct tccctttgat 20  
<210>3762  
<211>20  
<212>DNA  
<400>3762  
atctagtgtc acacgcttgc 20  
<210>3763  
<211>20  
<212>DNA  
<400>3763  
gagatgggtac gtgatttgcc 20  
<210>3764

```

<211>20
<212>DNA
<400>3764
ggagaatgta tctcctgctg      20
<210>3765
<211>20
<212>DNA
<400>3765
catggacgtc tcgactcctt      20
<210>3766
<211>20
<212>DNA
<400>3766
cacctttatc tgtcgagggtc      20
<210>3767
<211>20
<212>DNA
<400>3767
ctgagctcag tttcgaagag      20
<210>3768
<211>20
<212>DNA
<400>3768
ggatacctag ctggtccttag      20
<210>3769
<211>20
<212>DNA
<400>3769
ggttcttttta gggagcactg      20
<210>3770
<211>20
<212>DNA
<400>3770
ggaaaagcgc gtcctttact      20
<210>3771
<211>20
<212>DNA
<400>3771
ctcccatcta tacgaagcct      20
<210>3772
<211>20
<212>DNA
<400>3772
ggtcgaacca aagaggaact      20
<210>3773
<211>20
<212>DNA
<400>3773
agatgcgtcg catttttttc      20
<210>3774
<211>20
<212>DNA
<400>3774
gcaacgcagc agcgagttgc      20
<210>3775
<211>20
<212>DNA
<400>3775
cagctgccta aggaattgga      20
<210>3776
<211>20
<212>DNA
<400>3776
ggttgtatcg agaggagaga      20

```

## WO 99/27105

<210>3777  
 <211>20  
 <212>DNA  
 <400>3777  
 cagctgccta aggaattgga 20  
 <210>3778  
 <211>20  
 <212>DNA  
 <400>3778  
 ggggagcggg taaagaaatc 20  
 <210>3779  
 <211>20  
 <212>DNA  
 <400>3779  
 gcatgctttg tatcctgagg 20  
 <210>3780  
 <211>20  
 <212>DNA  
 <400>3780  
 gaggcacccc tgcattctat 20  
 <210>3781  
 <211>20  
 <212>DNA  
 <400>3781  
 cagcgagttg cagcatttga 20  
 <210>3782  
 <211>20  
 <212>DNA  
 <400>3782  
 ggattgcaca gctacgacaa 20  
 <210>3783  
 <211>20  
 <212>DNA  
 <400>3783  
 cgagaataag cccgtcttct 20  
 <210>3784  
 <211>20  
 <212>DNA  
 <400>3784  
 cctaaggcac ataagtcagg 20  
 <210>3785  
 <211>20  
 <212>DNA  
 <400>3785  
 gggattagag cccaacgttc 20  
 <210>3786  
 <211>20  
 <212>DNA  
 <400>3786  
 gcctggggat cttaggaaat 20  
 <210>3787  
 <211>20  
 <212>DNA  
 <400>3787  
 gatgggtatg atggtgcgct 20  
 <210>3788  
 <211>20  
 <212>DNA  
 <400>3788  
 cagacgagga gattcctgta 20  
 <210>3789  
 <211>20  
 <212>DNA  
 <400>3789

gattgcacag ctacgacaat 20  
 <210>3790  
 <211>20  
 <212>DNA  
 <400>3790  
 ggataggtct gatgtcctac 20  
 <210>3791  
 <211>20  
 <212>DNA  
 <400>3791  
 gcgtcgaaaa gtactcgcta 20  
 <210>3792  
 <211>20  
 <212>DNA  
 <400>3792  
 ccagaaggac ttttgaggag 20  
 <210>3793  
 <211>20  
 <212>DNA  
 <400>3793  
 cggttggtca tactactctc 20  
 <210>3794  
 <211>20  
 <212>DNA  
 <400>3794  
 cgaactacag cttgttcttc 20  
 <210>3795  
 <211>20  
 <212>DNA  
 <400>3795  
 acaacagttg cggagatgcc 20  
 <210>3796  
 <211>20  
 <212>DNA  
 <400>3796  
 cgtccactac cttttcaacc 20  
 <210>3797  
 <211>20  
 <212>DNA  
 <400>3797  
 cactatgtgt ctgcgatgtc 20  
 <210>3798  
 <211>20  
 <212>DNA  
 <400>3798  
 ggcagagctc tgtgaagaaa 20  
 <210>3799  
 <211>20  
 <212>DNA  
 <400>3799  
 gttgcagcct ctacatcctt 20  
 <210>3800  
 <211>20  
 <212>DNA  
 <400>3800  
 gcagcagctt ctatattggc 20  
 <210>3801  
 <211>20  
 <212>DNA  
 <400>3801  
 cctctacatc cagagcaaac 20  
 <210>3802  
 <211>20  
 <212>DNA

## WO 99/27105

<400>3802  
 gatgagcgaa agatttcacc 20  
 <210>3803  
 <211>20  
 <212>DNA  
 <400>3803  
 cacaacagcc tgggactgga 20  
 <210>3804  
 <211>20  
 <212>DNA  
 <400>3804  
 aagagaccga accgatggct 20  
 <210>3805  
 <211>20  
 <212>DNA  
 <400>3805  
 cagggaaaac ttcagcatcg 20  
 <210>3806  
 <211>20  
 <212>DNA  
 <400>3806  
 gcggcatttc ttccccaaat 20  
 <210>3807  
 <211>20  
 <212>DNA  
 <400>3807  
 cttctacgac tccacatcat 20  
 <210>3808  
 <211>20  
 <212>DNA  
 <400>3808  
 cttcttcctg ccgacgtttt 20  
 <210>3809  
 <211>20  
 <212>DNA  
 <400>3809  
 caaatagctg gacacgaggt 20  
 <210>3810  
 <211>20  
 <212>DNA  
 <400>3810  
 gggctgctct atataggcat 20  
 <210>3811  
 <211>20  
 <212>DNA  
 <400>3811  
 cgcataatc cgcataatca 20  
 <210>3812  
 <211>20  
 <212>DNA  
 <400>3812  
 ggccatcttc tctaattctc 20  
 <210>3813  
 <211>20  
 <212>DNA  
 <400>3813  
 gatgggttcc ttctccttca 20  
 <210>3814  
 <211>20  
 <212>DNA  
 <400>3814  
 gaggcctttg ccaaaagtaa 20  
 <210>3815  
 <211>20

<212>DNA  
<400>3815  
ggttcatctc caaagcgatt 20  
<210>3816  
<211>20  
<212>DNA  
<400>3816  
cctgcgagtt ttctctaaagg 20  
<210>3817  
<211>20  
<212>DNA  
<400>3817  
agttctgagg atcccttagg 20  
<210>3818  
<211>20  
<212>DNA  
<400>3818  
atttcacctt cgacagcgca 20  
<210>3819  
<211>20  
<212>DNA  
<400>3819  
acccagaaaa acgtgccgtt 20  
<210>3820  
<211>20  
<212>DNA  
<400>3820  
agcaagccga gcacaagaat 20  
<210>3821  
<211>20  
<212>DNA  
<400>3821  
gggtctcttg aacctgcatt 20  
<210>3822  
<211>20  
<212>DNA  
<400>3822  
cggagacaag caaaccaaga 20  
<210>3823  
<211>20  
<212>DNA  
<400>3823  
accttctcca gtaacactgc 20  
<210>3824  
<211>20  
<212>DNA  
<400>3824  
cagcattccc ccacaagata 20  
<210>3825  
<211>20  
<212>DNA  
<400>3825  
gggacttctc gtttcttcag 20  
<210>3826  
<211>20  
<212>DNA  
<400>3826  
ctgtgatgtc atcatgctca 20  
<210>3827  
<211>20  
<212>DNA  
<400>3827  
ggctacttct atagggtggg 20  
<210>3828



```

<211>20
<212>DNA
<400>3828
ttcggaccat agtcgcatga      20
<210>3829
<211>20
<212>DNA
<400>3829
gggtatcctc aaccacaaag      20
<210>3830
<211>20
<212>DNA
<400>3830
gcggagatag aagtacttgc      20
<210>3831
<211>20
<212>DNA
<400>3831
aaaccggaat ccccctggaa      20
<210>3832
<211>20
<212>DNA
<400>3832
ccaagagcgc gagatttact      20
<210>3833
<211>20
<212>DNA
<400>3833
gcggctgcct taaaatcttc      20
<210>3834
<211>20
<212>DNA
<400>3834
ccaagagcgc gagatttact      20
<210>3835
<211>20
<212>DNA
<400>3835
gcggctgcct taaaatcttc      20
<210>3836
<211>20
<212>DNA
<400>3836
ctcatcgttc tcattcagcc      20
<210>3837
<211>20
<212>DNA
<400>3837
ccatctgtag ccgatgatgt      20
<210>3838
<211>20
<212>DNA
<400>3838
ttccctggtc gtaagcaaag      20
<210>3839
<211>20
<212>DNA
<400>3839
gttatctcca gtatcagggc      20
<210>3840
<211>20
<212>DNA
<400>3840
ccaagccaaa atcttggggag      20

```

<210>3841  
<211>20  
<212>DNA  
<400>3841  
gtatcaccac ccggcatcct 20  
<210>3842  
<211>20  
<212>DNA  
<400>3842  
gctcctatcg tattgccttc 20  
<210>3843  
<211>20  
<212>DNA  
<400>3843  
gcgtgggtatc ctgcaatctt 20  
<210>3844  
<211>20  
<212>DNA  
<400>3844  
ctctcatcgc taattgccag 20  
<210>3845  
<211>20  
<212>DNA  
<400>3845  
gaacttccag gagacgcaat 20  
<210>3846  
<211>20  
<212>DNA  
<400>3846  
ggggaaaagaa gacttcattg 20  
<210>3847  
<211>20  
<212>DNA  
<400>3847  
ccttcgtttg cagtctccat 20  
<210>3848  
<211>20  
<212>DNA  
<400>3848  
gctcctgtga ccttattgtc 20  
<210>3849  
<211>20  
<212>DNA  
<400>3849  
ggactaaagc ttgtcttgcc 20  
<210>3850  
<211>20  
<212>DNA  
<400>3850  
ttcacgagct tctgttcctt 20  
<210>3851  
<211>20  
<212>DNA  
<400>3851  
atactaaggc acctgcagca 20  
<210>3852  
<211>20  
<212>DNA  
<400>3852  
gtgcaaagtc tgaacgctac 20  
<210>3853  
<211>20  
<212>DNA  
<400>3853

gaacttgtgc tccggtccat	20
<210>3854	
<211>20	
<212>DNA	
<400>3854	
gccgtcgcct taatgatagc	20
<210>3855	
<211>20	
<212>DNA	
<400>3855	
acctgcatct accgacagga	20
<210>3856	
<211>20	
<212>DNA	
<400>3856	
ctgccttgca tttcttcctg	20
<210>3857	
<211>20	
<212>DNA	
<400>3857	
gggatgactt gcacattcca	20
<210>3858	
<211>20	
<212>DNA	
<400>3858	
tccctccgc tcctggagat	20
<210>3859	
<211>20	
<212>DNA	
<400>3859	
gactaccac atcttgagca	20
<210>3860	
<211>20	
<212>DNA	
<400>3860	
gagaatgaac ctctgtgtc	20
<210>3861	
<211>20	
<212>DNA	
<400>3861	
tgtgggtcaa agcctgaagc	20
<210>3862	
<211>20	
<212>DNA	
<400>3862	
ggtctagaag gagctacttc	20
<210>3863	
<211>20	
<212>DNA	
<400>3863	
ctgagtaaga ctaaccctcg	20
<210>3864	
<211>20	
<212>DNA	
<400>3864	
cgttctctcc atgattatgc	20
<210>3865	
<211>20	
<212>DNA	
<400>3865	
gaacttgccg cacaaaaggc	20
<210>3866	
<211>20	
<212>DNA	

<400>3866  
 ggatgggtcag agctactaca 20  
 <210>3867  
 <211>20  
 <212>DNA  
 <400>3867  
 ggggatcatc aggtaatcca 20  
 <210>3868  
 <211>20  
 <212>DNA  
 <400>3868  
 ccttgaggaa tcagacgcat 20  
 <210>3869  
 <211>20  
 <212>DNA  
 <400>3869  
 gctgtctgct atgagcatag 20  
 <210>3870  
 <211>20  
 <212>DNA  
 <400>3870  
 ccttgatgaa gcgaacaacc 20  
 <210>3871  
 <211>20  
 <212>DNA  
 <400>3871  
 cgggtttgag gattagtgag 20  
 <210>3872  
 <211>20  
 <212>DNA  
 <400>3872  
 ggggatcatc aggtaatcca 20  
 <210>3873  
 <211>20  
 <212>DNA  
 <400>3873  
 gcctctccgc atacattaag 20  
 <210>3874  
 <211>20  
 <212>DNA  
 <400>3874  
 tcgacgttct ggactttcag 20  
 <210>3875  
 <211>20  
 <212>DNA  
 <400>3875  
 ccgacagacc cataactatc 20  
 <210>3876  
 <211>20  
 <212>DNA  
 <400>3876  
 gaagcgcaaa gtctctgaac 20  
 <210>3877  
 <211>20  
 <212>DNA  
 <400>3877  
 gccccaaaag atgcctctga 20  
 <210>3878  
 <211>20  
 <212>DNA  
 <400>3878  
 acgtgccgca acacaaaagc 20  
 <210>3879  
 <211>20

<212>DNA  
<400>3879  
gccaaagttga acccttggtc 20  
<210>3880  
<211>20  
<212>DNA  
<400>3880  
atctcctcca cccgtacaac 20  
<210>3881  
<211>20  
<212>DNA  
<400>3881  
cgtacgtgtt gatctatcca 20  
<210>3882  
<211>20  
<212>DNA  
<400>3882  
gactatgaag agcttcctgc 20  
<210>3883  
<211>20  
<212>DNA  
<400>3883  
gagtttccta tcatgcggaac 20  
<210>3884  
<211>20  
<212>DNA  
<400>3884  
cgccatgttc ctgattatgc 20  
<210>3885  
<211>20  
<212>DNA  
<400>3885  
cttaggaaaa agctctggca 20  
<210>3886  
<211>20  
<212>DNA  
<400>3886  
cttggaataat ctacccccta 20  
<210>3887  
<211>20  
<212>DNA  
<400>3887  
gctgcggatt aggagaaatc 20  
<210>3888  
<211>20  
<212>DNA  
<400>3888  
cttaggaaaa agctctggca 20  
<210>3889  
<211>20  
<212>DNA  
<400>3889  
cgaaacgatc gtaagagtcg 20  
<210>3890  
<211>20  
<212>DNA  
<400>3890  
gggacgtccc gttttcaata 20  
<210>3891  
<211>20  
<212>DNA  
<400>3891  
cgttcgcagg atttaatccc 20  
<210>3892

```

<211>20
<212>DNA
<400>3892
gcaactccct gaaaagagag      20
<210>3893
<211>20
<212>DNA
<400>3893
ggagtttcta cagaaatgcg      20
<210>3894
<211>20
<212>DNA
<400>3894
acgatctaca ggctctccaa      20
<210>3895
<211>20
<212>DNA
<400>3895
gcagttggtg tagtgctaca      20
<210>3896
<211>20
<212>DNA
<400>3896
ggaccagtct ttaccaggaa      20
<210>3897
<211>20
<212>DNA
<400>3897
gtgtcgggct ctctttttga      20
<210>3898
<211>20
<212>DNA
<400>3898
gagtctcggg ataaggagag      20
<210>3899
<211>20
<212>DNA
<400>3899
ccttacctcc aactctacct      20
<210>3900
<211>20
<212>DNA
<400>3900
gattaaataa cctcagcgca      20
<210>3901
<211>20
<212>DNA
<400>3901
atgctctgtg ctcttcttcc      20
<210>3902
<211>20
<212>DNA
<400>3902
gctacacaac cccaatatcc      20
<210>3903
<211>20
<212>DNA
<400>3903
ggtctctgcg tatttcagga      20
<210>3904
<211>20
<212>DNA
<400>3904
gtggagctcc caacataaga      20

```

<210>3905  
<211>20  
<212>DNA  
<400>3905  
gcacattggc acgactagaa 20  
<210>3906  
<211>20  
<212>DNA  
<400>3906  
ggctctcctt gaaacccaca 20  
<210>3907  
<211>20  
<212>DNA  
<400>3907  
ccttgcaaag aggctttagc 20  
<210>3908  
<211>20  
<212>DNA  
<400>3908  
gtcccgtaac ttctgttct 20  
<210>3909  
<211>20  
<212>DNA  
<400>3909  
gcagcggata cgctaagaaa 20  
<210>3910  
<211>20  
<212>DNA  
<400>3910  
gcctctccac aaatgctaac 20  
<210>3911  
<211>20  
<212>DNA  
<400>3911  
ggaattcgtg gtacagggaa 20  
<210>3912  
<211>20  
<212>DNA  
<400>3912  
ggcagcacta gaaaacacag 20  
<210>3913  
<211>20  
<212>DNA  
<400>3913  
ccatcgcgat caaacacata 20  
<210>3914  
<211>20  
<212>DNA  
<400>3914  
ccctgaagat ccagaagtca 20  
<210>3915  
<211>20  
<212>DNA  
<400>3915  
tcgagaagaa atcgacccta 20  
<210>3916  
<211>20  
<212>DNA  
<400>3916  
cccacctaca aagaacagag 20  
<210>3917  
<211>20  
<212>DNA  
<400>3917

```

ctcctccttg acgtcttgta 20
<210>3918
<211>20
<212>DNA
<400>3918
ggagcctccc accgtggtat 20
<210>3919
<211>20
<212>DNA
<400>3919
gcctctacaa cagagactgc 20
<210>3920
<211>20
<212>DNA
<400>3920
gccatcgcgga tcaaacacat 20
<210>3921
<211>20
<212>DNA
<400>3921
gactctttgt acgcacgttg 20
<210>3922
<211>20
<212>DNA
<400>3922
gctcctgata atgcaattcc 20
<210>3923
<211>20
<212>DNA
<400>3923
ttgtacctca tggatcaggc 20
<210>3924
<211>20
<212>DNA
<400>3924
cctcgactcg agatagcata 20
<210>3925
<211>20
<212>DNA
<400>3925
gcagtgagca cttctatgtc 20
<210>3926
<211>20
<212>DNA
<400>3926
ctgtggtgct atcggaatca 20
<210>3927
<211>20
<212>DNA
<400>3927
tctgcaatcg ctcttcgcta 20
<210>3928
<211>20
<212>DNA
<400>3928
cgatctcttg gaatctcctc 20
<210>3929
<211>20
<212>DNA
<400>3929
ctaagacaac cacttccgct 20
<210>3930
<211>20
<212>DNA

```



<400>3930  
 gatcaggccc tctagatacc 20  
 <210>3931  
 <211>20  
 <212>DNA  
 <400>3931  
 gtgatgccat cgtgaccaaa 20  
 <210>3932  
 <211>20  
 <212>DNA  
 <400>3932  
 tgatcggggg gtagctgtgg 20  
 <210>3933  
 <211>20  
 <212>DNA  
 <400>3933  
 ccagcccttg agtttcaaac 20  
 <210>3934  
 <211>20  
 <212>DNA  
 <400>3934  
 ctaaattctct gctcagcacg 20  
 <210>3935  
 <211>20  
 <212>DNA  
 <400>3935  
 gcgactatga aggaacacga 20  
 <210>3936  
 <211>20  
 <212>DNA  
 <400>3936  
 gagttgtaag tgatcatgcga 20  
 <210>3937  
 <211>20  
 <212>DNA  
 <400>3937  
 atatcagact caggaagccc 20  
 <210>3938  
 <211>20  
 <212>DNA  
 <400>3938  
 acagaaagag tgtgtcgagg 20  
 <210>3939  
 <211>20  
 <212>DNA  
 <400>3939  
 ccccttcgt tattgctttc 20  
 <210>3940  
 <211>20  
 <212>DNA  
 <400>3940  
 ggatcacgca ggtaaattgga 20  
 <210>3941  
 <211>20  
 <212>DNA  
 <400>3941  
 gtccccagg ctgatctgg 20  
 <210>3942  
 <211>20  
 <212>DNA  
 <400>3942  
 caaccgcctg ttaccttaaca 20  
 <210>3943  
 <211>20

<212>DNA  
<400>3943  
cagacctcat acgtatccga 20  
<210>3944  
<211>20  
<212>DNA  
<400>3944  
tcttctacga gtgcgattgc 20  
<210>3945  
<211>20  
<212>DNA  
<400>3945  
cttcaagctg tgcaggatct 20  
<210>3946  
<211>20  
<212>DNA  
<400>3946  
ctccttctct ctagagaaga 20  
<210>3947  
<211>20  
<212>DNA  
<400>3947  
cctcccgaag ccatataaac 20  
<210>3948  
<211>20  
<212>DNA  
<400>3948  
ttccttcgat ggatgagggg 20  
<210>3949  
<211>20  
<212>DNA  
<400>3949  
gagaacatga ggaacgagag 20  
<210>3950  
<211>20  
<212>DNA  
<400>3950  
caccgcacag tgtctatagt 20  
<210>3951  
<211>20  
<212>DNA  
<400>3951  
cctcggctcc aaatacgaat 20  
<210>3952  
<211>20  
<212>DNA  
<400>3952  
gcttggtctg gtataatcca 20  
<210>3953  
<211>20  
<212>DNA  
<400>3953  
ggagatttag cccaagtgtg 20  
<210>3954  
<211>20  
<212>DNA  
<400>3954  
ggctccaaag cgtcataatc 20  
<210>3955  
<211>20  
<212>DNA  
<400>3955  
gccgtgcttt aaagccaaac 20  
<210>3956

<211>20  
<212>DNA  
<400>3956  
cttgactctt tcgatcgcag 20  
<210>3957  
<211>20  
<212>DNA  
<400>3957  
cttggatcat gagtgcttgg 20  
<210>3958  
<211>20  
<212>DNA  
<400>3958  
gaagttctcc tcctgaatcc 20  
<210>3959  
<211>20  
<212>DNA  
<400>3959  
gagtccttga agaagggact 20  
<210>3960  
<211>20  
<212>DNA  
<400>3960  
ctcgggagtg tttgcctaaa 20  
<210>3961  
<211>20  
<212>DNA  
<400>3961  
gaatcgaggc ttgggatgcc 20  
<210>3962  
<211>20  
<212>DNA  
<400>3962  
agccacgccc attccgattc 20  
<210>3963  
<211>20  
<212>DNA  
<400>3963  
cgagcttcaa gagcttgtct 20  
<210>3964  
<211>20  
<212>DNA  
<400>3964  
cgccacgatg aattgctttg 20  
<210>3965  
<211>20  
<212>DNA  
<400>3965  
ggaggagtgt gatctgatgt 20  
<210>3966  
<211>20  
<212>DNA  
<400>3966  
cggatgtaat gtagaccgtg 20  
<210>3967  
<211>20  
<212>DNA  
<400>3967  
ggccggtcga gatctataat 20  
<210>3968  
<211>20  
<212>DNA  
<400>3968  
gcaaattctga cacgatgcaa 20

<210>3969  
<211>20  
<212>DNA  
<400>3969  
ctgacgatta cgcttggtgt 20  
<210>3970  
<211>20  
<212>DNA  
<400>3970  
aaacacgaat accttaggtc 20  
<210>3971  
<211>20  
<212>DNA  
<400>3971  
ggaccttaga gatcctgtct 20  
<210>3972  
<211>20  
<212>DNA  
<400>3972  
gattgtgtgg gatttgccat 20  
<210>3973  
<211>20  
<212>DNA  
<400>3973  
gatataaagg aaagaggccg 20  
<210>3974  
<211>20  
<212>DNA  
<400>3974  
ccctgaacct tttcaatgac 20  
<210>3975  
<211>20  
<212>DNA  
<400>3975  
cagaattgag gaggatcctg 20  
<210>3976  
<211>20  
<212>DNA  
<400>3976  
gggtgacata gagggctctt 20  
<210>3977  
<211>20  
<212>DNA  
<400>3977  
ctaggaaacg tcgccccacg 20  
<210>3978  
<211>20  
<212>DNA  
<400>3978  
gctagcattt caacgtgaac 20  
<210>3979  
<211>20  
<212>DNA  
<400>3979  
gtcccccttc tagtgaagtt 20  
<210>3980  
<211>20  
<212>DNA  
<400>3980  
gaggatcggg atggtggggg 20  
<210>3981  
<211>20  
<212>DNA  
<400>3981

cgggatctat ggtatcttcg 20  
 <210>3982  
 <211>20  
 <212>DNA  
 <400>3982  
 ctctacagca gcactgctta 20  
 <210>3983  
 <211>20  
 <212>DNA  
 <400>3983  
 caagcgatca accagcatca 20  
 <210>3984  
 <211>20  
 <212>DNA  
 <400>3984  
 gtccccctcat ttcgagtcta 20  
 <210>3985  
 <211>20  
 <212>DNA  
 <400>3985  
 ggtgctcttc atttccccta 20  
 <210>3986  
 <211>20  
 <212>DNA  
 <400>3986  
 aaacggatcc tgccacagcg 20  
 <210>3987  
 <211>20  
 <212>DNA  
 <400>3987  
 gttcagcatc ttcttgagag 20  
 <210>3988  
 <211>20  
 <212>DNA  
 <400>3988  
 ctggctggcc tagtgggtag 20  
 <210>3989  
 <211>20  
 <212>DNA  
 <400>3989  
 cgtgcttgct taccattca 20  
 <210>3990  
 <211>20  
 <212>DNA  
 <400>3990  
 cgtgcttgct taccattca 20  
 <210>3991  
 <211>20  
 <212>DNA  
 <400>3991  
 ttagctgcag gaggtttggc 20  
 <210>3992  
 <211>20  
 <212>DNA  
 <400>3992  
 aagactcgtc agtcagatgc 20  
 <210>3993  
 <211>20  
 <212>DNA  
 <400>3993  
 ccttccagcg aggaaaacta 20  
 <210>3994  
 <211>20  
 <212>DNA

<400>3994  
 ggcttatctt gagttgcagc 20  
 <210>3995  
 <211>20  
 <212>DNA  
 <400>3995  
 gccagcatct tgtaacttct 20  
 <210>3996  
 <211>20  
 <212>DNA  
 <400>3996  
 ggtaaaaaaa cggctccacg 20  
 <210>3997  
 <211>20  
 <212>DNA  
 <400>3997  
 cccgtttcat cggttaaacg 20  
 <210>3998  
 <211>20  
 <212>DNA  
 <400>3998  
 tctacctcta aacctgcagc 20  
 <210>3999  
 <211>20  
 <212>DNA  
 <400>3999  
 ataacgccct acacgtccta 20  
 <210>4000  
 <211>20  
 <212>DNA  
 <400>4000  
 ttctgtaggt tcggcagcaa 20  
 <210>4001  
 <211>20  
 <212>DNA  
 <400>4001  
 gaaagagagg tgatcagacc 20  
 <210>4002  
 <211>20  
 <212>DNA  
 <400>4002  
 gaaaacctct tctaaaccga 20  
 <210>4003  
 <211>20  
 <212>DNA  
 <400>4003  
 gcaacaacaa tagctccaga 20  
 <210>4004  
 <211>20  
 <212>DNA  
 <400>4004  
 cgcagcaaca ttcccaatct 20  
 <210>4005  
 <211>20  
 <212>DNA  
 <400>4005  
 ctgttcggaa acttcagtcc 20  
 <210>4006  
 <211>20  
 <212>DNA  
 <400>4006  
 gtctttcttcg gtacgacgat 20  
 <210>4007  
 <211>20

<212>DNA  
<400>4007  
ggctacttca ggagatgcaa 20  
<210>4008  
<211>20  
<212>DNA  
<400>4008  
gggttcttgg gccactttta 20  
<210>4009  
<211>20  
<212>DNA  
<400>4009  
aaaacaagag cactgcgcgg 20  
<210>4010  
<211>20  
<212>DNA  
<400>4010  
ccgacacagt agcatttcca 20  
<210>4011  
<211>20  
<212>DNA  
<400>4011  
ggaactaaga tccagaaccc 20  
<210>4012  
<211>20  
<212>DNA  
<400>4012  
ctcttcatgg ggacgtgtat 20  
<210>4013  
<211>20  
<212>DNA  
<400>4013  
cgatcttgag aagacttatg 20  
<210>4014  
<211>20  
<212>DNA  
<400>4014  
gagctatgct atgtgctttg 20  
<210>4015  
<211>20  
<212>DNA  
<400>4015  
tccgtcaaag cgtacacgta 20  
<210>4016  
<211>20  
<212>DNA  
<400>4016  
gattctggta gctgagtagg 20  
<210>4017  
<211>20  
<212>DNA  
<400>4017  
cctcgctcat aaaaagcagc 20  
<210>4018  
<211>20  
<212>DNA  
<400>4018  
cctgagcaag tttggttctg 20  
<210>4019  
<211>20  
<212>DNA  
<400>4019  
ccaccaaaaa cctggagagt 20  
<210>4020

```

<211>20
<212>DNA
<400>4020
gcgttctgct ggagataaca    20
<210>4021
<211>20
<212>DNA
<400>4021
cggggtccct aaaagagaat    20
<210>4022
<211>20
<212>DNA
<400>4022
gtctccctaa gaacgtgaca    20
<210>4023
<211>20
<212>DNA
<400>4023
cctcggagac aatatcttcg    20
<210>4024
<211>20
<212>DNA
<400>4024
gacctcaaca ccagctatgt    20
<210>4025
<211>20
<212>DNA
<400>4025
cctcctaatt cataggggaac    20
<210>4026
<211>20
<212>DNA
<400>4026
cctcggagac aatatcttcg    20
<210>4027
<211>20
<212>DNA
<400>4027
ccacatccta tagcacttcc    20
<210>4028
<211>20
<212>DNA
<400>4028
ccatgtcctt catctatccg    20
<210>4029
<211>20
<212>DNA
<400>4029
cgacacgaag cttataaggc    20
<210>4030
<211>20
<212>DNA
<400>4030
cacgggaagg catttccctca    20
<210>4031
<211>20
<212>DNA
<400>4031
ggaccattca ccaaagtcgt    20
<210>4032
<211>20
<212>DNA
<400>4032
cgggttctgt atcctgaaag    20

```



<210>4033  
 <211>20  
 <212>DNA  
 <400>4033  
 cctcctcaag ctgatgaatc 20  
 <210>4034  
 <211>20  
 <212>DNA  
 <400>4034  
 acaggaacaa caccaggatg 20  
 <210>4035  
 <211>20  
 <212>DNA  
 <400>4035  
 ggctttctga tcctcaagag 20  
 <210>4036  
 <211>20  
 <212>DNA  
 <400>4036  
 ggccactcgg taatctacat 20  
 <210>4037  
 <211>20  
 <212>DNA  
 <400>4037  
 gaggtgcct ctaaactctca 20  
 <210>4038  
 <211>20  
 <212>DNA  
 <400>4038  
 gcgtgtgatc atactgtcct 20  
 <210>4039  
 <211>20  
 <212>DNA  
 <400>4039  
 ggaaccactc ttcactaac 20  
 <210>4040  
 <211>20  
 <212>DNA  
 <400>4040  
 gggtcttggtg ctgtgtactc 20  
 <210>4041  
 <211>20  
 <212>DNA  
 <400>4041  
 cttcttcgat caactgggct 20  
 <210>4042  
 <211>20  
 <212>DNA  
 <400>4042  
 gtctgcagga ctttttagctc 20  
 <210>4043  
 <211>20  
 <212>DNA  
 <400>4043  
 gtagagcaat tagctgccag 20  
 <210>4044  
 <211>20  
 <212>DNA  
 <400>4044  
 cttcttcgat caactgggct 20  
 <210>4045  
 <211>20  
 <212>DNA  
 <400>4045

agccgagcac tttgtgcaac 20  
 <210>4046  
 <211>20  
 <212>DNA  
 <400>4046  
 cgatcaactg ggctatagaa 20  
 <210>4047  
 <211>20  
 <212>DNA  
 <400>4047  
 ccgagcactt tgtgcaactt 20  
 <210>4048  
 <211>20  
 <212>DNA  
 <400>4048  
 ctgcgcgtcgt tctcccacta 20  
 <210>4049  
 <211>20  
 <212>DNA  
 <400>4049  
 gagacaccgc atcttttggtt 20  
 <210>4050  
 <211>20  
 <212>DNA  
 <400>4050  
 cccataactca gaggcacaaa 20  
 <210>4051  
 <211>20  
 <212>DNA  
 <400>4051  
 gacaaggaag gacgaaagaa 20  
 <210>4052  
 <211>20  
 <212>DNA  
 <400>4052  
 cccaccgaca atgatcacta 20  
 <210>4053  
 <211>20  
 <212>DNA  
 <400>4053  
 caggttatgt gttccgctca 20  
 <210>4054  
 <211>20  
 <212>DNA  
 <400>4054  
 gaatgaaggc ttcggactct 20  
 <210>4055  
 <211>20  
 <212>DNA  
 <400>4055  
 ggaacaaatc ccatcgaagc 20  
 <210>4056  
 <211>20  
 <212>DNA  
 <400>4056  
 cgtctacttg ggacccccca 20  
 <210>4057  
 <211>20  
 <212>DNA  
 <400>4057  
 ctgaagaatt ccccatctgg 20  
 <210>4058  
 <211>20  
 <212>DNA

<400>4058  
gggcttctgg atcatagatg 20  
<210>4059  
<211>20  
<212>DNA  
<400>4059  
tgcacaacct cgtcttgtca 20  
<210>4060  
<211>20  
<212>DNA  
<400>4060  
tctacgcgcc tcctgaaaat 20  
<210>4061  
<211>20  
<212>DNA  
<400>4061  
gttgtggggg tgtatagggt 20  
<210>4062  
<211>20  
<212>DNA  
<400>4062  
ccagactcta tggtttctcc 20  
<210>4063  
<211>20  
<212>DNA  
<400>4063  
cccaacgtcc tatacgattg 20  
<210>4064  
<211>20  
<212>DNA  
<400>4064  
ctcctacctc tccaacagga 20  
<210>4065  
<211>20  
<212>DNA  
<400>4065  
cggaatcatt ctgaagaggc 20  
<210>4066  
<211>20  
<212>DNA  
<400>4066  
gagtttgtca aggacgagag 20  
<210>4067  
<211>20  
<212>DNA  
<400>4067  
tgatagccca atcacgagcg 20  
<210>4068  
<211>20  
<212>DNA  
<400>4068  
cggatagtcg agaatttggc 20  
<210>4069  
<211>20  
<212>DNA  
<400>4069  
cctgactcta agacacaatg 20  
<210>4070  
<211>20  
<212>DNA  
<400>4070  
ggcaacttct ccctatgtct 20  
<210>4071  
<211>20

<212>DNA  
<400>4071  
gtaaacgctt caccccagtt 20  
<210>4072  
<211>20  
<212>DNA  
<400>4072  
ctgtgcaggc tgtcttacat 20  
<210>4073  
<211>20  
<212>DNA  
<400>4073  
gctgacaaat cgcctagaag 20  
<210>4074  
<211>20  
<212>DNA  
<400>4074  
cgggtttaaact actcggcaac 20  
<210>4075  
<211>20  
<212>DNA  
<400>4075  
ggatctctcc catccatttc 20  
<210>4076  
<211>20  
<212>DNA  
<400>4076  
actcacggca ccattgagat 20  
<210>4077  
<211>20  
<212>DNA  
<400>4077  
tttcgaaact ggttcacgtc 20  
<210>4078  
<211>20  
<212>DNA  
<400>4078  
ggggaaacat gcttccagat 20  
<210>4079  
<211>20  
<212>DNA  
<400>4079  
caggacatag tcccctatac 20  
<210>4080  
<211>20  
<212>DNA  
<400>4080  
gctccctgct ttactaaagc 20  
<210>4081  
<211>20  
<212>DNA  
<400>4081  
cgaacttggg ctcggttgttt 20  
<210>4082  
<211>20  
<212>DNA  
<400>4082  
agctgaagtg acaggctctg 20  
<210>4083  
<211>20  
<212>DNA  
<400>4083  
ggaccataac gtcgtattgc 20  
<210>4084

<211>20  
<212>DNA  
<400>4084  
gccttcatga ggaagacaaa 20  
<210>4085  
<211>20  
<212>DNA  
<400>4085  
ccctgtacgc ttgatttaag 20  
<210>4086  
<211>20  
<212>DNA  
<400>4086  
gcaacacgat gcaaggatac 20  
<210>4087  
<211>20  
<212>DNA  
<400>4087  
cgtctcctaa caatctacgg 20  
<210>4088  
<211>20  
<212>DNA  
<400>4088  
ctccaggaaa tacctttccc 20  
<210>4089  
<211>20  
<212>DNA  
<400>4089  
caaccccaga aatcttagac 20  
<210>4090  
<211>20  
<212>DNA  
<400>4090  
gcctgacgat ccaaaagtct 20  
<210>4091  
<211>20  
<212>DNA  
<400>4091  
cgaacaagtt gacgcacttc 20  
<210>4092  
<211>20  
<212>DNA  
<400>4092  
ctttctttcc acagtagggc 20  
<210>4093  
<211>20  
<212>DNA  
<400>4093  
gcgggggaaa aaattggtga 20  
<210>4094  
<211>20  
<212>DNA  
<400>4094  
ggtacatatc cacgtactct 20  
<210>4095  
<211>20  
<212>DNA  
<400>4095  
cggtggcgat aaggtaatgc 20  
<210>4096  
<211>20  
<212>DNA  
<400>4096  
cctcgcactt tatgatgctc 20

<210>4097  
<211>20  
<212>DNA  
<400>4097  
cccaaccttt ggaactagga 20  
<210>4098  
<211>20  
<212>DNA  
<400>4098  
ccagcactcc ttagaagaac 20  
<210>4099  
<211>20  
<212>DNA  
<400>4099  
cctaagttgt ccgaagtcac 20  
<210>4100  
<211>20  
<212>DNA  
<400>4100  
gcacaaggga acatcgatct 20  
<210>4101  
<211>20  
<212>DNA  
<400>4101  
cataatctct gcacagctgc 20  
<210>4102  
<211>20  
<212>DNA  
<400>4102  
ctctggcttc aaagtcctct 20  
<210>4103  
<211>20  
<212>DNA  
<400>4103  
ccccaatctc ttccctaagc 20  
<210>4104  
<211>20  
<212>DNA  
<400>4104  
ccacaactag aaatagctcc 20  
<210>4105  
<211>20  
<212>DNA  
<400>4105  
cccaactccc gctagatcaa 20  
<210>4106  
<211>20  
<212>DNA  
<400>4106  
gcacttcaga tagatggctc 20  
<210>4107  
<211>20  
<212>DNA  
<400>4107  
ctctgcctag ttctcttcgg 20  
<210>4108  
<211>20  
<212>DNA  
<400>4108  
ccgtcatatt taaaaggcgg 20  
<210>4109  
<211>20  
<212>DNA  
<400>4109

ctcgaaaaaa cccccccat	20
<210>4110	
<211>20	
<212>DNA	
<400>4110	
gcattgctag gggcgatatt	20
<210>4111	
<211>20	
<212>DNA	
<400>4111	
cacggctatg aagagatgtc	20
<210>4112	
<211>20	
<212>DNA	
<400>4112	
gggagtcatt gcagtcatac	20
<210>4113	
<211>20	
<212>DNA	
<400>4113	
cacctactac ttccctgtag	20
<210>4114	
<211>20	
<212>DNA	
<400>4114	
gaaagcacct tcttgagtgc	20
<210>4115	
<211>20	
<212>DNA	
<400>4115	
cccacctccc ggagtatttt	20
<210>4116	
<211>20	
<212>DNA	
<400>4116	
cgcttttctg tgtgtattcg	20
<210>4117	
<211>20	
<212>DNA	
<400>4117	
ccatgtcacg cgctttctta	20
<210>4118	
<211>20	
<212>DNA	
<400>4118	
cgatggaaaa acatacgcac	20
<210>4119	
<211>20	
<212>DNA	
<400>4119	
ccccagagaa ataacagacc	20
<210>4120	
<211>20	
<212>DNA	
<400>4120	
ccccattcca cgttcttaca	20
<210>4121	
<211>20	
<212>DNA	
<400>4121	
gagacctttt tctttgggaa	20
<210>4122	
<211>20	
<212>DNA	

<400>4122  
 gctaccaaag caagcacaga 20  
 <210>4123  
 <211>20  
 <212>DNA  
 <400>4123  
 ggcgctatca tttgtcagca 20  
 <210>4124  
 <211>20  
 <212>DNA  
 <400>4124  
 caaaactctc agaggctctc 20  
 <210>4125  
 <211>20  
 <212>DNA  
 <400>4125  
 gaggtatcga caaagccgta 20  
 <210>4126  
 <211>20  
 <212>DNA  
 <400>4126  
 cccaagtcac tgtaggaaga 20  
 <210>4127  
 <211>20  
 <212>DNA  
 <400>4127  
 gtgaaatcat ggccgtccta 20  
 <210>4128  
 <211>20  
 <212>DNA  
 <400>4128  
 actcctcaca acagaagcct 20  
 <210>4129  
 <211>20  
 <212>DNA  
 <400>4129  
 cgctttgtta tcgtgattgc 20  
 <210>4130  
 <211>20  
 <212>DNA  
 <400>4130  
 cgtgctgagg tccttgTTTT 20  
 <210>4131  
 <211>20  
 <212>DNA  
 <400>4131  
 ccgaattctc tccctctcat 20  
 <210>4132  
 <211>20  
 <212>DNA  
 <400>4132  
 ggtctgactt cccactcaat 20  
 <210>4133  
 <211>20  
 <212>DNA  
 <400>4133  
 gccacagaaa aagtaggtcc 20  
 <210>4134  
 <211>20  
 <212>DNA  
 <400>4134  
 gtcgacagct ctagaaagca 20  
 <210>4135  
 <211>20



<212>DNA  
<400>4135  
ggaggcatct caacaactga 20  
<210>4136  
<211>20  
<212>DNA  
<400>4136  
gccgaattac aacccccatt 20  
<210>4137  
<211>20  
<212>DNA  
<400>4137  
ccccctacaa gcaaaccaaa 20  
<210>4138  
<211>20  
<212>DNA  
<400>4138  
tggcaagcag gacaacttga 20  
<210>4139  
<211>20  
<212>DNA  
<400>4139  
ccaaccagct cttcccttta 20  
<210>4140  
<211>20  
<212>DNA  
<400>4140  
cgatatccaa gtgttacgtg 20  
<210>4141  
<211>20  
<212>DNA  
<400>4141  
ggagggttag tagaccctcg 20  
<210>4142  
<211>20  
<212>DNA  
<400>4142  
atgaaggaga atggcgccta 20  
<210>4143  
<211>20  
<212>DNA  
<400>4143  
cggtagtttt ttgcgtcctg 20  
<210>4144  
<211>20  
<212>DNA  
<400>4144  
gaggctgcta cacaagtaac 20  
<210>4145  
<211>20  
<212>DNA  
<400>4145  
ccaccttggtg cttgtcaaac 20  
<210>4146  
<211>20  
<212>DNA  
<400>4146  
gcacttcgag atttctagag 20  
<210>4147  
<211>20  
<212>DNA  
<400>4147  
ccataaaatt caccccaagc 20  
<210>4148

<211>20  
<212>DNA  
<400>4148  
ccttgtgctt gtcaaacata 20  
<210>4149  
<211>20  
<212>DNA  
<400>4149  
taccgaagct cagctacacg 20  
<210>4150  
<211>20  
<212>DNA  
<400>4150  
ggggatagga agcaagaatg 20  
<210>4151  
<211>20  
<212>DNA  
<400>4151  
gcgcattccga aagacttttc 20  
<210>4152  
<211>20  
<212>DNA  
<400>4152  
cccctaaaca tacgccgaat 20  
<210>4153  
<211>20  
<212>DNA  
<400>4153  
ccgagtaagg agatagctac 20  
<210>4154  
<211>20  
<212>DNA  
<400>4154  
ggccatgaac tgtctggaaa 20  
<210>4155  
<211>20  
<212>DNA  
<400>4155  
gggaaaatgc cttgaggaag 20  
<210>4156  
<211>20  
<212>DNA  
<400>4156  
cgttgctctc tcctctgtat 20  
<210>4157  
<211>20  
<212>DNA  
<400>4157  
cccgaacgac gctgtatacg 20  
<210>4158  
<211>20  
<212>DNA  
<400>4158  
cccttgatgat agagaatcct 20  
<210>4159  
<211>20  
<212>DNA  
<400>4159  
cagagattct aggacgatgc 20  
<210>4160  
<211>20  
<212>DNA  
<400>4160  
cccttgatgat agagaatcct 20

<210>4161  
 <211>20  
 <212>DNA  
 <400>4161  
 cagagattct aggacgatgc 20  
 <210>4162  
 <211>20  
 <212>DNA  
 <400>4162  
 gccccaggat tattacgatg 20  
 <210>4163  
 <211>20  
 <212>DNA  
 <400>4163  
 cccacaattc cggatagcag 20  
 <210>4164  
 <211>20  
 <212>DNA  
 <400>4164  
 ttccagaggg acgatctccg 20  
 <210>4165  
 <211>20  
 <212>DNA  
 <400>4165  
 gccgtcctgt ttagtcgaat 20  
 <210>4166  
 <211>20  
 <212>DNA  
 <400>4166  
 cacctgggac gctcgattcc 20  
 <210>4167  
 <211>20  
 <212>DNA  
 <400>4167  
 ccccttcact agagattgct 20  
 <210>4168  
 <211>20  
 <212>DNA  
 <400>4168  
 ttttccggtg gctatcgct 20  
 <210>4169  
 <211>20  
 <212>DNA  
 <400>4169  
 gcttctgaga tttcccactg 20  
 <210>4170  
 <211>20  
 <212>DNA  
 <400>4170  
 gcacgagctg atctcatatc 20  
 <210>4171  
 <211>20  
 <212>DNA  
 <400>4171  
 ggcgatgttg atctcctcat 20  
 <210>4172  
 <211>20  
 <212>DNA  
 <400>4172  
 ccctaacaca ggacacaact 20  
 <210>4173  
 <211>20  
 <212>DNA  
 <400>4173

gcgatctcgt tcacttttcc 20  
 <210>4174  
 <211>20  
 <212>DNA  
 <400>4174  
 gcttgaaagc ttcgatgttc 20  
 <210>4175  
 <211>20  
 <212>DNA  
 <400>4175  
 gatttaggaa acgacggcac 20  
 <210>4176  
 <211>20  
 <212>DNA  
 <400>4176  
 ccacgttcca ttttcttccc 20  
 <210>4177  
 <211>20  
 <212>DNA  
 <400>4177  
 gcctcacgca cttcttgatt 20  
 <210>4178  
 <211>20  
 <212>DNA  
 <400>4178  
 ctcttcgctg atatgcggag 20  
 <210>4179  
 <211>20  
 <212>DNA  
 <400>4179  
 caggacgtac tttaagtctg 20  
 <210>4180  
 <211>20  
 <212>DNA  
 <400>4180  
 agaagcaaac gaacttcccc 20  
 <210>4181  
 <211>20  
 <212>DNA  
 <400>4181  
 ggtgggtgttg gaataccatc 20  
 <210>4182  
 <211>20  
 <212>DNA  
 <400>4182  
 ggtaggaaat tttggctaag 20  
 <210>4183  
 <211>20  
 <212>DNA  
 <400>4183  
 ctataccatg gcctaaactc 20  
 <210>4184  
 <211>20  
 <212>DNA  
 <400>4184  
 ggctgttggt tctacagcag 20  
 <210>4185  
 <211>20  
 <212>DNA  
 <400>4185  
 gcaggattcc cttccaactt 20  
 <210>4186  
 <211>20  
 <212>DNA

<400>4186  
ggaggtccat atggacctat 20  
<210>4187  
<211>20  
<212>DNA  
<400>4187  
caactgagtg aacagcttgc 20  
<210>4188  
<211>20  
<212>DNA  
<400>4188  
ggctatccgc tacttcttac 20  
<210>4189  
<211>20  
<212>DNA  
<400>4189  
ccctccagag ttgcaaaaac 20  
<210>4190  
<211>20  
<212>DNA  
<400>4190  
gatgcaaagg aacggctctt 20  
<210>4191  
<211>20  
<212>DNA  
<400>4191  
tatgcctagt gctcgcaatc 20  
<210>4192  
<211>20  
<212>DNA  
<400>4192  
tgctcgcaat ctccctccaa 20  
<210>4193  
<211>20  
<212>DNA  
<400>4193  
gtgtcgctgg tgtaggggta 20  
<210>4194  
<211>20  
<212>DNA  
<400>4194  
ctcaaggacc agacaatcct 20  
<210>4195  
<211>20  
<212>DNA  
<400>4195  
ctacagggtca ttgtcatctc 20  
<210>4196  
<211>20  
<212>DNA  
<400>4196  
gcggctcttc gaactacaaa 20  
<210>4197  
<211>20  
<212>DNA  
<400>4197  
ggcgtgagat aaccatcttg 20  
<210>4198  
<211>20  
<212>DNA  
<400>4198  
tctggggagc gcaatctctg 20  
<210>4199  
<211>20

<212>DNA  
 <400>4199  
 cgtactccga ttagccctat 20  
 <210>4200  
 <211>20  
 <212>DNA  
 <400>4200  
 cccccacaat tagagttagg 20  
 <210>4201  
 <211>20  
 <212>DNA  
 <400>4201  
 gcagcaaaac gaagacaacc 20  
 <210>4202  
 <211>20  
 <212>DNA  
 <400>4202  
 ggcagaaaag aggtgcatct 20  
 <210>4203  
 <211>20  
 <212>DNA  
 <400>4203  
 gcggaagaca ataatcgctc 20  
 <210>4204  
 <211>20  
 <212>DNA  
 <400>4204  
 ggaaggatcc cagctacaaa 20  
 <210>4205  
 <211>20  
 <212>DNA  
 <400>4205  
 agaggaaaga cctgtctagc 20  
 <210>4206  
 <211>20  
 <212>DNA  
 <400>4206  
 cgttttagctg caaccgtaga 20  
 <210>4207  
 <211>20  
 <212>DNA  
 <400>4207  
 cgagtgactt tctcgtctct 20  
 <210>4208  
 <211>20  
 <212>DNA  
 <400>4208  
 gcagcaaaac gaagacaacc 20  
 <210>4209  
 <211>20  
 <212>DNA  
 <400>4209  
 cgtgcttcgc aaacgttttc 20  
 <210>4210  
 <211>20  
 <212>DNA  
 <400>4210  
 ggcttaggggt tattaagccg 20  
 <210>4211  
 <211>20  
 <212>DNA  
 <400>4211  
 tgggaccata acacctcaat 20  
 <210>4212

<211>20  
 <212>DNA  
 <400>4212  
 gggaggggtgt ctcattaaat 20  
 <210>4213  
 <211>20  
 <212>DNA  
 <400>4213  
 ggacatgcct ccgaagtaat 20  
 <210>4214  
 <211>20  
 <212>DNA  
 <400>4214  
 ccatagcatt acgtgctgta 20  
 <210>4215  
 <211>20  
 <212>DNA  
 <400>4215  
 cgctataggc attggtcctt 20  
 <210>4216  
 <211>20  
 <212>DNA  
 <400>4216  
 gttcctgggg gagttgaagg 20  
 <210>4217  
 <211>20  
 <212>DNA  
 <400>4217  
 ccctgatcca aactcgagat 20  
 <210>4218  
 <211>20  
 <212>DNA  
 <400>4218  
 gcatacatgg aagaagcctt 20  
 <210>4219  
 <211>20  
 <212>DNA  
 <400>4219  
 gctgttgagt gtgtgactgt 20  
 <210>4220  
 <211>20  
 <212>DNA  
 <400>4220  
 gagtgctgtc gtcgtatatac 20  
 <210>4221  
 <211>20  
 <212>DNA  
 <400>4221  
 cctcgacttg gagataagac 20  
 <210>4222  
 <211>20  
 <212>DNA  
 <400>4222  
 acgcaagaac tggcacctat 20  
 <210>4223  
 <211>20  
 <212>DNA  
 <400>4223  
 gagtggggaa aagataggga 20  
 <210>4224  
 <211>20  
 <212>DNA  
 <400>4224  
 ccaagtctgt gagtgtcatc 20

<210>4225  
<211>20  
<212>DNA  
<400>4225  
cctcagggga atccttttgt 20  
<210>4226  
<211>20  
<212>DNA  
<400>4226  
gattcttggc gtccaacctt 20  
<210>4227  
<211>20  
<212>DNA  
<400>4227  
cttggatctc tttcctcctg 20  
<210>4228  
<211>20  
<212>DNA  
<400>4228  
ggaaagcgtt tcttcctctg 20  
<210>4229  
<211>20  
<212>DNA  
<400>4229  
ggctatggta cgtagaacac 20  
<210>4230  
<211>20  
<212>DNA  
<400>4230  
gaatctcggg gtgctttcat 20  
<210>4231  
<211>20  
<212>DNA  
<400>4231  
ccatctccag gtcgtttaga 20  
<210>4232  
<211>20  
<212>DNA  
<400>4232  
acaaccagca agccgcgtta 20  
<210>4233  
<211>20  
<212>DNA  
<400>4233  
tatagagcgt tttctgccgc 20  
<210>4234  
<211>20  
<212>DNA  
<400>4234  
ggctatggta cgtagaacac 20  
<210>4235  
<211>20  
<212>DNA  
<400>4235  
gcctcaagca gcaaagtctt 20  
<210>4236  
<211>20  
<212>DNA  
<400>4236  
agctcggagg ctttttctaatt 20  
<210>4237  
<211>20  
<212>DNA  
<400>4237



## WO 99/27105

```

agggggaatag acaagagcct      20
<210>4238
<211>20
<212>DNA
<400>4238
ctacaacaag ttccggagac      20
<210>4239
<211>20
<212>DNA
<400>4239
cctttcttgc tgaggatcca      20
<210>4240
<211>20
<212>DNA
<400>4240
gactgtctct gcaatggtct      20
<210>4241
<211>20
<212>DNA
<400>4241
ctcttctaag tcctcagcag      20
<210>4242
<211>20
<212>DNA
<400>4242
cgggatttac aggacagagc      20
<210>4243
<211>20
<212>DNA
<400>4243
cagccttctg agcttcttgt      20
<210>4244
<211>20
<212>DNA
<400>4244
gtataggagg ttagaatcac      20
<210>4245
<211>20
<212>DNA
<400>4245
aggcgtttgc taagatctgc      20
<210>4246
<211>20
<212>DNA
<400>4246
cccaagaggt ttctctctta      20
<210>4247
<211>20
<212>DNA
<400>4247
caggctggta cccattgtta      20
<210>4248
<211>20
<212>DNA
<400>4248
agcatctcca gcgtttgctt      20
<210>4249
<211>20
<212>DNA
<400>4249
ccacaatagc tacgattggc      20
<210>4250
<211>20
<212>DNA

```

<400>4250  
gacgttgctt ctgacctgtt 20  
<210>4251  
<211>20  
<212>DNA  
<400>4251  
tcccagaaag gggaagctat 20  
<210>4252  
<211>20  
<212>DNA  
<400>4252  
ggaacacaag taagcaaacc 20  
<210>4253  
<211>20  
<212>DNA  
<400>4253  
ggccttgaag cttcatttga 20  
<210>4254  
<211>20  
<212>DNA  
<400>4254  
ccgtcgaagt cgaatttctc 20  
<210>4255  
<211>20  
<212>DNA  
<400>4255  
ctgggctcac ttcccactgg 20  
<210>4256  
<211>20  
<212>DNA  
<400>4256  
gggagttgtg cttgtttag 20  
<210>4257  
<211>20  
<212>DNA  
<400>4257  
gtcgaaggcgc ttacaaatga 20  
<210>4258  
<211>20  
<212>DNA  
<400>4258  
tatctctcca gaaccctgga 20  
<210>4259  
<211>20  
<212>DNA  
<400>4259  
cttgagcgat gcgttagtgt 20  
<210>4260  
<211>20  
<212>DNA  
<400>4260  
cgaagagggt atgtgaatcc 20  
<210>4261  
<211>20  
<212>DNA  
<400>4261  
gggaagcttc catcgtaga 20  
<210>4262  
<211>20  
<212>DNA  
<400>4262  
cgatttctgc attgggggtt 20  
<210>4263  
<211>20

<212>DNA  
<400>4263  
cgaaaccttg cctactctgt 20  
<210>4264  
<211>20  
<212>DNA  
<400>4264  
ggcatcgttc cgacatcttt 20  
<210>4265  
<211>20  
<212>DNA  
<400>4265  
gttggcctgt tgtagagctt 20  
<210>4266  
<211>20  
<212>DNA  
<400>4266  
gaatccgcaa tggttttggg 20  
<210>4267  
<211>20  
<212>DNA  
<400>4267  
catagttag caggggggaa 20  
<210>4268  
<211>20  
<212>DNA  
<400>4268  
gtaattcgta cggttcctgg 20  
<210>4269  
<211>20  
<212>DNA  
<400>4269  
ggattgcagg gttctttgag 20  
<210>4270  
<211>20  
<212>DNA  
<400>4270  
gcaagttcag gaacgactcc 20  
<210>4271  
<211>20  
<212>DNA  
<400>4271  
gcgttggtgcc atctcttggt 20  
<210>4272  
<211>20  
<212>DNA  
<400>4272  
ccgtccgagg aaagagagta 20  
<210>4273  
<211>20  
<212>DNA  
<400>4273  
cggactccta gattttctgg 20  
<210>4274  
<211>20  
<212>DNA  
<400>4274  
cagcgaagaa acggagcata 20  
<210>4275  
<211>20  
<212>DNA  
<400>4275  
gctccataaa gcgctgtctt 20  
<210>4276

<211>20  
<212>DNA  
<400>4276  
gttgggcaat agaaagggtcc 20  
<210>4277  
<211>20  
<212>DNA  
<400>4277  
gttgctcttag ggtaatcacc 20  
<210>4278  
<211>20  
<212>DNA  
<400>4278  
ggtcggagtc cgtggtggat 20  
<210>4279  
<211>20  
<212>DNA  
<400>4279  
cttgaagtag acctcagctc 20  
<210>4280  
<211>20  
<212>DNA  
<400>4280  
cttgaagtag acctcagctc 20  
<210>4281  
<211>20  
<212>DNA  
<400>4281  
atccatgaga tccctcttcg 20  
<210>4282  
<211>20  
<212>DNA  
<400>4282  
cgagcatgga gagacaagaa 20  
<210>4283  
<211>20  
<212>DNA  
<400>4283  
gggaggttca caagatcaag 20  
<210>4284  
<211>20  
<212>DNA  
<400>4284  
ccgactagag caagatttcg 20  
<210>4285  
<211>20  
<212>DNA  
<400>4285  
gaaggcgagg gttcttttag 20  
<210>4286  
<211>20  
<212>DNA  
<400>4286  
accttacgtg ctctggggat 20  
<210>4287  
<211>20  
<212>DNA  
<400>4287  
ttgtgaagat ttggtagccc 20  
<210>4288  
<211>20  
<212>DNA  
<400>4288  
gaagcaagaa cattatgggg 20

<210>4289  
 <211>20  
 <212>DNA  
 <400>4289  
 gcgtgtggag tatcatcttc 20  
 <210>4290  
 <211>20  
 <212>DNA  
 <400>4290  
 ggagttctct tagacagact 20  
 <210>4291  
 <211>20  
 <212>DNA  
 <400>4291  
 ggtgggtaga gtttgtagag 20  
 <210>4292  
 <211>20  
 <212>DNA  
 <400>4292  
 gtgtgagtag tagtgtggag 20  
 <210>4293  
 <211>20  
 <212>DNA  
 <400>4293  
 tatttacgaa cccacgagg 20  
 <210>4294  
 <211>20  
 <212>DNA  
 <400>4294  
 gctccgaacc agatgaatgt 20  
 <210>4295  
 <211>20  
 <212>DNA  
 <400>4295  
 gaccaggtgg atgagtagtt 20  
 <210>4296  
 <211>20  
 <212>DNA  
 <400>4296  
 tcctgccata gcagtgagga 20  
 <210>4297  
 <211>20  
 <212>DNA  
 <400>4297  
 gctgagcgtc ccataagttt 20  
 <210>4298  
 <211>20  
 <212>DNA  
 <400>4298  
 ggctaaagtc aatgggattc 20  
 <210>4299  
 <211>20  
 <212>DNA  
 <400>4299  
 agtgcaccag ttgtggcttg 20  
 <210>4300  
 <211>20  
 <212>DNA  
 <400>4300  
 ggttgatcga cgctctcttt 20  
 <210>4301  
 <211>20  
 <212>DNA  
 <400>4301

ccaatgtaca ggcctcttct 20  
 <210>4302  
 <211>20  
 <212>DNA  
 <400>4302  
 ggggctgttt agttatgagg 20  
 <210>4303  
 <211>20  
 <212>DNA  
 <400>4303  
 cagagaagac ctttggtgct 20  
 <210>4304  
 <211>20  
 <212>DNA  
 <400>4304  
 ccaatgtaca ggcctcttct 20  
 <210>4305  
 <211>20  
 <212>DNA  
 <400>4305  
 ctccagttca gaggtgctat 20  
 <210>4306  
 <211>20  
 <212>DNA  
 <400>4306  
 ggctgtggag gattgtattg 20  
 <210>4307  
 <211>20  
 <212>DNA  
 <400>4307  
 agaaagtccg gcacgtcttt 20  
 <210>4308  
 <211>20  
 <212>DNA  
 <400>4308  
 aggaattccc agattagagc 20  
 <210>4309  
 <211>20  
 <212>DNA  
 <400>4309  
 ccgaagttat aggagggaac 20  
 <210>4310  
 <211>20  
 <212>DNA  
 <400>4310  
 gcacgtattc gcaagactct 20  
 <210>4311  
 <211>20  
 <212>DNA  
 <400>4311  
 cttggaaatc cttcccagtc 20  
 <210>4312  
 <211>20  
 <212>DNA  
 <400>4312  
 ggggatcttc ttctgtttgg 20  
 <210>4313  
 <211>20  
 <212>DNA  
 <400>4313  
 cgtcaciaaag attgctgacc 20  
 <210>4314  
 <211>20  
 <212>DNA

<400>4314  
 tgagtgcgat ttctgagcgt 20  
 <210>4315  
 <211>20  
 <212>DNA  
 <400>4315  
 aggcgctggt aggtacaata 20  
 <210>4316  
 <211>20  
 <212>DNA  
 <400>4316  
 cagagaaagt ctggaatcca 20  
 <210>4317  
 <211>20  
 <212>DNA  
 <400>4317  
 gaaccatgcg ccttcatcag 20  
 <210>4318  
 <211>20  
 <212>DNA  
 <400>4318  
 gccgatccat cctagagata 20  
 <210>4319  
 <211>20  
 <212>DNA  
 <400>4319  
 gaatatcggc gttggagtag 20  
 <210>4320  
 <211>20  
 <212>DNA  
 <400>4320  
 gaccctagct tgggatttct 20  
 <210>4321  
 <211>20  
 <212>DNA  
 <400>4321  
 gctacgtata ggtacttcgt 20  
 <210>4322  
 <211>20  
 <212>DNA  
 <400>4322  
 gaatatcggc gttggagtag 20  
 <210>4323  
 <211>20  
 <212>DNA  
 <400>4323  
 ccagactttt gcatgttgcg 20  
 <210>4324  
 <211>20  
 <212>DNA  
 <400>4324  
 cgctattgtg ggagggaaga 20  
 <210>4325  
 <211>20  
 <212>DNA  
 <400>4325  
 ccgtaggcgt ggattaattg 20  
 <210>4326  
 <211>20  
 <212>DNA  
 <400>4326  
 ggagaactgc ttgtgccata 20  
 <210>4327  
 <211>20

```

<212>DNA
<400>4327
cgggttttttg gggaactgct      20
<210>4328
<211>20
<212>DNA
<400>4328
ggttcggttaa tccctcgaga      20
<210>4329
<211>20
<212>DNA
<400>4329
tagggtagac gattctaggc      20
<210>4330
<211>20
<212>DNA
<400>4330
cagaatggag cgaatgatcg      20
<210>4331
<211>20
<212>DNA
<400>4331
gctgtagtcg gagactactt      20
<210>4332
<211>20
<212>DNA
<400>4332
ggttggtgggg ttggtggttg      20
<210>4333
<211>20
<212>DNA
<400>4333
gcagctcaag cattgctatg      20
<210>4334
<211>20
<212>DNA
<400>4334
ggctgccatt tgctgttgaa      20
<210>4335
<211>20
<212>DNA
<400>4335
ccaagaaatg cagggaggat      20
<210>4336
<211>20
<212>DNA
<400>4336
cttacaaagt tggctgaggg      20
<210>4337
<211>20
<212>DNA
<400>4337
gttaggcacg taagcttctc      20
<210>4338
<211>20
<212>DNA
<400>4338
ccttcttggt ctgcttggtgc      20
<210>4339
<211>20
<212>DNA
<400>4339
ctacatagaa tctcagggtgc      20
<210>4340

```



## WO 99/27105

```

<211>20
<212>DNA
<400>4340
ccaagaaatg cagggaggat      20
<210>4341
<211>20
<212>DNA
<400>4341
ctggatcctt caatgagacc      20
<210>4342
<211>20
<212>DNA
<400>4342
cgagcagaga gtatacagtc      20
<210>4343
<211>20
<212>DNA
<400>4343
gacgttgcct atatgcagca      20
<210>4344
<211>20
<212>DNA
<400>4344
cttcccaaga cagagtgtgt      20
<210>4345
<211>20
<212>DNA
<400>4345
ctagtctcca aatcgcggtt      20
<210>4346
<211>20
<212>DNA
<400>4346
gttaggcacg taagcttctc      20
<210>4347
<211>20
<212>DNA
<400>4347
tagtgtcagc ggcgctgttt      20
<210>4348
<211>20
<212>DNA
<400>4348
caggtgctag tacctgagta      20
<210>4349
<211>20
<212>DNA
<400>4349
gcagatgtga ggcctttctt      20
<210>4350
<211>20
<212>DNA
<400>4350
gcagctcagt gcttgtcttt      20
<210>4351
<211>20
<212>DNA
<400>4351
caaggactat gtttttgggc      20
<210>4352
<211>20
<212>DNA
<400>4352
gataccttgc tcaagagtgt      20

```

<210>4353  
<211>20  
<212>DNA  
<400>4353  
ggagtcgaag ctaaattctgg 20  
<210>4354  
<211>20  
<212>DNA  
<400>4354  
cgttcaagag attgggatct 20  
<210>4355  
<211>20  
<212>DNA  
<400>4355  
cgттаagccg ttgacgttct 20  
<210>4356  
<211>20  
<212>DNA  
<400>4356  
gcgtgcgggc aaaactccaa 20  
<210>4357  
<211>20  
<212>DNA  
<400>4357  
ggggtccatt tctagggaa 20  
<210>4358  
<211>20  
<212>DNA  
<400>4358  
cgттаagccg ttgacgttct 20  
<210>4359  
<211>20  
<212>DNA  
<400>4359  
gccaggggaat ctgtttttcc 20  
<210>4360  
<211>20  
<212>DNA  
<400>4360  
cttcctcttg cagagatgag 20  
<210>4361  
<211>20  
<212>DNA  
<400>4361  
gttgccatag tctcaatccc 20  
<210>4362  
<211>20  
<212>DNA  
<400>4362  
agtgaggtga tatagagcgg 20  
<210>4363  
<211>20  
<212>DNA  
<400>4363  
gaccatcttc tcctagtcct 20  
<210>4364  
<211>20  
<212>DNA  
<400>4364  
cataacttct atcccccccc 20  
<210>4365  
<211>20  
<212>DNA  
<400>4365

## WO 99/27105

cgacatgatg atgacagggg	20
<210>4366	
<211>20	
<212>DNA	
<400>4366	
gttgccatag tctcaatccc	20
<210>4367	
<211>20	
<212>DNA	
<400>4367	
ttcagtgggtg cgcagtaact	20
<210>4368	
<211>20	
<212>DNA	
<400>4368	
gttctcgacc atctcagcat	20
<210>4369	
<211>20	
<212>DNA	
<400>4369	
ccgcctcaca atctacaatc	20
<210>4370	
<211>20	
<212>DNA	
<400>4370	
taggaccgac attaggtgcc	20
<210>4371	
<211>20	
<212>DNA	
<400>4371	
aggaaactct tcttccttgc	20
<210>4372	
<211>20	
<212>DNA	
<400>4372	
gctgagagcc cttagctaaa	20
<210>4373	
<211>20	
<212>DNA	
<400>4373	
gctgtagttt gtgcagttgt	20
<210>4374	
<211>20	
<212>DNA	
<400>4374	
gcaataggca agctgtagtt	20
<210>4375	
<211>20	
<212>DNA	
<400>4375	
agaggggggaa gggttagaat	20
<210>4376	
<211>20	
<212>DNA	
<400>4376	
ccgcctcaca atctacaatc	20
<210>4377	
<211>20	
<212>DNA	
<400>4377	
ggcttgaacg gggaaatagt	20
<210>4378	
<211>20	
<212>DNA	

<400>4378  
gacagaaggc gaacatcact 20  
<210>4379  
<211>20  
<212>DNA  
<400>4379  
ccttctcgga ataatcgctc 20  
<210>4380  
<211>20  
<212>DNA  
<400>4380  
ggaaccgcaa ttcacggatt 20  
<210>4381  
<211>20  
<212>DNA  
<400>4381  
catagcttcc ctaagctgtc 20  
<210>4382  
<211>20  
<212>DNA  
<400>4382  
tctcctgctt atcaagtggg 20  
<210>4383  
<211>20  
<212>DNA  
<400>4383  
ctccccatac atagggaaag 20  
<210>4384  
<211>20  
<212>DNA  
<400>4384  
catggaccaa taacaagtag 20  
<210>4385  
<211>20  
<212>DNA  
<400>4385  
agccccagat ggtgttcata 20  
<210>4386  
<211>20  
<212>DNA  
<400>4386  
caggcttggc tttgcagttt 20  
<210>4387  
<211>20  
<212>DNA  
<400>4387  
ccagaactcg cttaggaaag 20  
<210>4388  
<211>20  
<212>DNA  
<400>4388  
gggcttccat aacagctcat 20  
<210>4389  
<211>20  
<212>DNA  
<400>4389  
ctagggaagg agtcttatcc 20  
<210>4390  
<211>20  
<212>DNA  
<400>4390  
caagggcagg taattgctac 20  
<210>4391  
<211>20

WO 99/27105

<212>DNA  
 <400>4391  
 ggggacatca tcacgaagtt 20  
 <210>4392  
 <211>20  
 <212>DNA  
 <400>4392  
 ctggagctaa gaaaggccaa 20  
 <210>4393  
 <211>20  
 <212>DNA  
 <400>4393  
 ggggatacag gagtttttag 20  
 <210>4394  
 <211>20  
 <212>DNA  
 <400>4394  
 ctagggaagg agtccttatcc 20  
 <210>4395  
 <211>20  
 <212>DNA  
 <400>4395  
 gtcgaccctt atgacccctga 20  
 <210>4396  
 <211>20  
 <212>DNA  
 <400>4396  
 gtggagtgggt tataggaacg 20  
 <210>4397  
 <211>20  
 <212>DNA  
 <400>4397  
 gggttgaagt catgcatcca 20  
 <210>4398  
 <211>20  
 <212>DNA  
 <400>4398  
 cgttaggggg aagaactgta 20  
 <210>4399  
 <211>20  
 <212>DNA  
 <400>4399  
 ccatcactca cttcatcagg 20  
 <210>4400  
 <211>20  
 <212>DNA  
 <400>4400  
 aaaggactca tccatggcaa 20  
 <210>4401  
 <211>20  
 <212>DNA  
 <400>4401  
 gggagtcaat gtaccttgga 20  
 <210>4402  
 <211>20  
 <212>DNA  
 <400>4402  
 gggagcttct tttggtagca 20  
 <210>4403  
 <211>20  
 <212>DNA  
 <400>4403  
 ctgtaggggg aaatactgcg 20  
 <210>4404

<211>20  
<212>DNA  
<400>4404  
cagcacttac tattggtcag 20  
<210>4405  
<211>20  
<212>DNA  
<400>4405  
cttacggtta ttcacactca 20  
<210>4406  
<211>20  
<212>DNA  
<400>4406  
cggagataat tctgccactc 20  
<210>4407  
<211>20  
<212>DNA  
<400>4407  
ggagggagga taaatgtcac 20  
<210>4408  
<211>20  
<212>DNA  
<400>4408  
gtacactggg gacctcaata 20  
<210>4409  
<211>20  
<212>DNA  
<400>4409  
ttgctacccc ccctcatgat 20  
<210>4410  
<211>20  
<212>DNA  
<400>4410  
gttgccctgc cttacgttga 20  
<210>4411  
<211>20  
<212>DNA  
<400>4411  
gaggggtattc aacgataggg 20  
<210>4412  
<211>20  
<212>DNA  
<400>4412  
gggcaacata gtggacttga 20  
<210>4413  
<211>20  
<212>DNA  
<400>4413  
tttgggggtg tcgcatagtg 20  
<210>4414  
<211>20  
<212>DNA  
<400>4414  
atggaacaat gttgtgcggg 20  
<210>4415  
<211>20  
<212>DNA  
<400>4415  
ctttcatcca cggaggattt 20  
<210>4416  
<211>20  
<212>DNA  
<400>4416  
ggcgccttcc tcaataacaa 20

## WO 99/27105

<210>4417  
 <211>20  
 <212>DNA  
 <400>4417  
 ccttgcttga gagcatggat 20  
 <210>4418  
 <211>20  
 <212>DNA  
 <400>4418  
 cccccacttc tttttcttca 20  
 <210>4419  
 <211>20  
 <212>DNA  
 <400>4419  
 gcagagacta ggcaactcat 20  
 <210>4420  
 <211>20  
 <212>DNA  
 <400>4420  
 gcttttcatcc acggaggatt 20  
 <210>4421  
 <211>20  
 <212>DNA  
 <400>4421  
 ggtcgaaccc gcaacttccg 20  
 <210>4422  
 <211>20  
 <212>DNA  
 <400>4422  
 gcagagacta ggcaactcat 20  
 <210>4423  
 <211>20  
 <212>DNA  
 <400>4423  
 gctgagggat cttctctatg 20  
 <210>4424  
 <211>20  
 <212>DNA  
 <400>4424  
 tcccgcaaatt ggacacgaca 20  
 <210>4425  
 <211>20  
 <212>DNA  
 <400>4425  
 gtgggtatgg taatagctgc 20  
 <210>4426  
 <211>20  
 <212>DNA  
 <400>4426  
 tgtccctaga gagacccctt 20  
 <210>4427  
 <211>20  
 <212>DNA  
 <400>4427  
 ggtaacagtg catgcgaaag 20  
 <210>4428  
 <211>20  
 <212>DNA  
 <400>4428  
 cggtgaaaag aaagccgttg 20  
 <210>4429  
 <211>20  
 <212>DNA  
 <400>4429

tggtatacca tcttctcccc	20
<210>4430	
<211>20	
<212>DNA	
<400>4430	
ctgatgcaca agaactaccc	20
<210>4431	
<211>20	
<212>DNA	
<400>4431	
accctgccaa tcccccaaca	20
<210>4432	
<211>20	
<212>DNA	
<400>4432	
gattgagaag ggcattgggt	20
<210>4433	
<211>20	
<212>DNA	
<400>4433	
cacagaagct cctaagagac	20
<210>4434	
<211>20	
<212>DNA	
<400>4434	
cattcgggtgt agatgtgcct	20
<210>4435	
<211>20	
<212>DNA	
<400>4435	
agcaccgcaa tcctagattc	20
<210>4436	
<211>20	
<212>DNA	
<400>4436	
ctttcttctc gggctgagaa	20
<210>4437	
<211>20	
<212>DNA	
<400>4437	
ttcaagtggc gtagtcaata	20
<210>4438	
<211>20	
<212>DNA	
<400>4438	
ctttcttctc gggctgagaa	20
<210>4439	
<211>20	
<212>DNA	
<400>4439	
ttcaagtggc gtagtcaata	20
<210>4440	
<211>20	
<212>DNA	
<400>4440	
gtcacatgcc ttttcgaagc	20
<210>4441	
<211>20	
<212>DNA	
<400>4441	
gctcctagag ctatatcgag	20
<210>4442	
<211>20	
<212>DNA	



<400>4442  
 gcgggttttgt gcggattcta 20  
 <210>4443  
 <211>20  
 <212>DNA  
 <400>4443  
 gcaacttggg ttatgcacct 20  
 <210>4444  
 <211>20  
 <212>DNA  
 <400>4444  
 tttgtcttca agtggcgtag 20  
 <210>4445  
 <211>20  
 <212>DNA  
 <400>4445  
 gacctacacc tttccttcct 20  
 <210>4446  
 <211>20  
 <212>DNA  
 <400>4446  
 gctcctagag ctatatcgag 20  
 <210>4447  
 <211>20  
 <212>DNA  
 <400>4447  
 caccaaactgt ggtggttga 20  
 <210>4448  
 <211>20  
 <212>DNA  
 <400>4448  
 gccgaccttt gttctaaggt 20  
 <210>4449  
 <211>20  
 <212>DNA  
 <400>4449  
 gctctacaag ttcaccgatg 20  
 <210>4450  
 <211>20  
 <212>DNA  
 <400>4450  
 ctgttacgga tcacgacagt 20  
 <210>4451  
 <211>20  
 <212>DNA  
 <400>4451  
 ctggtcttac ccatagtgt 20  
 <210>4452  
 <211>20  
 <212>DNA  
 <400>4452  
 ggtataaagg tcttgagag 20  
 <210>4453  
 <211>20  
 <212>DNA  
 <400>4453  
 gtccttcacg ctggaggaaa 20  
 <210>4454  
 <211>20  
 <212>DNA  
 <400>4454  
 gggatgtctc aagctatagg 20  
 <210>4455  
 <211>20

<212>DNA  
<400>4455  
ggggcgctcgt gtatttaaagt 20  
<210>4456  
<211>20  
<212>DNA  
<400>4456  
acagccccta aaaagggatt 20  
<210>4457  
<211>20  
<212>DNA  
<400>4457  
tggttcctctc actatcggag 20  
<210>4458  
<211>20  
<212>DNA  
<400>4458  
cagcaaacct ttctccaaag 20  
<210>4459  
<211>20  
<212>DNA  
<400>4459  
catgacgcct atccaggaaa 20  
<210>4460  
<211>20  
<212>DNA  
<400>4460  
ctgaaagcta tccacagctc 20  
<210>4461  
<211>20  
<212>DNA  
<400>4461  
ccagggtatt gtcaaggaac 20  
<210>4462  
<211>20  
<212>DNA  
<400>4462  
gcagaagaca gggaagaagt 20  
<210>4463  
<211>20  
<212>DNA  
<400>4463  
ggattgcgta gatagcacca 20  
<210>4464  
<211>20  
<212>DNA  
<400>4464  
cgtcaccaag aagttcgtct 20  
<210>4465  
<211>20  
<212>DNA  
<400>4465  
ggaagaagat ttccccaaga 20  
<210>4466  
<211>20  
<212>DNA  
<400>4466  
gaggcttgaa agaagcaagc 20  
<210>4467  
<211>20  
<212>DNA  
<400>4467  
ctcctacttt cagggttggtg 20  
<210>4468

<211>20  
<212>DNA  
<400>4468  
gctctactgg aatcagagga 20  
<210>4469  
<211>20  
<212>DNA  
<400>4469  
aaggcgcat tagaagcagg 20  
<210>4470  
<211>20  
<212>DNA  
<400>4470  
gaagctccag gagaagagat 20  
<210>4471  
<211>20  
<212>DNA  
<400>4471  
ccccaccaa gaccttgaaa 20  
<210>4472  
<211>20  
<212>DNA  
<400>4472  
gagtagggaa gaagactctc 20  
<210>4473  
<211>20  
<212>DNA  
<400>4473  
ccttctcatt gtctcctgtg 20  
<210>4474  
<211>20  
<212>DNA  
<400>4474  
gagaatccca agtgtcagac 20  
<210>4475  
<211>20  
<212>DNA  
<400>4475  
cctggctttt ggtgactcta 20  
<210>4476  
<211>20  
<212>DNA  
<400>4476  
gggagcttct ctcacagcta 20  
<210>4477  
<211>20  
<212>DNA  
<400>4477  
gaagccacaa tcgatgaagc 20  
<210>4478  
<211>20  
<212>DNA  
<400>4478  
gtgtgtttag gtaagcttgc 20  
<210>4479  
<211>20  
<212>DNA  
<400>4479  
gtgggtaaga acaccttcta 20  
<210>4480  
<211>20  
<212>DNA  
<400>4480  
gcagcctttt ctaaagggga 20

<210>4481  
<211>20  
<212>DNA  
<400>4481  
ctctagccag gttgagaaag 20  
<210>4482  
<211>20  
<212>DNA  
<400>4482  
gtaatggtgg agccgagagc 20  
<210>4483  
<211>20  
<212>DNA  
<400>4483  
ctccaggcaa acgggtaaata 20  
<210>4484  
<211>20  
<212>DNA  
<400>4484  
ccctatagga gctttcttgg 20  
<210>4485  
<211>20  
<212>DNA  
<400>4485  
gcaaccgagg ttgaagctat 20  
<210>4486  
<211>20  
<212>DNA  
<400>4486  
gccatagact aaagctgcgt 20  
<210>4487  
<211>20  
<212>DNA  
<400>4487  
gggatgaaag aacgcaaagg 20  
<210>4488  
<211>20  
<212>DNA  
<400>4488  
ctagttcggg tacctgttgg 20  
<210>4489  
<211>20  
<212>DNA  
<400>4489  
ctctgtagca atcgctagca 20  
<210>4490  
<211>20  
<212>DNA  
<400>4490  
gctcctccta cttgaaggat 20  
<210>4491  
<211>20  
<212>DNA  
<400>4491  
ctggggtggt taagatgagc 20  
<210>4492  
<211>20  
<212>DNA  
<400>4492  
gagagtgccg taacaaccta 20  
<210>4493  
<211>20  
<212>DNA  
<400>4493

ccaatcatag cctcagcata 20  
 <210>4494  
 <211>20  
 <212>DNA  
 <400>4494  
 gcctccacaa tggtttaaga 20  
 <210>4495  
 <211>20  
 <212>DNA  
 <400>4495  
 gtcttggtac ttttgctcag 20  
 <210>4496  
 <211>20  
 <212>DNA  
 <400>4496  
 ggagtggatc caaaagaagt 20  
 <210>4497  
 <211>20  
 <212>DNA  
 <400>4497  
 gtaggtatgg gacaagacct 20  
 <210>4498  
 <211>20  
 <212>DNA  
 <400>4498  
 cctcgagtt atcgagctat 20  
 <210>4499  
 <211>20  
 <212>DNA  
 <400>4499  
 ggcaggcatt caggaagagg 20  
 <210>4500  
 <211>20  
 <212>DNA  
 <400>4500  
 gtgtcacacg tggtaggaaa 20  
 <210>4501  
 <211>20  
 <212>DNA  
 <400>4501  
 ctgtcccaag agatgagttc 20  
 <210>4502  
 <211>20  
 <212>DNA  
 <400>4502  
 caggcattca ggaagaggat 20  
 <210>4503  
 <211>20  
 <212>DNA  
 <400>4503  
 ccaccacatg gccttcttta 20  
 <210>4504  
 <211>20  
 <212>DNA  
 <400>4504  
 ggggcctaaa ttaaggttag 20  
 <210>4505  
 <211>20  
 <212>DNA  
 <400>4505  
 cgaccctcga tcaatatcca 20  
 <210>4506  
 <211>20  
 <212>DNA

<400>4506  
 gactacgctc actagcaaca 20  
 <210>4507  
 <211>20  
 <212>DNA  
 <400>4507  
 gagacccttc acttacctca 20  
 <210>4508  
 <211>20  
 <212>DNA  
 <400>4508  
 tttcccgtcc taacaccggg 20  
 <210>4509  
 <211>20  
 <212>DNA  
 <400>4509  
 ctgcagcaga gacaaatcct 20  
 <210>4510  
 <211>20  
 <212>DNA  
 <400>4510  
 ccgataggct ttccatgtaa 20  
 <210>4511  
 <211>20  
 <212>DNA  
 <400>4511  
 ggactcaagc gtagtggaag 20  
 <210>4512  
 <211>20  
 <212>DNA  
 <400>4512  
 gcatgttgca ttgcctgaga 20  
 <210>4513  
 <211>20  
 <212>DNA  
 <400>4513  
 ggattcgata gacgggtgtca 20  
 <210>4514  
 <211>20  
 <212>DNA  
 <400>4514  
 gcttttaaact ctggcggaga 20  
 <210>4515  
 <211>20  
 <212>DNA  
 <400>4515  
 cctcttcagt cagaacctct 20  
 <210>4516  
 <211>20  
 <212>DNA  
 <400>4516  
 cccgtaaagg tctaagatcc 20  
 <210>4517  
 <211>20  
 <212>DNA  
 <400>4517  
 cattaggcaa agtggcctgt 20  
 <210>4518  
 <211>20  
 <212>DNA  
 <400>4518  
 tgacaatgcg gctcctattc 20  
 <210>4519  
 <211>20

<212>DNA  
<400>4519  
ccgtcaagaa caagagcttg 20  
<210>4520  
<211>20  
<212>DNA  
<400>4520  
gccccaacgt tttttggcta 20  
<210>4521  
<211>20  
<212>DNA  
<400>4521  
gtacatcgcc tactgcatga 20  
<210>4522  
<211>20  
<212>DNA  
<400>4522  
caataggggt gcctataacg 20  
<210>4523  
<211>20  
<212>DNA  
<400>4523  
gttggagaaa tagtagaccc 20  
<210>4524  
<211>20  
<212>DNA  
<400>4524  
cgctgcccac gaaaatgtga 20  
<210>4525  
<211>20  
<212>DNA  
<400>4525  
tacggctacg gtatacgcta 20  
<210>4526  
<211>20  
<212>DNA  
<400>4526  
tgaggcgtag acctgctgcc 20  
<210>4527  
<211>20  
<212>DNA  
<400>4527  
gatgataagc gccggtcttt 20  
<210>4528  
<211>20  
<212>DNA  
<400>4528  
gccttgtgag atactgatgg 20  
<210>4529  
<211>20  
<212>DNA  
<400>4529  
ggggaacatg atggcgattt 20  
<210>4530  
<211>20  
<212>DNA  
<400>4530  
gccatgttgt tctcctgagt 20  
<210>4531  
<211>20  
<212>DNA  
<400>4531  
gtccagcagt ggatcactaa 20  
<210>4532

<211>20  
<212>DNA  
<400>4532  
cgtcaggtag ccatgtactt 20  
<210>4533  
<211>20  
<212>DNA  
<400>4533  
gttacgggtt cttggggaat 20  
<210>4534  
<211>20  
<212>DNA  
<400>4534  
ggggaacatg atggcgattt 20  
<210>4535  
<211>20  
<212>DNA  
<400>4535  
ggggaatctt ggagctttgt 20  
<210>4536  
<211>20  
<212>DNA  
<400>4536  
gggaaagttt tagcagagga 20  
<210>4537  
<211>20  
<212>DNA  
<400>4537  
caactagaga agctgcgggg 20  
<210>4538  
<211>20  
<212>DNA  
<400>4538  
tggtcttttcg agccatggtc 20  
<210>4539  
<211>20  
<212>DNA  
<400>4539  
gcatagacgc taagtgttgt 20  
<210>4540  
<211>20  
<212>DNA  
<400>4540  
gggatgctaa tccccaaagaa 20  
<210>4541  
<211>20  
<212>DNA  
<400>4541  
gctgctcaag aaccaagtgc 20  
<210>4542  
<211>20  
<212>DNA  
<400>4542  
gctccctatg ccagttccta 20  
<210>4543  
<211>20  
<212>DNA  
<400>4543  
cgccaggctg tatttcgtta 20  
<210>4544  
<211>20  
<212>DNA  
<400>4544  
tgcgggggtg ttcttttgcta 20



```

<210>4545
<211>20
<212>DNA
<400>4545
caatattgcg acgttcaacg      20
<210>4546
<211>20
<212>DNA
<400>4546
gggtcttggt ttcttagctc     20
<210>4547
<211>20
<212>DNA
<400>4547
cagcagggaa catagcttca     20
<210>4548
<211>20
<212>DNA
<400>4548
gttcgcgtca tctcttaagg     20
<210>4549
<211>20
<212>DNA
<400>4549
cgatcacgaa agtcggtaag     20
<210>4550
<211>20
<212>DNA
<400>4550
cagtagcgta gtctgcatca     20
<210>4551
<211>20
<212>DNA
<400>4551
cccaagcttc tggcaataga     20
<210>4552
<211>20
<212>DNA
<400>4552
gatgatgaga acgacgaacg     20
<210>4553
<211>20
<212>DNA
<400>4553
cggcagtaaa cgaatgtctg     20
<210>4554
<211>20
<212>DNA
<400>4554
gcgagtcata attccttcag     20
<210>4555
<211>20
<212>DNA
<400>4555
cgaatcctag agaacctcct     20
<210>4556
<211>20
<212>DNA
<400>4556
gcgataaaac cagcagagac     20
<210>4557
<211>20
<212>DNA
<400>4557

```

gggcttttatt cgtgctgaag 20  
<210>4558  
<211>20  
<212>DNA  
<400>4558  
tacggccaat caacatgacc 20  
<210>4559  
<211>20  
<212>DNA  
<400>4559  
ccgttttttga ccatgaagcc 20  
<210>4560  
<211>20  
<212>DNA  
<400>4560  
cacctaacca gtctatggga 20  
<210>4561  
<211>20  
<212>DNA  
<400>4561  
ggtagggaaa acttcaatcg 20  
<210>4562  
<211>20  
<212>DNA  
<400>4562  
gctgcgtatg acactttagg 20  
<210>4563  
<211>20  
<212>DNA  
<400>4563  
ccgtgtcttt aaactcctgc 20  
<210>4564  
<211>20  
<212>DNA  
<400>4564  
gggaaatcgg tttctctctc 20  
<210>4565  
<211>20  
<212>DNA  
<400>4565  
agtcaacgat aggcggaggc 20  
<210>4566  
<211>20  
<212>DNA  
<400>4566  
gaagcccaaa cgttttgttc 20  
<210>4567  
<211>20  
<212>DNA  
<400>4567  
cgtcaaaccg ccaacaatgt 20  
<210>4568  
<211>20  
<212>DNA  
<400>4568  
cagctgcaaa gcacttgga 20  
<210>4569  
<211>20  
<212>DNA  
<400>4569  
cctatgagcg acaacgtatc 20  
<210>4570  
<211>20  
<212>DNA

## WO 99/27105

```

<400>4570
ccagcttctc cttttttccg      20
<210>4571
<211>20
<212>DNA
<400>4571
cgaggggaaga cttgcaacat      20
<210>4572
<211>20
<212>DNA
<400>4572
ggagtttgga ttccctcagc      20
<210>4573
<211>20
<212>DNA
<400>4573
cgtcttgagg tataatccct      20
<210>4574
<211>20
<212>DNA
<400>4574
ccatttacag agagagcagc      20
<210>4575
<211>20
<212>DNA
<400>4575
ggggaagagg ttttcttaga      20
<210>4576
<211>20
<212>DNA
<400>4576
ggactcgtat cttcaccagt      20
<210>4577
<211>20
<212>DNA
<400>4577
ggacttacgg gagcaaaaac      20
<210>4578
<211>20
<212>DNA
<400>4578
cctgtaagtg ggcactttct      20
<210>4579
<211>20
<212>DNA
<400>4579
ggtgagtagc aaaatggctg      20
<210>4580
<211>20
<212>DNA
<400>4580
gaggttatca ggagcttgag      20
<210>4581
<211>20
<212>DNA
<400>4581
ctctgttgga tcttgggttc      20
<210>4582
<211>20
<212>DNA
<400>4582
cgcatgtcct cattgcattg      20
<210>4583
<211>20

```

```

<212>DNA
<400>4583
ggagagtgtt ttccctaagg      20
<210>4584
<211>20
<212>DNA
<400>4584
gttgcgtcat gtgcatttag      20
<210>4585
<211>20
<212>DNA
<400>4585
gcgttcagga tctacaggaa      20
<210>4586
<211>20
<212>DNA
<400>4586
ggaacctgaa gccgttggtta      20
<210>4587
<211>20
<212>DNA
<400>4587
gcttttggtc aggagattca      20
<210>4588
<211>20
<212>DNA
<400>4588
agacagtcgg atccgagtga      20
<210>4589
<211>20
<212>DNA
<400>4589
ctgcgcattt tgtcacaacg      20
<210>4590
<211>20
<212>DNA
<400>4590
cgtggatgct aggatcttga      20
<210>4591
<211>20
<212>DNA
<400>4591
cgttttgact gggactgaga      20
<210>4592
<211>20
<212>DNA
<400>4592
gctcggttga ttatcgagag      20
<210>4593
<211>20
<212>DNA
<400>4593
ctccagtaag aacatagcgg      20
<210>4594
<211>20
<212>DNA
<400>4594
gggcatgact ttgattcctc      20
<210>4595
<211>20
<212>DNA
<400>4595
gggaagggtg tctttctcaa      20
<210>4596

```

```

<211>20
<212>DNA
<400>4596
gctcatttcg ggatacaacg      20
<210>4597
<211>20
<212>DNA
<400>4597
cttcgcgatg agggccaacg      20
<210>4598
<211>20
<212>DNA
<400>4598
ccttcatcgg agcacatctt      20
<210>4599
<211>20
<212>DNA
<400>4599
ctagaacgcg agcaataggt      20
<210>4600
<211>20
<212>DNA
<400>4600
cgaaggtgat ggtatctgtg      20
<210>4601
<211>20
<212>DNA
<400>4601
gggaacgtgc tcgattatcg      20
<210>4602
<211>20
<212>DNA
<400>4602
agactgtggt tctgcccttc      20
<210>4603
<211>20
<212>DNA
<400>4603
cctcgtcctt ggattgatgt      20
<210>4604
<211>20
<212>DNA
<400>4604
ccccaattcc agatggaagg      20
<210>4605
<211>20
<212>DNA
<400>4605
tccctacctt cgtaatgagc      20
<210>4606
<211>20
<212>DNA
<400>4606
ggtaagaagc tgcgtccta      20
<210>4607
<211>20
<212>DNA
<400>4607
gctgtcttgg ctttcagcat      20
<210>4608
<211>20
<212>DNA
<400>4608
ctgtgggtat tgtgcaggtt      20

```

<210>4609  
<211>20  
<212>DNA  
<400>4609  
ctcctagggga tggatatggat 20  
<210>4610  
<211>20  
<212>DNA  
<400>4610  
gagcgatttc ctagtatccg 20  
<210>4611  
<211>20  
<212>DNA  
<400>4611  
gctatttcct gttcaggtgc 20  
<210>4612  
<211>20  
<212>DNA  
<400>4612  
gatgatgtac atcgtgggta 20  
<210>4613  
<211>20  
<212>DNA  
<400>4613  
ggctgcgatc gtcttttgtg 20  
<210>4614  
<211>20  
<212>DNA  
<400>4614  
cagatttttag aatggcgggg 20  
<210>4615  
<211>20  
<212>DNA  
<400>4615  
gggtggctct tgaatgtcaa 20  
<210>4616  
<211>20  
<212>DNA  
<400>4616  
acaaaccctg aagctctctc 20  
<210>4617  
<211>20  
<212>DNA  
<400>4617  
cctctcagga tctttttgtt 20  
<210>4618  
<211>20  
<212>DNA  
<400>4618  
ggatgagttg ttttcagcga 20  
<210>4619  
<211>20  
<212>DNA  
<400>4619  
gccatgaaac ccacctttta 20  
<210>4620  
<211>20  
<212>DNA  
<400>4620  
ggtctatctc cagaagctca 20  
<210>4621  
<211>20  
<212>DNA  
<400>4621

gagcgcgaatt ttccaaaagg	20
<210>4622	
<211>20	
<212>DNA	
<400>4622	
cctctcagga tctttttgtt	20
<210>4623	
<211>20	
<212>DNA	
<400>4623	
gaagttcccc atgaactcac	20
<210>4624	
<211>20	
<212>DNA	
<400>4624	
gccacaagaa agagcgcgaat	20
<210>4625	
<211>20	
<212>DNA	
<400>4625	
cagtgcctacg actagcgtaa	20
<210>4626	
<211>20	
<212>DNA	
<400>4626	
gagtcgggca attgtcctaa	20
<210>4627	
<211>20	
<212>DNA	
<400>4627	
gatccaactt cagagtgcaa	20
<210>4628	
<211>20	
<212>DNA	
<400>4628	
ctaggctcat caatttgcgt	20
<210>4629	
<211>20	
<212>DNA	
<400>4629	
tgcttgggat tggctgtgtt	20
<210>4630	
<211>20	
<212>DNA	
<400>4630	
cttgggggaa tacttgttct	20
<210>4631	
<211>20	
<212>DNA	
<400>4631	
gggatacagt acagctaagg	20
<210>4632	
<211>20	
<212>DNA	
<400>4632	
gctacgagag ggagtagaat	20
<210>4633	
<211>20	
<212>DNA	
<400>4633	
gctctcttga aagcaagtgc	20
<210>4634	
<211>20	
<212>DNA	

```

<400>4634
cagtacctag gttccttaga 20
<210>4635
<211>20
<212>DNA
<400>4635
cccgtgatca atatgcgcta 20
<210>4636
<211>20
<212>DNA
<400>4636
ccctctcttt ttgaacgtcg 20
<210>4637
<211>20
<212>DNA
<400>4637
gtgcttttgg aggaggaaca 20
<210>4638
<211>20
<212>DNA
<400>4638
tcgactcgat ccaagagtat 20
<210>4639
<211>20
<212>DNA
<400>4639
tacggtaatc cccaagacgg 20
<210>4640
<211>20
<212>DNA
<400>4640
cgttagctca aggactgcga 20
<210>4641
<211>20
<212>DNA
<400>4641
cagagtcggg aactgtatgg 20
<210>4642
<211>20
<212>DNA
<400>4642
ttcaagcagg gaaacctgtg 20
<210>4643
<211>20
<212>DNA
<400>4643
cgcagactct ctgcatttcg 20
<210>4644
<211>20
<212>DNA
<400>4644
gggaaacggt ggtagacct 20
<210>4645
<211>20
<212>DNA
<400>4645
gagctatgga ttctcttcgc 20
<210>4646
<211>20
<212>DNA
<400>4646
aggtaggaag ggggtgccttg 20
<210>4647
<211>20

```



```

<212>DNA
<400>4647
gagcctgcat cagaagattc      20
<210>4648
<211>20
<212>DNA
<400>4648
cttgaagaga gaatccccga      20
<210>4649
<211>20
<212>DNA
<400>4649
cttccagcaa aacagatggc      20
<210>4650
<211>20
<212>DNA
<400>4650
gttacgagct gtgaaacacg      20
<210>4651
<211>20
<212>DNA
<400>4651
ggccatggag ttttccttct      20
<210>4652
<211>20
<212>DNA
<400>4652
gctgcgctat actccgtaaa      20
<210>4653
<211>20
<212>DNA
<400>4653
atcttggagg ctttaggagc      20
<210>4654
<211>20
<212>DNA
<400>4654
ggaattcacc tgagttcctt      20
<210>4655
<211>20
<212>DNA
<400>4655
gtcgggtgttt gctgatgaga      20
<210>4656
<211>20
<212>DNA
<400>4656
cgtattgatc gcagtctgga      20
<210>4657
<211>20
<212>DNA
<400>4657
aagcacgggt gattctgaga      20
<210>4658
<211>20
<212>DNA
<400>4658
gtacctaaga attcgtgcgt      20
<210>4659
<211>20
<212>DNA
<400>4659
catgttcgaa ttcgctgcgt      20
<210>4660

```

```

<211>20
<212>DNA
<400>4660
gggtagggag aacgatgttt      20
<210>4661
<211>20
<212>DNA
<400>4661
gaccgcagca attgctaatg      20
<210>4662
<211>20
<212>DNA
<400>4662
ggttttacggg ttctagttcc      20
<210>4663
<211>20
<212>DNA
<400>4663
agcagcgggt ccagaactta      20
<210>4664
<211>20
<212>DNA
<400>4664
gggtagggga ttagaatctg      20
<210>4665
<211>20
<212>DNA
<400>4665
gatcaggtat acggtcccaa      20
<210>4666
<211>20
<212>DNA
<400>4666
gggttctgtg gtggacataa      20
<210>4667
<211>20
<212>DNA
<400>4667
ctgtgactac tggagaagac      20
<210>4668
<211>20
<212>DNA
<400>4668
cacgggcatac gtcttttagt      20
<210>4669
<211>20
<212>DNA
<400>4669
gcagttacca tgatcttcgg      20
<210>4670
<211>20
<212>DNA
<400>4670
ggagatgcac ttgatgttcc      20
<210>4671
<211>20
<212>DNA
<400>4671
gcttgatgaa cagcagggt      20
<210>4672
<211>20
<212>DNA
<400>4672
ggccgagtgt ttcaggccat      20

```

```

<210>4673
<211>20
<212>DNA
<400>4673
tcttccatgg gtatgtgagc 20
<210>4674
<211>20
<212>DNA
<400>4674
gtgggggatg taggtgtaac 20
<210>4675
<211>20
<212>DNA
<400>4675
ctgcctcatt actcgacttg 20
<210>4676
<211>20
<212>DNA
<400>4676
caatctcagc gagtttggct 20
<210>4677
<211>20
<212>DNA
<400>4677
tcgtgacag atggaccaag 20
<210>4678
<211>20
<212>DNA
<400>4678
cctctcctaa gagatcttgc 20
<210>4679
<211>20
<212>DNA
<400>4679
ctcaagatcg gcgtaaggac 20
<210>4680
<211>20
<212>DNA
<400>4680
ggggatttttg gggatgcata 20
<210>4681
<211>20
<212>DNA
<400>4681
atcgaagggt acaacctgag 20
<210>4682
<211>20
<212>DNA
<400>4682
gcatgacctc gattcgtaag 20
<210>4683
<211>20
<212>DNA
<400>4683
ctctgcaagt tcgtgagaga 20
<210>4684
<211>20
<212>DNA
<400>4684
gcttgcgat agagagcttg 20
<210>4685
<211>20
<212>DNA
<400>4685

```

gagaccttgg tccccatgtt 20  
 <210>4686  
 <211>20  
 <212>DNA  
 <400>4686  
 gattttcttct tgggtgcctgc 20  
 <210>4687  
 <211>20  
 <212>DNA  
 <400>4687  
 gtgcaggcctt tatcataggc 20  
 <210>4688  
 <211>20  
 <212>DNA  
 <400>4688  
 gcgcttaaga tcaagaggag 20  
 <210>4689  
 <211>20  
 <212>DNA  
 <400>4689  
 gccgaaagat cacagttacc 20  
 <210>4690  
 <211>20  
 <212>DNA  
 <400>4690  
 gtgctttcgt cttgttcgta 20  
 <210>4691  
 <211>20  
 <212>DNA  
 <400>4691  
 ccggtatcat tgtcaggagt 20  
 <210>4692  
 <211>20  
 <212>DNA  
 <400>4692  
 ggacttaggt tctgtgaagc 20  
 <210>4693  
 <211>20  
 <212>DNA  
 <400>4693  
 cctgtgcttt agcatgccac 20  
 <210>4694  
 <211>20  
 <212>DNA  
 <400>4694  
 ggacttaggt tctgtgaagc 20  
 <210>4695  
 <211>20  
 <212>DNA  
 <400>4695  
 cgtgtctgtt cttcaacagc 20  
 <210>4696  
 <211>20  
 <212>DNA  
 <400>4696  
 cctatagtag ctgtggaaac 20  
 <210>4697  
 <211>20  
 <212>DNA  
 <400>4697  
 ttcggtagct tgggcacatc 20  
 <210>4698  
 <211>20  
 <212>DNA

<400>4698  
gtgaagatcc cttggggatt 20  
<210>4699  
<211>20  
<212>DNA  
<400>4699  
ggagaagagg ttgcaggttt 20  
<210>4700  
<211>20  
<212>DNA  
<400>4700  
gcatggctct aaaagccgtg 20  
<210>4701  
<211>20  
<212>DNA  
<400>4701  
cggggagatt gaactccttt 20  
<210>4702  
<211>20  
<212>DNA  
<400>4702  
caggggctat tacagcagca 20  
<210>4703  
<211>20  
<212>DNA  
<400>4703  
gacttctcgt ttttgtcctg 20  
<210>4704  
<211>20  
<212>DNA  
<400>4704  
gtagcttggg cacatcttga 20  
<210>4705  
<211>20  
<212>DNA  
<400>4705  
gacttctcgt ttttgtcctg 20  
<210>4706  
<211>20  
<212>DNA  
<400>4706  
ccaagggttc ttgtgtggat 20  
<210>4707  
<211>20  
<212>DNA  
<400>4707  
gccagaaata caaggagtt 20  
<210>4708  
<211>20  
<212>DNA  
<400>4708  
gcaaagatgg tttcaccgca 20  
<210>4709  
<211>20  
<212>DNA  
<400>4709  
aggtcgtccc ttgcaagccc 20  
<210>4710  
<211>20  
<212>DNA  
<400>4710  
gacttctcgt ttttgtcctg 20  
<210>4711  
<211>20

```

<212>DNA
<400>4711
gagacagtgt ggggaaatag      20
<210>4712
<211>20
<212>DNA
<400>4712
cctcaaggcg gtggtggaat      20
<210>4713
<211>20
<212>DNA
<400>4713
cctctccgtt agcctcatta      20
<210>4714
<211>20
<212>DNA
<400>4714
ggggtaaaga gggacttcta      20
<210>4715
<211>20
<212>DNA
<400>4715
gaagttctac aaggatgtgg      20
<210>4716
<211>20
<212>DNA
<400>4716
gaccaagcag ttctatggtg      20
<210>4717
<211>20
<212>DNA
<400>4717
ctaccaactt ctcagtggaa      20
<210>4718
<211>20
<212>DNA
<400>4718
gggtcagaga ttttgctcag      20
<210>4719
<211>20
<212>DNA
<400>4719
tacggtgatg ccttggttgc      20
<210>4720
<211>20
<212>DNA
<400>4720
ctagatcacc acaggaagtt      20
<210>4721
<211>20
<212>DNA
<400>4721
gactacgccg aaatccttac      20
<210>4722
<211>20
<212>DNA
<400>4722
cttgccagtg ttgcagatgt      20
<210>4723
<211>20
<212>DNA
<400>4723
gatctgcaca agtcgcactt      20
<210>4724

```

## WO 99/27105

```

<211>20
<212>DNA
<400>4724
cacgaagctg catctccaaa      20
<210>4725
<211>20
<212>DNA
<400>4725
tgaggacaac agcaacactc      20
<210>4726
<211>20
<212>DNA
<400>4726
acccgacttg tagagcgata      20
<210>4727
<211>20
<212>DNA
<400>4727
tcacctcagg tagcgaacac      20
<210>4728
<211>20
<212>DNA
<400>4728
aggtgctacc gcacccttta      20
<210>4729
<211>20
<212>DNA
<400>4729
cctagctcta gggcgattat      20
<210>4730
<211>20
<212>DNA
<400>4730
cctgacattc ggaatcttcc      20
<210>4731
<211>20
<212>DNA
<400>4731
cgcggaagaa acggctatgc      20
<210>4732
<211>20
<212>DNA
<400>4732
cgcaaccact aagagctaac      20
<210>4733
<211>20
<212>DNA
<400>4733
gggagaaaaga atgtgccgat      20
<210>4734
<211>20
<212>DNA
<400>4734
ggcaaggcta attcctgtca      20
<210>4735
<211>20
<212>DNA
<400>4735
ccctgatgat gccatttcct      20
<210>4736
<211>20
<212>DNA
<400>4736
gctaagcacc gagagaaaaa      20

```

<210>4737  
<211>20  
<212>DNA  
<400>4737  
cgtgtcatgt gtgccatttg 20  
<210>4738  
<211>20  
<212>DNA  
<400>4738  
gcccttttggga attcttaggt 20  
<210>4739  
<211>20  
<212>DNA  
<400>4739  
ctagagagcg ttcccctgtg 20  
<210>4740  
<211>20  
<212>DNA  
<400>4740  
aacacggtcg ccagggttgta 20  
<210>4741  
<211>20  
<212>DNA  
<400>4741  
cagtaacaag tcctggagca 20  
<210>4742  
<211>20  
<212>DNA  
<400>4742  
aggtcgcacc ccggaagggt 20  
<210>4743  
<211>20  
<212>DNA  
<400>4743  
gagatcctgc ctccaatgta 20  
<210>4744  
<211>20  
<212>DNA  
<400>4744  
gtgagcttgg cattgatacc 20  
<210>4745  
<211>20  
<212>DNA  
<400>4745  
ggtctcacca gtaattgctg 20  
<210>4746  
<211>20  
<212>DNA  
<400>4746  
gcatcggttg caccagatcat 20  
<210>4747  
<211>20  
<212>DNA  
<400>4747  
ggcaaagcct tagatcgtgt 20  
<210>4748  
<211>20  
<212>DNA  
<400>4748  
ccatatacctt ggatcatcacc 20  
<210>4749  
<211>20  
<212>DNA  
<400>4749



tagagagctc ccctagatga 20  
<210>4750  
<211>20  
<212>DNA  
<400>4750  
ggcaaagcct tagatcgtgt 20  
<210>4751  
<211>20  
<212>DNA  
<400>4751  
gatcaaccca atagcatgag 20  
<210>4752  
<211>20  
<212>DNA  
<400>4752  
cccgatttgt atccaactac 20  
<210>4753  
<211>20  
<212>DNA  
<400>4753  
gcctgaattg ggggtctttt 20  
<210>4754  
<211>20  
<212>DNA  
<400>4754  
tttctccctc actgcggatt 20  
<210>4755  
<211>20  
<212>DNA  
<400>4755  
gtacttcccc aaacatggac 20  
<210>4756  
<211>20  
<212>DNA  
<400>4756  
cctcgtaggc ttcaggaaat 20  
<210>4757  
<211>20  
<212>DNA  
<400>4757  
cctacggaca tggcaataac 20  
<210>4758  
<211>20  
<212>DNA  
<400>4758  
ccgctgttgt atcctaaggt 20  
<210>4759  
<211>20  
<212>DNA  
<400>4759  
cggctatcag gaagataagc 20  
<210>4760  
<211>20  
<212>DNA  
<400>4760  
ccccacaaaa cctggattga 20  
<210>4761  
<211>20  
<212>DNA  
<400>4761  
cgtcaggact actttaaggc 20  
<210>4762  
<211>20  
<212>DNA

```

<400>4762
cctacggaca tggcaataac      20
<210>4763
<211>20
<212>DNA
<400>4763
ggctgttctc tactcgcaat      20
<210>4764
<211>20
<212>DNA
<400>4764
cgaagcagct tccatgttga      20
<210>4765
<211>20
<212>DNA
<400>4765
ggcagtctgt actcaagatt      20
<210>4766
<211>20
<212>DNA
<400>4766
gtcccggaaa cgacattatg      20
<210>4767
<211>20
<212>DNA
<400>4767
tcgccgaggg agttcataat      20
<210>4768
<211>20
<212>DNA
<400>4768
gcgcttgata gaaactccga      20
<210>4769
<211>20
<212>DNA
<400>4769
gcttgtgtca acctcctcca      20
<210>4770
<211>20
<212>DNA
<400>4770
cttgggttaa ggtgacaggc      20
<210>4771
<211>20
<212>DNA
<400>4771
caccggtcac cacttatggc      20
<210>4772
<211>20
<212>DNA
<400>4772
tgcacgctag caatttaggg      20
<210>4773
<211>20
<212>DNA
<400>4773
cttcagggct tttaggaacc      20
<210>4774
<211>20
<212>DNA
<400>4774
gagatcgtag taaacggaag      20
<210>4775
<211>20

```

<212>DNA  
 <400>4775  
 cgccgtcata ttgcttcttt 20  
 <210>4776  
 <211>20  
 <212>DNA  
 <400>4776  
 ggaggcttct gttcgtagaa 20  
 <210>4777  
 <211>20  
 <212>DNA  
 <400>4777  
 tattgagggg cagacctacg 20  
 <210>4778  
 <211>20  
 <212>DNA  
 <400>4778  
 gctgtctatg cttttgtgga 20  
 <210>4779  
 <211>20  
 <212>DNA  
 <400>4779  
 gcgcctgact attttcacca 20  
 <210>4780  
 <211>20  
 <212>DNA  
 <400>4780  
 gtgaatggag aggatagaca 20  
 <210>4781  
 <211>20  
 <212>DNA  
 <400>4781  
 ccggagttct tcaatcacga 20  
 <210>4782  
 <211>20  
 <212>DNA  
 <400>4782  
 cgaggcctta aaaaaccgtc 20  
 <210>4783  
 <211>20  
 <212>DNA  
 <400>4783  
 gtagtgacct acggcatgaa 20  
 <210>4784  
 <211>20  
 <212>DNA  
 <400>4784  
 cagcaagcgc ctgactattt 20  
 <210>4785  
 <211>20  
 <212>DNA  
 <400>4785  
 gacgcttaag agtttcgtca 20  
 <210>4786  
 <211>20  
 <212>DNA  
 <400>4786  
 tacacccttc ctccgcagggt 20  
 <210>4787  
 <211>20  
 <212>DNA  
 <400>4787  
 ccactccttt aggaccgata 20  
 <210>4788

<211>20  
<212>DNA  
<400>4788  
gaggaccatt gaggaagaga 20  
<210>4789  
<211>20  
<212>DNA  
<400>4789  
gcgtctctgt ccaaagagaa 20  
<210>4790  
<211>20  
<212>DNA  
<400>4790  
ccccgagttg tattgcctat 20  
<210>4791  
<211>20  
<212>DNA  
<400>4791  
gcggacggta tgttttgaag 20  
<210>4792  
<211>20  
<212>DNA  
<400>4792  
ggcttggaag gggtttcaat 20  
<210>4793  
<211>20  
<212>DNA  
<400>4793  
cgtcggctcc tgacatat 20  
<210>4794  
<211>20  
<212>DNA  
<400>4794  
gcaggcaccc actctttttt 20  
<210>4795  
<211>20  
<212>DNA  
<400>4795  
ggaatatcag agtaggcgag 20  
<210>4796  
<211>20  
<212>DNA  
<400>4796  
ggtgatgata agaccacaa 20  
<210>4797  
<211>20  
<212>DNA  
<400>4797  
ctagtccggt agcccctcat 20  
<210>4798  
<211>20  
<212>DNA  
<400>4798  
ccgcaatcac cacgatgaaa 20  
<210>4799  
<211>20  
<212>DNA  
<400>4799  
gccccaaagag tttgatagga 20  
<210>4800  
<211>20  
<212>DNA  
<400>4800  
gctttcgccg tgactttggt 20

<210>4801  
<211>20  
<212>DNA  
<400>4801  
gatccttcct atagcgacca 20  
<210>4802  
<211>20  
<212>DNA  
<400>4802  
ggtatctcgt gtgaagaagc 20  
<210>4803  
<211>20  
<212>DNA  
<400>4803  
caagaaagct cgtgacgact 20  
<210>4804  
<211>20  
<212>DNA  
<400>4804  
gtcctgtatc aggagagggtt 20  
<210>4805  
<211>20  
<212>DNA  
<400>4805  
cttcagctcc ccagctttta 20  
<210>4806  
<211>20  
<212>DNA  
<400>4806  
agctgccccca agagtttgat 20  
<210>4807  
<211>20  
<212>DNA  
<400>4807  
gggatacctgc ctgggtttttt 20  
<210>4808  
<211>20  
<212>DNA  
<400>4808  
aaatggttga gtaccgcagc 20  
<210>4809  
<211>20  
<212>DNA  
<400>4809  
cctgcatgac aggaggccga 20  
<210>4810  
<211>20  
<212>DNA  
<400>4810  
ttctaacgac aagggtggga 20  
<210>4811  
<211>20  
<212>DNA  
<400>4811  
gatgaagtgc tgcaggaggc 20  
<210>4812  
<211>20  
<212>DNA  
<400>4812  
cgcagttgca caagaagtgt 20  
<210>4813  
<211>20  
<212>DNA  
<400>4813

```

aatcttcagc ggcctccac 20
<210>4814
<211>20
<212>DNA
<400>4814
ggtttgcagc tcagagaaga 20
<210>4815
<211>20
<212>DNA
<400>4815
ctgaagagcg acactatctg 20
<210>4816
<211>20
<212>DNA
<400>4816
gtcggttgcg ttttcgcttg 20
<210>4817
<211>20
<212>DNA
<400>4817
tcgcgctaac gcagggtttta 20
<210>4818
<211>20
<212>DNA
<400>4818
gcaagggtgca acagggattt 20
<210>4819
<211>20
<212>DNA
<400>4819
ggaggaaacg tccatgaaca 20
<210>4820
<211>20
<212>DNA
<400>4820
gectcctttt tcgccagttt 20
<210>4821
<211>20
<212>DNA
<400>4821
gggtgtgcct tttctatctc 20
<210>4822
<211>20
<212>DNA
<400>4822
ccagctctac ctacgggaat 20
<210>4823
<211>20
<212>DNA
<400>4823
ctctggaaga tgcacgcttt 20
<210>4824
<211>20
<212>DNA
<400>4824
ggaatggagt gggtgagaaa 20
<210>4825
<211>20
<212>DNA
<400>4825
gttacagaca gatgtcgagc 20
<210>4826
<211>20
<212>DNA

```

## WO 99/27105

<400>4826  
 cccccaagg ttaacagtag 20  
 <210>4827  
 <211>20  
 <212>DNA  
 <400>4827  
 tagaagcgca agggatcagg 20  
 <210>4828  
 <211>20  
 <212>DNA  
 <400>4828  
 ggacgtggag gaggattttt 20  
 <210>4829  
 <211>20  
 <212>DNA  
 <400>4829  
 cctgtgtcat agacatagcg 20  
 <210>4830  
 <211>20  
 <212>DNA  
 <400>4830  
 gacagatgtc gagcggtaat 20  
 <210>4831  
 <211>20  
 <212>DNA  
 <400>4831  
 gctcaggatt tcgtgacgaa 20  
 <210>4832  
 <211>20  
 <212>DNA  
 <400>4832  
 gccattcagg tatagctgag 20  
 <210>4833  
 <211>20  
 <212>DNA  
 <400>4833  
 ggagagagta aggaagatgg 20  
 <210>4834  
 <211>20  
 <212>DNA  
 <400>4834  
 gggtttatag ggggttggct 20  
 <210>4835  
 <211>20  
 <212>DNA  
 <400>4835  
 gagtgcgag aatcctgaga 20  
 <210>4836  
 <211>20  
 <212>DNA  
 <400>4836  
 gtcggcggat ggagtcacta 20  
 <210>4837  
 <211>20  
 <212>DNA  
 <400>4837  
 ccaccattcg cagttgttgt 20  
 <210>4838  
 <211>20  
 <212>DNA  
 <400>4838  
 ccgcattctga gggtttttgtt 20  
 <210>4839  
 <211>20

<212>DNA  
 <400>4839  
 tttgtgctga aggtcacggt 20  
 <210>4840  
 <211>20  
 <212>DNA  
 <400>4840  
 gcatggtgca ccaatagaga 20  
 <210>4841  
 <211>20  
 <212>DNA  
 <400>4841  
 ctcccgaagt ttcagcagta 20  
 <210>4842  
 <211>20  
 <212>DNA  
 <400>4842  
 cggtaaagcat ctacagcgta 20  
 <210>4843  
 <211>20  
 <212>DNA  
 <400>4843  
 ccccccatcc attaagatgc 20  
 <210>4844  
 <211>20  
 <212>DNA  
 <400>4844  
 ccaagagaca gaggacttca 20  
 <210>4845  
 <211>20  
 <212>DNA  
 <400>4845  
 cccactggac ttggtttcta 20  
 <210>4846  
 <211>20  
 <212>DNA  
 <400>4846  
 cgataaagga atgatctggg 20  
 <210>4847  
 <211>20  
 <212>DNA  
 <400>4847  
 gcttcatctg cagagagctt 20  
 <210>4848  
 <211>20  
 <212>DNA  
 <400>4848  
 gcctttccca gcatcgttta 20  
 <210>4849  
 <211>20  
 <212>DNA  
 <400>4849  
 ccgaagagct ggcagaaagc 20  
 <210>4850  
 <211>20  
 <212>DNA  
 <400>4850  
 cagcagcaaa cgcagagaaa 20  
 <210>4851  
 <211>20  
 <212>DNA  
 <400>4851  
 gcacttatgt ggcgaaaacc 20  
 <210>4852



<211>20  
<212>DNA  
<400>4852  
cggcgaaggc cagactttta 20  
<210>4853  
<211>20  
<212>DNA  
<400>4853  
cagcttcccc agagagttct 20  
<210>4854  
<211>20  
<212>DNA  
<400>4854  
taagacgggc ggagttcgtg 20  
<210>4855  
<211>20  
<212>DNA  
<400>4855  
cctcttggga aacttatgcc 20  
<210>4856  
<211>20  
<212>DNA  
<400>4856  
cctttcttgt taaaaacacg 20  
<210>4857  
<211>20  
<212>DNA  
<400>4857  
ctaatacggc tgcggattct 20  
<210>4858  
<211>20  
<212>DNA  
<400>4858  
gggctatttg tgctactggt 20  
<210>4859  
<211>20  
<212>DNA  
<400>4859  
gttccttctg aagtgatggg 20  
<210>4860  
<211>20  
<212>DNA  
<400>4860  
gggctatttg tgctactggt 20  
<210>4861  
<211>20  
<212>DNA  
<400>4861  
gttccttctg aagtgatggg 20  
<210>4862  
<211>20  
<212>DNA  
<400>4862  
cacaggcacc tataactccta 20  
<210>4863  
<211>20  
<212>DNA  
<400>4863  
gctggtcacg gctgaacata 20  
<210>4864  
<211>20  
<212>DNA  
<400>4864  
gtgactgtag gtgacatgag 20

<210>4865  
<211>20  
<212>DNA  
<400>4865  
cggaagcctt tgcgattttc 20  
<210>4866  
<211>20  
<212>DNA  
<400>4866  
gtatgggtcat ggtttcctcg 20  
<210>4867  
<211>20  
<212>DNA  
<400>4867  
gcacgtagag atgaaaccag 20  
<210>4868  
<211>20  
<212>DNA  
<400>4868  
ggcattttcc catttcttac 20  
<210>4869  
<211>20  
<212>DNA  
<400>4869  
cgtgggtgtc acagcaatct 20  
<210>4870  
<211>20  
<212>DNA  
<400>4870  
ctccattggg actctgcaca 20  
<210>4871  
<211>20  
<212>DNA  
<400>4871  
gcctcctgac gaagtaaagt 20  
<210>4872  
<211>20  
<212>DNA  
<400>4872  
tcctagagtg gcaaacttgg 20  
<210>4873  
<211>20  
<212>DNA  
<400>4873  
ggaaaggccc ttccctaata 20  
<210>4874  
<211>20  
<212>DNA  
<400>4874  
cccttccta ataaggagag 20  
<210>4875  
<211>20  
<212>DNA  
<400>4875  
tcgcgggttat ggacaaccg 20  
<210>4876  
<211>20  
<212>DNA  
<400>4876  
atagctccac ccttctccgc 20  
<210>4877  
<211>20  
<212>DNA  
<400>4877

cgggggtaca gaaaactcta 20  
 <210>4878  
 <211>20  
 <212>DNA  
 <400>4878  
 tcgcacccgc atcatttggt 20  
 <210>4879  
 <211>20  
 <212>DNA  
 <400>4879  
 gcggcgtaga tttgctcctg 20  
 <210>4880  
 <211>20  
 <212>DNA  
 <400>4880  
 ttgtcaggtc tgaggtaggt 20  
 <210>4881  
 <211>20  
 <212>DNA  
 <400>4881  
 cactgccatt cctatcttgc 20  
 <210>4882  
 <211>20  
 <212>DNA  
 <400>4882  
 gaagccattg caacgtgaag 20  
 <210>4883  
 <211>20  
 <212>DNA  
 <400>4883  
 cggggccgaga tcatatttct 20  
 <210>4884  
 <211>20  
 <212>DNA  
 <400>4884  
 ggctgttatg ggaaggattc 20  
 <210>4885  
 <211>20  
 <212>DNA  
 <400>4885  
 cttaaggcag cactttggct 20  
 <210>4886  
 <211>20  
 <212>DNA  
 <400>4886  
 cgacggtttg aggataacga 20  
 <210>4887  
 <211>20  
 <212>DNA  
 <400>4887  
 gagagtttcg tgaccaagcc 20  
 <210>4888  
 <211>20  
 <212>DNA  
 <400>4888  
 ctcttagag gactctctct 20  
 <210>4889  
 <211>20  
 <212>DNA  
 <400>4889  
 ggcgagata ttgcaaagag 20  
 <210>4890  
 <211>20  
 <212>DNA

<400>4890  
 caaagggtc cctgaaaact 20  
 <210>4891  
 <211>20  
 <212>DNA  
 <400>4891  
 tcccagacac accgttcgtc 20  
 <210>4892  
 <211>20  
 <212>DNA  
 <400>4892  
 cccagaggca ttgtctctat 20  
 <210>4893  
 <211>20  
 <212>DNA  
 <400>4893  
 ggcagcagtc tcttagttga 20  
 <210>4894  
 <211>20  
 <212>DNA  
 <400>4894  
 gtgcagaatc actatcccca 20  
 <210>4895  
 <211>20  
 <212>DNA  
 <400>4895  
 tcctgccccct catacctctt 20  
 <210>4896  
 <211>20  
 <212>DNA  
 <400>4896  
 cccatcccgt ttgttctcgg 20  
 <210>4897  
 <211>20  
 <212>DNA  
 <400>4897  
 ctcagtaccc ccaaactcaa 20  
 <210>4898  
 <211>20  
 <212>DNA  
 <400>4898  
 ggtatcgagg gttcttattg 20  
 <210>4899  
 <211>20  
 <212>DNA  
 <400>4899  
 agcttagggc tcgacttcct 20  
 <210>4900  
 <211>20  
 <212>DNA  
 <400>4900  
 catgtggctg tagtctgcaa 20  
 <210>4901  
 <211>20  
 <212>DNA  
 <400>4901  
 ctgtagacgt atcagcagga 20  
 <210>4902  
 <211>20  
 <212>DNA  
 <400>4902  
 gccatctatc gtatcgtacc 20  
 <210>4903  
 <211>20

<212>DNA  
<400>4903  
gagccactta tctctattcc 20  
<210>4904  
<211>20  
<212>DNA  
<400>4904  
gttccaagat cctagagcgg 20  
<210>4905  
<211>20  
<212>DNA  
<400>4905  
tggctccacc gttgctctgg 20  
<210>4906  
<211>20  
<212>DNA  
<400>4906  
cgctccctgt gttcacgaat 20  
<210>4907  
<211>20  
<212>DNA  
<400>4907  
aacagcaagg actccttgac 20  
<210>4908  
<211>20  
<212>DNA  
<400>4908  
cagaggatca agctctttgc 20  
<210>4909  
<211>20  
<212>DNA  
<400>4909  
gtgcagcgac atcgacaata 20  
<210>4910  
<211>20  
<212>DNA  
<400>4910  
aatcctgtaa gagtggagag 20  
<210>4911  
<211>20  
<212>DNA  
<400>4911  
ccggggatgc tattttgatg 20  
<210>4912  
<211>20  
<212>DNA  
<400>4912  
ctgagacaaa tgggtcgcac 20  
<210>4913  
<211>20  
<212>DNA  
<400>4913  
gcctgtgggtt tgtattgggtc 20  
<210>4914  
<211>20  
<212>DNA  
<400>4914  
cctcctgaac catttcctga 20  
<210>4915  
<211>20  
<212>DNA  
<400>4915  
gcgcagtttg attgtggact 20  
<210>4916

<211>20  
<212>DNA  
<400>4916  
ctgtcggacc gttatttttg 20  
<210>4917  
<211>20  
<212>DNA  
<400>4917  
ggctccaaca aagaaggaag 20  
<210>4918  
<211>20  
<212>DNA  
<400>4918  
gaggtaagat gcggattcct 20  
<210>4919  
<211>20  
<212>DNA  
<400>4919  
catgatagcg ccgccccaaag 20  
<210>4920  
<211>20  
<212>DNA  
<400>4920  
gtcttggtta gtgtcatccc 20  
<210>4921  
<211>20  
<212>DNA  
<400>4921  
cccgtagctt ccatatggaa 20  
<210>4922  
<211>20  
<212>DNA  
<400>4922  
taggagccat gacgatccac 20  
<210>4923  
<211>20  
<212>DNA  
<400>4923  
gcggctatat ggaggcaaca 20  
<210>4924  
<211>20  
<212>DNA  
<400>4924  
gggacttgta gctacaacga 20  
<210>4925  
<211>20  
<212>DNA  
<400>4925  
cgggatgtcg attcatcaag 20  
<210>4926  
<211>20  
<212>DNA  
<400>4926  
gcaatgtgac tgatcctgtc 20  
<210>4927  
<211>20  
<212>DNA  
<400>4927  
ggaatcgagg gatcgatttt 20  
<210>4928  
<211>20  
<212>DNA  
<400>4928  
cggttctcat cggaaggtga 20

<210>4929  
 <211>20  
 <212>DNA  
 <400>4929  
 gagacgagga tctctgcgga 20  
 <210>4930  
 <211>20  
 <212>DNA  
 <400>4930  
 gatcttgatg gtcccgtaga 20  
 <210>4931  
 <211>20  
 <212>DNA  
 <400>4931  
 ccctccttta gctactgtga 20  
 <210>4932  
 <211>20  
 <212>DNA  
 <400>4932  
 gtgcgagtac ttttccttcc 20  
 <210>4933  
 <211>20  
 <212>DNA  
 <400>4933  
 gggatccttg cttctgaaga 20  
 <210>4934  
 <211>20  
 <212>DNA  
 <400>4934  
 gtgcgagtac ttttccttcc 20  
 <210>4935  
 <211>20  
 <212>DNA  
 <400>4935  
 gtccaggggc gcatacgggtt 20  
 <210>4936  
 <211>20  
 <212>DNA  
 <400>4936  
 ggactttgtc tatcgtctgg 20  
 <210>4937  
 <211>20  
 <212>DNA  
 <400>4937  
 ctggattctg aaatccctgc 20  
 <210>4938  
 <211>20  
 <212>DNA  
 <400>4938  
 cgtcgtcgta ctaaggcata 20  
 <210>4939  
 <211>20  
 <212>DNA  
 <400>4939  
 gcacagctga aagctgtgat 20  
 <210>4940  
 <211>20  
 <212>DNA  
 <400>4940  
 agcgtatctt cctaaggagc 20  
 <210>4941  
 <211>20  
 <212>DNA  
 <400>4941

tgtagttgc aggggtttcc	20
<210>4942	
<211>20	
<212>DNA	
<400>4942	
gatctctgta gctatgatgc	20
<210>4943	
<211>20	
<212>DNA	
<400>4943	
gcagattcgt gagcagattc	20
<210>4944	
<211>20	
<212>DNA	
<400>4944	
cgcagagata actaagcgtg	20
<210>4945	
<211>20	
<212>DNA	
<400>4945	
ggatctccac gaatctctga	20
<210>4946	
<211>20	
<212>DNA	
<400>4946	
cgtttggttg caaggcttgg	20
<210>4947	
<211>20	
<212>DNA	
<400>4947	
gagaattcgc tttcgatgct	20
<210>4948	
<211>20	
<212>DNA	
<400>4948	
gttgccgttc tagaaccctc	20
<210>4949	
<211>20	
<212>DNA	
<400>4949	
ggcagatggt ccaagagaag	20
<210>4950	
<211>20	
<212>DNA	
<400>4950	
gagcagaacg tatcctatgg	20
<210>4951	
<211>20	
<212>DNA	
<400>4951	
tgtgagagac cactgccttc	20
<210>4952	
<211>20	
<212>DNA	
<400>4952	
gaagatccgg attttgtgcg	20
<210>4953	
<211>20	
<212>DNA	
<400>4953	
gcagctagcg gagtcttttt	20
<210>4954	
<211>20	
<212>DNA	



## WO 99/27105

```

<400>4954
gcgcggacgc tataatgata 20
<210>4955
<211>20
<212>DNA
<400>4955
gatatccaca tggtcggcag 20
<210>4956
<211>20
<212>DNA
<400>4956
gaagatccgg attttgtgcg 20
<210>4957
<211>20
<212>DNA
<400>4957
gcagctagcg gagtcttttt 20
<210>4958
<211>20
<212>DNA
<400>4958
gatcctcggg atacctgagc 20
<210>4959
<211>20
<212>DNA
<400>4959
ccaatcactt ccttgtgcga 20
<210>4960
<211>20
<212>DNA
<400>4960
gccaatacag agcgcaaagt 20
<210>4961
<211>20
<212>DNA
<400>4961
aagagcgtaa gctcagagcc 20
<210>4962
<211>20
<212>DNA
<400>4962
gaagaaaaac cacgcagttg 20
<210>4963
<211>20
<212>DNA
<400>4963
ggcagaggct ggaaagatcg 20
<210>4964
<211>20
<212>DNA
<400>4964
gttgccagag actactgaga 20
<210>4965
<211>20
<212>DNA
<400>4965
gcattggtac tcacgatggt 20
<210>4966
<211>20
<212>DNA
<400>4966
aacgtgcttt gcggttaacg 20
<210>4967
<211>20

```

<212>DNA  
<400>4967  
gcagaggctc tgtctttatg 20  
<210>4968  
<211>20  
<212>DNA  
<400>4968  
ctcgcgagga agaagaaact 20  
<210>4969  
<211>20  
<212>DNA  
<400>4969  
gaaggggaagt agcgggaaaa 20  
<210>4970  
<211>20  
<212>DNA  
<400>4970  
ccttcctgcg atcaatggat 20  
<210>4971  
<211>20  
<212>DNA  
<400>4971  
gccttccggt atggattcaa 20  
<210>4972  
<211>20  
<212>DNA  
<400>4972  
gcgcttctaa gactagcggt 20  
<210>4973  
<211>20  
<212>DNA  
<400>4973  
gaagacggga acaagagctt 20  
<210>4974  
<211>20  
<212>DNA  
<400>4974  
atgtgcagag gctctgtctt 20  
<210>4975  
<211>20  
<212>DNA  
<400>4975  
catcctgaat cgtgcatggt 20  
<210>4976  
<211>20  
<212>DNA  
<400>4976  
gcaggtaata gcgagagtag 20  
<210>4977  
<211>20  
<212>DNA  
<400>4977  
ccggatcatc tctggaacta 20  
<210>4978  
<211>20  
<212>DNA  
<400>4978  
atctccacgc acaaccgatt 20  
<210>4979  
<211>20  
<212>DNA  
<400>4979  
gagtgtcttg tagtttcggt 20  
<210>4980

<211>20  
 <212>DNA  
 <400>4980  
 gagatccctc cttctcttca 20  
 <210>4981  
 <211>20  
 <212>DNA  
 <400>4981  
 cagagcggag aaacgaacaa 20  
 <210>4982  
 <211>20  
 <212>DNA  
 <400>4982  
 gataagggtc aatccttatg 20  
 <210>4983  
 <211>20  
 <212>DNA  
 <400>4983  
 gtagctacgg cttgtatagc 20  
 <210>4984  
 <211>20  
 <212>DNA  
 <400>4984  
 gcgagcaatt ttcctagcct 20  
 <210>4985  
 <211>20  
 <212>DNA  
 <400>4985  
 gttgtccttg gtaacaagcg 20  
 <210>4986  
 <211>20  
 <212>DNA  
 <400>4986  
 ctccaaaagc caaagagAAC 20  
 <210>4987  
 <211>20  
 <212>DNA  
 <400>4987  
 gcgaggctgg aattatttcg 20  
 <210>4988  
 <211>20  
 <212>DNA  
 <400>4988  
 gcgtttccgg gacgcgtggt 20  
 <210>4989  
 <211>20  
 <212>DNA  
 <400>4989  
 ctgaaggtgt ggggacctca 20  
 <210>4990  
 <211>20  
 <212>DNA  
 <400>4990  
 gtgaggaaga gacggagtta 20  
 <210>4991  
 <211>20  
 <212>DNA  
 <400>4991  
 ggCGaatctc gtctcggaat 20  
 <210>4992  
 <211>20  
 <212>DNA  
 <400>4992  
 gtgattgata gtcaagagtc 20

<210>4993  
<211>20  
<212>DNA  
<400>4993  
ggctgccctg tttttaggta 20  
<210>4994  
<211>20  
<212>DNA  
<400>4994  
ctacaggctg ccctgttttt 20  
<210>4995  
<211>20  
<212>DNA  
<400>4995  
cttcagagta cttacggcca 20  
<210>4996  
<211>20  
<212>DNA  
<400>4996  
agtatcgcaa gcttcaggca 20  
<210>4997  
<211>20  
<212>DNA  
<400>4997  
ttcatcaaag tcgtctccac 20  
<210>4998  
<211>20  
<212>DNA  
<400>4998  
gggctttctc catgctttct 20  
<210>4999  
<211>20  
<212>DNA  
<400>4999  
cggcatctcg aaccattctt 20  
<210>5000  
<211>20  
<212>DNA  
<400>5000  
actgcttgac gttttgctgg 20  
<210>5001  
<211>20  
<212>DNA  
<400>5001  
gcaactcctt gatcagagaa 20  
<210>5002  
<211>20  
<212>DNA  
<400>5002  
gctgccgatg atgctgctgc 20  
<210>5003  
<211>20  
<212>DNA  
<400>5003  
gtagtgcagc ttaagtccgt 20  
<210>5004  
<211>20  
<212>DNA  
<400>5004  
cactcgtgaa ctgagtggct 20  
<210>5005  
<211>20  
<212>DNA  
<400>5005

ggatagattc tggaagagcg 20  
 <210>5006  
 <211>20  
 <212>DNA  
 <400>5006  
 agagagtgcg gatggcaaca 20  
 <210>5007  
 <211>20  
 <212>DNA  
 <400>5007  
 gggttgggtt aggaagttca 20  
 <210>5008  
 <211>20  
 <212>DNA  
 <400>5008  
 tcgaggtgcg tttggtctat 20  
 <210>5009  
 <211>20  
 <212>DNA  
 <400>5009  
 cgccgagctt gtttactcat 20  
 <210>5010  
 <211>20  
 <212>DNA  
 <400>5010  
 ggtaagcaga gcctcttttc 20  
 <210>5011  
 <211>20  
 <212>DNA  
 <400>5011  
 ggtttgggga tgtgttctct 20  
 <210>5012  
 <211>20  
 <212>DNA  
 <400>5012  
 gcgaaaaaga gaccgaagag 20  
 <210>5013  
 <211>20  
 <212>DNA  
 <400>5013  
 cggcgtctgt aaaagagcag 20  
 <210>5014  
 <211>20  
 <212>DNA  
 <400>5014  
 ctggtgctca atgcattcgt 20  
 <210>5015  
 <211>20  
 <212>DNA  
 <400>5015  
 ggaaatcggt cctaggatgt 20  
 <210>5016  
 <211>20  
 <212>DNA  
 <400>5016  
 gggatatagag ttttgtcccg 20  
 <210>5017  
 <211>20  
 <212>DNA  
 <400>5017  
 cgaaaagtgt ggctccgttc 20  
 <210>5018  
 <211>20  
 <212>DNA

<400>5018  
ccatcaagtt ttccgtggag 20  
<210>5019  
<211>20  
<212>DNA  
<400>5019  
ggctgaagtg atgttgaagc 20  
<210>5020  
<211>20  
<212>DNA  
<400>5020  
gggggcttcc caatctgtgg 20  
<210>5021  
<211>20  
<212>DNA  
<400>5021  
ggcacgtcgt catttgatga 20  
<210>5022  
<211>20  
<212>DNA  
<400>5022  
ggatcatctcg gaaataacgc 20  
<210>5023  
<211>20  
<212>DNA  
<400>5023  
cccagttgat gagccatctt 20  
<210>5024  
<211>20  
<212>DNA  
<400>5024  
ggcacgtcgt catttgatga 20  
<210>5025  
<211>20  
<212>DNA  
<400>5025  
gtgcgatcat acttactcgc 20  
<210>5026  
<211>20  
<212>DNA  
<400>5026  
gcactgagga tacgttggtt 20  
<210>5027  
<211>20  
<212>DNA  
<400>5027  
ggtcggagag gctctataaa 20  
<210>5028  
<211>20  
<212>DNA  
<400>5028  
gtcgagcatt gctgaggaaa 20  
<210>5029  
<211>20  
<212>DNA  
<400>5029  
cttcaaaggc gtccttttgc 20  
<210>5030  
<211>20  
<212>DNA  
<400>5030  
tcttcggatg aagagggtgc 20  
<210>5031  
<211>20

## WO 99/27105

```

<212>DNA
<400>5031
aagcccgcgc gctccgttta      20
<210>5032
<211>20
<212>DNA
<400>5032
ccgaacgagc ctttggtgga      20
<210>5033
<211>20
<212>DNA
<400>5033
gcttctgctc ttgttggtgc      20
<210>5034
<211>20
<212>DNA
<400>5034
cgaggccgca aaaaatcttc      20
<210>5035
<211>20
<212>DNA
<400>5035
gcgacaaatc aacctcgaga      20
<210>5036
<211>20
<212>DNA
<400>5036
gcttctgctc ttgttggtgc      20
<210>5037
<211>20
<212>DNA
<400>5037
gggggagtggt ttgttgatga      20
<210>5038
<211>20
<212>DNA
<400>5038
ggaaggagat ttgcaactcc      20
<210>5039
<211>20
<212>DNA
<400>5039
ggcttcgtct ttagaagtcc      20
<210>5040
<211>20
<212>DNA
<400>5040
gactttgggt atgggtatcg      20
<210>5041
<211>20
<212>DNA
<400>5041
agagaatgcg ggctgaagag      20
<210>5042
<211>20
<212>DNA
<400>5042
gcttggtatt tacgagcgggt      20
<210>5043
<211>20
<212>DNA
<400>5043
tacgctagta aagcttggcg      20
<210>5044

```

<211>20  
<212>DNA  
<400>5044  
cccaatagct atggtggtag 20  
<210>5045  
<211>20  
<212>DNA  
<400>5045  
gcgacgttct ttgtttgctg 20  
<210>5046  
<211>20  
<212>DNA  
<400>5046  
gccaaaaata cagggttccc 20  
<210>5047  
<211>20  
<212>DNA  
<400>5047  
cctgagcatt gacttgggat 20  
<210>5048  
<211>20  
<212>DNA  
<400>5048  
ggaatgcgat acatgtgaag 20  
<210>5049  
<211>20  
<212>DNA  
<400>5049  
atttagcggc tctctcggac 20  
<210>5050  
<211>20  
<212>DNA  
<400>5050  
cagatagggt ttgcatgcct 20  
<210>5051  
<211>20  
<212>DNA  
<400>5051  
ggagaagtga atcgcatgcc 20  
<210>5052  
<211>20  
<212>DNA  
<400>5052  
gccccatcata cgttatcctg 20  
<210>5053  
<211>20  
<212>DNA  
<400>5053  
cggccgttac tgcattgat 20  
<210>5054  
<211>20  
<212>DNA  
<400>5054  
gggatattgt aggtacaccc 20  
<210>5055  
<211>20  
<212>DNA  
<400>5055  
cgagtcggca aaagaaactg 20  
<210>5056  
<211>20  
<212>DNA  
<400>5056  
ggaggtatga ttactctggg 20



<210>5057  
<211>20  
<212>DNA  
<400>5057  
tgtgggttagc agaggctttg 20  
<210>5058  
<211>20  
<212>DNA  
<400>5058  
cctgatcacg cagcaataac 20  
<210>5059  
<211>20  
<212>DNA  
<400>5059  
tgggagcctt gccttctggg 20  
<210>5060  
<211>20  
<212>DNA  
<400>5060  
gttggttcgtc aacgttgggt 20  
<210>5061  
<211>20  
<212>DNA  
<400>5061  
ctctctgggc atgttttttg 20  
<210>5062  
<211>20  
<212>DNA  
<400>5062  
gcttttcctg agagacgtat 20  
<210>5063  
<211>20  
<212>DNA  
<400>5063  
gttcccttct agagtatgcg 20  
<210>5064  
<211>20  
<212>DNA  
<400>5064  
caagtgaact tagaggctgc 20  
<210>5065  
<211>20  
<212>DNA  
<400>5065  
gcgatagaag acggttcata 20  
<210>5066  
<211>20  
<212>DNA  
<400>5066  
cctcctaggt taaggtagtc 20  
<210>5067  
<211>20  
<212>DNA  
<400>5067  
cacgacaggg gttttgaacg 20  
<210>5068  
<211>20  
<212>DNA  
<400>5068  
caaatcccgt aagaagactc 20  
<210>5069  
<211>20  
<212>DNA  
<400>5069

gctgtgtttt ggctgaggaa 20  
<210>5070  
<211>20  
<212>DNA  
<400>5070  
caggaggcca agaatcaca 20  
<210>5071  
<211>20  
<212>DNA  
<400>5071  
cgatcatcacg aaaatcgtgc 20  
<210>5072  
<211>20  
<212>DNA  
<400>5072  
ggatggacac cttgctttgt 20  
<210>5073  
<211>20  
<212>DNA  
<400>5073  
gacttggtat gttgcttgga 20  
<210>5074  
<211>20  
<212>DNA  
<400>5074  
gaaagcagat cgatcatcacg 20  
<210>5075  
<211>20  
<212>DNA  
<400>5075  
gctccttgga tagtaatggc 20  
<210>5076  
<211>20  
<212>DNA  
<400>5076  
ggagaacatc gtttgctcgt 20  
<210>5077  
<211>20  
<212>DNA  
<400>5077  
gggaatgaaa gatccacggc 20  
<210>5078  
<211>20  
<212>DNA  
<400>5078  
gctccttgga tagtaatggc 20  
<210>5079  
<211>20  
<212>DNA  
<400>5079  
gcagcaaaaa cagctgtagc 20  
<210>5080  
<211>20  
<212>DNA  
<400>5080  
agacgcggga tctccgaagg 20  
<210>5081  
<211>20  
<212>DNA  
<400>5081  
agagagccca cctccatgtt 20  
<210>5082  
<211>20  
<212>DNA

<400>5082  
 tcctgaggcg agagagagcc 20  
 <210>5083  
 <211>20  
 <212>DNA  
 <400>5083  
 gtgggtggag ctactgttgc 20  
 <210>5084  
 <211>20  
 <212>DNA  
 <400>5084  
 gaagcgggtga tcttaggaaa 20  
 <210>5085  
 <211>20  
 <212>DNA  
 <400>5085  
 gccgatgcaa agagctagaa 20  
 <210>5086  
 <211>20  
 <212>DNA  
 <400>5086  
 ggtttggttc cccgcggaat 20  
 <210>5087  
 <211>20  
 <212>DNA  
 <400>5087  
 gagcccctac aaaagccacc 20  
 <210>5088  
 <211>20  
 <212>DNA  
 <400>5088  
 gccgatgcaa agagctagaa 20  
 <210>5089  
 <211>20  
 <212>DNA  
 <400>5089  
 caagccgaaa cggtagagat 20  
 <210>5090  
 <211>20  
 <212>DNA  
 <400>5090  
 gcaaggaacc gggtgtggca 20  
 <210>5091  
 <211>20  
 <212>DNA  
 <400>5091  
 ggggaagttg cttcggataa 20  
 <210>5092  
 <211>20  
 <212>DNA  
 <400>5092  
 ctctcccgaa gaagacttag 20  
 <210>5093  
 <211>20  
 <212>DNA  
 <400>5093  
 ggggaacctc attgtctcta 20  
 <210>5094  
 <211>20  
 <212>DNA  
 <400>5094  
 gttcgtcaga gagggaccgc 20  
 <210>5095  
 <211>20

<212>DNA  
<400>5095  
gcgaactaca ggtcaacgat 20  
<210>5096  
<211>20  
<212>DNA  
<400>5096  
ggggaagttg cttcggataa 20  
<210>5097  
<211>20  
<212>DNA  
<400>5097  
caacgaccct tgtcaacgta 20  
<210>5098  
<211>20  
<212>DNA  
<400>5098  
ggcgaagaat tcgaaatctc 20  
<210>5099  
<211>20  
<212>DNA  
<400>5099  
cgttcgccac atgtggataa 20  
<210>5100  
<211>20  
<212>DNA  
<400>5100  
ccatgcagaa gaggaaggaa 20  
<210>5101  
<211>20  
<212>DNA  
<400>5101  
ggacagacca tcatttctgg 20  
<210>5102  
<211>20  
<212>DNA  
<400>5102  
agcgatccca tctaccgcat 20  
<210>5103  
<211>20  
<212>DNA  
<400>5103  
ctcaaagagc gttgtgcaga 20  
<210>5104  
<211>20  
<212>DNA  
<400>5104  
taggaccaat tcctctgcct 20  
<210>5105  
<211>20  
<212>DNA  
<400>5105  
ctgtagccgt atttgacgcc 20  
<210>5106  
<211>20  
<212>DNA  
<400>5106  
ggtagcagta attaccccag 20  
<210>5107  
<211>20  
<212>DNA  
<400>5107  
catcgtatgg cggaagcaaa 20  
<210>5108

<211>20  
 <212>DNA  
 <400>5108  
 gtgaagacac ccatcgatatg 20  
 <210>5109  
 <211>20  
 <212>DNA  
 <400>5109  
 ctgggaaaca tcgacctgtt 20  
 <210>5110  
 <211>20  
 <212>DNA  
 <400>5110  
 gctagcgaac gtaggaattg 20  
 <210>5111  
 <211>20  
 <212>DNA  
 <400>5111  
 gcgtgatttt ccttcgtaca 20  
 <210>5112  
 <211>20  
 <212>DNA  
 <400>5112  
 gcctatatgt gtggtgaagg 20  
 <210>5113  
 <211>20  
 <212>DNA  
 <400>5113  
 ctacgcatag acggacaagt 20  
 <210>5114  
 <211>20  
 <212>DNA  
 <400>5114  
 ggttacataa atcgcggctc 20  
 <210>5115  
 <211>20  
 <212>DNA  
 <400>5115  
 gcgcggttgc tctgcttcac 20  
 <210>5116  
 <211>20  
 <212>DNA  
 <400>5116  
 ggaagcagac tcaatccaga 20  
 <210>5117  
 <211>20  
 <212>DNA  
 <400>5117  
 ctccctagacg atcttcagca 20  
 <210>5118  
 <211>20  
 <212>DNA  
 <400>5118  
 cgatcagctt gtccatcatc 20  
 <210>5119  
 <211>20  
 <212>DNA  
 <400>5119  
 ccacgtacga gatcagatgt 20  
 <210>5120  
 <211>20  
 <212>DNA  
 <400>5120  
 gctcgatgat gggatcctta 20

<210>5121  
 <211>20  
 <212>DNA  
 <400>5121  
 caactcctac aagtgatggg 20  
 <210>5122  
 <211>20  
 <212>DNA  
 <400>5122  
 ccgctctgct ttaggatagc 20  
 <210>5123  
 <211>20  
 <212>DNA  
 <400>5123  
 ggcagatgca aacagtaagg 20  
 <210>5124  
 <211>20  
 <212>DNA  
 <400>5124  
 gtgtaactct caaagcccac 20  
 <210>5125  
 <211>20  
 <212>DNA  
 <400>5125  
 ctcacgtcct cagaggggaa 20  
 <210>5126  
 <211>20  
 <212>DNA  
 <400>5126  
 cctgatgacg cttccttttg 20  
 <210>5127  
 <211>20  
 <212>DNA  
 <400>5127  
 cgttggtgcg ggatccaatg 20  
 <210>5128  
 <211>20  
 <212>DNA  
 <400>5128  
 gctccaaatt tcgaacctcc 20  
 <210>5129  
 <211>20  
 <212>DNA  
 <400>5129  
 cccatatgca gggactctaa 20  
 <210>5130  
 <211>20  
 <212>DNA  
 <400>5130  
 gcgatattca gggcgtgttt 20  
 <210>5131  
 <211>20  
 <212>DNA  
 <400>5131  
 ccaggtagc tatccaaaag 20  
 <210>5132  
 <211>20  
 <212>DNA  
 <400>5132  
 agaccgctaa ctttcattcg 20  
 <210>5133  
 <211>20  
 <212>DNA  
 <400>5133

gcaccacctc	tggtgttggt	20
<210>5134		
<211>20		
<212>DNA		
<400>5134		
ttcagccgca	cggtaatgac	20
<210>5135		
<211>20		
<212>DNA		
<400>5135		
ccttcgctag	cgccttatatt	20
<210>5136		
<211>20		
<212>DNA		
<400>5136		
gacagtcggt	tggtgttgga	20
<210>5137		
<211>20		
<212>DNA		
<400>5137		
cggatgctac	tatcatccag	20
<210>5138		
<211>20		
<212>DNA		
<400>5138		
cccgcatagt	gtaactccta	20
<210>5139		
<211>20		
<212>DNA		
<400>5139		
gagcttgga	aggtctccta	20
<210>5140		
<211>20		
<212>DNA		
<400>5140		
catgacgagc	aaaggagtag	20
<210>5141		
<211>20		
<212>DNA		
<400>5141		
gtgagtctaa	ggtatccagc	20
<210>5142		
<211>20		
<212>DNA		
<400>5142		
cgatcgcaact	aaacgtgctt	20
<210>5143		
<211>20		
<212>DNA		
<400>5143		
catgctttga	gctcggcaat	20
<210>5144		
<211>20		
<212>DNA		
<400>5144		
gcgttcgcaa	cttcttgagt	20
<210>5145		
<211>20		
<212>DNA		
<400>5145		
gcatcgttgg	aaacagtgg	20
<210>5146		
<211>20		
<212>DNA		

<400>5146  
cattgcttcc ataaccaggg 20  
<210>5147  
<211>20  
<212>DNA  
<400>5147  
aaagcttcgg ggaagcgtag 20  
<210>5148  
<211>20  
<212>DNA  
<400>5148  
aggctcttga ggaagctcag 20  
<210>5149  
<211>20  
<212>DNA  
<400>5149  
gatgttcac cagggttcct 20  
<210>5150  
<211>20  
<212>DNA  
<400>5150  
agcgctgtga ttcattggggc 20  
<210>5151  
<211>20  
<212>DNA  
<400>5151  
gcctcctttt ggtctgcatt 20  
<210>5152  
<211>20  
<212>DNA  
<400>5152  
gctctcgaag ctgaaatctt 20  
<210>5153  
<211>20  
<212>DNA  
<400>5153  
ggagtgccag gacctgtatg 20  
<210>5154  
<211>20  
<212>DNA  
<400>5154  
ggttgatagg agctgccata 20  
<210>5155  
<211>20  
<212>DNA  
<400>5155  
ttcctgttcc cgttcccgtg 20  
<210>5156  
<211>20  
<212>DNA  
<400>5156  
caatccgagt ggatgggttc 20  
<210>5157  
<211>20  
<212>DNA  
<400>5157  
gtagaacctg gaagcgtact 20  
<210>5158  
<211>20  
<212>DNA  
<400>5158  
gtcagggtgc gactttagt 20  
<210>5159  
<211>20



<212>DNA  
<400>5159  
ccttctggag tcgttggttc 20  
<210>5160  
<211>20  
<212>DNA  
<400>5160  
cctaagtttc aggacctcgt 20  
<210>5161  
<211>20  
<212>DNA  
<400>5161  
agcgatgctc gacggcgagc 20  
<210>5162  
<211>20  
<212>DNA  
<400>5162  
cgttcttttag atcggcagga 20  
<210>5163  
<211>20  
<212>DNA  
<400>5163  
gaggtctctt tgacctcgat 20  
<210>5164  
<211>20  
<212>DNA  
<400>5164  
ccatcatgcg ctgatttcca 20  
<210>5165  
<211>20  
<212>DNA  
<400>5165  
ctagagccaa agactttggc 20  
<210>5166  
<211>20  
<212>DNA  
<400>5166  
ccttctggag tcgttggttc 20  
<210>5167  
<211>20  
<212>DNA  
<400>5167  
gcaaaggagg tcaccacaaa 20  
<210>5168  
<211>20  
<212>DNA  
<400>5168  
gacgaaacat caatgggcct 20  
<210>5169  
<211>20  
<212>DNA  
<400>5169  
ttgtctagcg aacagatccc 20  
<210>5170  
<211>20  
<212>DNA  
<400>5170  
cgtcaagggg agtctttaga 20  
<210>5171  
<211>20  
<212>DNA  
<400>5171  
aaaaggacgt gctccatcgt 20  
<210>5172

<211>20  
<212>DNA  
<400>5172  
caagaatagg aaggggtggct 20  
<210>5173  
<211>20  
<212>DNA  
<400>5173  
ggtaagatag cgtgcatgga 20  
<210>5174  
<211>20  
<212>DNA  
<400>5174  
gcgacgctct ccaggaatgg 20  
<210>5175  
<211>20  
<212>DNA  
<400>5175  
cgggtggagat ccgtaaaatc 20  
<210>5176  
<211>20  
<212>DNA  
<400>5176  
gcgtttgcaa atagaggggtg 20  
<210>5177  
<211>20  
<212>DNA  
<400>5177  
tgcgagccga gatcttggtg 20  
<210>5178  
<211>20  
<212>DNA  
<400>5178  
tctgggtcac ccgagaaaat 20  
<210>5179  
<211>20  
<212>DNA  
<400>5179  
gggagaacat cggtaaagga 20  
<210>5180  
<211>20  
<212>DNA  
<400>5180  
caaggaaaag gcccttcttc 20  
<210>5181  
<211>20  
<212>DNA  
<400>5181  
gggtgctgct gctcctactg 20  
<210>5182  
<211>20  
<212>DNA  
<400>5182  
tagagaaccc cttcgggagt 20  
<210>5183  
<211>20  
<212>DNA  
<400>5183  
ccaaaccatt tccctctctc 20  
<210>5184  
<211>20  
<212>DNA  
<400>5184  
gggagaacat cggtaaagga 20

<210>5185  
 <211>20  
 <212>DNA  
 <400>5185  
 gagaaggctt ggcgtaagca 20  
 <210>5186  
 <211>20  
 <212>DNA  
 <400>5186  
 ggctcagaga aaatgctgtg 20  
 <210>5187  
 <211>20  
 <212>DNA  
 <400>5187  
 cccctggatg gattcatttt 20  
 <210>5188  
 <211>20  
 <212>DNA  
 <400>5188  
 ctgagactta ctgggattgc 20  
 <210>5189  
 <211>20  
 <212>DNA  
 <400>5189  
 caggaattgc tgcgcagtta 20  
 <210>5190  
 <211>20  
 <212>DNA  
 <400>5190  
 tatcgctcga cggcccatct 20  
 <210>5191  
 <211>20  
 <212>DNA  
 <400>5191  
 caagctaaag cgagcatgtc 20  
 <210>5192  
 <211>20  
 <212>DNA  
 <400>5192  
 gtgaggtaag aagttccgag 20  
 <210>5193  
 <211>20  
 <212>DNA  
 <400>5193  
 tctagctggc ggatagcctc 20  
 <210>5194  
 <211>20  
 <212>DNA  
 <400>5194  
 gggttacgtg atgctttagg 20  
 <210>5195  
 <211>20  
 <212>DNA  
 <400>5195  
 cctctttagtag cgagtcaaac 20  
 <210>5196  
 <211>20  
 <212>DNA  
 <400>5196  
 cctttacgca taagcagagg 20  
 <210>5197  
 <211>20  
 <212>DNA  
 <400>5197

gtgatgtccc cctcctttat 20  
 <210>5198  
 <211>20  
 <212>DNA  
 <400>5198  
 ggtcagttta ggaaggcgtg 20  
 <210>5199  
 <211>20  
 <212>DNA  
 <400>5199  
 tttaccgatt gcgccagacc 20  
 <210>5200  
 <211>20  
 <212>DNA  
 <400>5200  
 ggggttggggt gtatggaata 20  
 <210>5201  
 <211>20  
 <212>DNA  
 <400>5201  
 ggacggggat tctttatggg 20  
 <210>5202  
 <211>20  
 <212>DNA  
 <400>5202  
 gtaggcagtg caacgcataa 20  
 <210>5203  
 <211>20  
 <212>DNA  
 <400>5203  
 ctcaagcatc tttggacgac 20  
 <210>5204  
 <211>20  
 <212>DNA  
 <400>5204  
 ctaagagagg ggagataagc 20  
 <210>5205  
 <211>20  
 <212>DNA  
 <400>5205  
 agtgacgtgg cagatttctc 20  
 <210>5206  
 <211>20  
 <212>DNA  
 <400>5206  
 gcattaggat ggggaatcgt 20  
 <210>5207  
 <211>20  
 <212>DNA  
 <400>5207  
 aggtctaagt tgagttctgc 20  
 <210>5208  
 <211>20  
 <212>DNA  
 <400>5208  
 tgaaggaggc ctccagaata 20  
 <210>5209  
 <211>20  
 <212>DNA  
 <400>5209  
 gctttggtag tcgcagggtat 20  
 <210>5210  
 <211>20  
 <212>DNA

<400>5210  
 ggcatagcga gaacaccata 20  
 <210>5211  
 <211>20  
 <212>DNA  
 <400>5211  
 cctggcatgg agagatcttt 20  
 <210>5212  
 <211>20  
 <212>DNA  
 <400>5212  
 tgaggcaggg ctgacctttt 20  
 <210>5213  
 <211>20  
 <212>DNA  
 <400>5213  
 gcacagtcac gattaagtcg 20  
 <210>5214  
 <211>20  
 <212>DNA  
 <400>5214  
 cctttactag tcacctggca 20  
 <210>5215  
 <211>20  
 <212>DNA  
 <400>5215  
 ggttcagcga atgttgtagg 20  
 <210>5216  
 <211>20  
 <212>DNA  
 <400>5216  
 cagactcagc tacgaatagc 20  
 <210>5217  
 <211>20  
 <212>DNA  
 <400>5217  
 cggagggaga gtgggcacat 20  
 <210>5218  
 <211>20  
 <212>DNA  
 <400>5218  
 ccatgtttgc agccagtga 20  
 <210>5219  
 <211>20  
 <212>DNA  
 <400>5219  
 gggaaaacag tcattccagc 20  
 <210>5220  
 <211>20  
 <212>DNA  
 <400>5220  
 acgcacaact cgcttatagc 20  
 <210>5221  
 <211>20  
 <212>DNA  
 <400>5221  
 agcggtatcg tcttcctaa 20  
 <210>5222  
 <211>20  
 <212>DNA  
 <400>5222  
 gcctatgcag tactctggga 20  
 <210>5223  
 <211>20

<212>DNA  
<400>5223  
cctccgatga agagattgct 20  
<210>5224  
<211>20  
<212>DNA  
<400>5224  
cgctcttcta gctcctgtaa 20  
<210>5225  
<211>20  
<212>DNA  
<400>5225  
gatattgttc tcctcccagg 20  
<210>5226  
<211>20  
<212>DNA  
<400>5226  
ggcgaagaag aaaacttggg 20  
<210>5227  
<211>20  
<212>DNA  
<400>5227  
taatgggtat tgggccgaca 20  
<210>5228  
<211>20  
<212>DNA  
<400>5228  
gagcttttgc tgcccttcct 20  
<210>5229  
<211>20  
<212>DNA  
<400>5229  
cggaggcctc aaattttgag 20  
<210>5230  
<211>20  
<212>DNA  
<400>5230  
gggaaaagact gtgagattcg 20  
<210>5231  
<211>20  
<212>DNA  
<400>5231  
cgggtcaagct gtagcaattc 20  
<210>5232  
<211>20  
<212>DNA  
<400>5232  
gggcaaaagg ttatctcctc 20  
<210>5233  
<211>20  
<212>DNA  
<400>5233  
cacacgcgat tgctgtgaat 20  
<210>5234  
<211>20  
<212>DNA  
<400>5234  
cacttggtcc acaggggaata 20  
<210>5235  
<211>20  
<212>DNA  
<400>5235  
ctccagctca gattcgtaga 20  
<210>5236

<211>20  
<212>DNA  
<400>5236  
tggcgtgctt cctatgagta 20  
<210>5237  
<211>20  
<212>DNA  
<400>5237  
caagccatag cagccaaagt 20  
<210>5238  
<211>20  
<212>DNA  
<400>5238  
gaacctaccc cgctattgat 20  
<210>5239  
<211>20  
<212>DNA  
<400>5239  
actagtgaga gagaagatgg 20  
<210>5240  
<211>20  
<212>DNA  
<400>5240  
gtggtttgat tcagtgatcc 20  
<210>5241  
<211>20  
<212>DNA  
<400>5241  
ggcacgaaga tactccctat 20  
<210>5242  
<211>20  
<212>DNA  
<400>5242  
ccacgatggt aggtcgagaa 20  
<210>5243  
<211>20  
<212>DNA  
<400>5243  
gctgacgatg tgattgcaag 20  
<210>5244  
<211>20  
<212>DNA  
<400>5244  
gaaggccaaa caagaaggct 20  
<210>5245  
<211>20  
<212>DNA  
<400>5245  
tgtgattcct ggcactctgt 20  
<210>5246  
<211>20  
<212>DNA  
<400>5246  
ctgatgctgt agcaaccttg 20  
<210>5247  
<211>20  
<212>DNA  
<400>5247  
gggcaagatc ttacagtag 20  
<210>5248  
<211>20  
<212>DNA  
<400>5248  
cgtggctctc gggtttctat 20

<210>5249  
 <211>20  
 <212>DNA  
 <400>5249  
 cttcggatcg agagcaaadc 20  
 <210>5250  
 <211>20  
 <212>DNA  
 <400>5250  
 ccctctcttt ccgaataacc 20  
 <210>5251  
 <211>20  
 <212>DNA  
 <400>5251  
 gttcaatagg atgcagacgc 20  
 <210>5252  
 <211>20  
 <212>DNA  
 <400>5252  
 cgtatcgatt tgacatcccc 20  
 <210>5253  
 <211>20  
 <212>DNA  
 <400>5253  
 atgcccgcata ttctcgatgc 20  
 <210>5254  
 <211>20  
 <212>DNA  
 <400>5254  
 cgtccccct ccactatagc 20  
 <210>5255  
 <211>20  
 <212>DNA  
 <400>5255  
 gctatgggtcc tagaaacgca 20  
 <210>5256  
 <211>20  
 <212>DNA  
 <400>5256  
 caaatcctgc agaagctgct 20  
 <210>5257  
 <211>20  
 <212>DNA  
 <400>5257  
 cagagatcaa ccgtttgaag 20  
 <210>5258  
 <211>20  
 <212>DNA  
 <400>5258  
 ggcattcagg ctttagcagc 20  
 <210>5259  
 <211>20  
 <212>DNA  
 <400>5259  
 gtctgtagca gaatgagtgg 20  
 <210>5260  
 <211>20  
 <212>DNA  
 <400>5260  
 gctcagcgtg atatcctcat 20  
 <210>5261  
 <211>20  
 <212>DNA  
 <400>5261



gctatcggca gatgatgcta	20
<210>5262	
<211>20	
<212>DNA	
<400>5262	
gagaaaggta tggctatgcc	20
<210>5263	
<211>20	
<212>DNA	
<400>5263	
gaggttatgg aagtccgtga	20
<210>5264	
<211>20	
<212>DNA	
<400>5264	
gtcttttcgt gctcagatgg	20
<210>5265	
<211>20	
<212>DNA	
<400>5265	
ttcgactcta cacatggacg	20
<210>5266	
<211>20	
<212>DNA	
<400>5266	
gacttgaccg tcaggttaga	20
<210>5267	
<211>20	
<212>DNA	
<400>5267	
cagttggaag tcgatctacg	20
<210>5268	
<211>20	
<212>DNA	
<400>5268	
gacaagctaa aggtggagac	20
<210>5269	
<211>20	
<212>DNA	
<400>5269	
cgaggtcaga gacatagact	20
<210>5270	
<211>20	
<212>DNA	
<400>5270	
gagactattg gcgaacttgt	20
<210>5271	
<211>20	
<212>DNA	
<400>5271	
cggtactgca atgcttatcg	20
<210>5272	
<211>20	
<212>DNA	
<400>5272	
cgtgctttga tatctgctgg	20
<210>5273	
<211>20	
<212>DNA	
<400>5273	
ctgggtgtgg ttccttacat	20
<210>5274	
<211>20	
<212>DNA	

<400>5274  
 gcatcagcag gtaaagtagg 20  
 <210>5275  
 <211>20  
 <212>DNA  
 <400>5275  
 ttacggcctg tagagtgggt 20  
 <210>5276  
 <211>20  
 <212>DNA  
 <400>5276  
 cgactgaact ctctgctaca 20  
 <210>5277  
 <211>20  
 <212>DNA  
 <400>5277  
 aggggggagga gttcctttat 20  
 <210>5278  
 <211>20  
 <212>DNA  
 <400>5278  
 tgtctgcttc gtgtggattc 20  
 <210>5279  
 <211>20  
 <212>DNA  
 <400>5279  
 gaagttcttg tccatcacga 20  
 <210>5280  
 <211>20  
 <212>DNA  
 <400>5280  
 gaagagttcc tacaagaggg 20  
 <210>5281  
 <211>20  
 <212>DNA  
 <400>5281  
 cgcgctatgc .gtgtgttttt 20  
 <210>5282  
 <211>20  
 <212>DNA  
 <400>5282  
 catcacgatg gagcacagtt 20  
 <210>5283  
 <211>20  
 <212>DNA  
 <400>5283  
 cccttcgtgg aattcgtatg 20  
 <210>5284  
 <211>20  
 <212>DNA  
 <400>5284  
 cttcccgttt ccactctatc 20  
 <210>5285  
 <211>20  
 <212>DNA  
 <400>5285  
 cgaagggtgta aacgttcgca 20  
 <210>5286  
 <211>20  
 <212>DNA  
 <400>5286  
 ggctcgagaa cctattctac 20  
 <210>5287  
 <211>20

<212>DNA  
 <400>5287  
 cgttggttcga gtagaaagga 20  
 <210>5288  
 <211>20  
 <212>DNA  
 <400>5288  
 cgcgctatgc gtgtgttttt 20  
 <210>5289  
 <211>20  
 <212>DNA  
 <400>5289  
 cgacgacgat ttagatgcgt 20  
 <210>5290  
 <211>20  
 <212>DNA  
 <400>5290  
 cgacttccgc ggatttttcta 20  
 <210>5291  
 <211>20  
 <212>DNA  
 <400>5291  
 gcaggattaa gtaaggaggc 20  
 <210>5292  
 <211>20  
 <212>DNA  
 <400>5292  
 cgaaggtgta aacgttcgca 20  
 <210>5293  
 <211>20  
 <212>DNA  
 <400>5293  
 gtcctgggtt ggtaattgga 20  
 <210>5294  
 <211>20  
 <212>DNA  
 <400>5294  
 gggagacgtt atcaaagctg 20  
 <210>5295  
 <211>20  
 <212>DNA  
 <400>5295  
 gccgggcctg tctacaagcg 20  
 <210>5296  
 <211>20  
 <212>DNA  
 <400>5296  
 ggtgttggtg tctcggcaaa 20  
 <210>5297  
 <211>20  
 <212>DNA  
 <400>5297  
 gatgatcggc catacgtttg 20  
 <210>5298  
 <211>20  
 <212>DNA  
 <400>5298  
 gttaagcgag tggaaagggt 20  
 <210>5299  
 <211>20  
 <212>DNA  
 <400>5299  
 gaaccctgta gatcatcccc 20  
 <210>5300

<211>20  
<212>DNA  
<400>5300  
ccgagattgc tcgttctgaa 20  
<210>5301  
<211>20  
<212>DNA  
<400>5301  
gtggtgagtt gcgcggtacg 20  
<210>5302  
<211>20  
<212>DNA  
<400>5302  
ggaacagctg ggattttctc 20  
<210>5303  
<211>20  
<212>DNA  
<400>5303  
ctcctaaaac tcagtcagcg 20  
<210>5304  
<211>20  
<212>DNA  
<400>5304  
gtttgttgat caccacctcc 20  
<210>5305  
<211>20  
<212>DNA  
<400>5305  
gcgaagttga agtagcagac 20  
<210>5306  
<211>20  
<212>DNA  
<400>5306  
gtgtagatgg caaagctgga 20  
<210>5307  
<211>20  
<212>DNA  
<400>5307  
ctcctggtcg ttgtttccct 20  
<210>5308  
<211>20  
<212>DNA  
<400>5308  
ggagagggaa agaaaaaggg 20  
<210>5309  
<211>20  
<212>DNA  
<400>5309  
ttgctccgct gcaatttctg 20  
<210>5310  
<211>20  
<212>DNA  
<400>5310  
gcaatgttga gtgtcgtagc 20  
<210>5311  
<211>20  
<212>DNA  
<400>5311  
cattcggtgt tttagctccg 20  
<210>5312  
<211>20  
<212>DNA  
<400>5312  
gcgatcgact cctggtcggt 20

<210>5313  
<211>20  
<212>DNA  
<400>5313  
gcaagggttc tacgaactca 20  
<210>5314  
<211>20  
<212>DNA  
<400>5314  
ggcagaaaac aaagtctggc 20  
<210>5315  
<211>20  
<212>DNA  
<400>5315  
agtaaagcgt cagaccccca 20  
<210>5316  
<211>20  
<212>DNA  
<400>5316  
cattcggtgt tttacgtccg 20  
<210>5317  
<211>20  
<212>DNA  
<400>5317  
accattggaa gtggaaaccc 20  
<210>5318  
<211>20  
<212>DNA  
<400>5318  
agggagccat ttgcttgac 20  
<210>5319  
<211>20  
<212>DNA  
<400>5319  
ctgctggtgt attgataggc 20  
<210>5320  
<211>20  
<212>DNA  
<400>5320  
tttgctacgc gattagccct 20  
<210>5321  
<211>20  
<212>DNA  
<400>5321  
cgctattctg gagtgggaat 20  
<210>5322  
<211>20  
<212>DNA  
<400>5322  
ctgctggtgt attgataggc 20  
<210>5323  
<211>20  
<212>DNA  
<400>5323  
cttcccgaag gtaaggcatt 20  
<210>5324  
<211>20  
<212>DNA  
<400>5324  
gggggatgtt tggataatgc 20  
<210>5325  
<211>20  
<212>DNA  
<400>5325

cgctatcgag atgcttcgat 20  
 <210>5326  
 <211>20  
 <212>DNA  
 <400>5326  
 cagtctgcct caggtaacta 20  
 <210>5327  
 <211>20  
 <212>DNA  
 <400>5327  
 acaaccagcc cattcctgtc 20  
 <210>5328  
 <211>20  
 <212>DNA  
 <400>5328  
 actgtggatt ctctaggtcg 20  
 <210>5329  
 <211>20  
 <212>DNA  
 <400>5329  
 aaaccctgtc cgttttagctg 20  
 <210>5330  
 <211>20  
 <212>DNA  
 <400>5330  
 tacttcccta gaagtcgggg 20  
 <210>5331  
 <211>20  
 <212>DNA  
 <400>5331  
 gaccctggaa gaagtgcaaa 20  
 <210>5332  
 <211>20  
 <212>DNA  
 <400>5332  
 gcctatcttc aatgggcatc 20  
 <210>5333  
 <211>20  
 <212>DNA  
 <400>5333  
 cttttctatc tggaacaggc 20  
 <210>5334  
 <211>20  
 <212>DNA  
 <400>5334  
 gcctaagcca cgattttgtg 20  
 <210>5335  
 <211>20  
 <212>DNA  
 <400>5335  
 tgcgcattcc catgcaaaa 20  
 <210>5336  
 <211>20  
 <212>DNA  
 <400>5336  
 cagtcccacc aaaagaacct 20  
 <210>5337  
 <211>20  
 <212>DNA  
 <400>5337  
 agggttcctt catcaatggc 20  
 <210>5338  
 <211>20  
 <212>DNA

<400>5338  
cgtgaggtaa gacaacccat 20  
<210>5339  
<211>20  
<212>DNA  
<400>5339  
catgtagcat agtcggttgcc 20  
<210>5340  
<211>20  
<212>DNA  
<400>5340  
cttgccatct tcaggcacct 20  
<210>5341  
<211>20  
<212>DNA  
<400>5341  
cggaggtagc atcaaagggtt 20  
<210>5342  
<211>20  
<212>DNA  
<400>5342  
gagcctatct tgcttcctct 20  
<210>5343  
<211>20  
<212>DNA  
<400>5343  
ggatgctcaa ggattcacag 20  
<210>5344  
<211>20  
<212>DNA  
<400>5344  
gggattgcct taggggttaga 20  
<210>5345  
<211>20  
<212>DNA  
<400>5345  
gctcaaaagc gtattgagcc 20  
<210>5346  
<211>20  
<212>DNA  
<400>5346  
gaatggtcgc aacatttgcg 20  
<210>5347  
<211>20  
<212>DNA  
<400>5347  
taatgtgctt tggagggttg 20  
<210>5348  
<211>20  
<212>DNA  
<400>5348  
gcgcgggtttt tctccaatac 20  
<210>5349  
<211>20  
<212>DNA  
<400>5349  
aagctatgga tgcacaggct 20  
<210>5350  
<211>20  
<212>DNA  
<400>5350  
gaaaaaccct ttccaccccc 20  
<210>5351  
<211>20

<212>DNA  
<400>5351  
actctccacg ggtttcatag 20  
<210>5352  
<211>20  
<212>DNA  
<400>5352  
acactcgcaa ccaatgatgg 20  
<210>5353  
<211>20  
<212>DNA  
<400>5353  
ctttgccatg cttgcgggta 20  
<210>5354  
<211>20  
<212>DNA  
<400>5354  
cgaagatcgt gtgcgctcatt 20  
<210>5355  
<211>20  
<212>DNA  
<400>5355  
gcatgacgaa agtgctagag 20  
<210>5356  
<211>20  
<212>DNA  
<400>5356  
caaaacgctg ggtggaaagc 20  
<210>5357  
<211>20  
<212>DNA  
<400>5357  
ctctgcgttc tttccgcttt 20  
<210>5358  
<211>20  
<212>DNA  
<400>5358  
ggatgggttag gatgctgctt 20  
<210>5359  
<211>20  
<212>DNA  
<400>5359  
ggaaagagag tcctgcatgt 20  
<210>5360  
<211>20  
<212>DNA  
<400>5360  
gaactccttc cagagatagc 20  
<210>5361  
<211>20  
<212>DNA  
<400>5361  
gatgatgtaa cccatgggga 20  
<210>5362  
<211>20  
<212>DNA  
<400>5362  
ttctaagtct cctctatggg 20  
<210>5363  
<211>20  
<212>DNA  
<400>5363  
acaaggggca tagaaaggct 20  
<210>5364



```

<211>20
<212>DNA
<400>5364
tttggctcgt tcctgagctt      20
<210>5365
<211>20
<212>DNA
<400>5365
cgatcctggt cccctgaaaa      20
<210>5366
<211>20
<212>DNA
<400>5366
aataccttcc cagagtcggc      20
<210>5367
<211>20
<212>DNA
<400>5367
gcgagtgcaa aagagcatct      20
<210>5368
<211>20
<212>DNA
<400>5368
gtggtatgct tttccttctg      20
<210>5369
<211>20
<212>DNA
<400>5369
gccgaggatt tccaaacgat      20
<210>5370
<211>20
<212>DNA
<400>5370
cgccctgtgg gataaaatga      20
<210>5371
<211>20
<212>DNA
<400>5371
ctgcggaacc tccatacttt      20
<210>5372
<211>20
<212>DNA
<400>5372
aagactatcg ctcgcatccc      20
<210>5373
<211>20
<212>DNA
<400>5373
cacctcaacc tcctacggcg      20
<210>5374
<211>20
<212>DNA
<400>5374
gaagctgcag ttgcatttgc      20
<210>5375
<211>20
<212>DNA
<400>5375
cttacagagg tagtacgcac      20
<210>5376
<211>20
<212>DNA
<400>5376
gagaactcgg tgcggctgta      20

```

<210>5377  
<211>20  
<212>DNA  
<400>5377  
ctccctgaac tttagatggt 20  
<210>5378  
<211>20  
<212>DNA  
<400>5378  
ctcaggcctg tctctctaag 20  
<210>5379  
<211>20  
<212>DNA  
<400>5379  
ccgcagaact ctcttcctac 20  
<210>5380  
<211>20  
<212>DNA  
<400>5380  
cccaggcttt ggtctatctt 20  
<210>5381  
<211>20  
<212>DNA  
<400>5381  
cgaggcggaa attatggaag 20  
<210>5382  
<211>20  
<212>DNA  
<400>5382  
ggatgggctc agcattaaca 20  
<210>5383  
<211>20  
<212>DNA  
<400>5383  
tgggggtactg ttggcggtgt 20  
<210>5384  
<211>20  
<212>DNA  
<400>5384  
ccataccaag cactgttcct 20  
<210>5385  
<211>20  
<212>DNA  
<400>5385  
agagagttgg tgggggtaga 20  
<210>5386  
<211>20  
<212>DNA  
<400>5386  
ggcagataaa gcacgcttgc 20  
<210>5387  
<211>20  
<212>DNA  
<400>5387  
ctcctcagat aaccctacca 20  
<210>5388  
<211>20  
<212>DNA  
<400>5388  
taagaaccca gaggtgagag 20  
<210>5389  
<211>20  
<212>DNA  
<400>5389

cctgtacgtc caggatttca 20  
 <210>5390  
 <211>20  
 <212>DNA  
 <400>5390  
 ccgtaagtaa gttgtggcct 20  
 <210>5391  
 <211>20  
 <212>DNA  
 <400>5391  
 ctaggctaag agcgtcttct 20  
 <210>5392  
 <211>20  
 <212>DNA  
 <400>5392  
 gagegccatg gcaatgcaaa 20  
 <210>5393  
 <211>20  
 <212>DNA  
 <400>5393  
 tcgatagagt tgaagcccac 20  
 <210>5394  
 <211>20  
 <212>DNA  
 <400>5394  
 ctaggctaag agcgtcttct 20  
 <210>5395  
 <211>20  
 <212>DNA  
 <400>5395  
 cgatcacacg tagtagggtt 20  
 <210>5396  
 <211>20  
 <212>DNA  
 <400>5396  
 cctgtacgtc caggatttca 20  
 <210>5397  
 <211>20  
 <212>DNA  
 <400>5397  
 ggaaagaata ggggtagtga 20  
 <210>5398  
 <211>20  
 <212>DNA  
 <400>5398  
 ggaagctcta cccgtcgtta 20  
 <210>5399  
 <211>20  
 <212>DNA  
 <400>5399  
 cgtctgcgat aggatcttct 20  
 <210>5400  
 <211>20  
 <212>DNA  
 <400>5400  
 aactgggaac gagagtggga 20  
 <210>5401  
 <211>20  
 <212>DNA  
 <400>5401  
 gcaaaagaga acgagccttt 20  
 <210>5402  
 <211>20  
 <212>DNA

<400>5402  
cccataccttt ggatctaggt 20  
<210>5403  
<211>20  
<212>DNA  
<400>5403  
tcctgaagag atgcagacga 20  
<210>5404  
<211>20  
<212>DNA  
<400>5404  
ggtgatagat gccgttgcta 20  
<210>5405  
<211>20  
<212>DNA  
<400>5405  
ccagagattc ctggagtcaa 20  
<210>5406  
<211>20  
<212>DNA  
<400>5406  
gatagaaaca gacgaggtga 20  
<210>5407  
<211>20  
<212>DNA  
<400>5407  
gatccatggt ttttgtcggg 20  
<210>5408  
<211>20  
<212>DNA  
<400>5408  
tcttggagaa ataccgagag 20  
<210>5409  
<211>20  
<212>DNA  
<400>5409  
gctgctctac gtaatgaacc 20  
<210>5410  
<211>20  
<212>DNA  
<400>5410  
gcctatacgg atccgaagat 20  
<210>5411  
<211>20  
<212>DNA  
<400>5411  
cgacctgatt tgtctgatgg 20  
<210>5412  
<211>20  
<212>DNA  
<400>5412  
gcatgtaagc gccttagtgt 20  
<210>5413  
<211>20  
<212>DNA  
<400>5413  
gatgtctagc aaccgcgtact 20  
<210>5414  
<211>20  
<212>DNA  
<400>5414  
gactggatcg ggaatatggt 20  
<210>5415  
<211>20

<212>DNA  
<400>5415  
gcggaagatt ctaaagcgg 20  
<210>5416  
<211>20  
<212>DNA  
<400>5416  
ggaggagcca ttattgcgtt 20  
<210>5417  
<211>20  
<212>DNA  
<400>5417  
ggtcgaaaac atagtctccg 20  
<210>5418  
<211>20  
<212>DNA  
<400>5418  
caagaaagcg tggcttcaga 20  
<210>5419  
<211>20  
<212>DNA  
<400>5419  
caacgccttt atagcccttg 20  
<210>5420  
<211>20  
<212>DNA  
<400>5420  
cctcactacc ttctcaagtc 20  
<210>5421  
<211>20  
<212>DNA  
<400>5421  
gggattccaa gctttgtacc 20  
<210>5422  
<211>20  
<212>DNA  
<400>5422  
cgcaaactgg attaaggggt 20  
<210>5423  
<211>20  
<212>DNA  
<400>5423  
ccagtcggga taaacgcatt 20  
<210>5424  
<211>20  
<212>DNA  
<400>5424  
attaatgcag tgccgttggc 20  
<210>5425  
<211>20  
<212>DNA  
<400>5425  
cagagggaaa agaaaaaccc 20  
<210>5426  
<211>20  
<212>DNA  
<400>5426  
cccatttgat ctgccgatac 20  
<210>5427  
<211>20  
<212>DNA  
<400>5427  
tgatctcggg ttactgctgc 20  
<210>5428

<211>20  
<212>DNA  
<400>5428  
cttcgacttc aggctgtaag 20  
<210>5429  
<211>20  
<212>DNA  
<400>5429  
gagcttggaa gcagtaatcc 20  
<210>5430  
<211>20  
<212>DNA  
<400>5430  
ctaaccgctg agctaaagac 20  
<210>5431  
<211>20  
<212>DNA  
<400>5431  
gtaagagtcg gccgtataac 20  
<210>5432  
<211>20  
<212>DNA  
<400>5432  
ggggagtgct ttttagagga 20  
<210>5433  
<211>20  
<212>DNA  
<400>5433  
atcctggttc gatccctctt 20  
<210>5434  
<211>20  
<212>DNA  
<400>5434  
gccgtggaat agcttctgac 20  
<210>5435  
<211>20  
<212>DNA  
<400>5435  
tgtcacgatc gtttcccacg 20  
<210>5436  
<211>20  
<212>DNA  
<400>5436  
gagttgttgc agttcgtaag 20  
<210>5437  
<211>20  
<212>DNA  
<400>5437  
ctcatcactc ctcagggtaa 20  
<210>5438  
<211>20  
<212>DNA  
<400>5438  
cttttcccca ggattagga 20  
<210>5439  
<211>20  
<212>DNA  
<400>5439  
cgtagatatt tctctgcgcc 20  
<210>5440  
<211>20  
<212>DNA  
<400>5440  
ccctcaacgc tcattagctt 20